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(54) **MICROARRAY ANALYSIS OF LIGHT CHAIN VARIABLE GENE EXPRESSION AND METHODS OF USE**

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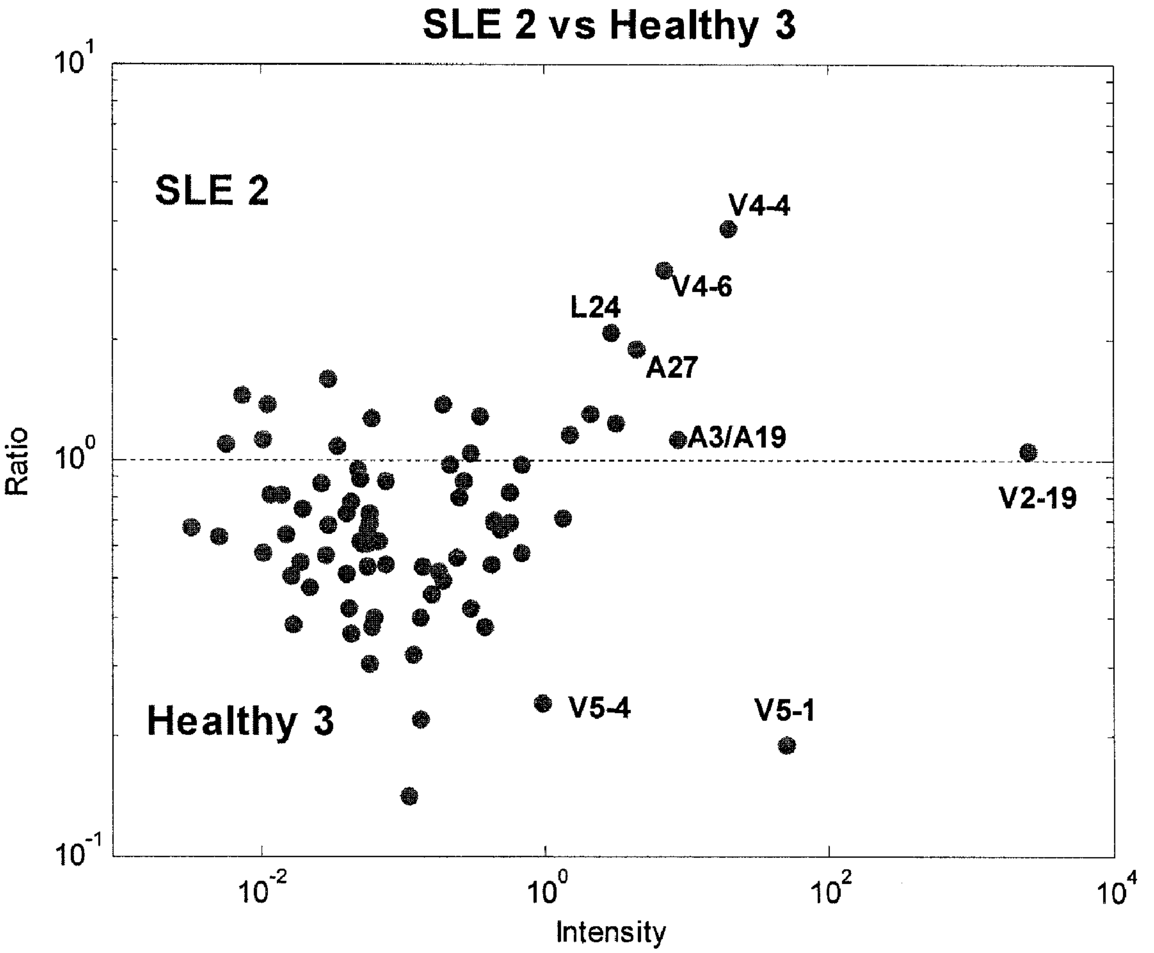
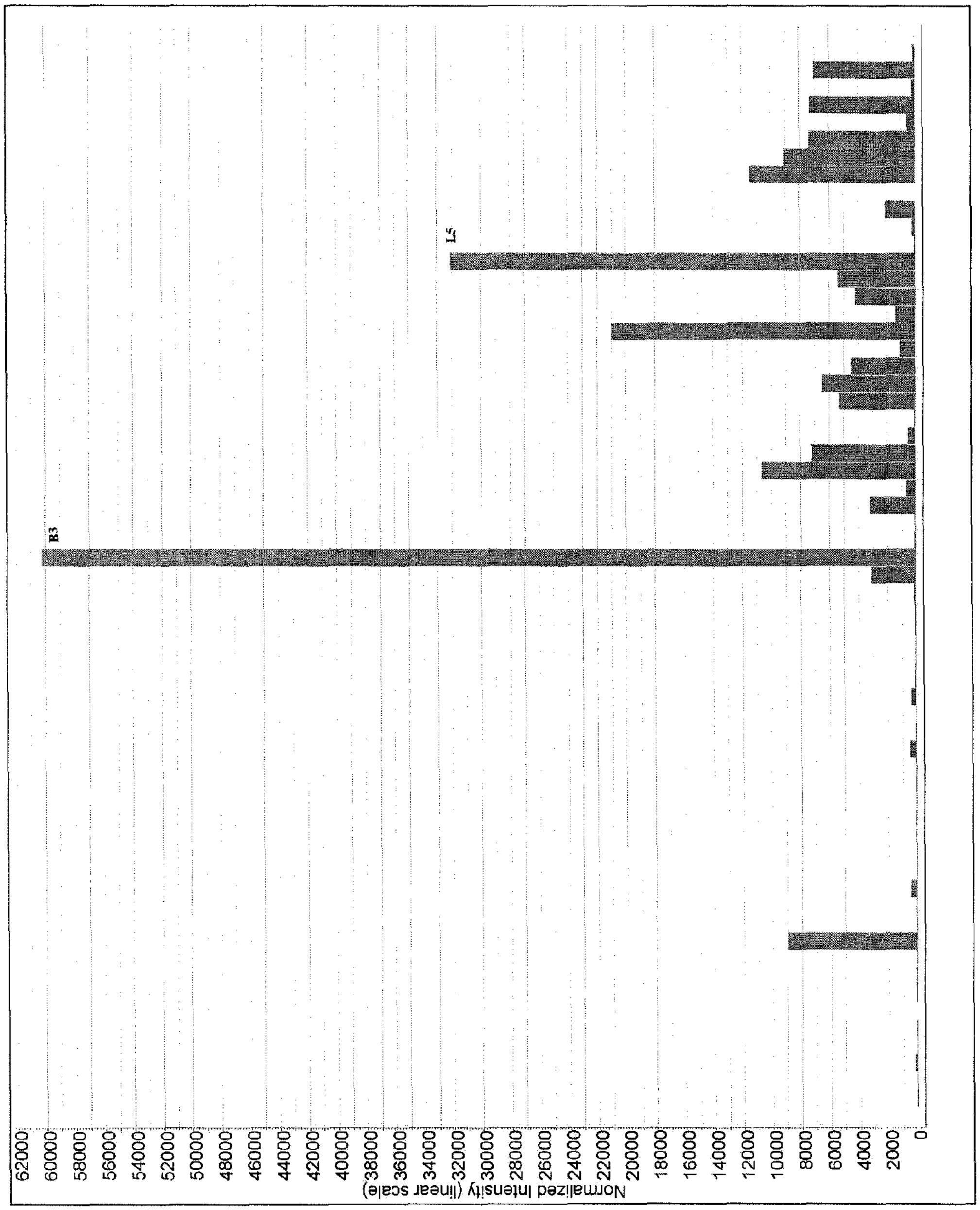
(52) **U.S. Cl.** **435/6**

(57) **ABSTRACT**

Disclosed are microarrays comprising a plurality of oligonucleotide species capable of hybridizing to a polynucleotide comprising a sequence encoding at least a portion of a light chain variable region or a complement thereof. Also disclosed are methods of identifying light chain variable genes associated with a disease, methods of diagnosing a disease and methods of monitoring a disease. Methods of evaluating the ability of a therapeutic agent or a treatment to alter expression of the light chain variable gene are also provided.




Normalized Intensity (linear scale)
62000
60000
58000
56000
54000
52000
50000
48000
46000
44000
42000
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34000
32000
30000
28000
26000
24000
22000
20000
18000
16000
14000
12000
10000
8000
6000
4000
2000
0
B3
L5

FIG. 1

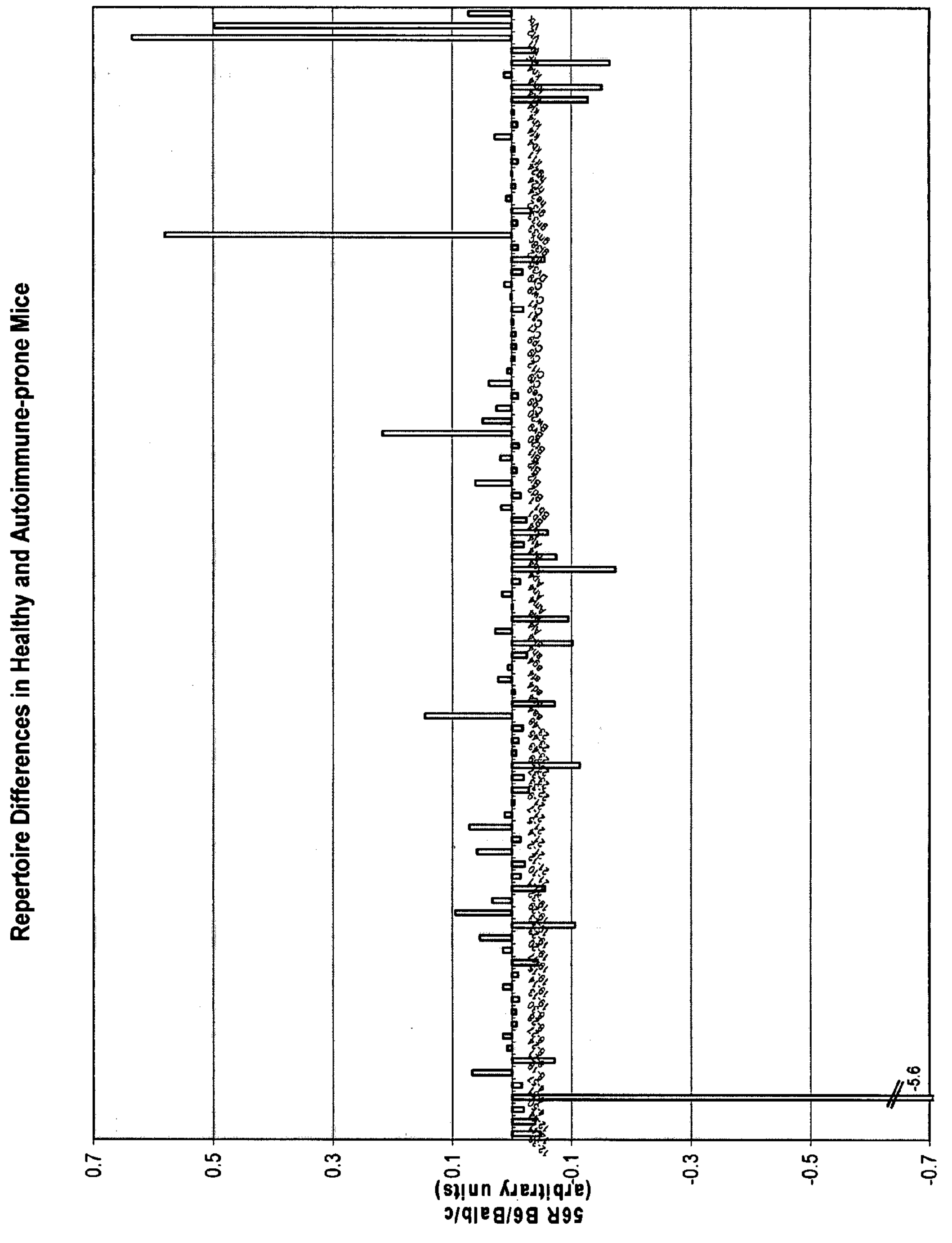
Repertoire Differences in Healthy and Autoimmune-prone Mice
56R B6/Balb/c
(arbitrary units)
0.7
0.5
0.3
0.1
-0.1
-0.3
-0.5
-0.7
-5.6

FIG. 2

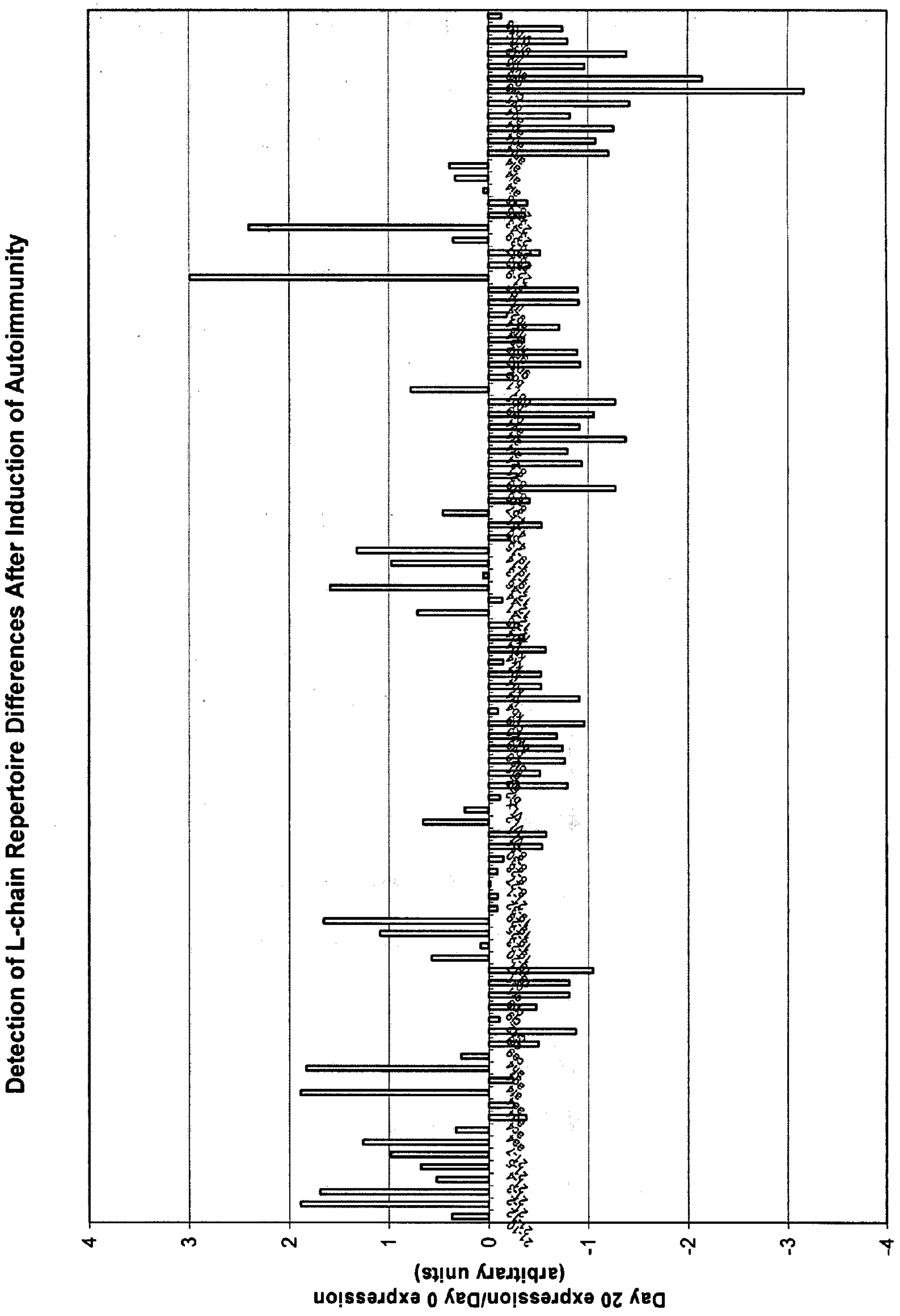
Detection of L-chain Repertoire Differences After Induction of Autoimmunity
4
3
2
1
0
-1
-2
-3
-4
Day 20 expression/Day 0 expression
(arbitrary units)

FIG. 3

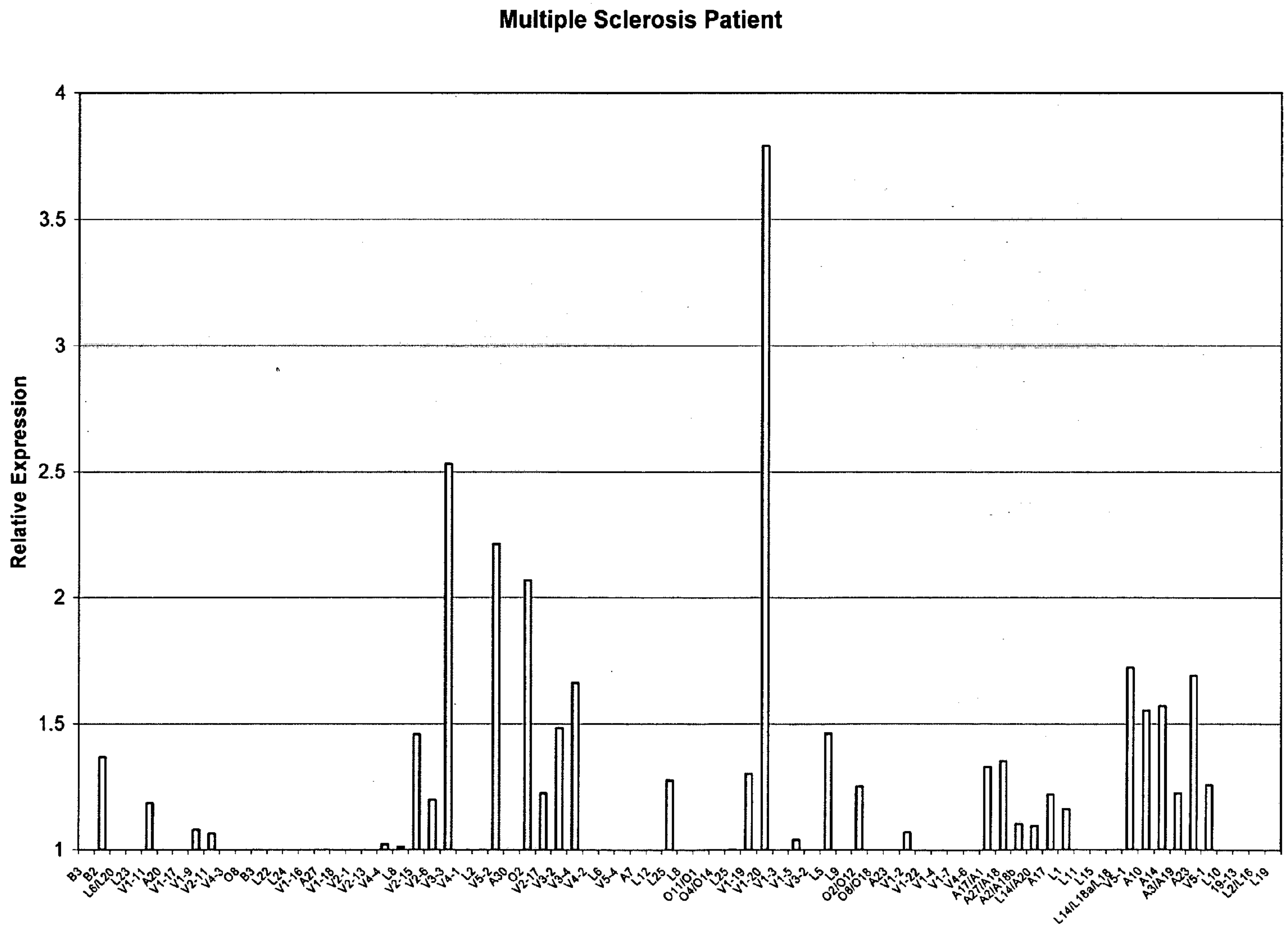
Multiple Sclerosis Patient
Relative Expression
4
3.5
3
2.5
2
1.5
1
B3
B2
L6/L20
L23
V1-11
A20
V1-17
V1-9
V2-11
V4-3
O8
B3
L22
L24
V1-16
A27
V1-18
V2-1
V2-13
V4-4
L8
V2-15
V2-6
V3-3
V4-1
L2
V5-2
A30
O2
V2-17
V3-2
V3-4
V4-2
L6
V5-4
A7
L12
L25
L8
O11/O1
O4/O14
L25
V1-19
V1-20
V1-3
V1-5
V3-2
L5
L9
O2/O12
O8/O18
A23
V1-2
V1-22
V1-4
V1-7
V4-6
A17/A1
A27/A18
A2/A18b
L14/A20
A17
L1
L11
L15
L14/L18a/L18
V5-1
A10
A14
A3/A19
A23
V5-1
L10
19-13
L2/L16
L19

FIG. 4

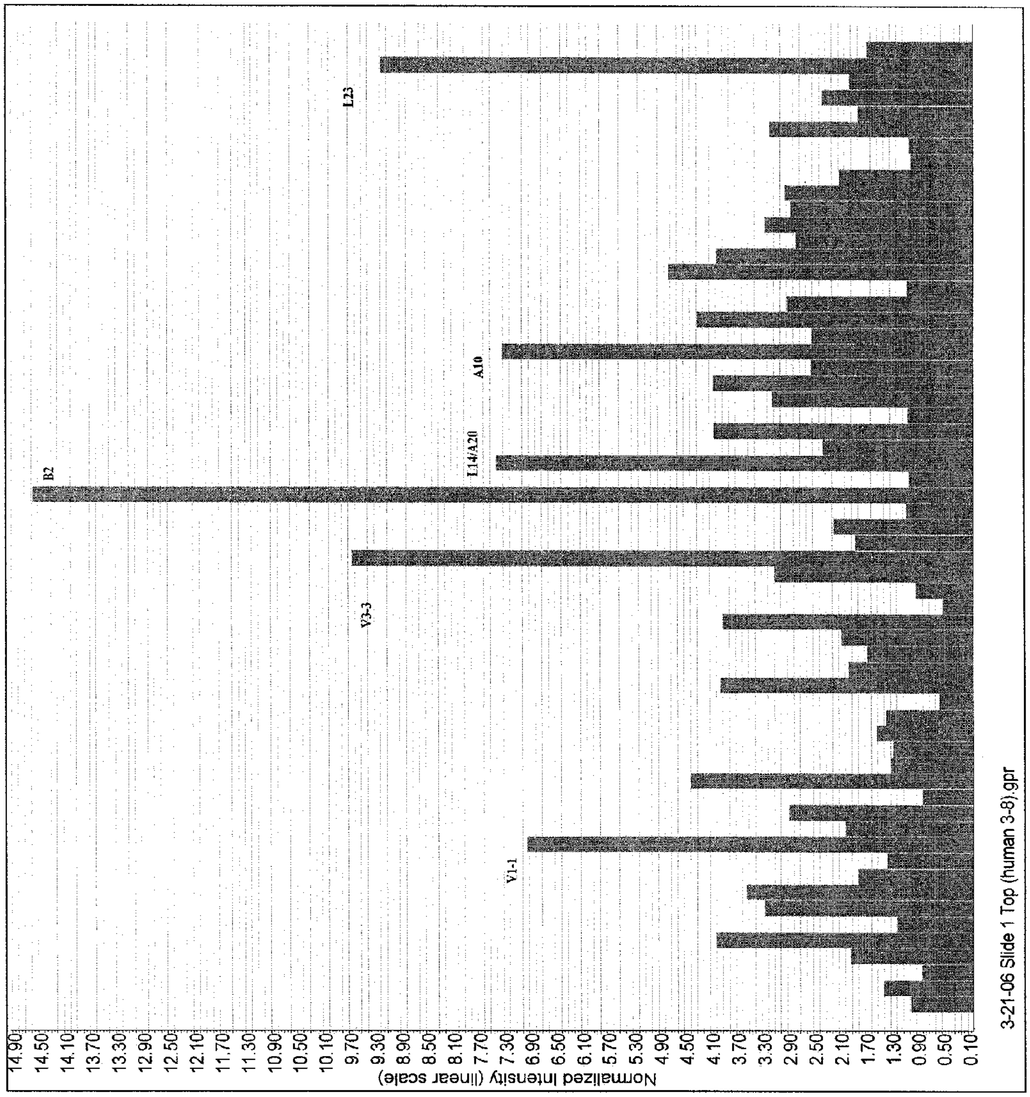
Normalized Intensity (linear scale)
14.90
14.50
14.10
13.70
13.30
12.90
12.50
12.10
11.70
11.30
10.90
10.50
10.10
9.70
9.30
8.90
8.50
8.10
7.70
7.30
6.90
6.50
6.10
5.70
5.30
4.90
4.50
4.10
3.70
3.30
2.90
2.50
2.10
1.70
1.30
0.90
0.50
0.10
V1-1
V3-3
B2
L14/A20
A10
L23
3-21-06 Slide 1 Top (human 3-8).gpr

FIG. 5

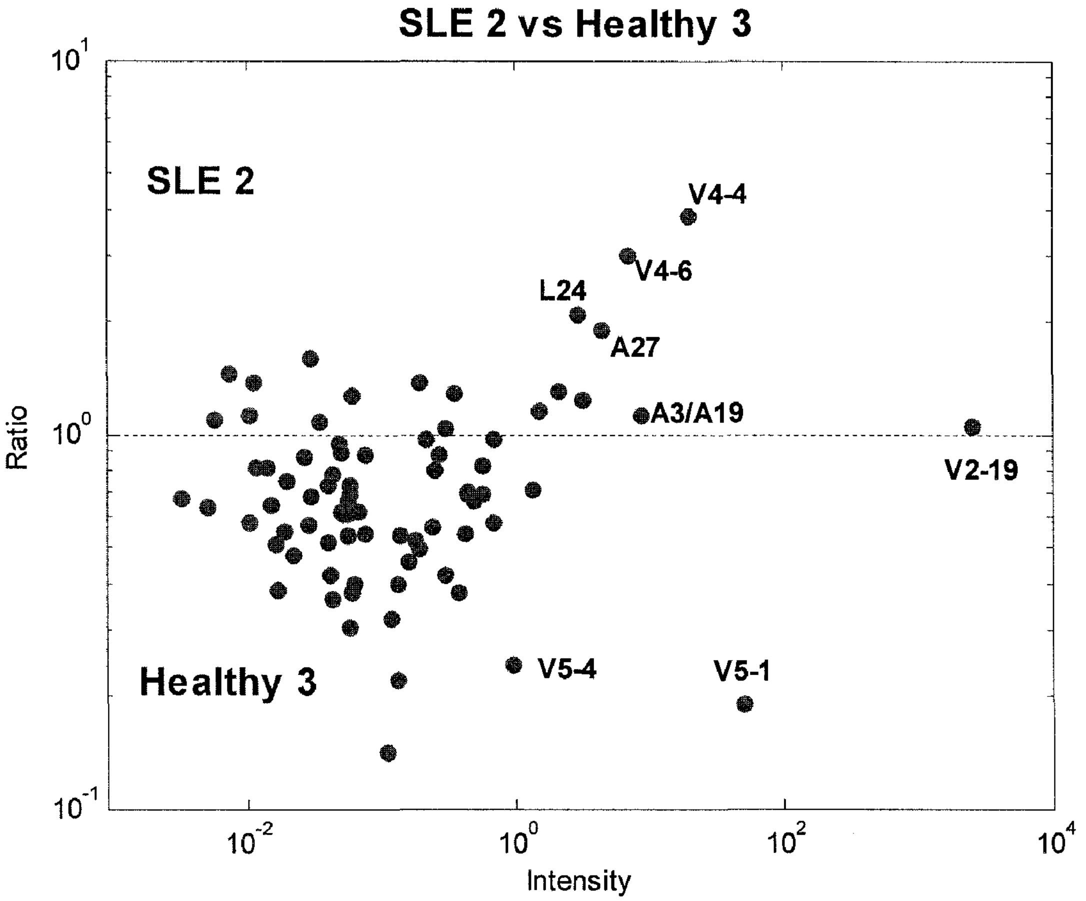
SLE 2 vs Healthy 3
SLE 2
Healthy 3
V4-4
V4-6
L24
A27
A3/A19
V2-19
V5-4
V5-1
Ratio
10^1
10^0
10^{-1}
10^{-2}
10^0
10^2
10^4
Intensity

FIG. 6

MICROARRAY ANALYSIS OF LIGHT CHAIN VARIABLE GENE EXPRESSION AND METHODS OF USE

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Application No. 60/803,099 filed on May 24, 2006, which is incorporated by reference in its entirety.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

[0002] Not applicable.

INTRODUCTION

[0003] Immunoglobulins are comprised of a heavy chain and a light chain. Both heavy chains and light chains are encoded by a series of gene segments that are rearranged by genomic recombination events that occur during B cell development. The resulting immunoglobulins are expressed on the cell surface as B cell receptors and may be secreted as antibodies. The genomic recombination events cause expression patterns of the various immunoglobulin gene segments to vary from one individual to another.

[0004] There are numerous pathologic conditions caused by the formation of auto-antibodies, which recognize self-antigens. In systemic autoimmune diseases, the immune system of an organism launches an immune response against the organism's own tissues, causing inflammation and tissue damage. Examples of diseases caused by immune dysfunction include rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis, scleroderma, psoriasis, and Sjorgen's syndrome. Additionally, there are other B cell related diseases in which immunoglobulin expression may play a role, such as multiple myeloma.

[0005] Relatively little is known about the role of light chain variable region expression in autoimmune diseases or other B cell related diseases. Thus, there is a need in the art for improved understanding of the relationship between immunoglobulin expression and disease.

SUMMARY

[0006] The present invention provides a microarray comprising a plurality of oligonucleotide species at least 20 nucleotides long and capable of hybridizing to a polynucleotide comprising a sequence that encodes at least a portion of a light chain variable (LCV) region, or a complement thereof.

[0007] Also provided is a method of characterizing the light chain variable gene expression in a subject. First, B cells are isolated from the subject and target polynucleotides are prepared from the B cells. Then target polynucleotides are hybridized to a microarray of the invention. Finally, light chain variable gene expression is characterized by detecting hybridization of the target polynucleotides to one or more oligonucleotide species.

[0008] In another aspect, the invention provides methods of identifying light chain variable genes associated with a disease by comparing the light chain variable gene expression in a first subject with the disease to the light chain variable gene expression in a second subject that does not have the disease. The light chain variable gene expression can be assessed using a microarray according to the present invention. A difference in light chain variable gene expression between the first and the second subject indicating that expression of the light chain variable gene is associated with the disease.

[0009] In still another aspect, methods of monitoring a disease state in a subject are provided. The expression in the subject of a light chain variable gene associated with the disease is compared at two or more time points.

[0010] In a further aspect, methods of evaluating the effect of a therapy or a therapeutic agent on expression of a light chain variable gene associated with a disease in a subject are provided. The expression of the light chain variable gene in the subject is compared before and after treatment.

[0011] In a still further aspect, kits comprising the microarray are provided.

BRIEF DESCRIPTION OF THE DRAWINGS

[0012] FIG. **1** is a graph showing fluorescence intensity of labeled human B3 light chain DNA after hybridization to the human light chain variable genes.

[0013] FIG. **2** is a graph demonstrating the light chain variable gene repertoire differences in B6 56R transgenic mice as compared to Balb/c mice. The microarray fluorescent intensity data was normalized to the kappa constant region for each sample and then the Balb/c normalized values were subtracted from the B6 56R transgenic normalized values. A positive number indicates an over-representation of the light chain variable region in the B6 56R transgenic mouse.

[0014] FIG. **3** is a graph demonstrating the light chain variable gene repertoire differences in B6 56R transgenic mice before and after induction of autoimmunity. The microarray fluorescent intensity data were normalized to the kappa constant region for each sample.

[0015] FIG. **4** is a graph demonstrating the light chain variable expression in B cells harvested from the cerebral spinal fluid of a patient with multiple sclerosis. The data are normalized to the kappa constant region.

[0016] FIG. **5** is a graph demonstrating the overrepresentation of light chain variable genes in B cells isolated from the cerebral spinal fluid of an individual with multiple sclerosis normalized to light chain variable expression in B cells isolated from the cerebral spinal fluid of three individuals not suffering from an autoimmune disease.

[0017] FIG. **6** is a graph comparing the peripheral B cell repertoires of a healthy individual and a systemic lupus erythematosus (SLE) patient. The x-axis is the sum of the intensities for a given light chain gene in both samples. The y-axis is the ratio (SLE:healthy) of intensities between the samples. Global intensity dependent normalization was performed for each sample.

DETAILED DESCRIPTION

[0018] As described in detail below, the light chain variable gene repertoire expressed by an individual may provide information concerning that individual's risk of developing a disease, his prognosis, or his response to a particular treatment. A light chain variable gene associated with a disease can be determined by comparing expression of light chain variable genes of individuals with the disease to the expression of light chain variable genes of individuals who do not have the disease, and identifying genes that are differentially expressed among a subpopulation of individuals with the disease.

[0019] The present invention provides a new approach to evaluating autoimmune disease using microarray analysis of light chain variable (V) gene usage. Microarrays suitable for use in this analysis include oligonucleotide species capable of hybridizing to a polynucleotide encoding at least a portion of an antibody light chain variable region, or to a complement thereof. Microarray analysis provides a rapid and relatively inexpensive method of characterizing light chain variable gene expression in a subject. By this method, the light chain variable repertoire of a subject can be determined. Information can be obtained by comparing light chain variable gene repertoires between subjects or by evaluating changes in expression in a single subject over time.

[0020] The light chain variable region repertoire of a subject refers to the light chain variable genes expressed by a subject. Characterization of the light chain variable gene repertoire includes, but is not limited to, detection and/or quantification of one or more of the light chain variable genes expressed in a subject. The subject can be any subject capable of expressing light chain variable genes, e.g. vertebrates. In the Examples, mouse and human subjects were used.

[0021] The methods of the invention can identify and distinguish light chain variable gene repertoires and provide information on relative expression of individual light chain variable genes in both humans and mice. This information is useful in identifying those light chain variable genes associated with a disease, such as autoimmune diseases or other B cell related diseases. Once a light chain variable gene is identified as being associated with a particular disease, the expression of that light chain variable gene can be used to diagnose the disease and to predict or assess the course of disease (e.g., severity, flares, or remission). The microarray may also be used to evaluate the effect of a therapy or therapeutic agent on expression of light chain variable genes associated with disease, or to predict an individual's response to treatment. Light chain variable gene expression may also be used to predict auto-antibody structures or susceptibility to autoimmune disease. Microarrays according to the invention may also allow evaluation of the overall immune system function and/or status of a subject.

[0022] Mouse models of systemic autoimmune diseases described below demonstrate that certain light chain V genes have unique properties and the expression of certain sequences are associated with disease activity. Table 1 includes the light chain V regions of anti-DNA antibodies isolated from a mouse model of lupus. As can be seen in Table 1, these light chain variable regions have an unusually high frequency of acidic amino acids clustered in the complementarity determining regions (CDRs). Expression of these light chains in a subject with an autoimmune disease were studied using microarrays. Importantly, human counterparts to the mouse light chain variable genes discussed above have been identified, and were found to have similar structural features to those of mice (See Table 1, bottom panel). These light chains may also be important in autoimmune pathology, susceptibility and disease course in humans.

[0023] The human B2 gene encodes a κIII domain that displays four aspartic acids in a five amino acid segment of CDR1 (Table 1) and is thus of particular interest. A database of almost 300 human kappa light chain variable domain sequences derived from patients with monoclonal dyscrasias reveals no example of such an aspartic acid cluster, although studies suggest that B2 products are functional. One of the aspartic acids in B2 is located at amino acid position 31, which has been linked to the formation of amyloid fibrils in approximately 10% of patients with multiple myeloma. Specifically, mutations that generated an aspartic acid at position 31 are highly correlated with amyloid formation. Thus, light chain variable gene expression may also be related to symptomology or sequelae of a disease such as multiple myeloma.

[0024] Subsets of light chain variable regions have been found to be associated with particular diseases as described in detail below. Briefly, auto-antibodies found in individuals with systemic autoimmune diseases such as lupus, rheumatoid arthritis and multiple sclerosis (MS) have a restricted light chain repertoire. These auto-antibodies appear to be associated with pathogenesis and/or correlate with disease activity in systemic autoimmune diseases. Knowledge of antibodies associated with pathogenesis will yield important information concerning the structure and expression patterns of these light chain variable genes. Light chain variable gene expression is also relevant to other diseases such as multiple myeloma and other B cell-related diseases.

[0025] The development of a rapid, sensitive, reliable and relatively inexpensive means of analyzing immunoglobulin light chain expression in subjects is needed to determine whether particular light chain variable genes are related to a particular disease. Development of such methods will allow for improved diagnosis of these diseases and may aid in determining disease prognosis and etiology, monitoring disease progression and evaluating therapeutic agents and treatment regimens.

TABLE 1

Comparison of mouse light chain V genes (top) identified in lupus models as having unique properties and human light chains (bottom) with similar properties. Highlighted are the relevant residues that confer autoreactivity.

BT20	STTVTQSPASLSMAIGEKVTIRCITSTDIDD----DMNWYQQKPGEPPKLLISE----GNTLRPGVPSRFSSSGYGTDFVFTIENMLSEDVADYYCLQSDNLP----	SEQ ID NO: 1

TABLE 1-continued

Comparison of mouse light chain V genes (top) identified in lupus models as having unique properties and human light chains (bottom) with similar properties. Highlighted are the relevant residues that confer autoreactivity.

BW20	ETTVTQSPASLSVATGEKVTIRCITSTDIDD----DMNWYQQKPGEPPKLLISE---- GNTLRPGVPSRFSSSGYGTDFVFTIENTLSEDVADYYCLQSDNMP----	SEQ ID NO: 2
GJ39C	DIQMTQSPSSLSASLGGKVTITCKASQDINK----YIAWYQHKPGKGPRLLIHY---- TSTLQPGIPSRFSGSGSGRDYSFSISNLEPEDIATYYCLQYDNLL----	SEQ ID NO: 3
VLX	QLVLTQ-SSSASFSLGASAKLTCTLSSQHST--- YTIEW- YQQQ- PLKPP- KYVMELKKDGSHSTGDGIPDRFSGSSSGADRYLSISNIQPEDEAIYIC GVGDTIKEQFV	SEQ ID NO: 4
21-4	DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKILIYA---- ASNLESGIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDP----	SEQ ID NO: 5
12-38	DIQMTQSPASLAASVGETVTITCRASENIYY----SLAWYQQKQGKSPQLLIYN---- ANSLEDGVPSRFSGSGSGTQYSMKINSMQPEDTATYFCKQAYDVP----	SEQ ID NO: 6
12-46	DIQMTQSPASLSVSVGETVTITCRASENIYS----NLAWYQQKQGKSPQLLVYA---- ATNLADGVPSRFSGSGSGTQYSLKINSLQSEDFGSYYCQHFWGTP----	SEQ ID NO: 7
08/018	DIQMTQSPSSLSASVGDRVTITCQASQDISN--YLNWYQQKYGKAPKLLIYDASN---- LETGVPSRFSGSG-SGTDFTFTISSLQPEDIATYYCQQYDNLP----	SEQ ID NO: 8
L25	EIVMTQSPATLSLSPGERATLSCRASQSVSSSY-LSWYQQKPGQAPRLLIYGAST---- RATGIPARFSGSG-SGTDFTLTISSLQPEDFAVYYCQQDYNLP----	SEQ ID NO: 9
B2	ETTLTQSPAFMSATPGDKVNISCKASQDIDD--DMNWYQQKPGEAAIFIIQEATT---- LVPGIPPRFSGSG-YGTDFTLTINNIESEDAAYYFCLQHDNFP----	SEQ ID NO: 10
L11	AIQMTQSPSSLSASVGDRVTITCRASQGIRN--DLGWYQQKPGKAPKLLIYAASS---- LQSGVPSRFSGSG-SGTDFTLTISSLQPEDFATYYCLQDYNYP----	SEQ ID NO: 11
L10	EIVMTQSPPTLSLSPGERVTLSCRASQSVSSSY-LTWYQQKPGQAPRLLIYGAST---- RATSIPARESGSG-SGTDFTLTISSLQPEDFAVYYCQQDHNLPP---	SEQ ID NO: 12
V2-19	SYELTQPSSVSVSPGQTARITCSGDVLAKKY---ARWFQQKYGQAPVLVIYKDSE---- RPSGIPERFSGSS-SGTTVTLTISGAQVEDEADYYCYSAADNNL---	SEQ ID NO: 13
V2-15	SYELTQLPSVSVSPGQTARITCSGDVLGENY---ADWYQQKPGQAPELVIYEDSE---- RYPGIPERFSGST-SGNTTTLTISRVLTEDEADYYCLSGDEDNP---	SEQ ID NO: 14
V5-4	QPVLTQSSSASASLGSSVKLTCTLSSGHSS-- YIIAWHQQQPGKAPRYLMKLEGSGSYNKGSGVPDRFSGS- SSGADRYLTISNLQFEDEADYYCETWDSNT----	SEQ ID NO: 15

[0026] The microarray of the present invention includes a plurality of oligonucleotide species capable of hybridizing to a polynucleotide comprising a sequence encoding at least a portion of an antibody light chain variable region, or a complement thereof. As described in the Examples below, a bioinformatics approach was used to select oligonucleotide sequences for use in the microarray from the variable regions of the 99 mouse and 82 human light chain variable genes. The oligonucleotide sequences were selected to minimize cross-hybridization with each of the other light chain variable genes. Generally, the oligonucleotide sequences selected were between 60 and 80 nucleotides long. Computer programs suitable for use in the selection process are described in detail in the Examples section. However, as one skilled in the art will appreciate, any suitable program for selecting oligonucleotide sequences can be used, and many different programs are known to those of skill in the art. The light chain variable regions from all species identified to date are similar in structure such that one of skill in the art would expect the microarray and methods described herein could be adapted for use in any species capable of producing antibodies.

[0027] The human and mouse light chain variable gene specific oligonucleotides listed in Table 2 and Table 3, respectively, were selected from the germline sequences for the genes based on several criteria. The oligonucleotides were chosen from the most variable regions of each light chain variable gene, and were selected to be sufficiently unique to allow identification of individual light chain variable regions with minimal cross-hybridization. The oligonucleotides were also selected to maximize the likelihood that all of the sequences would hybridize to their target sequences under similar conditions by choosing a group of oligonucleotides that have similar G-C content and similar melting temperatures. Finally, oligonucleotides that have a low potential to self-fold were selected. Any suitable criteria could be used to select oligonucleotides for use in the microarray. Additional potential oligonucleotides are listed in Tables 4 and 5.

[0028] One of skill in the art will appreciate that the present invention is not limited to the oligonucleotides listed in Tables 2-5. Additional oligonucleotides for use in the microarray and methods of the invention include, but are not limited to, the complements of the oligonucleotides listed in the Tables, oligonucleotides substantially similar to the oligonucleotides listed in the Tables and any other oligonucleotides derived from the germline sequences of the light chain variable regions. The light chain variable region gene sequences are publicly available in GenBank under the heading "Ig Germline Genes". "Substantially similar oligonucleotides" includes oligonucleotides with at least 90% nucleotide identity to the oligonucleotides of Table 2-5. Suitably the oligonucleotides have at least 95% nucleotide identity to the oligonucleotides of Tables 2-5. Also included are light chain variable oligonucleotides containing portions of the sequences of the oligonucleotides listed in Tables 2-5.

[0029] In the Examples, oligonucleotides between 60 and 80 nucleotides long were used to minimize cross-hybridization with multiple light chain variable regions. One of skill in the art would appreciate that shorter or longer oligonucleotides could be used. Use of shorter oligonucleotides may result in a loss of specificity for a single light chain variable region, but such a loss of specificity can be compensated for by selecting and using multiple shorter oligonucleotides for each light chain variable region and then using a computer program that compensates for the cross-hybridization in the analysis of the microarray data. For example, the oligonucleotides included in the microarray may suitably be at least 20 nucleotides long, 30 nucleotides long, 40 nucleotides long, 50 nucleotides long, 60 nucleotides long, 70 nucleotides long, 80 nucleotides long, or 100 nucleotides long. Quantification of cross-hybridization between light chain variable region oligonucleotides and all target polynucleotides can be tested using target polynucleotides complementary to each of the oligonucleotide species on the microarray. These target polynucleotides may be synthetically produced or produced from B cell clones expressing known light chain variable regions. The results from such cross-hybridization experiments can then be applied to experimental data to eliminate experimental artifacts due to cross-hybridization. Other methods to minimize or compensate for cross-hybridization may also be used as would be apparent to those of skill in the art.

TABLE 2

Human light chain V gene selected oligonucleotides. The complements of these sequences may also be used.

Gene	Sequence	
A17/A1	CTGCAGGTCTAGTCAAAGCCTCGTATACAGTGATGGAAACACCTACTTGAATTGGTTTCAGCAGAGG	SEQ ID NO: 16
A10	CTCACCATCAATAGCCTGGAAGCTGAAGATGCTGCAACGTATTACTGTCATCAGAGTAGTAGTTTAC	SEQ ID NO: 17
A27/A11	GACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTATG	SEQ ID NO: 18
A14	GATCTGGGACAGATTTCACCTTTACCATCAGTAGCCTGGAAGCTGAAGATGCTGCAACATATTACTG	SEQ ID NO: 19
A2/A18b	CATCTCCTGCAAGTCTAGTCAGAGCCTCCTGCATAGTGATGGAAAGACCTATTTGTATTGGTACCTG	SEQ ID NO: 20
A3/A19	GATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTG	SEQ ID NO: 21
L14/A20	TCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCAATTATTTAG	SEQ ID NO: 22
A23	CTACTTGAGTTGGCTTCAGCAGAGGCGAGGCCAGCCTCCAAGACTGCTAATTTATAAGATTTCTAAC	SEQ ID NO: 23
A30	CTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAGCATAATAGTTA	SEQ ID NO: 24
A7	CATCTCCTTCAGGTCTAGTCAAAGCCTCGTACACAGTGATGGAAACACCTACTTGAGTTGGCTTCAG	SEQ ID NO: 25
B2	GAGAAGCTGCTATTTTCATTATTCAAGAAGCTACTAGTCTCGTTCCTGGAATCCCACCTCGATTCAG	SEQ ID NO: 26
B3	CATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCTCCAACAATAAGAACTACTTAGCTTGGTAC	SEQ ID NO: 27
L1	GTAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTTTC	SEQ ID NO: 28

TABLE 2-continued

Human light chain V gene selected oligonucleotides. The complements of these sequences may also be used.

Gene	Sequence	
L10	CTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAGTTTATTACTGTCAGGAGGATCATAACTTAC	SEQ ID NO: 29
L11	CTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAAGATTACAATTA	SEQ ID NO: 30
L12	TGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGATGCCTCCAGTTTGGAAAGTG	SEQ ID NO: 31
L15	CTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGCCAACAGTATAATAGTTA	SEQ ID NO: 32
L2/L16	CTCTCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTATAATAACTG	SEQ ID NO: 33
L14/18a/L18	TGGTATCAGCAGAAACCAGGGAAAGCTCCTAAGCTCCTGATCTATGATGCCTCCAGTTTGGAAAGTG	SEQ ID NO: 34
L19	CATCTTCTGTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAG	SEQ ID NO: 35
L6/L20	TTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGCGTAGCA	SEQ ID NO: 36
L22	GTAGGAGACAGAGTCAGTATCATTTGCTGGGCAAGTGAGGGCATTAGCAGTAATTTAGCCTGGTATC	SEQ ID NO: 37
L23	CTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCAACAGTATTATAGTAC	SEQ ID NO: 38
L24	CATCTACAGGAGACAGAGTCACCATCAGTTGTCGGATGAGTCAGGGCATTAGCAGTTATTTAGCCTG	SEQ ID NO: 39
L25	CTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAGTTTATTACTGTCAGCAGGATTATAACTTAC	SEQ ID NO: 40
L5	GACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAG	SEQ ID NO: 41
L8	CTCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCAACAGCTTAATAGTTA	SEQ ID NO: 42
L9	CATCTACAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGTTATTTAGCCTG	SEQ ID NO: 43
O11/O1-72	GTCTAGTCAGAGCCTCTTGGATAGTGATGATGGAAACACCTATTTGGACTGGTACCTGCAGAAGCCA	SEQ ID NO: 44
O2/O12	GAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTAT	SEQ ID NO: 45
O4/O14	CAGTTATTTAAATTGGTATCGGCAGAAACCAGGGAAAGTTCCTAAGCTCCTGATCTATAGTGCATCC	SEQ ID NO: 46
O8/O18	GTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGTCAGGACATTAGCAACTATTTAAATTGGTATC	SEQ ID NO: 47
V1-11	GCAGAGGGTCACCATCTCCTGTTCTGGAAGCAGCTCCAACATCGGAAATAATGCTGTAAACTGGTAC	SEQ ID NO: 48
V1-16	GCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGTAATACTGTAAACTGGTAC	SEQ ID NO: 49
V1-17	GCAGAGGGTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGTAATTATGTATACTGGTAC	SEQ ID NO: 50
V1-18	CTCCCTGGCCATCACTGGACTCCAGTCTGAGGATGAGGCTGATTATTACTGCAAAGCATGGGATAAC	SEQ ID NO: 51
V1-19	CAAACTCCTCATTTATGACAATAATAAGCGACCCTCAGGGATTCCTGACCGATTCTCTGGCTCCAAG	SEQ ID NO: 52

TABLE 2-continued

Human light chain V gene selected oligonucleotides. The complements of these sequences may also be used.

Gene	Sequence	
V1-2	GTCAGTCACCATCTCCTGCACTGGAACCAGCAGTGACGTTGGTGGTTATAACTATGTCTCCTGGTAC	SEQ ID NO: 53
V1-20	CCACCCTCCCAAACTCCTATCCTACAGGAATAACAACCGGCCCTCAGGGATCTCAGAGAGATTCTCT	SEQ ID NO: 54
V1-22	CTGTGATCTATGAGGATAACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCTGGCTCCATCGACAG	SEQ ID NO: 55
V1-3	GTCAGTCACCATCTCCTGCACTGGAACCAGCAGTGATGTTGGTGGTTATAACTATGTCTCCTGGTAC	SEQ ID NO: 56
V1-4	CAAACTCATGATTTATGAGGTCAGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCAAG	SEQ ID NO: 57
V1-5	CTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCAGCTTATATACAAGCAGCAGCACTTTC	SEQ ID NO: 58
V1-7	CTGACAATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCTGCTCATATGCAGGTAGTAG	SEQ ID NO: 59
V1-9	CTCTGGGCTCAAGTCCGAGGTTGAGGCTAATTATCACTGCAGCTTATATTCAAGTAGTTACACTTTC	SEQ ID NO: 60
V2-1	GATAAATATGCTTGCTGGTATCAGCAGAAGCCAGGCCAGTCCCCTGTGCTGGTCATCTATCAAGATAG	SEQ ID NO: 61
V2-11	TAGTCACATTGACCATCAGTGGAGTCCAGGCAGAAGACGAGGCTGACTATTACTGTCTATCAGCAGA	SEQ ID NO: 62
V2-13	CTTGGGACAGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAAGCTATTATGCAAGCTGGTAC	SEQ ID NO: 63
V2-15	CTGAGTTGGTGATATACGAAGATAGTGAGCGGTACCCTGGAATCCCTGAACGATTCTCTGGGTCCAC	SEQ ID NO: 64
V2-17	GACAACAGTCACGTTGACCATCAGTGGAGTCCAGGCAGAAGATGAGGCTGACTATTACTGTCAATCAG	SEQ ID NO: 65
V2-6	CTGGGACAGACGGCCAGGATTACCTGTGGGGGAAACAACATTGGAAGTAAAAATGTGCACTGGTACC	SEQ ID NO: 66
V3-2	GTTACTATCCAAACTGGTTCCAGCAGAAACCTGGACAAGCACCCAGGGCACTGATTTATAGTACAAG	SEQ ID NO: 67
V3-3	GACACTGATTTATGATAGAAGCAACAAACACTCCTGGACACCTGCCCGGTTCTCAGGCTCCCTCCTT	SEQ ID NO: 68
V3-4	CTGGAGGGACAGTCACACTCACTTGTGGCTTGAGCTCTGGCTCAGTCTCTACTAGTTACTACCCCAG	SEQ ID NO: 69
V4-1	AATACAGGGATTTTACTCATCTCCGGGCTCCAGTCTGAGGATGAGGCTGACTATTACTGTATGATTT	SEQ ID NO: 70
V4-2	AATGCAGGGATTTTACTCATCTCTGGGCTCCAGTCTGAGGATGAGGCTGACTATTACTGTATGATTT	SEQ ID NO: 71
V4-3	AATGCAGGGATTTTAGTCATCTCTGGGCTCCAGTCTGAGGATGAGGCTGACTATTACTGTATGATTT	SEQ ID NO: 72
V4-4	GGTACCAACAAAAGCCAGGGAACCCTCCCCGGTATCTCCTGTACTACCACTCAGACTCCAATAAGGG	SEQ ID NO: 73
V4-6	GTACCAGCAGAAGCCAGGGAGCTCTCCCAGGTTATTCCTGTATCACTACTCAGACTCAGACAAGCAG	SEQ ID NO: 74
V5-1	CATCGAATGGTATCAACAGAGACCAGGGAGGTCCCCCCAGTATATAATGAAGGTTAAGAGTGATGGC	SEQ ID NO: 75

TABLE 2-continued

Human light chain V gene selected oligonucleotides. The complements of these sequences may also be used.

Gene	Sequence	
V5-2	GAATCGGTACCTGACCATCAAGAACATCCAGGAAGAAGATGAGAGTGACTACCACTGTGGGGCAGAC	SEQ ID NO: 76
V5-4	CTACCTCACCATCTCCAACCTCCAGTTTGAGGATGAGGCTGATTATTACTGTGAGACCTGGGACAGT	SEQ ID NO: 77
V1-13_146	TCATCTATGGTAACAGCAATCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCTCCAAGTCTGGCACCTCA	SEQ ID NO: 78
V2-14_127	CCTGTGCTGGTCGTCTATGATGATAGCGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACT	SEQ ID NO: 79
V2-19_209	TCACCTTGACCATCAGCGGGGCCCAGGTTGAGGATGAGGCTGACTATTACTGTTACTCTGCGGCTGACAACA	SEQ ID NO: 80
V2-7_150	CAGCAAACGACCCTCCGGGATCCCTGAGAGATTCTCTGGCTCCAGCTCAGGGACAATGGCCACCTTGACTATC	SEQ ID NO: 81
V2-8_129	TGTGCTGGTCATCTATAGCGATAGCAACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGCTCCAACCCAG	SEQ ID NO: 82
V5-6_121	GAGAAGGGCCCTCGGTACTTGATGAAGCTTAACAGTGATGGCAGCCACAGCAAGGGGGACGGGATCCCTGATC	SEQ ID NO: 83
actin_beta	TTTTAATAGTCATTCCAAATATGAGATGCGTTGTTACAGGAAGTCCCTTGCCATCCTAAAAGCCACC	SEQ ID NO: 84
CD19	GCTGTGACTTTGGCTTATGTGATCTTCTGCCTGTGTTCCCTTGTGGGCATTCTTCATCTTCAAAGAG	SEQ ID NO: 85
CD20	CAATACAGAACCCATTCCATTTATCTTTGTACAGGGCTGACATTGTGGCACATTCTTAGAGTTACCA	SEQ ID NO: 86
hk_con	GAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAAC	SEQ ID NO: 87

[0030]

TABLE 3

Mouse light chain V gene selected oligonucleotides. The complements of these sequences may also be used.

Gene	Sequence	
12-38	CTGGGACACAGTATTCTATGAAGATCAACAGCATGCAGCCTGAAGATACCGCAACTTATTTCTGTAAACA	SEQ ID NO: 88
12-41	GCAAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCA	SEQ ID NO: 89
12-44	AGTTTTCTCTGAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATCATTATGG	SEQ ID NO: 90
12-46	GCAACAAACTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGCACACAGTATTCCCTCA	SEQ ID NO: 91
19-13	TTTCACTCTCACCATCAGCAATATGCAGTCTGAAGACCTGGCAGATTATTTCTGCCAGCAATATAGCAGC	SEQ ID NO: 92
19-14	CTCTCACCATTAGCAATGTGCAATCTGAAGACCTGGCAGATTATTTCTGTCTGCAACATTGGAATTATCC	SEQ ID NO: 93
19-15	GGTACTAATGTAGCCTGGTATCAACAGAAACCAGGGCAATCTCCTAAAGCACTGATTTACTCGGCATCCT	SEQ ID NO: 94

TABLE 3-continued

Mouse light chain V gene selected oligonucleotides. The complements of these sequences may also be used.

Gene	Sequence	
19-17	GGACGGATTTCACTTTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAACA	SEQ ID NO: 95
19-20	CACTGGGGTCCCCGATCGCTTCACAGGCAGTGGATCTGCAACAGATTTCACTCTGACCATCAGCAGTGTG	SEQ ID NO: 96
19-23	CTCTCACCATTAGCAATGTGCAGTCTGAAGACTTGGCAGATTATTTCTGTCAGCAATATAGCAGCTATCC	SEQ ID NO: 97
19-25	TATACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCACTTTATTACTGTCAGCAACATTATAGCA	SEQ ID NO: 98
19-29	ACCCTGGGGTCCCTGATCGCTTCACAGGCAGTGGATCTGCAACAGATTTCACTCTGACCATCAGCAGTCT	SEQ ID NO: 99
19-32	ATTCCTGCTTGTATCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATGAT	SEQ ID NO: 100
21-1	CACCATCTCCTGCAGAGCCAGTGAAAGTGTTGAATATTATGGCACAAGTTTAATGCAGTGGTACCAACAG	SEQ ID NO: 101
21-10	TCACCCTCACCATTGATCCTGTGGAGGCTGATGATGCTGCAACCTATTACTGTCAGCAAAATAATGAGGA	SEQ ID NO: 102
21-12	CTGGCTATAGTTATATGCACTGGTACCAACAGAAACCAGGACAGCCACCCAAACTCCTCATCTATCTTGC	SEQ ID NO: 103
21-2	GCCACCATCTCCTGCAGAGCCAGCGAAAGTGTTGATAATTATGGCATTAGTTTTATGAACTGGTTCCAAC	SEQ ID NO: 104
21-3	GAGCCACTATCTTCTGCAGAGCCAGCCAGAGTGTCGATTATAATGGAATTAGTTATATGCACTGGTTCCA	SEQ ID NO: 105
21-4	GCCACCATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATATGAACTGGTACCAAC	SEQ ID NO: 106
21-5	CTCACCATTAATCCTGTGGAGGCTGATGATGTTGCAACCTATTACTGTCAGCAAAGTAATGAGGATCCTC	SEQ ID NO: 107
21-7	CTAGCTATAGTTATATGCACTGGTACCAACAGAAACCAGGACAGCCACCCAAACTCCTCATCAAGTATGC	SEQ ID NO: 108
21-9	GACAGAGGGCCACCATATCCTGCCAAGCCAGCGAAAGTGTCAGTTTTGCTGGTACAAGTTTAATGCACTG	SEQ ID NO: 109
22-33	AGTAAGAAGGTCACCATTAGTTGCACGGCCAGTGAGAGCCTTTATTCAAGCAAACACAAGGTGCACTACT	SEQ ID NO: 110
23-37	GATTACACTCTCAGTATCAACAGTGTGAAGCCCGAAGATGAAGGAATATATTACTGTCTTCAAGGTTACA	SEQ ID NO: 111
23-39	CTCTCAGTATCAACAGTGTGGAACCTGAAGATGTTGGAGTGTATTACTGTCAAAATGGTCACAGCTTTCC	SEQ ID NO: 112
23-43	CAGGAGATAGCGTCAGTCTTTCCTGCAGGGCCAGCCAAAGTATTAGCAACAACCTACACTGGTATCAACA	SEQ ID NO: 113
23-45	GGAGATAGAGTCAGTCTTTCCTGCAGGGCCAGTCAAAGTATTAGCAACTACCTACACTGGTATCAACAAA	SEQ ID NO: 114
23-48	TTCTCCTGCAGGGCCAGTCAGAGCATTGGCACAAGCATACACTGGTATCAGCAAAGAACAAATGGTTCTC	SEQ ID NO: 115
4-50	GTACTGGTACCAGCAGAAGTCAGATGCCTCCCCCAAACTATGGATTTATTACACATCCAACCTGGCTCCT	SEQ ID NO: 116
4-51	GGGGCTGGGATCTCTTACTCTCTCACAATCAGCAGCATGGAGGCTGAAAATGATGCAACTTATTACTGCC	SEQ ID NO: 117
4-57	TGTCTGCATCTCCAGGGGAAAAGGTCACCATGACCTGCAGGGCCAGCTCAAGTGTAAGTTCCAGTTACTT	SEQ ID NO: 118

TABLE 3-continued

Mouse light chain V gene selected oligonucleotides. The complements of these sequences may also be used.

Gene	Sequence	
8-16	ATCAGAATCTTTTATGGAGTGGAAACCAAAGGTACTGTTTGGTCTGGCACCAGTGGAAACCAGGGCAAAC	SEQ ID NO: 119
8-19	CTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGAATGATTATAGTTATCC	SEQ ID NO: 120
8-21	GGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTGGCTTGG	SEQ ID NO: 121
8-24	TCCTCCCTGGCTATGTCAGTAGGACAGAAGGTCACTATGAGCTGCAAGTCCAGTCAGAGCCTTTTAAATA	SEQ ID NO: 122
8-27	GAAAAGGTCACTATGAGCTGTAAGTCCAGTCAAAGTGTTTTATACAGTTCAAATCAGAAGAACTACTTGG	SEQ ID NO: 123
8-28	CCGATTTCACTCTTACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGAATGATCA	SEQ ID NO: 124
8-30	CCCTAGCTGTGTCAGTTGGAGAGAAGGTTACTATGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTAG	SEQ ID NO: 125
8-34	TAGCTAGTGGCAACCAAAATAACTACTTGGCCTGGCACCAGCAGAAACCAGGACGATCTCCTAAAATGCT	SEQ ID NO: 126
RF	GAGAAACCTGGGAAAACTAATAAGCTTCTTATCTACTCTGGATCCACTTTGCAATCTGGAATTCCATCAA	SEQ ID NO: 127
VL1	AACTATGCCAACTGGGTCCAAGAAAAAGCAGATCATTTATTCACTGGTCTAATAGGTGGTACCAACAACC	SEQ ID NO: 128
VL2	TAACTATGCCAACTGGGTTCAAGAAAAACCAGATCATTTATTCACTGGTCTAATAGGTGGTACCAGCAAC	SEQ ID NO: 129
VLx	ACAGCCACTCAAGCCTCCTAAGTATGTGATGGAGCTTAAGAAAGATGGAAGCCACAGCACAGGTGATGGG	SEQ ID NO: 130
aa4	CTCAAGTGTAAGTTACATGTACTGGTACCAGCAGAAGCCAGGATCCTCCCCCAAACCCTGGATTTATCGC	SEQ ID NO: 131
ac4	TCACGATCAGCAGCATGGAGGCTGAAGATGTTGCCACTTATTACTGTTTTCAGGGGAGTGGGTACCCACT	SEQ ID NO: 132
ad4	TATTCTCTCACAATCAGCAGCATGGAGGCTGAAGATGCTGCCACTTTTTACTGCCAGCAGTACAGTGGTT	SEQ ID NO: 133
ae4	ACTCTCTCACAATCAGCAGCATGGAGGCTGAAGATGCTGCCTCTTATTTCTGCCATCAGTGGAGTAGTTA	SEQ ID NO: 134
af4	CAATCATGTCTGCATCTCTAGGGGAGGAGATCACCCTAACCTGCAGTGCCAGCTCGAGTGTAAGTTACAT	SEQ ID NO: 135
ag4	CACTTCTACCAAATTCTGGATTTATAGGACATCCAACCTGGCTTCAGAAGTCCCAGCTCCCTTCAGTGGC	SEQ ID NO: 136
ah4	TACTTGTACTGGTACCAGCAGAAGTCAGGATCCTCCCCAAAACTCTGGATTTATAGCATATCCAACCTGG	SEQ ID NO: 137
ai4	CTCTCACAATCAGCAGCATGGAGGCTGAAGATGCTGCCACTTATTACTGCCACCAGTATCATCGTTCCCC	SEQ ID NO: 138
aj4	TACATGTAATGGTTCCAGCAGAAGCGAGGATCCTCCCCCAAACTCTGGATTTATAGCATATCCAACCTGG	SEQ ID NO: 139
al4	CATGCACTGGTACCAGCAGAAGCCAGGATCCTCCCCCAGACTCTGGATTTATTTAACATTCAACTTGGCT	SEQ ID NO: 140
am4	TTGTTCTCTCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTCACAATGACTTGCAGGGC	SEQ ID NO: 141

TABLE 3-continued

Mouse light chain V gene selected oligonucleotides. The complements of these sequences may also be used.

Gene	Sequence	
an4	GACATCTTTCTCTTTCACAATCAACAGCATGGAGGCTGAAGATGTTGCCACTTATTACTGTCAGCAAAGG	SEQ ID NO: 142
ap4	GCCAGCTCAAGTGTAAGTTACATGCACTGGTTCCAGCAGAAGCCAGGCACTTCTCCCAAACTCTGGATTT	SEQ ID NO: 143
aq4	GTAAGTTACATGTACTGGTACCAGCAGAAGCCAAGATCCTCCCCCAAACCCTGGATTTATCTCACATCCA	SEQ ID NO: 144
ar4	TGTAAGTTACATGTACAGGTACCAGCAGAAGCCAGGATCCTCACCCAAACCCTGGATTTATGGCACATCC	SEQ ID NO: 145
at4	GTAAGTTACATGTACTGGTACCAGCAGAAGCCAGGATCCTCCCCCAGACTCCTGATTTATGACACATCCA	SEQ ID NO: 146
ay4	GGTCTGAGAGCTCTTACACTCTGACAATCAGCTGCATGCAGGACGAAGTTGCTGCCACTTACTATTGTCA	SEQ ID NO: 147
ba4	CCATGTATGCATCTCTAGGAGAGAGAGTCACTATCACTTGCAAGGCGAGTCAGGACATTAATAGCTATTT	SEQ ID NO: 148
bb1	CACCTATTTACATTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAAC	SEQ ID NO: 149
bb1.1	AATGGAAACACCTATTTATATTGGTACCTGCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTACAGGG	SEQ ID NO: 150
bd2	GTCAGAGCCTCTTAGATAGTGATGGAAAGACATATTTGAATTGGTTGTTACAGAGGCCAGGCCAGTCTCC	SEQ ID NO: 151
bi2	TTACAACAGAGGCCTGGCCAGGCTCCAAAGCACCTAATGTATCAGGTGTCCAAACTGGACCCTGGCATCC	SEQ ID NO: 152
bj2	ATATAGTAATGGAAAAACCTATTTGAATTGGTTATTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATC	SEQ ID NO: 153
bl1	CAGGTCTAGTCAGAGCCTTGAAAACAGTAATGGAAACACCTATTTGAACTGGTACCTCCAGAAACCAGGC	SEQ ID NO: 154
bt20	CATCCCTGTCCATGGCTATAGGAGAAAAAGTCACCATCAGATGCATAACCAGCACTGATATTGATGATGA	SEQ ID NO: 155
bv9	ACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCAGATGGAACTATTAAACGCCTGATCTACGCCAC	SEQ ID NO: 156
bw20	CCTGTCCGTGGCTACAGGAGAAAAAGTCACTATCAGATGCATAACCAGCACTGATATTGATGATGATATG	SEQ ID NO: 157
cb9	GGGAGACAGAATAACCATCACTTGCCAGGCAACTCAAGACATTGTTAAGAATTTAAACTGGTATCAGCAG	SEQ ID NO: 158
ce9	CTCTCACCATTAGCAACCTGGAGCAAGAAGATATTGCCACTTACTTTTGCCAACAGGGTAATACGCTTCC	SEQ ID NO: 159
cf9	TTGCAGCAGAAACCAGGGAAATCATTTAAGGGCCTGATCTATCATGGAACCAACTTGGAAGATGGAGTTC	SEQ ID NO: 160
ci12	TCTGGGAGAAAGTGTCACCATCACATGCCTGGCAAGTCAGACCATTGGTACATGGTTAGCATGGTATCAG	SEQ ID NO: 161
cj9	CCGGGCAAGTCAGGACATTCATGGTTATTTAAACTTGTTTCAGCAGAAACCAGGTGAAACTATTAAACAC	SEQ ID NO: 162
cp9	TTCTCTCACCATCAGCAACCTGGAACCTGAAGATATTGCCACTTACTATTGTCAGCAGTATAGTAAGCTT	SEQ ID NO: 163
cr1	CTAGTCAGAGCATTGTACATAGTAATGGAAACACCTATTTAGAATGGTACCTGCAGAAACCAGGCCAGTC	SEQ ID NO: 164
cs1	CACTCAAGATCAGCACAATAAAGCCTGAGGACTTGGGAATGTATTACTGCTTACAAGGTACACATCAGCC	SEQ ID NO: 165

TABLE 3-continued

Mouse light chain V gene selected oligonucleotides. The complements of these sequences may also be used.

Gene	Sequence	
cv1	AGATCAAGCCTCTATCTCTTGCAAGTCTACTAAGAGTCTTCTGAATAGTGATGGATTCACTTATTTGGAC	SEQ ID NO: 166
cw9	AAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCAGATGGAACTATTAAACGCCTGATCTACGCCGC	SEQ ID NO: 167
cy9	CAGTCTCTCTTGTCGGGCTAGTCAGGGCATTAGAGGTAATTTAGACTGGTATCAGCAGAAACCAGGTGGA	SEQ ID NO: 168
dv-36	GCAGAAAGCAGAGCAAGTTCCCCGGCTCCTTATCCATAGTGCCTCCACTAGGGCCGGTGGTGTCCCAGTC	SEQ ID NO: 169
fl12	AGTATTCTCTCAAGATCAGTAGCCTGCATCCTGACGATGTTGCAACGTATTACTGTCAAAATGTGTTAAG	SEQ ID NO: 170
gj38c	ACCAACACAAGCCTGGAAAAGGTCCTAGGCTGCTCATACATTACACATCTACATTACAGCCAGGCATCCC	SEQ ID NO: 171
gm33	CTCCTTTCTGTATCTCTAGGAGACAGAGTCACCATTACTTGCAAGGCAAGTGAGGACATATATAATCGG	SEQ ID NO: 172
gn33	CTACTTGTCTGTATCTCTAGGAGGCAGAGTCACCATTACTTGCAAGGCAAGTGACCACATTAATAATTGG	SEQ ID NO: 173
gr32	CCAGGAAATATTCCTAAACTATTGATCTATAAGGCTTCCAACTTGCACACAGGCGTCCCATCAAGGTTTA	SEQ ID NO: 174
he24	TATTGTGATGACGCAGGCTGCATTCTCCAATCCAGTCACTCTTGGAACATCAGCTTCCATCTCCTGCAGG	SEQ ID NO: 175
hf24	ATATTGTGATGACTCAGGCTGCACCCTCTGTACCTGTCACTCCTGGAGAGTCAGTATCCATCTCCTGCAG	SEQ ID NO: 176
hg24	TCTAGTAAGAGTCTCCTATATAAGGATGGGAAGACATACTTGAATTGGTTTCTGCAGAGACCAGGACAAT	SEQ ID NO: 177
if11	TGACTTGCCAGGCAAGTCAGGGCACTAGCATTAATTTAAACTGGTTTCAGCAAAAACCAGGGAAAGCTCC	SEQ ID NO: 178
kb4	AATTGTGCTCACTCAGTCTCCAGCCATCACAGCTGCATCTCTGGGGCAAAAGGTCACCATCACCTGCAGT	SEQ ID NO: 179
kf4	CCCGGGGAGAAGATCACTATCACCTGCAGTGCCAGCTCAAGTATAAGTTCCAATTACTTGCATTGGTATC	SEQ ID NO: 180
kh4	GCTCAAGTATAAGTTCCAGCAACTTGCACTGGTACCAGCAGAAGTCAGAAACCTCCCCCAAACCCTGGAT	SEQ ID NO: 181
kj4	TTACTTGCACTGGTACGAGCAGAAGTCAGGCGCTTCCCCCAAACCCTTGATTCATAGGACATCCAACCTG	SEQ ID NO: 182
kk4	CTCAAGTGTAAGTTACATGCACTGGTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGAC	SEQ ID NO: 183
km4	AGGATCCTCGCCCAAACCCTGGATTTATGACACATCCAACCTGGCTTCTGGATTCCCTGCTCGCTTCAGT	SEQ ID NO: 184
kn4	CCAGCTCAAGTATAAGTTACATGCACTGGTACCAGCAGAAGCCAGGCACCTCCCCCAAAAGATGGATTTA	SEQ ID NO: 185
Kappa Constant	CTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGGTCCTGAGACGCCACCACCAG	SEQ ID NO: 186
Lambda1 Constant	AGAAACATGCCCAAGTGTATCCTTGGTGCTTTTGCCTACCATAGCCCTTCTCTCTACCCTCAAAATGCAC	SEQ ID NO: 187
Lambda2 Constant	CCGTGTTTCCACCTTCCTCTGAGGAGCTCAAGGAAAACAAAGCCACACTGGTGTGTCTGATTTCCAACTT	SEQ ID NO: 188

TABLE 3-continued

Mouse light chain V gene selected oligonucleotides. The complements of these sequences may also be used.

Gene	Sequence	
Lambda3 Constant	AATCCCTTCTTTCATTCACACAGGTCAGCCCAAGTCCACTCCCAGACTCACCATGTTTCCACCTTCCCCT	SEQ ID NO: 189
Actin Beta	CGTGCACCGCAAGTGCTTCTAGGCGGACTGTTACTGAGCTGCGTTTTACACCCTTTCTTTGACAAAACCT	SEQ ID NO: 190

[0031]

TABLE 4

Additional human light chain V gene oligonucleotides. The complements of these sequences may also be used.

Sequence Name	Secondary Sequence	
>A1_134	AGGCCAATCTCCAAGGCGCCTAATTTATAAGGTTTCTAACTGGGACTCTGGGGTCCCAGACAGATTCAGC	SEQ ID NO: 191
>A11_93	AGCTACTTAGCCTGGTACCAGCAGAAACCTGGCCTGGCGCCCAGGCTCCTCATCTATGATGCATCCAGCA	SEQ ID NO: 192
>A14_28	TCCTCTCTGTGACTCCAGGGGAGAAAGTCACCATCACCTGCCAGGCCAGTGAAGGCATTGGCAACTACTT	SEQ ID NO: 193
>A17_134	AGGCCAATCTCCAAGGCGCCTAATTTATAAGGTTTCTAACCGGGACTCTGGGGTCCCAGACAGATTCAGC	SEQ ID NO: 194
>A18b_109	CTATTTGTATTGGTACCTGCAGAAGCCAGGCCAGTCTCCACAGCTCCTAATCTATGAAGTTTCCAGCCGG	SEQ ID NO: 195
>A19_159	TATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCAGTGGCAGTGGATCAGGCACAGATTTTA	SEQ ID NO: 196
>A2_109	ATTTGTATTGGTACCTGCAGAAGCCAGGCCAGCCTCCACAGCTCCTGATCTATGAAGTTTCCAACCGGTT	SEQ ID NO: 197
>A20_123	AAAGTTCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAATCAGGGGTCCCATCTCGGTTCAGTGGCA	SEQ ID NO: 198
>A23_143	TCCAAGACTCCTAATTTATAAGATTTCTAACCGGTTCTCTGGGGTCCCAGACAGATTCAGTGGCAGTGGG	SEQ ID NO: 199
>A26_65	CTGCCGGGCCAGTCAGAGCATTGGTAGTAGCTTACACTGGTACCAGCAGAAACCAGATCAGTCTCCAAAG	SEQ ID NO: 200
>A27_1	AAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAG	SEQ ID NO: 201
>A30_85	TTAGAAATGATTTAGGCTGGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCGCCTGATCTATGCTGCATC	SEQ ID NO: 202
>A5_101	ATACACCTATTTGTATTGGTTTCTGCAGAAAGCCAGGCCAGTCTCCACACTCCTGATCTATGAAGTTTCC	SEQ ID NO: 203
>A7_222	GATTTCACACTGAAAATCAGCAGGGTGGAAGCTGAGGATGTCGGGGTTTATTACTGCACGCAAGCTACAC	SEQ ID NO: 204
>B2_214	CCCTCACAATTAATAACATAGAATCTGAGGATGCTGCATATTACTTCTGTCTACAACATGATAATTTCCC	SEQ ID NO: 205
>B3_27	TCCCTGGCTGTGTCTCTGGGCGAGAGGGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTATACAGCT	SEQ ID NO: 206
>L1_71	GGCGAGTCAGGGCATTAGCAATTATTTAGCCTGGTTTCAGCAGAAACCAGGGAAAGCCCCTAAGTCCCTG	SEQ ID NO: 207

TABLE 4-continued

Additional human light chain V gene oligonucleotides. The complements of these sequences may also be used.

Sequence Name	Secondary Sequence	
>L10_92	CAGCTACTTAACCTGGTATCAGCAGAAACCTGGCCAGGCGCCCAGGCTCCTCATCTATGGTGCATCCACC	SEQ ID NO: 208
>L11_217	TCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCTACAAGATTACAATTACCCTCC	SEQ ID NO: 209
>L12_47	AGACAGAGTCACCATCACTTGCCGGGCCAGTCAGAGTATTAGTAGCTGGTTGGCCTGGTATCAGCAGAAA	SEQ ID NO: 210
>L14_68	TCGGGCGAGGCAGGGCATTAGCAATTATTTAGCCTGGTTTCAGCAGAAACCAGGGAAAGTCCCTAAGCAC	SEQ ID NO: 211
>L15_92	CTGGTTAGCCTGGTATCAGCAGAAACCAGAGAAAGCCCCTAAGTCCCTGATCTATGCTGCATCCAGTTTG	SEQ ID NO: 212
>L16_217	TCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTATAATAACTGACCTCC	SEQ ID NO: 213
>L18_216	CTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCAACAGTTTAATAATTACCCTC	SEQ ID NO: 214
>L19_206	AGATTTCACTCTCACTATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCAACAGGCTAAC	SEQ ID NO: 215
>L2_217	TCACCATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTATAATAACTGGCCTCC	SEQ ID NO: 216
>L20_193	GTGGGCCTGGGACAGACTTCACTCTCACCATCAGCAGCCTAGAGCCTGAAGATTTTGCAGTTTATTACTG	SEQ ID NO: 217
>L22_113	GAAACCAGGGAAATCCCCTAAGCTCTTCCTCTATGATGCAAAAGATTTGCACCCTGGGGTCTCATCGAGG	SEQ ID NO: 218
>L23_104	GTATCAGCAAAAACCAGCAAAAGCCCCTAAGCTCTTCATCTATTATGCATCCAGTTTGCAAAGTGGGGTC	SEQ ID NO: 219
>L24_24	TCCTTACTCTCTGCATCTACAGGAGACAGAGTCACCATCAGTTGTCGGATGAGTCAGGGCATTAGCAGTT	SEQ ID NO: 220
>L25_92	CAGCTACTTATCCTGGTACCAGCAGAAACCTGGGCAGGCTCCCAGGCTCCTCATCTATGGTGCATCCACC	SEQ ID NO: 221
>L4/18a_216	CTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCAACAGTTTAATAGTTACCCTC	SEQ ID NO: 222
>L5_196	GATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTACTATTGTCA	SEQ ID NO: 223
>L6_49	AAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCTACTTAGCCTGGTACCAACAGAAACC	SEQ ID NO: 224
>L8_215	TCTCACAATCAGCAGCCTGCAGCCTGAAGATTTTGCAACTTATTACTGTCAACAGCTTAATAGTTACCCT	SEQ ID NO: 225
>L9_28	CATTCTCTGCATCTACAGGAGACAGAGTCACCATCACTTGTCGGGCGAGTCAGGGTATTAGCAGTTATTT	SEQ ID NO: 226
>O1_159	ATCTATACGCTTTCCTATCGGGCCTCTGGAGTCCCAGACAGGTTCAGTGGCAGTGGGTCAGGCACTGATT	SEQ ID NO: 227
>O2_215	TCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCT	SEQ ID NO: 228
>O4_217	TCACTATCAGCAGCCTGCAGCCTGAAGATGTTGCAACTTATTACGGTCAACGGACTTACAATGCCCCTCC	SEQ ID NO: 229
>O8_145	ACGATGCATCCAATTTGGAAACAGGGGTCCCATCAAGGTTCAGTGGAAGTGGATCTGGGACAGATTTTAC	SEQ ID NO: 230

TABLE 4-continued

Additional human light chain V gene oligonucleotides. The complements of these sequences may also be used.

Sequence Name	Secondary Sequence	
>V1-11_121	CAGGAAAGGCTCCCAAACTCCTCATCTATTATGATGATCTGCTGCCCTCAGGGGTCTCTGACCGATTCTC	SEQ ID NO: 231
>V1-13_228	ATCACTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCAGCCTGAGTGGTT	SEQ ID NO: 232
>V1-16_51	GTCACCATCTCTTGTTCTGGAAGCAGCTCCAACATCGGAAGTAATACTGTAAACTGGTACCAGCAGCTCC	SEQ ID NO: 233
>V1-17_93	AATTATGTATACTGGTACCAGCAGCTCCCAGGAACGGCCCCCAAACTCCTCATCTATAGTAATAATCAGC	SEQ ID NO: 234
>V1-18_226	CCATCACTGGACTCCAGTCTGAGGATGAGGCTGATTATTACTGCAAAGCATGGGATAACAGGCTGAATGC	SEQ ID NO: 235
>V1-19_225	ATCACCGGACTCCAGACTGGGGACGAGGCCGATTATTACTGCGGAACATGGGATAGCAGCCTGAGTGCTG	SEQ ID NO: 236
>V1-2_227	CGTCTCTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCAGCTCATATGCAGGCAGCAACAATTTC	SEQ ID NO: 237
>V1-20_91	ACCAAGGAGCAGCTTGGCTGCAGCAGCACCAGGGCCACCCTGCCAAACTCCTATCCTACAGGAATAACAA	SEQ ID NO: 238
>V1-22_36	TCTCCGGGGAAGACGGTAACCATCTCCTGCACCCGCAGCAGTGGCAGCATTGCCAGCAACTATGTGCAGT	SEQ ID NO: 239
>V1-3_227	CATCTCTGGGCTCCAGGCTGAGGATGAGGCTGATTATTACTGCTGCTCATATGCAGGCAGCTACACTTTC	SEQ ID NO: 240
>V1-4_143	CATGATTTATGAGGTCAGTAATCGGCCCTCAGGGGTTTCTAATCGCTTCTCTGGCTCCAAGTCTGGCAAC	SEQ ID NO: 241
>V1-5_85	TTGGTAGTTATAACCGTGTCTCCTGGTACCAGCAGCCCCCAGGCACAGCCCCCAAACTCATGATTTATGA	SEQ ID NO: 242
>V1-7_227	AATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCTGCTCATATGCAGGTAGTAGCACTTTC	SEQ ID NO: 243
>V1-9_83	CGTTGGGGATTATGATCATGTCTTCTGGTACCAAAAGCGTCTCAGCACTACCTCCAGACTCCTGATTTAC	SEQ ID NO: 244
>V2-1_30	TCCGTGTCCCCAGGACAGACAGCCAGCATCACCTGCTCTGGAGATAAATTGGGGGATAAATATGCTTGCT	SEQ ID NO: 245
>V2-11_84	AAAAAATATGCTTATTGGTACCAGCAGAAGCCAGGCCAGTTCCCTGTGCTGGTGATATATAAAGACAGCG	SEQ ID NO: 246
>V2-13_44	ACAGACAGTCAGGATCACATGCCAAGGAGACAGCCTCAGAAGCTATTATGCAAGCTGGTACCAGCAGAAG	SEQ ID NO: 247
>V2-14_218	CATCAGCAGGGTCGAAGCCGGGGATGAGGCCGACTATTACTGTCAGGTGTGGGATAGTAGTAGTGATCAT	SEQ ID NO: 248
>V2-15_125	CCCTGAGTTGGTGATATACGAAGATAGTGAGCGGTACCCTGGAATCCCTGAACGATTCTCTGGGTCCACC	SEQ ID NO: 249
>V2-17_204	ACAGTCACGTTGACCATCAGTGGAGTCCAGGCAGAAGATGAGGCTGACTATTACTGTCAATCAGCAGACA	SEQ ID NO: 250
>V2-19_211	CCTTGACCATCAGCGGGGCCCAGGTTGAGGATGAGGCTGACTATTACTGTTACTCTGCGGCTGACAACAA	SEQ ID NO: 251
>V2-6_215	GACCATCAGCAGAGCCCAAGCCGGGGATGAGGCTGACTATTACTGTCAGGTGTGGGACAGCAGCACTGCA	SEQ ID NO: 252
>V2-7_220	TCAGTGGGGCCCAGGTGGAGGATGAAGCTGACTACTACTGTTACTCAACAGACAGCAGTGGTAATCATAG	SEQ ID NO: 253

TABLE 4-continued

Additional human light chain V gene oligonucleotides. The complements of these sequences may also be used.

Sequence Name	Secondary Sequence	
>V2-8_189	TCCAACCCAGGGAACACCGCCACCCTAACCATCAGCAGGATCGAGGCTGGGGATGAGGCTGACTATTACT	SEQ ID NO: 254
>V3-2_224	GACACTGTCAGGTGTGCAGCCTGAGGACGAGGCTGAGTATTACTGCCTGCTCTACTATGGTGGTGCTCAG	SEQ ID NO: 255
>V3-3_95	TCATTATCCCTACTGGTTCCAGCAGAAGCCTGGCCAAGCCCCCAGGACACTGATTTATGATACAAGCAAC	SEQ ID NO: 256
>V3-4_209	GAACAAAGCTGCCCTCACCATCACGGGGGCCCAGGCAGATGATGAATCTGATTATTACTGTGTGCTGTAT	SEQ ID NO: 257
>V4-1_20	ACCTTCCTCCTCCGCATCTCCTGGAGAATCCGCCAGACTCACCTGCACCTTGCCCAGTGACATCAATGTT	SEQ ID NO: 258
>V4-2_110	GTACCAGCAGAAGCCAGGGAGTCCTCCCCAGTATCTCCTGAGGTACAAATCAGACTCAGATAAGCAGCAG	SEQ ID NO: 259
>V4-3_110	GTACCAGCAGAAGCCAGAGAGCCCTCCCCGGTATCTCCTGAGCTACTACTCAGACTCAAGTAAGCATCAG	SEQ ID NO: 260
>V4-4_66	ATGCTGAGCAGTGGCTTCAGTGTTGGGGACTTCTGGATAAGGTGGTACCAACAAAAGCCAGGGAACCCTC	SEQ ID NO: 261
>V4-6_182	ACCTGGGGTCCCCAGTCGAGTCTCTGGCTCCAAGGAGACCTCAAGTAACACAGCGTTTTTGCTCATCTCT	SEQ ID NO: 262
>V5-1_77	TGAGCACAGCACCTACACCATCGAATGGTATCAACAGAGACCAGGGAGGTCCCCCCAGTATATAATGAAG	SEQ ID NO: 263
>V5-2_237	ATCAAGAACATCCAGGAAGAAGATGAGAGTGACTACCACTGTGGGGCAGACCATGGCAGTGGGAGCAACT	SEQ ID NO: 264
>V5-4_117	CCAGGGAAGGCCCCTCGGTACTTGATGAAGCTTGAAGGTAGTGGAAGCTACAACAAGGGGAGGGGAGTTC	SEQ ID NO: 265
>V5-6_120	GAGAAGGGCCCTCGGTACTTGATGAAGCTTAACAGTGATGGCAGCCACAGCAAGGGGGACGGGATCCCTG	SEQ ID NO: 266

[0032]

TABLE 5

Additional mouse light chain V gene selected oligonucleotides. The complements of these sequences may also be used.

	Secondary Sequence	
12-38-65	CATGTCGAGCAAGTGAGAACATTTACTACAGTTTAGCATGGTATCAGCAGAAGCAAGGGAAATCTCC	SEQ ID NO: 267
12-41-86	TTCACAATTATTTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGGTCCTGGTCTATAATGC	SEQ ID NO: 268
12-44-70	CGAGCAAGTGAGAATATTTACAGTTATTTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGC	SEQ ID NO: 269
12-46-70	CGAGCAAGTGAGAATATTTACAGTAATTTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGC	SEQ ID NO: 270
19-13-103	TGGTATCAACAGAAACCAGGACAATCTCCTAAACTACTGATTTACTCGGCATCCAATCGGTACACTG	SEQ ID NO: 271
19-14-197	GATCTGGGACAGATTTCACTCTCACCATTAGCAATGTGCAATCTGAAGACCTGGCAGATTATTTCTG	SEQ ID NO: 272

TABLE 5-continued

Additional mouse light chain V gene selected oligonucleotides. The complements of these sequences may also be used.

	Secondary Sequence	
19-15-217	CTCACCATCAGCAATGTGCAGTCTGAAGACTTGGCAGAGTATTTCTGTCAGCAATATAACAGCTATC	SEQ ID NO: 273
19-17-215	CTTTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCAGTTTATTACTGTCAGCAACATTATAGTAC	SEQ ID NO: 274
19-20-69	CAAGGCCAGTGAGAATGTGGGTACTTATGTATCCTGGTATCAACAGAAACCAGAGCAGTCTCCTAAA	SEQ ID NO: 275
19-23-206	CAGATTTCACTCTCACCATTAGCAATGTGCAGTCTGAAGACTTGGCAGATTATTTCTGTCAGCAATATAG	SEQ ID NO: 276
19-25-209	ATTATACTCTCACCATCAGCAGTGTGCAGGCTGAAGACCTGGCACTTTATTACTGTCAGCAACATTATA	SEQ ID NO: 277
19-29-69	CAAGGCCAGTGAGAATGTGGGTACTTATGTATCCTGGTATCAACAGAAACCAGAGCAGTCTCCTAAA	SEQ ID NO: 278
19-32-124	CAGTCTCCTAAACTGCTGATATACTATGCATCCAATCGCTACACTGGAGTCCCTGATCGCTTCACTG	SEQ ID NO: 279
21-1-117	GTACCAACAGAAACCAGGACAGCCACCCAAACTCCTCATCTATGCTGCATCCAACGTAGAATCTGGG	SEQ ID NO: 280
21-10-210	GTCTAGGACAGACTTCACCCTCACCATTGATCCTGTGGAGGCTGATGATGCTGCAACCTATTACTGT	SEQ ID NO: 281
21-12-117	GTACCAACAGAAACCAGGACAGCCACCCAAACTCCTCATCTATCTTGCATCCAACCTAGAATCTGGG	SEQ ID NO: 282
21-2-229	CTCAACATCCATCCTATGGAGGAGGATGATACTGCAATGTATTTCTGTCAGCAAAGTAAGGAGGTTC	SEQ ID NO: 283
21-3-66	CTGCAGAGCCAGCCAGAGTGTCGATTATAATGGAATTAGTTATATGCACTGGTTCCAACAGAAACCA	SEQ ID NO: 284
21-4-117	GTACCAACAGAAACCAGGACAGCCACCCAAACTCCTCATCTATGCTGCATCCAATCTAGAATCTGGG	SEQ ID NO: 285
21-5-196	TTCAGTGGCAGTGGGTCTAGGACAGACTTCACCCTCACCATTAATCCTGTGGAGGCTGATGATGTTG	SEQ ID NO: 286
21-7-229	CTCAACATCCATCCTGTGGAGGAGGAGGATACTGCAACATATTACTGTCAGCACAGTTGGGAGATTC	SEQ ID NO: 287
21-9-212	CTGAGTCAGACTTCACTCTCACCATCGATCCTGTGGAGGAAGATGATGCTGCAATGTATTACTGTAT	SEQ ID NO: 288
22-33-217	TCTGGGACAGATTTCACTCTGACCATCAGCAGTGTACAGGTTGAAGACCTCACACATTATTACTGTG	SEQ ID NO: 289
23-37-81	GAGTATTTACAAGAACCTACACTGGTATCAACAGAAATCACATCGGTCTCCAAGGCTTCTCATCAAGTATG	SEQ ID NO: 290
23-39-202	GGGTCAGATTTCACTCTCAGTATCAACAGTGTGGAACCTGAAGATGTTGGAGTGTATTACTGTCAAA	SEQ ID NO: 291
23-43-195	TGGATCAGGGACAGATTTCACTCTCAGTATCAACAGTGTGGAGACTGAAGATTTTGGAATGTATTTCT	SEQ ID NO: 292
23-45-76	AGTCAAAGTATTAGCAACTACCTACACTGGTATCAACAAAAATCACATGAGTCTCCAAGGCTTCTCA	SEQ ID NO: 293
23-48-184	TTTAGTGGCAGTGGATCAGGGACAGATTTTACTCTTAGCATCAACAGTGTGGAGTCTGAAGATATTG	SEQ ID NO: 294
4-50-103	TACCAGCAGAAGTCAGATGCCTCCCCCAAACTATGGATTTATTACACATCCAACCTGGCTCCTGGAG	SEQ ID NO: 295
4-51-207	GATCTCTTACTCTCTCACAATCAGCAGCATGGAGGCTGAAAATGATGCAACTTATTACTGCCAGCAG	SEQ ID NO: 296

TABLE 5-continued

Additional mouse light chain V gene selected oligonucleotides. The complements of these sequences may also be used.

	Secondary Sequence	
4-57-210	CTCTTACTCTCTCACAATCAGCAGTGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTAC	SEQ ID NO: 297
8-16-170	CATCTGATAGGTACTCTGGAGTCCCTGATCGTTTCATAGGCAGTGGATCTGTGACAGATTTCACTCT	SEQ ID NO: 298
8-19	GAGAGAAGGTCACTATGAGCTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTA	SEQ ID NO: 299
8-21	GAAGGTCACTATGAGCTGCAAATCCAGTCAGAGTCTGCTCAACAGTAGAACCCGAAAGAACTACTTG	SEQ ID NO: 300
8-24	GACAGAAGGTCACTATGAGCTGCAAGTCCAGTCAGAGCCTTTTAAATAGTAGCAATCAAAAGAACTA	SEQ ID NO: 301
8-27	GCAGGAGAAAAGGTCACTATGAGCTGTAAGTCCAGTCAAAGTGTTTTATACAGTTCAAATCAGAAGAAC	SEQ ID NO: 302
8-28	GAGAGAAGGTCACTATGAGCTGCAAGTCCAGTCAGAGTCTGTTAAACAGTGGAAATCAAAAGAACTA	SEQ ID NO: 303
8-30	TTGGAGAGAAGGTTACTATGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTAGCAATCAAAAGAACTACTT	SEQ ID NO: 304
8-34-143	GATCTCCTAAAATGCTGATAATTTGGGCATCCACTAGGGTATCTGGAGTCCCTGATCGCTTCATAGG	SEQ ID NO: 305
RF-40	TCTCCTGGAGAAACCATTACTATTAATTGCAGGGCAAGTAAGAGCATTAGCAAATATTTAGCCTGGTATCAAG	SEQ ID NO: 306
aa4-1	CAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATATCCT	SEQ ID NO: 307
ac4-197	CTGGAAACTCTTACTCTCTCACGATCAGCAGCATGGAGGCTGAAGATGTTGCCACTTATTACTGTTT	SEQ ID NO: 308
ad4-26	CAATCATGTCTGCATCTCCTGGGGAGAAGGTCACCATGACCTGCAGTGCCAGATCAAGTGTAAGTTC	SEQ ID NO: 309
ae4-1	CAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCTGGGGAGAAGGTCACCTTGACCT	SEQ ID NO: 310
af4-120	CACTTCTCCCAAACTCTTGATTTATAGCACATCCAACCTGGCTTCTGGAGTCCCTTCTCGCTTCAGT	SEQ ID NO: 311
ag4-128	CTTCTACCAAATTCTGGATTTATAGGACATCCAACCTGGCTTCAGAAGTCCCAGCTCCCTTCAGTGG	SEQ ID NO: 312
ah4-125	GATCCTCCCCAAAACTCTGGATTTATAGCATATCCAACCTGGCTTCTGGAGTCCCAGCTCGCTTCAG	SEQ ID NO: 313
ai4-1	CAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCTAGGGGAACGGGTCACCATGACCT	SEQ ID NO: 314
aj4-119	GATCCTCCCCCAAACTCTGGATTTATAGCATATCCAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAG	SEQ ID NO: 315
al4-133	CTCTGGATTTATTTAACATTCAACTTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTG	SEQ ID NO: 316
am4-212	CTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTAGTAA	SEQ ID NO: 317
an4-203	CATCTTTCTCTTTCACAATCAACAGCATGGAGGCTGAAGATGTTGCCACTTATTACTGTCAGCAAAG	SEQ ID NO: 318
ap4-80	CAAGTGTAAGTTACATGCACTGGTTCCAGCAGAAGCCAGGCACTTCTCCCAAACTCTGGATTTATAG	SEQ ID NO: 319

TABLE 5-continued

Additional mouse light chain V gene selected oligonucleotides. The complements of these sequences may also be used.

	Secondary Sequence	
aq4-38	CATCTCGAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGTACTGGTA	SEQ ID NO: 320
ar4-180	CTTCAGTGGCAGTGGATCTGGGACCTCTTATTCTCTCACAATCAGCAGCATGGAGGCTGAAGATGCT	SEQ ID NO: 321
at4-38	CATCTCCAGGGGAGAAGGTCACCATGACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGTACTGGTA	SEQ ID NO: 322
ay4-44	GAGGGGAGAAGGTCACCATCACCTGCCGTGCCAGCTCAAGTATAAGTTCCAATTACTTACACTGGTA	SEQ ID NO: 323
ba9-195	TGGATCTGGGCAAGATTATTCTCTCACCATCAGCAGCCTGGAGTATGAAGATATGGGAATTTATTATT	SEQ ID NO: 324
bb1-60	CATCTCTTGCAGATCTAGTCAGAGCCTTGTACACAGTAATGGAAACACCTATTTACATTGGTACCTG	SEQ ID NO: 325
bb1.1-59	CCATCTCTTGCAGATCTAGTCAGAGCCTTGTACACAGTAATGGAAACACCTATTTATATTGGTACCTG	SEQ ID NO: 326
bd2-85	CTCTTAGATAGTGATGGAAAGACATATTTGAATTGGTTGTTACAGAGGCCAGGCCAGTCTCCAAAGC	SEQ ID NO: 327
bi2-172	AAACTGGACCCTGGCATCCCTGACAGGTTCAGTGGCAGTGGATCAGAAACAGATTTTACACTTAAAAT	SEQ ID NO: 328
bj2-108	CTATTTGAATTGGTTATTACAGAGGCCAGGCCAGTCTCCAAAGCGCCTAATCTATCTGGTGTCTAAA	SEQ ID NO: 329
bl1-57	CTCCATCTCTTGCAGGTCTAGTCAGAGCCTTGAAAACAGTAATGGAAACACCTATTTGAACTGGTAC	SEQ ID NO: 330
bt20-123	GGAACCTCCTAAGCTCCTTATTTCAGAAGGCAATACTCTTCGTCCTGGAGTCCCATCCCGATTCTCC	SEQ ID NO: 331
bv9-81	GGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCAGATGGAACTATTAAACGCCTGATCTAC	SEQ ID NO: 332
bw20-123	GGAACCTCCTAAGCTCCTTATTTCAGAAGGCAATACTCTTCGTCCTGGAGTCCCATCCCGATTCTCC	SEQ ID NO: 333
cb9-42	TCTGGGAGACAGAATAACCATCACTTGCCAGGCAACTCAAGACATTGTTAAGAATTTAAACTGGTAT	SEQ ID NO: 334
ce9-184	TTCAGTGGCAGTGGGTCTGGAACAGATTATTCTCTCACCATTAGCAACCTGGAGCAAGAAGATATTG	SEQ ID NO: 335
cf9-109	CAGCAGAAACCAGGGAAATCATTTAAGGGCCTGATCTATCATGGAACCAACTTGGAAGATGGAGTTC	SEQ ID NO: 336
ci12-81	GACCATTGGTACATGGTTAGCATGGTATCAGCAGAAACCAGGGAAATCTCCTCAGCTCCTGATTTAT	SEQ ID NO: 337
cj9	ACCTGATCTATGAAACATCCAATTTAGATTCTGGTGTCCCAAAAAGGTTCAGTGGCAGTAGGTCTGG	SEQ ID NO: 338
cp9	TTATTCTCTCACCATCAGCAACCTGGAACCTGAAGATATTGCCACTTACTATTGTCAGCAGTATAGT	SEQ ID NO: 339
cr1	GGAGATCAAGCCTCCATCTCTTGCAGATCTAGTCAGAGCATTGTACATAGTAATGGAAACACCTATTTAGAAT	SEQ ID NO: 340
cs1	GATTTCACACTCAAGATCAGCACAATAAAGCCTGAGGACTTGGGAATGTATTACTGCTTACAAGGTA	SEQ ID NO: 341
cv1	CTCAAGATCAGCAGAGTGGAGGCTGAGGATTTGGGAGTTTATTATTGCTTCCAGAGTAACTATCTTC	SEQ ID NO: 342
cw9	GGAAATTAGTGGTTACTTAAGCTGGCTTCAGCAGAAACCAGATGGAACTATTAAACGCCTGATCTAC	SEQ ID NO: 343

TABLE 5-continued

Additional mouse light chain V gene selected oligonucleotides. The complements of these sequences may also be used.

	Secondary Sequence	
cy9	CTAGTCAGGGCATTAGAGGTAATTTAGACTGGTATCAGCAGAAACCAGGTGGAACTATTAAACTCCTG	SEQ ID NO: 344
dv-36	GAAACAACACAGGCTCCAGCTTCTCTGAGTTTTTCTCTTGGTGAAACAGCAACACTGTCATGCAGGTC	SEQ ID NO: 345
fl12	CAAGTGAGAATATTTACGGTGCTTTAAATTGGTATCAGCGGAAACAGGGAAAATCTCCTCAGCTCCT	SEQ ID NO: 346
gj38c	CTGCTCATACATTACACATCTACATTACAGCCAGGCATCCCATCAAGGTTCAGTGGAAGTGGGTCTG	SEQ ID NO: 347
gm33	GTTCCTTCAAGATTCAGTGGCAGTGGATCTGGAAAGGATTACACTCTCAGCATTACCAGTCTTCAGA	SEQ ID NO: 348
gn33	GACATCCAGATGACACAATCTTCATCCTACTTGTCTGTATCTCTAGGAGGCAGAGTCACCATTACTT	SEQ ID NO: 349
gr32	GGAAATATTCCTAAACTATTGATCTATAAGGCTTCCAACTTGCACACAGGCGTCCCATCAAGGTTTA	SEQ ID NO: 350
he24	GATATTGTGATGACGCAGGCTGCATTCTCCAATCCAGTCACTCTTGGAACATCAGCTTCCATCTCCT	SEQ ID NO: 351
hf24	CTGAGAATCAGTAGAGTGGAGGCTGAGGATGTGGGTGTTTATTACTGTATGCAACATCTAGAATATCC	SEQ ID NO: 352
hg24	CTGGAAATCAGTAGAGTGAAGGCTGAGGATGTGGGTGTGTATTACTGTGAACAACTTGTAGAGTATC	SEQ ID NO: 353
if11	TCTCACCATCAGCAGCCTGGAGGATGAAGATATGGCAACTTATTTCTGTCTACAGCATAGTTATCTC	SEQ ID NO: 354
kb4	CATGGATTTATGAAATATCCAAACTGGCTTCTGGAGTCCCAGCTCGCTTCAGTGGCAGTGGGTCTGG	SEQ ID NO: 355
kf4	CAATTACTTGCATTGGTATCAGCAGAAGCCAGGATTCTCCCCTAAACTCTTGATTTATAGGACATCC	SEQ ID NO: 356
kh4	CTTCTGGAGTCCCTGTTCGCTTCAGTGGCAGTGGATCTGGGACCTCTTATTCTCTCACAATCAGCAG	SEQ ID NO: 357
kj4	GGTCTGGGACCTCTTACTCTCTCACAATCAGCAGCGTGGAGGCTGAAGATGATGCAACTTATTACTG	SEQ ID NO: 358
kk4	CCCAAAAGATGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTG	SEQ ID NO: 359
km4	CAAATTCTTCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATGACCT	SEQ ID NO: 360
kn4	CCCAAAAGATGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTG	SEQ ID NO: 361
ko4	CTTCAGTGGCAGTGGATCTGGGACCTCTTATTCTCTCACAATCAGCAGCATGGAGGCTGAAGATGCT	SEQ ID NO: 362
VL1	AAGTACTGGGGCTGTTACAACTAGTAACTATGCCAACTGGGTCCAAGAAAAACCAGATCATTTATTC	SEQ ID NO: 363
VL2	GTACTGGGGCTGTTACAACTAGTAACTATGCCAACTGGGTTCAAGAAAAACCAGATCATTTATTCACT	SEQ ID NO: 364
VLx	TTAGCATTTCCAACATCCAGCCTGAAGATGAAGCAATATACATCTGTGGTGTGGGTGATACAATTAA	SEQ ID NO: 365

[0033] One of skill in the art appreciates that whether an oligonucleotide is "capable of hybridizing" to another polynucleotide depends in part on the stringency of the conditions used during hybridization. As used herein "capable of hybridizing" to a polynucleotide encoding the light chain variable region, or the complement thereof, is one that hybridizes under high stringency conditions. In the Examples, high stringency hybridization was carried out at 45° C. in a buffer containing 50% formamide, 5×SSC, 0.1% SDS and 0.1 mg/mL BSA. After hybridization, the microarrays were washed in 2×SSC, 0.1% SDS at 42° C. for 5 minutes, two times in 1×SSC at room temperature, two times in 0.1×SSC, and in water for 30 seconds. One of skill in the art would appreciate that the hybridization and washing conditions can be altered while maintaining high stringency conditions.

[0034] Oligonucleotides corresponding to the sequences in Table 2 and Table 3 were generated and printed onto a glass slide to form the microarray used in the Examples. One of skill in the art would appreciate that a microarray having a subset of the oligonucleotides of Tables 2 and 3 may also be useful. For example, a microarray comprising a subset of oligonucleotides capable of hybridizing to a polynucleotide comprising a sequence encoding at least a portion of a light chain variable region that is associated with a disease, or a complement thereof, may be used in the methods of the invention. The subset of oligonucleotides capable of hybridizing to the light chain variable regions associated with a systemic autoimmune disease, such as the light chain variable regions listed in Table 1, may also be useful in the methods of the invention. One of skill in the art would also appreciate that two or more oligonucleotides capable of hybridizing to a single light chain variable gene could be used in the microarray. Use of multiple oligonucleotides specific for the same gene improves resolution and minimizes problems with cross-hybridization.

[0035] In addition to the oligonucleotides capable of hybridizing to the light chain variable regions, or complements thereof, appropriate quality control reporter oligonucleotides may be included in the microarrays of the present invention. Tables 2 and 3 include several oligonucleotides that were used as controls in the Examples. These include oligonucleotides capable of hybridizing to polynucleotides encoding beta actin, CD19, CD20, the kappa constant region and several lambda constant regions. The controls chosen for use in the Examples are not limiting. One of skill in the art could design control oligonucleotides from a wide variety of cellular genes.

[0036] Each oligonucleotide species used is immobilized at a distinct location or domain on a substantially planar solid surface of a substrate to form a microarray. Any suitable substrate may be used, including, but not limited to, glass, silicon, nitrocellulose, paper or other solid surface materials. The oligonucleotide species can be RNA or DNA. The oligonucleotide species can be immobilized by depositing or synthesizing oligonucleotides at specific locations on the microarray by methods known to those of skill in the art. Generally each oligonucleotide species is present in replicates on the microarray. Alternatively, pools of multiple oligonucleotide species could be used. In the Examples, each oligonucleotide species was printed either six times or ten times in distinct locations to serve as an internal control for even hybridization of the target polynucleotides to the slide. The replicate oligonucleotide species can be printed near each other, in a set pattern or randomly on the microarray. This generates a microarray chip that serves as a platform for identification and quantification of light chain variable region usage.

[0037] In the Examples, the microarray was used to detect the expression of light chain variable genes in B cells. However, the microarrays could also be used to detect light chain variable gene expression in plasma cells or plasmablasts. The cells may be harvested from any source, as long as the cell sample contains B cells. Peripheral blood is one source for obtaining cells from the subject. Cells may also be harvested from a body fluid of the subject, including, but not limited to synovial fluid, cerebrospinal fluid, lymph, bronchioalveolar lavage fluid, gastrointestinal secretions, saliva, urine, and tears. The cells may also be derived from a tissue of the individual, e.g., by performing a tissue biopsy on tissues, including, but not limited to, the spleen and lymph nodes. When assaying for a particular disease condition the selection of appropriate cell sources will be apparent to those of ordinary skill in the art. For example, to assay for autoimmune disorders affecting the joints (e.g., rheumatoid arthritis), synovial fluid is a suitable source of cells. In a patient with multiple sclerosis, cerebral spinal fluid is a suitable source of cells. In the Examples, the B cells were harvested from cerebral spinal fluid and peripheral blood.

[0038] Fluorescent activated cell sorting (FACS) was used in the Examples to harvest and select B cells by expression of specific cell surface markers, namely CD19 and CD20, and lack of expression of other markers that are indicative of plasma cells, memory B cells and plasmablasts, namely CD138, CD27 and CD38. One of skill in the art will appreciate that other methods of sorting cells may be used, including, but not limited to, magnetic cell sorting, and density gradient centrifugation.

[0039] In the Examples, about 100 of the relevant B cells were pooled as a sample. One of skill in the art appreciates that the number of B cells used can be as few as one or as many as millions. Use of about 100 B cells produced a representative sample of the B cell light chain variable repertoire with little risk of contamination by plasma cells and required only a minimal level of amplification for detection in the microarray.

[0040] Contamination of the B cell samples by plasma cells is a concern because the concentration of light chain mRNA in plasma cells is several thousand fold higher than that of B cells. Contamination by a single plasma cell significantly biases the results of the microarray experiment. The FACS protocol used in the Examples was developed to minimize the chance of plasma cell contamination, but any suitable method of separating plasma cells from the B cells could be used. To reduce plasma cell contamination, after the B cells were sorted and RNA extracted, each sample was tested for the presence of plasma cells using RT-PCR to rule out plasma cell contamination. Importantly, this RT-PCR procedure was optimized using a single cell RT-PCR approach to detect even a single plasma cell in a sample of 100 cells. Samples with detectable plasma cell contamination were not used.

[0041] RNA may be harvested from the B cells by any suitable method. In the examples, sufficient amounts of nucleic acid for downstream applications was generated from only 100 cells by amplifying the target nucleic acid using an established antisense RNA (aRNA) amplification protocol. Alternatively, cDNA or amplified cDNA could be generated and amplified using any suitable method.

[0042] The resulting target polynucleotides were then labeled with a marker. In the Examples, a fluorescent marker was added to the target polynucleotides. Amplified target polynucleotides can be labeled by any suitable method. For example, labeled nucleotides such as biotinylated UTP or CTP can be incorporated during in vitro transcription. Labeling target molecules may occur after the amplification reaction e.g., by enzymatically modifying the 5' end of the amplified nucleic acids. The label may be any label known to those of skill in the art, suitably the label is a fluorescent label, a radioactive label, or a luminescent label.

[0043] The labeled target polynucleotides are then contacted with the microarray under suitable hybridization conditions. Hybridization buffers and conditions may be altered to increase or decrease the stringency of the conditions as is well-known to those of skill in the art. After hybridization and washing, the microarray was analyzed for presence of bound target polynucleotide by assessing the presence of the label using a commercially available microarray scanner, such as the Axon GenePix 4000B produced by Molecular Devices or another comparable microarray scanner. Commercially available computer programs may be used to analyze the data.

[0044] Several methods are also provided for using the microarray described herein. The microarray may be used to identify light chain variable genes associated with a particular disease by comparing the light chain variable gene usage in subjects with a particular disease to subjects that do not have the disease. Such an analysis may allow identification of light chain variable genes whose expression correlates with the disease in subjects. Diseases that may correlate to particular light chain variable gene usage include, but are not limited to, systemic autoimmune diseases, cancer, especially B cell cancers, such as multiple myeloma, and immunodeficiency diseases. Systemic autoimmune diseases include, but are not limited to, systemic lupus erythematosus, multiple sclerosis, rheumatoid arthritis, scleroderma, Sjogren's syndrome, amylodosis, psoriasis, mixed connective tissue disease, polymyositis, dermatomyositis, thrombocytopenia, Wegener's granulomatosis, and autoimmune nephritis.

[0045] After expression of a particular light chain variable gene is identified as correlating with a disease, the expression of the light chain variable genes may be used to diagnose the disease, monitor disease progression, aid in prognosis, identify likely or potential sequelae of the disease associated with a particular light chain variable gene, predict the etiology of the disease or the response of the disease to particular forms of therapy. For example, a disease could be diagnosed if the pattern of detected hybridization complexes of the subject tested resembles the pattern of detected hybridization complexes of a diseased subject. As mentioned above, light chain variable gene B2 is associated with formation of amyloid fibrils in 10% of multiple myeloma patients. As an example, the microarray could be used to determine if individuals suffering from multiple myeloma are expressing light chain variable gene B2 using the microarray and tailor treatment options and determine disease prognosis based on the results.

[0046] As one of skill in the art will appreciate, expression of a particular light chain variable gene may be evaluated by any suitable means. For example, expression could be measured directly by measuring hybridization to an oligonucleotide encoding the light chain variable gene, or a complement thereof. Either the oligonucleotide or the target sample may be detectably labeled to visualize hybridization, and hybridization may be performed in any suitable format. Alternatively, expression may be detected by performing real time PCR on the target DNA using a pair of primers that hybridize to sequences within, partially overlapping or flanking the sequence encoding the light chain variable gene. Once a particular light chain variable gene of interest is identified, primer pairs may be designed using available sequence information.

[0047] The present invention also provides methods of evaluating the ability of a therapeutic agent to alter the expression of a light chain variable gene or the repertoire as a whole. First, the light chain variable gene expression of a subject with a disease is assessed using the microarray. Then the subject is treated with the therapeutic agent or undergoes a therapeutic treatment. The light chain variable gene expression is assessed again after treatment and compared to the light chain variable expression prior to treatment to determine whether the therapeutic agent or treatment affected the light chain variable repertoire. A change in light chain variable expression is indicative of effectiveness of the therapeutic agent or treatment.

[0048] The present invention also provides kits for performing the methods described herein. A kit may comprise a microarray comprising oligonucleotide species capable of hybridizing to a sequence encoding at least a portion of a light chain variable region, or a complement thereof. Suitably kits may also comprise antibodies used to sort for B cells, primers for generating the target polynucleotides, reagents needed to label the target polynucleotides and/or other reagents necessary to perform the methods described herein.

[0049] The following examples are meant to be illustrative only and are not intended as a limitation on the concepts and principles of the invention.

EXAMPLES

[0050] Oligonucleotide sequence selection. There are 82 human and 99 mouse functional light chain variable genes. In humans, 6 pairs have identical sequences, i.e., they are duplicate genes, and are not distinguishable. There are reports of pseudogenes in both mouse and human, but these genes were not included because they are considered to be nonfunctional. However, these and other genes may be included if they are found to be misclassified and are indeed functional. Oligonucleotides specific for each of the functional mouse and human light chain variable genes were selected from the genetic sequences that are available on the NCBI website under the heading "Ig Germline Genes".

[0051] Unique sequences ranging from 65-70 base pairs from each V region light chain (both kappa and lambda) were identified by genome scans of germline sequences. The sequence length was chosen to allow for use of high stringency hybridization conditions and thus optimize the specificity. The oligonucleotide set used in the microarray experiments described herein is shown in Table 2 and Table 3. The oligonucleotides were chosen to have minimal cross-hybridization with other variable light chain genes, to have melting temperatures of 70° C.+/−3° C. and a G-C content of 35% to 55%. The oligonucleotides were also selected to have low potential to self-fold, therefore maximizing their target size for spotting onto the slide. See Wang et al. Genome Biology 4:R5 (2003), which is incorporated herein by reference in its entirety. The following computer programs were also used in selection of the oligonucleotides:

[0052] 1. Oligowiz

[0053] 2. Array designer

[0054] 3. NCBI mouse gene database

[0055] 4. Blast

[0056] 5. Mfold

[0057] 6. Repeatmasker

[0058] 7. Bioperl Project

[0059] 8. EMBOSS.

[0060] In addition to the light chain variable region oligonucleotides, positive and negative control oligonucleotides were selected based on the same criteria. The kappa and lambda constant region oligonucleotides were used to normalize the samples for the amount of light chain present in each sample. Other control oligonucleotides included Beta actin, CD19, CD20, B220, CD 138, and Blimp-1.

[0061] Preparation of the microarray. Each of the oligonucleotides listed in Table 2 and Table 3 was generated (Integrated DNA Technologies, Coralville, Iowa). These oligonucleotides were suspended in microarray printing buffer (150 mM sodium phosphate) and printed at the University of Illinois, Urbana-Champagne using an OmniGrid 100 Microarrayer (Gene Machines, San Carlos, Calif.) onto an UltraGAPS Coated Slide (Corning, Acton, Mass.). Both positive control (CD19, CD20, B220, actin and GAPDH) and negative control (CD138, blank and Blimp-1) genes were incorporated into the microarray. Each oligonucleotide was printed in ten replicates onto a glass slide (either randomly or next to each other) and stored in vacuum sealed packaging until ready for use. Before the sample was applied to the microarray, the microarray was prehybridized in 5×SSC, 0.1% SDS and 0.1 mg/mL BSA at 42° C. for 45 minutes.

[0062] Isolation of B cells. B cells were sorted, based on the cell phenotype of CD19+ CD20+CD138− (mouse B cells sorts used CD19+CD138−), using fluorescent activated cell sorting (FACS). Human B cells were sorted by gating on CD19+, CD20+, CD138− cells. Mouse B cells were sorted by gating on CD19+, CD 138− cells. Cells were sorted directly into RNAlater (Ambion, Austin, Tex.) which prevents RNA degradation and allows samples to be stored indefinitely.

[0063] Plasma cells express CD138 and are a source of potential contamination because they express 1,000-10,000 fold more light chain than B cells and a single plasma cell could mask differential light chain variable region expression. Thus, several additional measures were taken to ensure that plasma cells were not present in the samples. First, the FACS selects against incorporation of plasma cells by selecting only CD138− cells. Additionally, only 100 cells are sorted into one sample (but many samples are collected from one individual) to minimize contamination. Finally, a reverse transcriptase-polymerase chain reaction (RT-PCR) capable of detecting plasma cell specific gene expression with single cell sensitivity was utilized to ensure the samples were plasma cell free. The PCR detects plasma cell-specific Blimp-1 gene expression (forward primer: TCTGTTCAAGCCGAGGCATCCTTA (SEQ ID NO:366) and reverse primer: TCCAAAGCGTGTTCCCTTCGGTAT (SEQ ID NO:367)). 1 μL of cDNA from the aRNA protocol (before any amplification) is used as the template with Platinum Taq DNA Polymerase using the recommended protocol (Invitrogen, Carlsbad, Calif.). If plasma cell contamination was detected in a sample, the sample was discarded.

[0064] Preparation of the target polynucleotides from B cells. RNA was isolated from the sorted B cells using TRIZOL (Invitrogen, Carlsbad, Calif.). Samples containing 100 B cells do not contain sufficient RNA for direct analysis in a microarray. Therefore, an established antisense RNA (aRNA) amplification protocol designed to minimize introduction of bias was used (MEGAscript T7 Kit, Ambion, Austin, Tex.). Two rounds of amplification provided sufficient RNA for hybridization. Amide-modified UTP was incorporated in the second round product and was used for fluorescent labeling of the samples. The RNA samples were labeled using ULYSIS dyes according to the manufacturer's instructions (Invitrogen-Molecular Probes, Eugene Oreg.).

[0065] Hybridization of the target polynucleotides to the microarray and scanning. Labeled aRNA samples were mixed with 1 μg of poly-A RNA as a blocking reagent and hybridization buffer (50% formamide, 5×SSC, 0.1% SDS and 0.1 mg/mL BSA) and added to the microarray slide. Hybridizations were performed in a 45° C. water bath overnight. After hybridization, microarrays were washed in 2×SSC, 0.1% SDS at 42° C. for 5 minutes, two times in 1×SSC at room temperature, two times in 0.1×SSC, and water for 30 seconds. Slides were then dried by centrifugation at 2,500 RPMs and immediately scanned using Axon GenePix 4000B (Molecular Devices, Sunnyvale, Calif.). Data analysis was performed on the scanned image using commercially available software and software designed in our lab. (GeneSpring, Agilent, Palo Alto).

[0066] Specificity of the microarray. To establish that the selected oligonucleotide sequences (represented in Table 2) were specific for the indicated light chain variable regions, RNA prepared from human light chain variable gene clones was used in the array. The B cell clones were obtained through a Material Transfer Agreement with the Mayo Clinic (Rochester, Minn.) and each of the light chain variable regions is known. FIG. **1** is a representative example of microarray data from a single B cell clone known to express the B3 light chain. This experiment allows for assessment of the level of cross-hybridization of the oligonucleotides in the microarray and provides an example of how this method can be used to characterize the light chain in plasma cell diseases. Similar experiments have been performed using the L12 light chain clone and are planned for the O8/18, V1-19, V1-16 and V1-22 light chains. Specificity of the mouse light chain oligonucleotides has been determined using RNA from hybridomas.

[0067] Use of Reference Sequence in Light Chain Microarray. A reference sequence is used to control for differences in probe hybridization efficiency, spotting inconsistencies and print batch differences and other variations that may influence spot intensity. The reference sequence is composed of equal-molar concentrations of DNA oligonucleotides complementary to the light chain probes. A large amount of the reference sequence has been synthesized and stored. It could also be re-synthesized if necessary. The reference sample is labeled with one fluorophore and the sample nucleic acid is labeled with a second fluorophore. Thus, spots or probe hybridization efficiency will be reflected in the intensity reading of the reference sample (a spot/probe with low hybridization efficiency will have a low intensity, while a spot/probe with high hybridization efficiency will have a high intensity). Thus, the sample of interest can be normalized on a probe-by-probe (gene-by-gene) basis according to the reference sample intensity of a particular probe.

[0068] Cross-hybridization Quantification and Incorporation into Data Analysis. The relatedness of the light chain V genes is reflected in the germline sequence similarity. In some cases, V genes have been duplicated and have not diverged (for example, O2 and O12 are identical, as are others). Other V genes have diverged slightly and share significant sequence similarity. While the oligonucleotide species described above were designed to exploit all possible differences, some of them are very similar to V genes other than the gene they were designed to interrogate. Thus, cross-hybridization between an oligonucleotide species and a related V gene is a concern. One example of this cross-hybridization is demonstrated in FIG. **1** where the B3 nucleic acid hybridizes to other oligonucleotide species, including the oligonucleotide species designed to hybridize to L5. We are currently in the process of testing each V gene sequence individually to determine the extent of cross-hybridization with all of the oligonucleotides species (we have completed over 60% of these hybridizations). When cloned V gene sequences were not available, the complementary sequence to that probe was synthesized, labeled and hybridized to the array. The data from these hybridizations is being compiled in a matrix. This matrix of cross-hybridization will then contain all of the information necessary to distinguish a real signal from cross-hybridization. This will be done by crossing the data generated by a sample with the inverse of this matrix. The output of this computation is the true signal.

[0069] Repertoire differences in autoimmune-prone and non-autoimmune prone mice. C57/B6 mice with the 56R heavy-chain transgene develop auto-antibodies at a very young age, while Balb/c mice (without any transgene) remain healthy and do not develop auto-antibodies. See Sekiguchi et al., J. Immunol. 176:6879-6887 (2006). The repertoire from two 56R transgenic C57/B6 mice with detectable auto-antibodies was compared with six Balb/c mice without any evidence of autoimmunity using the light chain variable region microarray and the results are depicted in FIG. **2**.

[0070] Briefly, B cells were sorted for each mouse independently, RNA was prepared and hybridization with the microarray performed as described in detail above. After hybridization, image analysis was completed using Axon GenePix and the median intensity for all replicate spots averaged. Intensity levels across samples were normalized by comparison with kappa-constant values from the same sample. These normalized values were then averaged for the 56R transgenic C57/B6 mice and the Balb/c mice. The Balb/c normalized and averaged values were then subtracted from the 56R transgenic C57/B6 normalized and averaged values for each gene. Thus, a positive value in FIG. **2** corresponds to a light chain being overrepresented in a 56R transgenic C57/B6 autoimmune mouse, while a negative value corresponds to overrepresentation of a light chain variable region in Balb/c mice. The following L-chain V gene spots had values below background and were not included in the analysis: 12-46, 21-3, 8-16, 8-34, ae4 and ba9.

[0071] As shown in FIG. **2**, several of the light chain variable genes were overrepresented in the autoimmune prone transgenic mice, namely 23-48, Bt20, gj38c, V11, and V12. Several of these light chain variable genes, including Bt20 and gj38c have been linked to autoimmune disease in this mouse model using traditional B cell cloning and sequencing or PCR-based analysis of the light chain variable gene. See Li et al., Immunity 15:947:957 (2001) and Table 1.

[0072] L-chain repertoire changes with induced autoimmunity. Chronic graft-versus-host (cGvH) disease was induced by injection of allogenic CD4+ T cells from a bm12 mouse into a 56R heavy-chain transgenic B6 mouse as previously described. See Sekiguchi et. al., Proc. Natl. Acad. Sci. U.S.A. 84:9150-9154 (2003) which is incorporated herein by reference in its entirety. The B cell light chain repertoire was sampled 20 days post-induction using the light chain variable gene microarray as described above and the results are presented in FIG. **3**. Anti-DNA antibodies were increased at day 20 post-induction in this mouse compared with day 0 and were higher than a littermate control 56R transgenic mouse that did not undergo cGvH induction as measured by ELISA.

[0073] Briefly, RNA was prepared from 100 B cells from a cGvH-induced 56R transgenic mouse and a control 56R transgenic mouse. The RNA was labeled and hybridized to the array. The microarray image was analyzed using the Axon GenePix, and the median intensity for all replicate spots was averaged for each sample. Intensity levels were normalized by comparing the average intensity of each light chain variable gene with the kappa-constant gene intensity for the same sample. These values from the control (no cGvH) 56R mouse were then subtracted from the day 20 cGvH 56R values for each gene and plotted on the y-axis. Positive values correspond to an expansion of light chain variable genes after induced autoimmunity, and negative values correspond to light chain variable genes that are underrepresented after induction of autoimmunity.

[0074] As shown in FIG. **3**, several of the light chain variable genes were overrepresented in the autoimmune mice at day 20 post-induction, while other light chain variable genes were underrepresented in these animals as compared to untreated control transgenic mice. The light chain variable genes overrepresented and underrepresented in this model were distinct from those identified as overrepresented in 56R as compared to Balb/c mice in FIG. **2** and are distinct from the previously reported light chain variable genes linked to autoimmunity Sekiguchi et al., J. Immunol. 176:6879-6887 (2006), Table 1, and unpublished data.

[0075] Light Chain Variable Detection in Human Autoimmune Disease. Reports in the literature suggest multiple sclerosis (MS) patients display a restricted cerebral-spinal fluid (CSF) B cell repertoire. See Monson et al., J. Neuroimmunol. 158:170-181 (2005) and Colombo et al., J. Immunol. 164:2782-2789 (2000) which are incorporated herein by reference in their entireties. Therefore, this disease was chosen to test the microarray and determine if the light chain variable regions identified in Table 1 were found in MS patients. B cells were harvested from the CSF of an untreated MS patient and from three individuals who do not have MS. The cells were sorted, the RNA isolated, amplified, labeled and hybridized to the microarray as described above. FIG. **4** depicts the light chain variable gene expression from the MS patient normalized to the kappa constant gene after averaging the replicates. The data demonstrate that a subset of light chain variable genes is expressed in the MS patient. Notably, several of the expressed genes correlate to the light chains hypothesized to be important in autoimmune pathology listed in Table 1, namely B2, O8/O18, L25 and V2-15. FIG. **5** shows the light chain variable gene expression as fluorescence intensity normalized to the kappa constant region as a ratio to the light chain variable gene expression in three healthy individuals. The light chain variable regions that were differentially expressed are noted in the Figure. As depicted in FIG. **5**, the B2 light chain was overrepresented in the MS patient as compared to the healthy individuals and this chain has structural properties similar to pathogenic light chains in the mouse as indicated in Table 1.

[0076] Light Chain Repertoire Differences in SLE. This method has detected V gene light chain repertoire differences between an individual with a clinical diagnosis of SLE and a healthy individual with no know autoimmunity. In this example, peripheral blood was isolated from these two individuals. B cells of the $CD20^{+}CD138^{-}CD27^{-}CD38^{-}$ phenotype were sorted and prepared as described above. Each sample was labeled with Alexa 647 dyes and mixed with a reference sequence labeled with Alexa 555 (Invitrogen-Molecular Probes, Eugene Oreg.). The samples were independently hybridized, washed and scanned. Comparisons were made by performing global intensity normalization for each fluorescent channel on each array. These were used to generate a ratio of sample:reference, and this sample:reference ratio was compared between arrays to generate FIG. **6**. As can be seen from this figure, some V genes are overrepresented in this SLE patient compared with this healthy individual (the points above the line such as V4-4, V4-6, L24 and A27). Additionally, some V genes are underrepresented in this SLE patient such as V5-4 and V5-1.

[0077] Various features of the invention are set forth in the following claims.

SEQUENCE LISTING

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Glu Lys Val Thr Ile Arg Cys Ile Thr Ser Thr Asp Ile Asp Asp Asp
            20                  25                  30

Met Asn Trp Tyr Gln Gln Lys Pro Gly Glu Pro Pro Lys Leu Leu Ile
        35                  40                  45

Ser Glu Gly Asn Thr Leu Arg Pro Gly Val Pro Ser Arg Phe Ser Ser
    50                  55                  60

Ser Gly Tyr Gly Thr Asp Phe Val Phe Thr Ile Glu Asn Met Leu Ser
65                  70                  75                  80

Glu Asp Val Ala Asp Tyr Tyr Cys Leu Gln Ser Asp Asn Leu Pro
                85                  90                  95


<210> SEQ ID NO 2
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 2

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            20                  25                  30

Met Asn Trp Tyr Gln Gln Lys Pro Gly Glu Pro Pro Lys Leu Leu Ile
        35                  40                  45

Ser Glu Gly Asn Thr Leu Arg Pro Gly Val Pro Ser Arg Phe Ser Ser
    50                  55                  60

Ser Gly Tyr Gly Thr Asp Phe Val Phe Thr Ile Glu Asn Thr Leu Ser
65                  70                  75                  80

Glu Asp Val Ala Asp Tyr Tyr Cys Leu Gln Ser Asp Asn Met Pro
                85                  90                  95


<210> SEQ ID NO 3
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 3

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
1               5                   10                  15

Gly Lys Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Ile Asn Lys Tyr
            20                  25                  30

Ile Ala Trp Tyr Gln His Lys Pro Gly Lys Gly Pro Arg Leu Leu Ile
        35                  40                  45

His Tyr Thr Ser Thr Leu Gln Pro Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Arg Asp Tyr Ser Phe Ser Ile Ser Asn Leu Glu Pro
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Tyr Cys Leu Gln Tyr Asp Asn Leu Leu
                85                  90                  95


<210> SEQ ID NO 4
<211> LENGTH: 103
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 4

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

Ser Ala Lys Leu Thr Cys Thr Leu Ser Ser Gln His Ser Thr Tyr Thr
            20                  25                  30

Ile Glu Trp Tyr Gln Gln Gln Pro Leu Lys Pro Pro Lys Tyr Val Met
        35                  40                  45

Glu Leu Lys Lys Asp Gly Ser His Ser Thr Gly Asp Gly Ile Pro Asp
    50                  55                  60

Arg Phe Ser Gly Ser Ser Ser Gly Ala Asp Arg Tyr Leu Ser Ile Ser
65                  70                  75                  80

Asn Ile Gln Pro Glu Asp Glu Ala Ile Tyr Ile Cys Gly Val Gly Asp
                85                  90                  95

Thr Ile Lys Glu Gln Phe Val
            100


<210> SEQ ID NO 5
<211> LENGTH: 99
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 5
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Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp
            20                  25                  30

Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45

Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala
    50                  55                  60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His
65                  70                  75                  80

Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn
                85                  90                  95

Glu Asp Pro


<210> SEQ ID NO 6
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Asp Ile Gln Met Thr Gln Ser Pro Ala Ser Leu Ala Ala Ser Val Gly
1               5                   10                  15

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

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Ile
        35                  40                  45

Tyr Asn Ala Asn Ser Leu Glu Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Gln Tyr Ser Met Lys Ile Asn Ser Met Gln Pro
65                  70                  75                  80

Glu Asp Thr Ala Thr Tyr Phe Cys Lys Gln Ala Tyr Asp Val Pro
                85                  90                  95


<210> SEQ ID NO 7
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 7

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

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

Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
        35                  40                  45

Tyr Ala Ala Thr Asn Leu Ala Asp Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Gln Tyr Ser Leu Lys Ile Asn Ser Leu Gln Ser
65                  70                  75                  80

Glu Asp Phe Gly Ser Tyr Tyr Cys Gln His Phe Trp Gly Thr Pro
                85                  90                  95


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<213> ORGANISM: Homo sapiens

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Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asp Asn Leu Pro
                85                  90                  95


<210> SEQ ID NO 9
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

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

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20                  25                  30

Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asp Tyr Asn Leu Pro
                85                  90                  95


<210> SEQ ID NO 10
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

Glu Thr Thr Leu Thr Gln Ser Pro Ala Phe Met Ser Ala Thr Pro Gly
1               5                   10                  15

Asp Lys Val Asn Ile Ser Cys Lys Ala Ser Gln Asp Ile Asp Asp Asp
            20                  25                  30

Met Asn Trp Tyr Gln Gln Lys Pro Gly Glu Ala Ala Ile Phe Ile Ile
        35                  40                  45

Gln Glu Ala Thr Thr Leu Val Pro Gly Ile Pro Pro Arg Phe Ser Gly
    50                  55                  60

Ser Gly Tyr Gly Thr Asp Phe Thr Leu Thr Ile Asn Asn Ile Glu Ser
65                  70                  75                  80

Glu Asp Ala Ala Tyr Tyr Phe Cys Leu Gln His Asp Asn Phe Pro
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

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

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Arg Asn Asp
            20                  25                  30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Asn Tyr Pro
                85                  90                  95


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<211> LENGTH: 97
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

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

Glu Arg Val Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
            20                  25                  30

Tyr Leu Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
        35                  40                  45

Ile Tyr Gly Ala Ser Thr Arg Ala Thr Ser Ile Pro Ala Arg Phe Ser
    50                  55                  60

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
65                  70                  75                  80

Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Asp His Asn Leu Pro
                85                  90                  95

Pro


<210> SEQ ID NO 13
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1               5                   10                  15

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

Arg Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
        35                  40                  45

Lys Asp Ser Glu Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60

Ser Ser Gly Thr Thr Val Thr Leu Thr Ile Ser Gly Ala Gln Val Glu
65                  70                  75                  80
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Asp Glu Ala Asp Tyr Tyr Cys Tyr Ser Ala Ala Asp Asn Asn Leu
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 14

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1               5                   10                  15

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

Asp Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Glu Leu Val Ile Tyr
        35                  40                  45

Glu Asp Ser Glu Arg Tyr Pro Gly Ile Pro Glu Arg Phe Ser Gly Ser
    50                  55                  60

Thr Ser Gly Asn Thr Thr Thr Leu Thr Ile Ser Arg Val Leu Thr Glu
65                  70                  75                  80

Asp Glu Ala Asp Tyr Tyr Cys Leu Ser Gly Asp Glu Asp Asn Pro
                85                  90                  95


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<213> ORGANISM: Homo sapiens

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1               5                   10                  15

Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gly His Ser Ser Tyr Ile
            20                  25                  30

Ile Ala Trp His Gln Gln Gln Pro Gly Lys Ala Pro Arg Tyr Leu Met
        35                  40                  45

Lys Leu Glu Gly Ser Gly Ser Tyr Asn Lys Gly Ser Gly Val Pro Asp
    50                  55                  60

Arg Phe Ser Gly Ser Ser Ser Gly Ala Asp Arg Tyr Leu Thr Ile Ser
65                  70                  75                  80

Asn Leu Gln Phe Glu Asp Glu Ala Asp Tyr Tyr Cys Glu Thr Trp Asp
                85                  90                  95

Ser Asn Thr


<210> SEQ ID NO 16
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 16

ctgcaggtct agtcaaagcc tcgtatacag tgatggaaac acctacttga attggtttca     60

gcagagg                                                               67


<210> SEQ ID NO 17
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 17
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ctcaccatca atagcctgga agctgaagat gctgcaacgt attactgtca tcagagtagt 60

agtttac 67

<210> SEQ ID NO 18
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 18

gacttcactc tcaccatcag cagactggag cctgaagatt ttgcagtgta ttactgtcag 60

cagtatg 67

<210> SEQ ID NO 19
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 19

gatctgggac agatttcacc tttaccatca gtagcctgga agctgaagat gctgcaacat 60

attactg 67

<210> SEQ ID NO 20
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

catctcctgc aagtctagtc agagcctcct gcatagtgat ggaaagacct atttgtattg 60

gtacctg 67

<210> SEQ ID NO 21
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 21

gatcaggcac agattttaca ctgaaaatca gcagagtgga ggctgaggat gttggggttt 60

attactg 67

<210> SEQ ID NO 22
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

tctgcatctg taggagacag agtcaccatc acttgccggg cgagtcaggg cattagcaat 60

tatttag 67

<210> SEQ ID NO 23
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 23

ctacttgagt tggcttcagc agaggccagg ccagcctcca agactcctaa tttataagat 60

ttctaac 67

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<210> SEQ ID NO 24
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 24

ctctcacaat cagcagcctg cagcctgaag attttgcaac ttattactgt ctacagcata 60

atagtta 67

<210> SEQ ID NO 25
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 25

catctccttc aggtctagtc aaagcctcgt acacagtgat ggaaacacct acttgagttg 60

gcttcag 67

<210> SEQ ID NO 26
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 26

gagaagctgc tattttcatt attcaagaag ctactactct cgttcctgga atcccacctc 60

gattcag 67

<210> SEQ ID NO 27
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 27

catcaactgc aagtccagcc agagtgtttt atacagctcc aacaataaga actacttagc 60

ttggtac 67

<210> SEQ ID NO 28
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 28

gtaggagaca gagtcaccat cacttgtcgg gcgagtcagg gcattagcaa ttatttagcc 60

tggtttc 67

<210> SEQ ID NO 29
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 29

ctcaccatca gcagcctgca gcctgaagat tttgcagttt attactgtca gcaggatcat 60

aacttac 67

<210> SEQ ID NO 30
<211> LENGTH: 67

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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 30

ctctcaccat cagcagcctg cagcctgaag attttgcaac ttattactgt ctacaagatt 60

acaatta 67

<210> SEQ ID NO 31
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 31

tggtatcagc agaaaccagg gaaagcccct aagctcctga tctatgatgc ctccagtttg 60

gaaagtg 67

<210> SEQ ID NO 32
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 32

ctctcaccat cagcagcctg cagcctgaag attttgcaac ttattactgc caacagtata 60

atagtta 67

<210> SEQ ID NO 33
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 33

ctctcaccat cagcagcctg cagtctgaag attttgcagt ttattactgt cagcagtata 60

ataactg 67

<210> SEQ ID NO 34
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 34

tggtatcagc agaaaccagg gaaagctcct aagctcctga tctatgatgc ctccagtttg 60

gaaagtg 67

<210> SEQ ID NO 35
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 35

catcttctgt gtctgcatct gtaggagaca gagtcaccat cacttgtcgg gcgagtcagg 60

gtattag 67

<210> SEQ ID NO 36
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 36

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ttcactctca ccatcagcag cctagagcct gaagattttg cagtttatta ctgtcagcag     60

cgtagca                                                               67


<210> SEQ ID NO 37
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 37

gtaggagaca gagtcagtat catttgctgg gcaagtgagg gcattagcag taatttagcc     60

tggtatc                                                               67


<210> SEQ ID NO 38
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 38

ctctcaccat cagcagcctg cagcctgaag attttgcaac ttattactgt caacagtatt     60

atagtac                                                               67


<210> SEQ ID NO 39
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 39

catctacagg agacagagtc accatcagtt gtcggatgag tcagggcatt agcagttatt     60

tagcctg                                                               67


<210> SEQ ID NO 40
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 40

ctcaccatca gcagcctgca gcctgaagat tttgcagttt attactgtca gcaggattat     60

aacttac                                                               67


<210> SEQ ID NO 41
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 41

gacagatttc actctcacca tcagcagcct gcagcctgaa gattttgcaa cttactattg     60

tcaacag                                                               67


<210> SEQ ID NO 42
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 42

ctctcacaat cagcagcctg cagcctgaag attttgcaac ttattactgt caacagctta     60

atagtta                                                               67
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<210> SEQ ID NO 43
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 43

catctacagg agacagagtc accatcactt gtcgggcgag tcagggtatt agcagttatt 60

tagcctg 67

<210> SEQ ID NO 44
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 44

gtctagtcag agcctcttgg atagtgatga tggaaacacc tatttggact ggtacctgca 60

gaagcca 67

<210> SEQ ID NO 45
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 45

gagcattagc agctatttaa attggtatca gcagaaacca gggaaagccc ctaagctcct 60

gatctat 67

<210> SEQ ID NO 46
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 46

cagttattta aattggtatc ggcagaaacc agggaaagtt cctaagctcc tgatctatag 60

tgcatcc 67

<210> SEQ ID NO 47
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 47

gtaggagaca gagtcaccat cacttgccag gcgagtcagg acattagcaa ctatttaaat 60

tggtatc 67

<210> SEQ ID NO 48
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 48

gcagagggtc accatctcct gttctggaag cagctccaac atcggaaata atgctgtaaa 60

ctggtac 67

<210> SEQ ID NO 49
<211> LENGTH: 67

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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 49

gcagagggtc accatctctt gttctggaag cagctccaac atcggaagta atactgtaaa 60

ctggtac 67

<210> SEQ ID NO 50
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 50

gcagagggtc accatctctt gttctggaag cagctccaac atcggaagta attatgtata 60

ctggtac 67

<210> SEQ ID NO 51
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 51

ctccctggcc atcactggac tccagtctga ggatgaggct gattattact gcaaagcatg 60

ggataac 67

<210> SEQ ID NO 52
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 52

caaactcctc atttatgaca ataataagcg accctcaggg attcctgacc gattctctgg 60

ctccaag 67

<210> SEQ ID NO 53
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 53

gtcagtcacc atctcctgca ctggaaccag cagtgacgtt ggtggttata actatgtctc 60

ctggtac 67

<210> SEQ ID NO 54
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 54

ccaccctccc aaactcctat cctacaggaa taacaaccgg ccctcaggga tctcagagag 60

attctct 67

<210> SEQ ID NO 55
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 55

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ctgtgatcta tgaggataac caaagaccct ctggggtccc tgatcggttc tctggctcca 60

tcgacag 67

<210> SEQ ID NO 56
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 56

gtcagtcacc atctcctgca ctggaaccag cagtgatgtt ggtggttata actatgtctc 60

ctggtac 67

<210> SEQ ID NO 57
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 57

caaactcatg atttatgagg tcagtaatcg gccctcaggg gtttctaatc gcttctctgg 60

ctccaag 67

<210> SEQ ID NO 58
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 58

ctctgggctc caggctgagg acgaggctga ttattactgc agcttatata caagcagcag 60

cactttc 67

<210> SEQ ID NO 59
<211> LENGTH: 68
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 59

ctgacaatct ctgggctcca ggctgaggac gaggctgatt attactgctg ctcatatgca 60

ggtagtag 68

<210> SEQ ID NO 60
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 60

ctctgggctc aagtccgagg ttgaggctaa ttatcactgc agcttatatt caagtagtta 60

cactttc 67

<210> SEQ ID NO 61
<211> LENGTH: 68
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 61

gataaatatg cttgctggta tcagcagaag ccaggccagt cccctgtgct ggtcatctat 60

caagatag 68

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<210> SEQ ID NO 62
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 62

tagtcacatt gaccatcagt ggagtccagg cagaagacga ggctgactat tactgtctat 60

cagcaga 67

<210> SEQ ID NO 63
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 63

cttgggacag acagtcagga tcacatgcca aggagacagc ctcagaagct attatgcaag 60

ctggtac 67

<210> SEQ ID NO 64
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 64

ctgagttggt gatatacgaa gatagtgagc ggtaccctgg aatccctgaa cgattctctg 60

ggtccac 67

<210> SEQ ID NO 65
<211> LENGTH: 68
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 65

gacaacagtc acgttgacca tcagtggagt ccaggcagaa gatgaggctg actattactg 60

tcaatcag 68

<210> SEQ ID NO 66
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 66

ctgggacaga cggccaggat tacctgtggg ggaaacaaca ttggaagtaa aaatgtgcac 60

tggtacc 67

<210> SEQ ID NO 67
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 67

gttactatcc aaactggttc cagcagaaac ctggacaagc acccagggca ctgatttata 60

gtacaag 67

<210> SEQ ID NO 68
<211> LENGTH: 67

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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 68

gacactgatt tatgatacaa gcaacaaaca ctcctggaca cctgcccggt tctcaggctc     60

cctcctt                                                               67


<210> SEQ ID NO 69
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 69

ctggagggac agtcacactc acttgtggct tgagctctgg ctcagtctct actagttact     60

accccag                                                               67


<210> SEQ ID NO 70
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 70

aatacaggga ttttactcat ctccgggctc cagtctgagg atgaggctga ctattactgt     60

atgattt                                                               67


<210> SEQ ID NO 71
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 71

aatgcaggga ttttactcat ctctgggctc cagtctgagg atgaggctga ctattactgt     60

atgattt                                                               67


<210> SEQ ID NO 72
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 72

aatgcaggga ttttagtcat ctctgggctc cagtctgagg atgaggctga ctattactgt     60

atgattt                                                               67


<210> SEQ ID NO 73
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 73

ggtaccaaca aaagccaggg aaccctcccc ggtatctcct gtactaccac tcagactcca     60

ataaggg                                                               67


<210> SEQ ID NO 74
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 74
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gtaccagcag aagccaggga gctctcccag gttattcctg tatcactact cagactcaga 60

caagcag 67

<210> SEQ ID NO 75
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 75

catcgaatgg tatcaacaga gaccagggag gtccccccag tatataatga aggttaagag 60

tgatggc 67

<210> SEQ ID NO 76
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 76

gaatcggtac ctgaccatca agaacatcca ggaagaagat gagagtgact accactgtgg 60

ggcagac 67

<210> SEQ ID NO 77
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 77

ctacctcacc atctccaacc tccagtttga ggatgaggct gattattact gtgagacctg 60

ggacagt 67

<210> SEQ ID NO 78
<211> LENGTH: 71
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 78

tcatctatgg taacagcaat cggccctcag ggtccctga ccgattctct ggctccaagt 60

ctggcacctc a 71

<210> SEQ ID NO 79
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 79

cctgtgctgg tcgtctatga tgatagcgac cggccctcag ggatccctga gcgattctct 60

ggctccaact 70

<210> SEQ ID NO 80
<211> LENGTH: 72
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 80

tcaccttgac catcagcggg gcccaggttg aggatgaggc tgactattac tgttactctg 60

cggctgacaa ca 72

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<210> SEQ ID NO 81
<211> LENGTH: 73
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 81

cagcaaacga ccctccggga tccctgagag attctctggc tccagctcag ggacaatggc     60

caccttgact atc                                                        73


<210> SEQ ID NO 82
<211> LENGTH: 71
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 82

tgtgctggtc atctatagcg atagcaaccg gccctcaggg atccctgagc gattctctgg     60

ctccaaccca g                                                          71


<210> SEQ ID NO 83
<211> LENGTH: 73
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 83

gagaagggcc ctcggtactt gatgaagctt aacagtgatg gcagccacag caaggggac      60

gggatccctg atc                                                        73


<210> SEQ ID NO 84
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 84

ttttaatagt cattccaaat atgagatgcg ttgttacagg aagtcccttg ccatcctaaa     60

agccacc                                                               67


<210> SEQ ID NO 85
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 85

gctgtgactt tggcttatct gatcttctgc ctgtgttccc ttgtgggcat tcttcatctt     60

caaagag                                                               67


<210> SEQ ID NO 86
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 86

caatacagaa cccattccat ttatctttct acagggctga cattgtggca cattcttaga     60

gttacca                                                               67


<210> SEQ ID NO 87
<211> LENGTH: 67
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 87

gaataacttc tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc     60

gggtaac                                                               67


<210> SEQ ID NO 88
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 88

ctgggacaca gtattctatg aagatcaaca gcatgcagcc tgaagatacc gcaacttatt     60

tctgtaaaca                                                            70


<210> SEQ ID NO 89
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 89

gcaaaaacct tagcagatgg tgtgccatca aggttcagtg gcagtggatc aggaacacaa     60

tattctctca                                                            70


<210> SEQ ID NO 90
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 90

agttttctct gaagatcaac agcctgcagc ctgaagattt tgggagttat tactgtcaac     60

atcattatgg                                                            70


<210> SEQ ID NO 91
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 91

gcaacaaact tagcagatgg tgtgccatca aggttcagtg gcagtggatc aggcacacag     60

tattccctca                                                            70


<210> SEQ ID NO 92
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 92

tttcactctc accatcagca atatgcagtc tgaagacctg gcagattatt tctgccagca     60

atatagcagc                                                            70


<210> SEQ ID NO 93
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 93
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ctctcaccat tagcaatgtg caatctgaag acctggcaga ttatttctgt ctgcaacatt     60

ggaattatcc                                                            70


<210> SEQ ID NO 94
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 94

ggtactaatg tagcctggta tcaacagaaa ccagggcaat ctcctaaagc actgatttac     60

tcggcatcct                                                            70


<210> SEQ ID NO 95
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 95

ggacggattt cactttcacc atcagcagtg tgcaggctga agacctggca gtttattact     60

gtcagcaaca                                                            70


<210> SEQ ID NO 96
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 96

cactggggtc cccgatcgct tcacaggcag tggatctgca acagatttca ctctgaccat     60

cagcagtgtg                                                            70


<210> SEQ ID NO 97
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 97

ctctcaccat tagcaatgtg cagtctgaag acttggcaga ttatttctgt cagcaatata     60

gcagctatcc                                                            70


<210> SEQ ID NO 98
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 98

tatactctca ccatcagcag tgtgcaggct gaagacctgg cactttatta ctgtcagcaa     60

cattatagca                                                            70


<210> SEQ ID NO 99
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 99

accctggggt ccctgatcgc ttcacaggca gtggatctgc aacagatttc actctgacca     60

tcagcagtct                                                            70
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<210> SEQ ID NO 100
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 100

attcctgctt gtatcagcag gagacagggt taccataacc tgcaaggcca gtcagagtgt 60

gagtaatgat 70

<210> SEQ ID NO 101
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 101

caccatctcc tgcagagcca gtgaaagtgt tgaatattat ggcacaagtt taatgcagtg 60

gtaccaacag 70

<210> SEQ ID NO 102
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 102

tcaccctcac cattgatcct gtggaggctg atgatgctgc aacctattac tgtcagcaaa 60

ataatgagga 70

<210> SEQ ID NO 103
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 103

ctggctatag ttatatgcac tggtaccaac agaaaccagg acagccaccc aaactcctca 60

tctatcttgc 70

<210> SEQ ID NO 104
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 104

gccaccatct cctgcagagc cagcgaaagt gttgataatt atggcattag ttttatgaac 60

tggttccaac 70

<210> SEQ ID NO 105
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 105

gagccactat cttctgcaga gccagccaga gtgtcgatta taatggaatt agttatatgc 60

actggttcca 70

<210> SEQ ID NO 106
<211> LENGTH: 70

<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 106

gccaccatct cctgcaaggc cagccaaagt gttgattatg atggtgatag ttatatgaac 60

tggtaccaac 70

<210> SEQ ID NO 107
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 107

ctcaccatta atcctgtgga ggctgatgat gttgcaacct attactgtca gcaaagtaat 60

gaggatcctc 70

<210> SEQ ID NO 108
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 108

ctagctatag ttatatgcac tggtaccaac agaaaccagg acagccaccc aaactcctca 60

tcaagtatgc 70

<210> SEQ ID NO 109
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 109

gacagagggc caccatatcc tgccaagcca gcgaaagtgt cagttttgct ggtacaagtt 60

taatgcactg 70

<210> SEQ ID NO 110
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 110

agtaagaagg tcaccattag ttgcacggcc agtgagagcc tttattcaag caaacacaag 60

gtgcactact 70

<210> SEQ ID NO 111
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 111

gattacactc tcagtatcaa cagtgtgaag cccgaagatg aaggaatata ttactgtctt 60

caaggttaca 70

<210> SEQ ID NO 112
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 112

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ctctcagtat caacagtgtg gaacctgaag atgttggagt gtattactgt caaaatggtc     60

acagctttcc                                                            70


<210> SEQ ID NO 113
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 113

caggagatag cgtcagtctt tcctgcaggg ccagccaaag tattagcaac aacctacact     60

ggtatcaaca                                                            70


<210> SEQ ID NO 114
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 114

ggagatagag tcagtctttc ctgcagggcc agtcaaagta ttagcaacta cctacactgg     60

tatcaacaaa                                                            70


<210> SEQ ID NO 115
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 115

ttctcctgca gggccagtca gagcattggc acaagcatac actggtatca gcaaagaaca     60

aatggttctc                                                            70


<210> SEQ ID NO 116
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 116

gtactggtac cagcagaagt cagatgcctc ccccaaacta tggatttatt acacatccaa     60

cctggctcct                                                            70


<210> SEQ ID NO 117
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 117

ggggctggga tctcttactc tctcacaatc agcagcatgg aggctgaaaa tgatgcaact     60

tattactgcc                                                            70


<210> SEQ ID NO 118
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 118

tgtctgcatc tccaggggaa aaggtcacca tgacctgcag ggccagctca agtgtaagtt     60

ccagttactt                                                            70
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<210> SEQ ID NO 119
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 119

atcagaatct tttatggagt ggaaaccaaa ggtactgttt ggtctggcac cagtggaaac 60

cagggcaaac 70

<210> SEQ ID NO 120
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 120

ctctcaccat cagcagtgtg caggctgaag acctggcagt ttattactgt cagaatgatt 60

atagttatcc 70

<210> SEQ ID NO 121
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 121

ggtcactatg agctgcaaat ccagtcagag tctgctcaac agtagaaccc gaaagaacta 60

cttggcttgg 70

<210> SEQ ID NO 122
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 122

tcctccctgg ctatgtcagt aggacagaag gtcactatga gctgcaagtc cagtcagagc 60

cttttaaata 70

<210> SEQ ID NO 123
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 123

gaaaaggtca ctatgagctg taagtccagt caaagtgttt tatacagttc aaatcagaag 60

aactacttgg 70

<210> SEQ ID NO 124
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 124

ccgatttcac tcttaccatc agcagtgtgc aggctgaaga cctggcagtt tattactgtc 60

agaatgatca 70

<210> SEQ ID NO 125
<211> LENGTH: 70

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<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 125

ccctagctgt gtcagttgga gagaaggtta ctatgagctg caagtccagt cagagccttt     60

tatatagtag                                                            70


<210> SEQ ID NO 126
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 126

tagctagtgg caaccaaaat aactacttgg cctggcacca gcagaaacca ggacgatctc     60

ctaaaatgct                                                            70


<210> SEQ ID NO 127
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 127

gagaaacctg ggaaaactaa taagcttctt atctactctg gatccacttt gcaatctgga     60

attccatcaa                                                            70


<210> SEQ ID NO 128
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 128

aactatgcca actgggtcca agaaaaacca gatcatttat tcactggtct aataggtggt     60

accaacaacc                                                            70


<210> SEQ ID NO 129
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 129

taactatgcc aactgggttc aagaaaaacc agatcattta ttcactggtc taataggtgg     60

taccagcaac                                                            70


<210> SEQ ID NO 130
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 130

acagccactc aagcctccta agtatgtgat ggagcttaag aaagatggaa gccacagcac     60

aggtgatggg                                                            70


<210> SEQ ID NO 131
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 131
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ctcaagtgta agttacatgt actggtacca gcagaagcca ggatcctccc ccaaaccctg 60

gatttatcgc 70

<210> SEQ ID NO 132
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 132

tcacgatcag cagcatggag gctgaagatg ttgccactta ttactgtttt caggggagtg 60

ggtacccact 70

<210> SEQ ID NO 133
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 133

tattctctca caatcagcag catggaggct gaagatgctg ccacttttta ctgccagcag 60

tacagtggtt 70

<210> SEQ ID NO 134
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 134

actctctcac aatcagcagc atggaggctg aagatgctgc ctcttatttc tgccatcagt 60

ggagtagtta 70

<210> SEQ ID NO 135
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 135

caatcatgtc tgcatctcta ggggaggaga tcaccctaac ctgcagtgcc agctcgagtg 60

taagttacat 70

<210> SEQ ID NO 136
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 136

cacttctacc aaattctgga tttataggac atccaacctg gcttcagaag tcccagctcc 60

cttcagtggc 70

<210> SEQ ID NO 137
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 137

tacttgtact ggtaccagca gaagtcagga tcctccccaa aactctggat ttatagcata 60

tccaacctgg 70

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<210> SEQ ID NO 138
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 138

ctctcacaat cagcagcatg gaggctgaag atgctgccac ttattactgc caccagtatc     60

atcgttcccc                                                            70


<210> SEQ ID NO 139
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 139

tacatgtaat ggttccagca gaagccagga tcctccccca aactctggat ttatagcata     60

tccaacctgg                                                            70


<210> SEQ ID NO 140
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 140

catgcactgg taccagcaga agccaggatc ctcccccaga ctctggattt atttaacatt     60

caacttggct                                                            70


<210> SEQ ID NO 141
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 141

ttgttctctc ccagtctcca gcaatcctgt ctgcatctcc aggggagaag gtcacaatga     60

cttgcagggc                                                            70


<210> SEQ ID NO 142
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 142

gacatctttc tctttcacaa tcaacagcat ggaggctgaa gatgttgcca cttattactg     60

tcagcaaagg                                                            70


<210> SEQ ID NO 143
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 143

gccagctcaa gtgtaagtta catgcactgg ttccagcaga agccaggcac ttctcccaaa     60

ctctggattt                                                            70


<210> SEQ ID NO 144
<211> LENGTH: 70
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<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 144

gtaagttaca tgtactggta ccagcagaag ccaagatcct cccccaaacc ctggatttat 60

ctcacatcca 70

<210> SEQ ID NO 145
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 145

tgtaagttac atgtacaggt accagcagaa gccaggatcc tcacccaaac cctggattta 60

tggcacatcc 70

<210> SEQ ID NO 146
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 146

gtaagttaca tgtactggta ccagcagaag ccaggatcct cccccagact cctgatttat 60

gacacatcca 70

<210> SEQ ID NO 147
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 147

ggtctgagag ctcttacact ctgacaatca gctgcatgca ggacgaagtt gctgccactt 60

actattgtca 70

<210> SEQ ID NO 148
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 148

ccatgtatgc atctctagga gagagagtca ctatcacttg caaggcgagt caggacatta 60

atagctattt 70

<210> SEQ ID NO 149
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 149

cacctattta cattggtacc tgcagaagcc aggccagtct ccaaagctcc tgatctacaa 60

agtttccaac 70

<210> SEQ ID NO 150
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 150

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aatggaaaca cctatttata ttggtacctg cagaagccag gccagtctcc aaagctcctg 60

atctacaggg 70

<210> SEQ ID NO 151
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 151

gtcagagcct cttagatagt gatggaaaga catatttgaa ttggttgtta cagaggccag 60

gccagtctcc 70

<210> SEQ ID NO 152
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 152

ttacaacaga ggcctggcca ggctccaaag cacctaatgt atcaggtgtc caaactggac 60

cctggcatcc 70

<210> SEQ ID NO 153
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 153

atatagtaat ggaaaaacct atttgaattg gttattacag aggccaggcc agtctccaaa 60

gcgcctaatc 70

<210> SEQ ID NO 154
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 154

caggtctagt cagagccttg aaaacagtaa tggaaacacc tatttgaact ggtacctcca 60

gaaaccaggc 70

<210> SEQ ID NO 155
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 155

catccctgtc catggctata ggagaaaaag tcaccatcag atgcataacc agcactgata 60

ttgatgatga 70

<210> SEQ ID NO 156
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 156

acattggtag tagcttaaac tggcttcagc aggaaccaga tggaactatt aaacgcctga 60

tctacgccac 70

<210> SEQ ID NO 157
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 157

cctgtccgtg gctacaggag aaaaagtcac tatcagatgc ataaccagca ctgatattga 60

tgatgatatg 70

<210> SEQ ID NO 158
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 158

gggagacaga ataaccatca cttgccaggc aactcaagac attgttaaga atttaaactg 60

gtatcagcag 70

<210> SEQ ID NO 159
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 159

ctctcaccat tagcaacctg gagcaagaag atattgccac ttacttttgc caacagggta 60

atacgcttcc 70

<210> SEQ ID NO 160
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 160

ttgcagcaga aaccagggaa atcatttaag ggcctgatct atcatggaac caacttggaa 60

gatggagttc 70

<210> SEQ ID NO 161
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 161

tctgggagaa agtgtcacca tcacatgcct ggcaagtcag accattggta catggttagc 60

atggtatcag 70

<210> SEQ ID NO 162
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 162

ccgggcaagt caggacattc atggttattt aaacttgttt cagcagaaac caggtgaaac 60

tattaaacac 70

<210> SEQ ID NO 163
<211> LENGTH: 70

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<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 163

ttctctcacc atcagcaacc tggaacctga agatattgcc acttactatt gtcagcagta     60

tagtaagctt                                                            70


<210> SEQ ID NO 164
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 164

ctagtcagag cattgtacat agtaatggaa acacctattt agaatggtac ctgcagaaac     60

caggccagtc                                                            70


<210> SEQ ID NO 165
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 165

cactcaagat cagcacaata aagcctgagg acttgggaat gtattactgc ttacaaggta     60

cacatcagcc                                                            70


<210> SEQ ID NO 166
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 166

agatcaagcc tctatctctt gcaagtctac taagagtctt ctgaatagtg atggattcac     60

ttatttggac                                                            70


<210> SEQ ID NO 167
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 167

aaattagtgg ttacttaagc tggcttcagc agaaaccaga tggaactatt aaacgcctga     60

tctacgccgc                                                            70


<210> SEQ ID NO 168
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 168

cagtctctct tgtcgggcta gtcagggcat tagaggtaat ttagactggt atcagcagaa     60

accaggtgga                                                            70


<210> SEQ ID NO 169
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 169
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gcagaaagca gagcaagttc cccggctcct tatccatagt gcctccacta gggccggtgg     60

tgtcccagtc                                                            70


<210> SEQ ID NO 170
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 170

agtattctct caagatcagt agcctgcatc ctgacgatgt tgcaacgtat tactgtcaaa     60

atgtgttaag                                                            70


<210> SEQ ID NO 171
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 171

accaacacaa gcctggaaaa ggtcctaggc tgctcataca ttacacatct acattacagc     60

caggcatccc                                                            70


<210> SEQ ID NO 172
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 172

ctccttttct gtatctctag gagacagagt caccattact tgcaaggcaa gtgaggacat     60

atataatcgg                                                            70


<210> SEQ ID NO 173
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 173

ctacttgtct gtatctctag gaggcagagt caccattact tgcaaggcaa gtgaccacat     60

taataattgg                                                            70


<210> SEQ ID NO 174
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 174

ccaggaaata ttcctaaact attgatctat aaggcttcca acttgcacac aggcgtccca     60

tcaaggttta                                                            70


<210> SEQ ID NO 175
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 175

tattgtgatg acgcaggctg cattctccaa tccagtcact cttggaacat cagcttccat     60

ctcctgcagg                                                            70
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<210> SEQ ID NO 176
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 176

atattgtgat gactcaggct gcaccctctg tacctgtcac tcctggagag tcagtatcca 60

tctcctgcag 70

<210> SEQ ID NO 177
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 177

tctagtaaga gtctcctata taaggatggg aagacatact tgaattggtt tctgcagaga 60

ccaggacaat 70

<210> SEQ ID NO 178
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 178

tgacttgcca ggcaagtcag ggcactagca ttaatttaaa ctggtttcag caaaaaccag 60

ggaaagctcc 70

<210> SEQ ID NO 179
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 179

aattgtgctc actcagtctc cagccatcac agctgcatct ctggggcaaa aggtcaccat 60

cacctgcagt 70

<210> SEQ ID NO 180
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 180

cccggggaga agatcactat cacctgcagt gccagctcaa gtataagttc caattacttg 60

cattggtatc 70

<210> SEQ ID NO 181
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 181

gctcaagtat aagttccagc aacttgcact ggtaccagca gaagtcagaa acctccccca 60

aaccctggat 70

<210> SEQ ID NO 182
<211> LENGTH: 70

<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 182

ttacttgcac tggtaccagc agaagtcagg cgcttccccc aaacccttga ttcataggac 60

atccaacctg 70

<210> SEQ ID NO 183
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 183

ctcaagtgta agttacatgc actggtacca gcagaagtca ggcacctccc ccaaaagatg 60

gatttatgac 70

<210> SEQ ID NO 184
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 184

aggatcctcg cccaaaccct ggatttatga cacatccaac ctggcttctg gattccctgc 60

tcgcttcagt 70

<210> SEQ ID NO 185
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 185

ccagctcaag tataagttac atgcactggt accagcagaa gccaggcacc tcccccaaaa 60

gatggattta 70

<210> SEQ ID NO 186
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 186

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ccaccaccag 70

<210> SEQ ID NO 187
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 187

agaaacatgc ccaagtgtat ccttggtgct tttgcctacc atagcccttc tctctaccct 60

caaaatgcac 70

<210> SEQ ID NO 188
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 188

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ccgtgtttcc accttcctct gaggagctca aggaaaacaa agccacactg gtgtgtctga 60

tttccaactt 70

<210> SEQ ID NO 189
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 189

aatcccttct ttcattcaca caggtcagcc caagtccact cccacactca ccatgtttcc 60

accttcccct 70

<210> SEQ ID NO 190
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 190

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gacaaaacct 70

<210> SEQ ID NO 191
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 191

aggccaatct ccaaggcgcc taatttataa ggtttctaac tgggactctg ggtcccaga 60

cagattcagc 70

<210> SEQ ID NO 192
<211> LENGTH: 70
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 192

agctacttag cctggtacca gcagaaacct ggcctggcgc ccaggctcct catctatgat 60

gcatccagca 70

<210> SEQ ID NO 193
<211> LENGTH: 70
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 193

tcctctctgt gactccaggg gagaaagtca ccatcacctg ccaggccagt gaaggcattg 60

gcaactactt 70

<210> SEQ ID NO 194
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 194

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cagattcagc 70

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<210> SEQ ID NO 195
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 195

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ttccagccgg 70

<210> SEQ ID NO 196
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 196

tatttgggtt ctaatcgggc ctccggggtc cctgacaggt tcagtggcag tggatcaggc 60

acagatttta 70

<210> SEQ ID NO 197
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 197

atttgtattg gtacctgcag aagccaggcc agcctccaca gctcctgatc tatgaagttt 60

ccaaccggtt 70

<210> SEQ ID NO 198
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 198

aaagttccta agctcctgat ctatgctgca tccactttgc aatcaggggt cccatctcgg 60

ttcagtggca 70

<210> SEQ ID NO 199
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 199

tccaagactc ctaatttata agatttctaa ccggttctct ggggtcccag acagattcag 60

tggcagtggg 70

<210> SEQ ID NO 200
<211> LENGTH: 70
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 200

ctgccgggcc agtcagagca ttggtagtag cttacactgg taccagcaga aaccagatca 60

gtctccaaag 70

<210> SEQ ID NO 201
<211> LENGTH: 70

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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 201

aaattgtgtt gacgcagtct ccaggcaccc tgtctttgtc tccaggggaa agagccaccc 60

tctcctgcag 70

<210> SEQ ID NO 202
<211> LENGTH: 70
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 202

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atgctgcatc 70

<210> SEQ ID NO 203
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<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 203

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tgaagtttcc 70

<210> SEQ ID NO 204
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 204

gatttcacac tgaaaatcag cagggtggaa gctgaggatg tcggggttta ttactgcacg 60

caagctacac 70

<210> SEQ ID NO 205
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 205

ccctcacaat taataacata gaatctgagg atgctgcata ttacttctgt ctacaacatg 60

ataatttccc 70

<210> SEQ ID NO 206
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 206

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ttatacagct 70

<210> SEQ ID NO 207
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 207

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taagtccctg 70

<210> SEQ ID NO 208
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 208

cagctactta acctggtatc agcagaaacc tggccaggcg cccaggctcc tcatctatgg 60

tgcatccacc 70

<210> SEQ ID NO 209
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 209

tcaccatcag cagcctgcag cctgaagatt ttgcaactta ttactgtcta caagattaca 60

attaccctcc 70

<210> SEQ ID NO 210
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 210

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tcagcagaaa 70

<210> SEQ ID NO 211
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 211

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ccctaagcac 70

<210> SEQ ID NO 212
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 212

ctggttagcc tggtatcagc agaaaccaga gaaagcccct aagtccctga tctatgctgc 60

atccagtttg 70

<210> SEQ ID NO 213
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 213

tcaccatcag cagcctgcag tctgaagatt ttgcagttta ttactgtcag cagtataata 60

actgacctcc 70

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<210> SEQ ID NO 214
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 214

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aattaccctc 70

<210> SEQ ID NO 215
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 215

agatttcact ctcactatca gcagcctgca gcctgaagat tttgcaactt actattgtca 60

acaggctaac 70

<210> SEQ ID NO 216
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 216

tcaccatcag cagcctgcag tctgaagatt ttgcagttta ttactgtcag cagtataata 60

actggcctcc 70

<210> SEQ ID NO 217
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 217

gtgggcctgg gacagacttc actctcacca tcagcagcct agagcctgaa gattttgcag 60

tttattactg 70

<210> SEQ ID NO 218
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 218

gaaaccaggg aaatccccta agctcttcct ctatgatgca aaagatttgc accctggggt 60

ctcatcgagg 70

<210> SEQ ID NO 219
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 219

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aagtggggtc 70

<210> SEQ ID NO 220
<211> LENGTH: 70

<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 220

tccttactct ctgcatctac aggagacaga gtcaccatca gttgtcggat gagtcagggc 60

attagcagtt 70

<210> SEQ ID NO 221
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 221

cagctactta tcctggtacc agcagaaacc tgggcaggct cccaggctcc tcatctatgg 60

tgcatccacc 70

<210> SEQ ID NO 222
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 222

ctcaccatca gcagcctgca gcctgaagat tttgcaactt attactgtca acagtttaat 60

agttaccctc 70

<210> SEQ ID NO 223
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 223

gatctgggac agatttcact ctcaccatca gcagcctgca gcctgaagat tttgcaactt 60

actattgtca 70

<210> SEQ ID NO 224
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 224

aaagagccac cctctcctgc agggccagtc agagtgttag cagctactta gcctggtacc 60

aacagaaacc 70

<210> SEQ ID NO 225
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 225

tctcacaatc agcagcctgc agcctgaaga ttttgcaact tattactgtc aacagcttaa 60

tagttaccct 70

<210> SEQ ID NO 226
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 226

cattctctgc atctacagga gacagagtca ccatcacttg tcgggcgagt cagggtatta 60

gcagttattt 70

<210> SEQ ID NO 227
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 227

atctatacgc tttcctatcg ggcctctgga gtcccagaca ggttcagtgg cagtgggtca 60

ggcactgatt 70

<210> SEQ ID NO 228
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 228

tctcaccatc agcagtctgc aacctgaaga ttttgcaact tactactgtc aacagagtta 60

cagtacccct 70

<210> SEQ ID NO 229
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 229

tcactatcag cagcctgcag cctgaagatg ttgcaactta ttacggtcaa cggacttaca 60

atgcccctcc 70

<210> SEQ ID NO 230
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 230

acgatgcatc caatttggaa acaggggtcc catcaaggtt cagtggaagt ggatctggga 60

cagattttac 70

<210> SEQ ID NO 231
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 231

caggaaaggc tcccaaactc ctcatctatt atgatgatct gctgccctca ggggtctctg 60

accgattctc 70

<210> SEQ ID NO 232
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 232

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ctgagtggtt 70

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<210> SEQ ID NO 233
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 233

gtcaccatct cttgttctgg aagcagctcc aacatcggaa gtaatactgt aaactggtac 60

cagcagctcc 70

<210> SEQ ID NO 234
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 234

aattatgtat actggtacca gcagctccca ggaacggccc ccaaactcct catctatagt 60

aataatcagc 70

<210> SEQ ID NO 235
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 235

ccatcactgg actccagtct gaggatgagg ctgattatta ctgcaaagca tgggataaca 60

gcctgaatgc 70

<210> SEQ ID NO 236
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 236

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ctgagtgctg 70

<210> SEQ ID NO 237
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 237

cgtctctggg ctccaggctg aggatgaggc tgattattac tgcagctcat atgcaggcag 60

caacaatttc 70

<210> SEQ ID NO 238
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 238

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ggaataacaa 70

<210> SEQ ID NO 239
<211> LENGTH: 70

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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 239

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tatgtgcagt 70

<210> SEQ ID NO 240
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 240

catctctggg ctccaggctg aggatgaggc tgattattac tgctgctcat atgcaggcag 60

ctacactttc 70

<210> SEQ ID NO 241
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 241

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gtctggcaac 70

<210> SEQ ID NO 242
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 242

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tgatttatga 70

<210> SEQ ID NO 243
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 243

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tagcactttc 70

<210> SEQ ID NO 244
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 244

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cctgatttac 70

<210> SEQ ID NO 245
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 245

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tccgtgtccc caggacagac agccagcatc acctgctctg gagataaatt gggggataaa 60

tatgcttgct 70

<210> SEQ ID NO 246
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 246

aaaaaatatg cttattggta ccagcagaag ccaggccagt tccctgtgct ggtgatatat 60

aaagacagcg 70

<210> SEQ ID NO 247
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 247

acagacagtc aggatcacat gccaaggaga cagcctcaga agctattatg caagctggta 60

ccagcagaag 70

<210> SEQ ID NO 248
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 248

catcagcagg gtcgaagccg gggatgaggc cgactattac tgtcaggtgt gggatagtag 60

tagtgatcat 70

<210> SEQ ID NO 249
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 249

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tgggtccacc 70

<210> SEQ ID NO 250
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 250

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tcagcagaca 70

<210> SEQ ID NO 251
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 251

ccttgaccat cagcggggcc caggttgagg atgaggctga ctattactgt tactctgcgg 60

ctgacaacaa 70

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<210> SEQ ID NO 252
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 252

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cagcactgca 70

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<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 253

tcagtggggc ccaggtggag gatgaagctg actactactg ttactcaaca gacagcagtg 60

gtaatcatag 70

<210> SEQ ID NO 254
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 254

tccaacccag ggaacaccgc caccctaacc atcagcagga tcgaggctgg ggatgaggct 60

gactattact 70

<210> SEQ ID NO 255
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 255

gacactgtca ggtgtgcagc ctgaggacga ggctgagtat tactgcctgc tctactatgg 60

tggtgctcag 70

<210> SEQ ID NO 256
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 256

tcattatccc tactggttcc agcagaagcc tggccaagcc cccaggacac tgatttatga 60

tacaagcaac 70

<210> SEQ ID NO 257
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 257

gaacaaagct gccctcacca tcacgggggc ccaggcagat gatgaatctg attattactg 60

tgtgctgtat 70

<210> SEQ ID NO 258
<211> LENGTH: 70

<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 258

acctteetcc tccgcatctc ctggagaatc cgccagactc acctgcacct tgcccagtga 60

catcaatgtt 70

<210> SEQ ID NO 259
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 259

gtaccagcag aagccaggga gtcctcccca gtatctcctg aggtacaaat cagactcaga 60

taagcagcag 70

<210> SEQ ID NO 260
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 260

gtaccagcag aagccagaga gccctccccg gtatctcctg agctactact cagactcaag 60

taagcatcag 70

<210> SEQ ID NO 261
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 261

atgctgagca gtggcttcag tgttggggac ttctggataa ggtggtacca acaaaagcca 60

gggaaccctc 70

<210> SEQ ID NO 262
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 262

acctggggtc cccagtcgag tctctggctc caaggagacc tcaagtaaca cagcgttttt 60

gctcatctct 70

<210> SEQ ID NO 263
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 263

tgagcacagc acctacacca tcgaatggta tcaacagaga ccagggaggt ccccccagta 60

tataatgaag 70

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<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 264

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atcaagaaca tccaggaaga agatgagagt gactaccact gtggggcaga ccatggcagt 60

gggagcaact 70

<210> SEQ ID NO 265
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 265

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agcggagttc 70

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<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 266

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gggatccctg 70

<210> SEQ ID NO 267
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 267

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aatctcc 67

<210> SEQ ID NO 268
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 268

ttcacaatta tttagcatgg tatcagcaga aacagggaaa atctcctcag ctcctggtct 60

ataatgc 67

<210> SEQ ID NO 269
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 269

cgagcaagtg agaatattta cagttattta gcatggtatc agcagaaaca gggaaaatct 60

cctcagc 67

<210> SEQ ID NO 270
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 270

cgagcaagtg agaatattta cagtaattta gcatggtatc agcagaaaca gggaaaatct 60

cctcagc 67

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<210> SEQ ID NO 271
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 271

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tacactg                                                               67


<210> SEQ ID NO 272
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 272

gatctgggac agatttcact ctcaccatta gcaatgtgca atctgaagac ctggcagatt     60

atttctg                                                               67


<210> SEQ ID NO 273
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 273

ctcaccatca gcaatgtgca gtctgaagac ttggcagagt atttctgtca gcaatataac     60

agctatc                                                               67


<210> SEQ ID NO 274
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 274

ctttcaccat cagcagtgtg caggctgaag acctggcagt ttattactgt cagcaacatt     60

atagtac                                                               67


<210> SEQ ID NO 275
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 275

caaggccagt gagaatgtgg gtacttatgt atcctggtat caacagaaac cagagcagtc     60

tcctaaa                                                               67


<210> SEQ ID NO 276
<211> LENGTH: 70
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 276

cagatttcac tctcaccatt agcaatgtgc agtctgaaga cttggcagat tatttctgtc     60

agcaatatag                                                            70


<210> SEQ ID NO 277
<211> LENGTH: 69
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<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 277

attatactct caccatcagc agtgtgcagg ctgaagacct ggcactttat tactgtcagc 60

aacattata 69

<210> SEQ ID NO 278
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 278

caaggccagt gagaatgtgg gtacttatgt atcctggtat caacagaaac cagagcagtc 60

tcctaaa 67

<210> SEQ ID NO 279
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 279

cagtctccta aactgctgat atactatgca tccaatcgct acactggagt ccctgatcgc 60

ttcactg 67

<210> SEQ ID NO 280
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 280

gtaccaacag aaaccaggac agccacccaa actcctcatc tatgctgcat ccaacgtaga 60

atctggg 67

<210> SEQ ID NO 281
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 281

gtctaggaca gacttcaccc tcaccattga tcctgtggag gctgatgatg ctgcaaccta 60

ttactgt 67

<210> SEQ ID NO 282
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 282

gtaccaacag aaaccaggac agccacccaa actcctcatc tatcttgcat ccaacctaga 60

atctggg 67

<210> SEQ ID NO 283
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 283

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ctcaacatcc atcctatgga ggaggatgat actgcaatgt atttctgtca gcaaagtaag   60

gaggttc   67

<210> SEQ ID NO 284
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 284

ctgcagagcc agccagagtg tcgattataa tggaattagt tatatgcact ggttccaaca   60

gaaacca   67

<210> SEQ ID NO 285
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 285

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atctggg   67

<210> SEQ ID NO 286
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 286

ttcagtggca gtgggtctag gacagacttc accctcacca ttaatcctgt ggaggctgat   60

gatgttg   67

<210> SEQ ID NO 287
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 287

ctcaacatcc atcctgtgga ggaggaggat actgcaacat attactgtca gcacagttgg   60

gagattc   67

<210> SEQ ID NO 288
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 288

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actgtat   67

<210> SEQ ID NO 289
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 289

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tactgtg   67

<210> SEQ ID NO 290
<211> LENGTH: 71
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 290

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catcaagtat g 71

<210> SEQ ID NO 291
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 291

gggtcagatt tcactctcag tatcaacagt gtggaacctg aagatgttgg agtgtattac 60

tgtcaaa 67

<210> SEQ ID NO 292
<211> LENGTH: 68
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 292

tggatcaggg acagatttca ctctcagtat caacagtgtg gagactgaag attttggaat 60

gtatttct 68

<210> SEQ ID NO 293
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 293

agtcaaagta ttagcaacta cctacactgg tatcaacaaa aatcacatga gtctccaagg 60

cttctca 67

<210> SEQ ID NO 294
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 294

tttagtggca gtggatcagg gacagatttt actcttagca tcaacagtgt ggagtctgaa 60

gatattg 67

<210> SEQ ID NO 295
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 295

taccagcaga agtcagatgc ctcccccaaa ctatggattt attacacatc caacctggct 60

cctggag 67

<210> SEQ ID NO 296
<211> LENGTH: 67

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<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 296

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ccagcag                                                               67


<210> SEQ ID NO 297
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 297

ctcttactct ctcacaatca gcagtgtgga ggctgaagat gctgccactt attactgcca     60

gcagtac                                                               67


<210> SEQ ID NO 298
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 298

catctgatag gtactctgga gtccctgatc gtttcatagg cagtggatct gtgacagatt     60

tcactct                                                               67


<210> SEQ ID NO 299
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 299

gagagaaggt cactatgagc tgcaagtcca gtcagagtct gttaaacagt ggaaatcaaa     60

agaacta                                                               67


<210> SEQ ID NO 300
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 300

gaaggtcact atgagctgca aatccagtca gagtctgctc aacagtagaa cccgaaagaa     60

ctacttg                                                               67


<210> SEQ ID NO 301
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 301

gacagaaggt cactatgagc tgcaagtcca gtcagagcct tttaaatagt agcaatcaaa     60

agaacta                                                               67


<210> SEQ ID NO 302
<211> LENGTH: 69
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 302
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gcaggagaaa aggtcactat gagctgtaag tccagtcaaa gtgttttata cagttcaaat 60

cagaagaac 69

<210> SEQ ID NO 303
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 303

gagagaaggt cactatgagc tgcaagtcca gtcagagtct gttaaacagt ggaaatcaaa 60

agaacta 67

<210> SEQ ID NO 304
<211> LENGTH: 73
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 304

ttggagagaa ggttactatg agctgcaagt ccagtcagag ccttttatat agtagcaatc 60

aaaagaacta ctt 73

<210> SEQ ID NO 305
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 305

gatctcctaa aatgctgata atttgggcat ccactagggt atctggagtc cctgatcgct 60

tcatagg 67

<210> SEQ ID NO 306
<211> LENGTH: 73
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 306

tctcctggag aaaccattac tattaattgc agggcaagta agagcattag caaatattta 60

gcctggtatc aag 73

<210> SEQ ID NO 307
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 307

caaattgttc tcacccagtc tccagcaatc atgtctgcat ctccagggga gaaggtcacc 60

atatcct 67

<210> SEQ ID NO 308
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 308

ctggaaactc ttactctctc acgatcagca gcatggaggc tgaagatgtt gccacttatt 60

actgttt 67

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<210> SEQ ID NO 309
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 309

caatcatgtc tgcatctcct ggggagaagg tcaccatgac ctgcagtgcc agatcaagtg 60

taagttc 67

<210> SEQ ID NO 310
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 310

caaattgttc tcacccagtc tccagcaatc atgtctgcat ctcctgggga gaaggtcacc 60

ttgacct 67

<210> SEQ ID NO 311
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 311

cacttctccc aaactcttga tttatagcac atccaacctg gcttctggag tcccttctcg 60

cttcagt 67

<210> SEQ ID NO 312
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 312

cttctaccaa attctggatt tataggacat ccaacctggc ttcagaagtc ccagctccct 60

tcagtgg 67

<210> SEQ ID NO 313
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 313

gatcctcccc aaaactctgg atttatagca tatccaacct ggcttctgga gtcccagctc 60

gcttcag 67

<210> SEQ ID NO 314
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 314

caaattgttc tcacccagtc tccagcaatc atgtctgcat ctctagggga acgggtcacc 60

atgacct 67

<210> SEQ ID NO 315
<211> LENGTH: 67

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<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 315

gatcctcccc caaactctgg atttatagca tatccaacct ggcttctgga gtccctgctc 60

gcttcag 67

<210> SEQ ID NO 316
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 316

ctctggattt atttaacatt caacttggct tctggagtcc ctgctcgctt cagtggcagt 60

gggtctg 67

<210> SEQ ID NO 317
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 317

ctctcacaat cagcagagtg gaggctgaag atgctgccac ttattactgc cagcagtgga 60

gtagtaa 67

<210> SEQ ID NO 318
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 318

catctttctc tttcacaatc aacagcatgg aggctgaaga tgttgccact tattactgtc 60

agcaaag 67

<210> SEQ ID NO 319
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 319

caagtgtaag ttacatgcac tggttccagc agaagccagg cacttctccc aaactctgga 60

tttatag 67

<210> SEQ ID NO 320
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 320

catctccagg ggagaaggtc accatgacct gcagtgccag ctcaagtgta agttacatgt 60

actggta 67

<210> SEQ ID NO 321
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 321

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cttcagtggc agtggatctg ggacctctta ttctctcaca atcagcagca tggaggctga     60

agatgct                                                               67


<210> SEQ ID NO 322
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 322

catctccagg ggagaaggtc accatgacct gcagtgccag ctcaagtgta agttacatgt     60

actggta                                                               67


<210> SEQ ID NO 323
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 323

gaggggagaa ggtcaccatc acctgccgtg ccagctcaag tataagttcc aattacttac     60

actggta                                                               67


<210> SEQ ID NO 324
<211> LENGTH: 68
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 324

tggatctggg caagattatt ctctcaccat cagcagcctg gagtatgaag atatgggaat     60

ttattatt                                                              68


<210> SEQ ID NO 325
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 325

catctcttgc agatctagtc agagccttgt acacagtaat ggaaacacct atttacattg     60

gtacctg                                                               67


<210> SEQ ID NO 326
<211> LENGTH: 68
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 326

ccatctcttg cagatctagt cagagccttg tacacagtaa tggaaacacc tatttatatt     60

ggtacctg                                                              68


<210> SEQ ID NO 327
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 327

ctcttagata gtgatggaaa gacatatttg aattggttgt tacagaggcc aggccagtct     60

ccaaagc                                                               67
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<210> SEQ ID NO 328
<211> LENGTH: 68
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 328

aaactggacc ctggcatccc tgacaggttc agtggcagtg gatcagaaac agattttaca 60

cttaaaat 68

<210> SEQ ID NO 329
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 329

ctatttgaat tggttattac agaggccagg ccagtctcca aagcgcctaa tctatctggt 60

gtctaaa 67

<210> SEQ ID NO 330
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 330

ctccatctct tgcaggtcta gtcagagcct tgaaaacagt aatggaaaca cctatttgaa 60

ctggtac 67

<210> SEQ ID NO 331
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 331

ggaacctcct aagctcctta tttcagaagg caatactctt cgtcctggag tcccatcccg 60

attctcc 67

<210> SEQ ID NO 332
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 332

ggacattggt agtagcttaa actggcttca gcaggaacca gatggaacta ttaaacgcct 60

gatctac 67

<210> SEQ ID NO 333
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 333

ggaacctcct aagctcctta tttcagaagg caatactctt cgtcctggag tcccatcccg 60

attctcc 67

<210> SEQ ID NO 334
<211> LENGTH: 67

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<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 334

tctgggagac agaataacca tcacttgcca ggcaactcaa gacattgtta agaatttaaa 60

ctggtat 67

<210> SEQ ID NO 335
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 335

ttcagtggca gtgggtctgg aacagattat tctctcacca ttagcaacct ggagcaagaa 60

gatattg 67

<210> SEQ ID NO 336
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 336

cagcagaaac cagggaaatc atttaagggc ctgatctatc atggaaccaa cttggaagat 60

ggagttc 67

<210> SEQ ID NO 337
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 337

gaccattggt acatggttag catggtatca gcagaaacca gggaaatctc ctcagctcct 60

gatttat 67

<210> SEQ ID NO 338
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 338

acctgatcta tgaaacatcc aatttagatt ctggtgtccc aaaaaggttc agtggcagta 60

ggtctgg 67

<210> SEQ ID NO 339
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 339

ttattctctc accatcagca acctggaacc tgaagatatt gccacttact attgtcagca 60

gtatagt 67

<210> SEQ ID NO 340
<211> LENGTH: 73
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 340

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ggagatcaag cctccatctc ttgcagatct agtcagagca ttgtacatag taatggaaac     60

acctatttag aat                                                        73


<210> SEQ ID NO 341
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 341

gatttcacac tcaagatcag cacaataaag cctgaggact tgggaatgta ttactgctta     60

caaggta                                                               67


<210> SEQ ID NO 342
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 342

ctcaagatca gcagagtgga ggctgaggat ttgggagttt attattgctt ccagagtaac     60

tatcttc                                                               67


<210> SEQ ID NO 343
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 343

ggaaattagt ggttacttaa gctggcttca gcagaaacca gatggaacta ttaaacgcct     60

gatctac                                                               67


<210> SEQ ID NO 344
<211> LENGTH: 68
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 344

ctagtcaggg cattagaggt aatttagact ggtatcagca gaaaccaggt ggaactatta     60

aactcctg                                                              68


<210> SEQ ID NO 345
<211> LENGTH: 68
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 345

gaaacaacac aggctccagc ttctctgagt ttttctcttg gtgaaacagc aacactgtca     60

tgcaggtc                                                              68


<210> SEQ ID NO 346
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 346

caagtgagaa tatttacggt gctttaaatt ggtatcagcg gaaacaggga aaatctcctc     60

agctcct                                                               67
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<210> SEQ ID NO 347
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 347

ctgctcatac attacacatc tacattacag ccaggcatcc catcaaggtt cagtggaagt     60

gggtctg                                                               67


<210> SEQ ID NO 348
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 348

gttccttcaa gattcagtgg cagtggatct ggaaaggatt acactctcag cattaccagt     60

cttcaga                                                               67


<210> SEQ ID NO 349
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 349

gacatccaga tgacacaatc ttcatcctac ttgtctgtat ctctaggagg cagagtcacc     60

attactt                                                               67


<210> SEQ ID NO 350
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 350

ggaaatattc ctaaactatt gatctataag gcttccaact tgcacacagg cgtcccatca     60

aggttta                                                               67


<210> SEQ ID NO 351
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 351

gatattgtga tgacgcaggc tgcattctcc aatccagtca ctcttggaac atcagcttcc     60

atctcct                                                               67


<210> SEQ ID NO 352
<211> LENGTH: 68
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 352

ctgagaatca gtagagtgga ggctgaggat gtgggtgttt attactgtat gcaacatcta     60

gaatatcc                                                              68


<210> SEQ ID NO 353
<211> LENGTH: 67
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<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 353

ctggaaatca gtagagtgaa ggctgaggat gtgggtgtgt attactgtca acaacttgta 60

gagtatc 67

<210> SEQ ID NO 354
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 354

tctcaccatc agcagcctgg aggatgaaga tatggcaact tatttctgtc tacagcatag 60

ttatctc 67

<210> SEQ ID NO 355
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 355

catggattta tgaaatatcc aaactggctt ctggagtccc agctcgcttc agtggcagtg 60

ggtctgg 67

<210> SEQ ID NO 356
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 356

caattacttg cattggtatc agcagaagcc aggattctcc cctaaactct tgatttatag 60

gacatcc 67

<210> SEQ ID NO 357
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 357

cttctggagt ccctgttcgc ttcagtggca gtggatctgg gacctcttat tctctcacaa 60

tcagcag 67

<210> SEQ ID NO 358
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 358

ggtctgggac ctcttactct ctcacaatca gcagcgtgga ggctgaagat gatgcaactt 60

attactg 67

<210> SEQ ID NO 359
<211> LENGTH: 67
<212> TYPE: DNA
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 359

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ggcagtg                                                               67


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<400> SEQUENCE: 360

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agatgct                                                               67


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<400> SEQUENCE: 364

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tattcact                                                              68


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<400> SEQUENCE: 365

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<400> SEQUENCE: 366

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<400> SEQUENCE: 367

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We claim:

1. A microarray comprising a plurality of oligonucleotide species, each species capable of hybridizing to a polynucleotide comprising a sequence or a complement thereof, the sequence encoding at least a portion of a light chain variable region, and wherein each of the plurality of oligonucleotide species is at least 20 nucleotides long.

2. The microarray of claim 1, wherein the light chain variable region is a vertebrate light chain variable region.

3. The microarray of claim 1, wherein the light chain variable region is a human light chain variable region.

4. The microarray of claim 1, wherein each of the plurality of oligonucleotide species is at least 40 nucleotides long.

5. The microarray of claim 1, wherein each of the plurality of oligonucleotide species is at least 60 nucleotides long.

6. The microarray of claim 1, wherein the plurality of oligonucleotide species comprises at least two oligonucleotide species substantially similar to the oligonucleotides of Table 2, Table 3, Table 4, or Table 5, or complements of the oligonucleotides of Table 2, Table 3, Table 4, or Table 5.

7. The microarray of claim 1, wherein the plurality of oligonucleotide species comprise at least 20 of the oligonucleotides of Table 2, Table 3, Table 4, or Table 5, or complements of the oligonucleotides of Table 2, Table 3, Table 4, or Table 5.

8. The microarray of claim 1, wherein each oligonucleotide species is immobilized at a distinct address on a substrate.

9. The microarray of claim 1, wherein at least one of the light chain variable regions is associated with a disease.

10. The microarray of claim 9, wherein the at least one light chain variable region is associated with a systemic autoimmune disease.

11. The microarray of claim 1, wherein the plurality of oligonucleotide species comprises an oligonucleotide comprising a sequence encoding at least a portion of a light chain variable region of mBT20, mBW20, mGJ38C, mVLX, m21-4, m12-38, m12-46, O8, O18, L25, B2, L11, L22, L10, V2-8, V2-14, V2-15, V2-19, A5, or complements of mBT20, mBW20, mGJ38C, mVLX, m21-4, m12-38, m12-46, O8, O18, L25, B2, L11, L22, L10, V2-8, V2-14, V2-15, V2-19, or A5.

12. A method of characterizing the light chain variable gene expression in a subject comprising:

a) isolating B cells from the subject;

b) preparing target polynucleotides from the B cells;

c) hybridizing the target polynucleotides to a microarray comprising a plurality of oligonucleotide species at least 20 nucleotides long, each species capable of hybridizing to at least one of the target polynucleotides comprising a sequence or a complement thereof, the sequence encoding at least a portion of a light chain variable region; and

d) detecting the hybridization.

13. A method of identifying light chain variable genes associated with a disease, comprising comparing the light chain variable gene expression in a first subject with the disease to the light chain variable gene expression in a second subject that does not have the disease, a difference in light chain variable gene expression between the first and second subjects indicating that expression of the light chain variable gene is associated with the disease.

14. The method of claim 13, wherein the disease is a systemic autoimmune disease.

15. The method of claim 14, wherein the systemic autoimmune disease is selected from the group consisting of systemic lupus erythematosus, multiple sclerosis, rheumatoid arthritis, scleroderma, Sjogren's syndrome, mixed connective tissue disease, amyloidosis, and psoriasis.

16. The method of claim 13, wherein the disease is cancer.

17. The method of claim 16, wherein the cancer is a B cell cancer.

18. The method of claim 13, wherein the disease is an immunodeficiency disease.

19. A method of monitoring a disease state in a subject comprising comparing expression in the subject of a light chain variable gene associated with the disease at two or more different time points.

20. A method of a evaluating the effect of a therapy or therapeutic agent on expression of a light chain variable gene associated with a disease in a subject, comprising comparing expression of the light chain variable gene expression in the subject before and after treatment.

21. A kit comprising the microarray of claim 1.

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