

HIGH EFFICIENCY GENE TRANSFER AND EXPRESSION IN MAMMALIAN CELLS BY A MULTIPLE TRANSFECTION PROCEDURE OF MATRIX ATTACHMENT REGION SEQUENCES

FIELD OF THE INVENTION

The present invention relates to purified and isolated DNA sequences having protein production increasing activity and more specifically to the use of matrix attachment regions (MARs) for increasing protein production activity in a eukaryotic cell. Also disclosed is a method for the identification of said active regions, in particular MAR nucleotide sequences, and the use of these characterized active MAR sequences in a new multiple transfection method.

BACKGROUND OF THE INVENTION

Nowadays, the model of loop domain organization of eukaryotic chromosomes is well accepted (Boulikas T, "Nature of DNA sequences at the attachment regions of genes to the nuclear matrix", *J. Cell Biochem.*, 52:14-22, 1993). According to this model chromatin is organized in loops that span 50-100 kb attached to the nuclear matrix, a proteinaceous network made up of RNPs and other nonhistone proteins (Bode J, Stengert-Iber M, Kay V, Schalke T and Dietz-Pfeilstetter A, *Crit. Rev. Euk. Gene Exp.*, 6:115-138, 1996).

The DNA regions attached to the nuclear matrix are termed SAR or MAR for respectively scaffold (during metaphase) or matrix (interphase) attachment regions (Hart C and Laemmli U (1998), "Facilitation of chromatin dynamics by SARs" *Curr Opin Genet Dev* 8, 519-525.)

As such, these regions may define boundaries of independent chromatin domains, such that only the encompassing cis-regulatory elements control the expression of the genes within the domain.

However, their ability to fully shield a chromosomal locus from nearby chromatin elements, and thus confer position-independent gene expression, has not been seen in stably transfected cells (Poljak L, Seum C, Mattioni T and Laemmli U. (1994) "SARs stimulate but do not confer position independent gene expression", *Nucleic Acids Res* 22, 4386-4394). On the other hand, MAR (or S/MAR) sequences have been shown to interact with enhancers to increase local chromatin accessibility (Jenuwein T, Forrester W, Fernandez-Herrero L, Laible G, Dull M, and Grosschedl R. (1997) "Extension of chromatin accessibility by nuclear matrix attachment regions" *Nature* 385, 269-272). Specifically, MAR elements can enhance expression of heterologous genes in cell culture lines (Kalos M and Fournier R (1995) "Position-independent transgene expression mediated by boundary elements from the apolipoprotein B chromatin domain" *Mol Cell Biol* 15, 198-207), transgenic mice (Castilla J, Pintado B, Sola I, Sanchez-Morgado J, and Enjuanes L (1998) "Engineering passive immunity in transgenic mice secreting virus-neutralizing antibodies in milk" *Nat Biotechnol* 16, 349-354) and plants (Allen G, Hall GJ, Michalowski S, Newman W, Spiker S, Weissinger A, and Thompson W (1996), "High-level transgene expression in plant cells: effects of a strong scaffold attachment region from tobacco" *Plant Cell* 8, 899-913). The utility of MAR sequences for developing improved vectors for gene therapy is also recognized (Agarwal M, Austin T, Morel F, Chen J, Bohnlein E, and Plavec I (1998), "Scaffold attachment region-mediated enhancement of retroviral vector expression in primary T

cells" *J Virol* 72, 3720-3728).

Recently, it has been shown that chromatin-structure modifying sequences including
MARs, as exemplified by the chicken lysozyme 5' MAR is able to significantly enhance
reporter expression in pools of stable Chinese Hamster Ovary (CHO) cells (Zahn-Zabal
M, et al., "Development of stable cell lines for production or regulated expression using
matrix attachment regions" *J Biotechnol*, 2001, 87(1): p. 29-42). This property was used
to increase the proportion of high-producing clones, thus reducing the number of clones
that need to be screened. These benefits have been observed both for constructs with
MARs flanking the transgene expression cassette, as well as when constructs are co-
transfected with the MAR on a separate plasmid. However, expression levels upon co-
transfection with MARs were not as high as those observed for a construct in which two
MARs delimit the transgene expression unit. A third and preferable process was shown
to be the transfection of transgenes with MARs both linked to the transgene and on a
separate plasmid (Girod et al., submitted for publication). However, one persisting
limitation of this technique is the quantity of DNA that can be transfected per cell.
Many multiples transfection protocols have been developed in order to achieve a high
transfection efficiency to characterize the function of genes of interest. The protocol
applied by Yamamoto et al, 1999 ("High efficiency gene transfer by multiple transfection
protocol", *Histochem. J.* 31(4), 241-243) leads to a transfection efficiency of about 80 %
after 5 transfections events, whereas the conventional transfection protocol only
achieved a rate of <40%. While this technique may be useful when one wishes to
increase the proportion of expressing cells, it does not lead to cells with a higher
intrinsic productivity. Therefore, it cannot be used to generate high producer
monoclonal cell lines. Hence, the previously described technique has two major
drawbacks:

- i) this technique does not generate a homogenous population of transfected
cells, since it cannot favour the integration of further gene copy, nor does it
direct the transgenes to favorable chromosomal loci,
- ii) the use of the same selectable marker in multiple transfection events does
not permit the selection of doubly or triply transfected cells.

In patent application WO02/074969, the utility of MARs for the development of stable
eukaryotic cell lines has also been demonstrated. However, this application does not
disclose neither any conserved homology for MAR DNA element nor any technique for
predicting the ability for a DNA sequence to be a MAR sequence.

In fact no clear-cut MAR consensus sequence has been found (Boulikas T, "Nature of
DNA sequences at the attachment regions of genes to the nuclear matrix", *J. Cell
Biochem.*, 52:14-22, 1993) but evolutionarily, the structure of these sequences seem to
be functionally conserved in eukaryotic genomes, since animal MARs can bind to plant
nuclear scaffolds and vice versa (Mielke C, Kohwi Y, Kohwi-Shigematsu T and Bode J,
"Hierarchical binding of DNA fragments derived from scaffold-attached regions:
correlation of properties in vitro and function in vivo", *Biochemistry*, 29:7475-7485,
1990).

The identification of MARs by biochemical studies is a long and unpredictable process;
various results can be obtained depending on the assay (Razin SV, "Functional
architecture of chromosomal DNA domains", *Crit Rev Eukaryot Gene Expr.*, 6:247-269,
1996). Considering the huge number of expected MARs in a eukaryotic genome and
the amount of sequences issued from genome projects, a tool able to filter potential
MARs in order to perform targeted experiments would be greatly useful.

Currently two different predictive tools for MARs are available via the Internet. The first one, MAR-Finder (<http://futuresoft.org/MarFinder>; Singh GB, Kramer JA and Krawetz SA, "Mathematical model to predict regions of chromatin attachment to the nuclear matrix", *Nucleic Acid Research*, 25:1419-1425, 1997) is based on set of patterns identified within several MARs and a statistical analysis of the co-occurrence of these patterns. MAR-Finder predictions are dependent of the sequence context, meaning that predicted MARs depend on the context of the submitted sequence. The other predictive software, SMARTest (<http://www.genomatix.de>; Frisch M, Frech K, Klingenhoff A, Cartharius K, Liebich I and Werner T, "In silico prediction of scaffold/matrix attachment regions in large genomic sequences", *Genome Research*, 12:349-354, 2001), use weight-matrices derived from experimentally identified MARs. SMARTest is said to be suitable to perform large-scale analyses. But actually aside its relative poor specificity, the amount of hypothetical MARs rapidly gets huge when doing large scale analyses with it, and in having no way to increase its specificity to restrain the number of hypothetical MARs, SMARTest becomes almost useless to screen for potent MARs from large DNA sequences. Some other softwares, not available via the Internet, also exists; they are based as well on the frequency of MAR motifs (MRS criterion; Van Drunen CM et al., "A bipartite sequence element associated with matrix/scaffold attachment regions", *Nucleic Acids Res*, 27:2924-2930, 1999), (ChrClass; Glazko GV et al., "Comparative study and prediction of DNA fragments associated with various elements of the nuclear matrix", *Biochim. Biophys. Acta*, 1517:351-356, 2001) or based on the identification of sites of stress-induced DNA duplex (SIDD; Benham C and al., "Stress-induced duplex DNA destabilization in scaffold/matrix attachment regions", *J. Mol. Biol.*, 274:181-196, 1997). However, their suitability to analyze complete genome sequences remains unknown, and whether these tools may allow the identification of protein production-increasing sequences has not been reported.

Furthermore, due to the relatively poor specificity of these softwares (Frisch M, Frech K, Klingenhoff A, Cartharius K, Liebich I and Werner T, "In silico prediction of scaffold/matrix attachment regions in large genomic sequences", *Genome Research*, 12:349-354, 2001), the amount of hypothetical MARs identified in genomes rapidly gets unmanageable when doing large scale analyses, especially if most of these have no or poor activity in practice. Thus, having no way to increase prediction specificity to restrain the number of hypothetical MARs, many of the available programs become almost useless to identify potent genetic elements in view of efficiently increasing recombinant protein production.

Since all the above available predictive methods have some drawbacks that prevent large-scale analyses of genomes to identify reliably novel and potent MARs, the object of this invention is to 1) understand the functional features of MARs that allow improved recombinant protein expression; 2) get a new Bioinformatic tool compiling MAR structural features as a prediction of function, in order to 3) perform large scale analyses of genomes to identify novel and more potent MARs, and, finally 4) to demonstrate improved efficiency to increase the production of recombinant proteins from eukaryotic cells or organisms when using the newly identified MAR sequences.

SUMMARY OF THE INVENTION

This object has been achieved by providing an improved and reliable method for the identification of DNA sequences having protein production increasing activity, in

particular MAR nucleotide sequences, and the use of these characterized active MAR sequences in a new multiple transfection method to increase the production of recombinant proteins in eukaryotic cells.

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BRIEF DESCRIPTION OF THE FIGURES

Fig. 1 shows the distribution plots of MARs and non-MARs sequences. Histograms are density plots (relative frequency divided by the bin width) relative to the score of the observed parameter. The density histogram for human MARs in the SMART DB database is shown in black, while the density histogram for the human chromosome 22 are in grey.

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Fig. 2 shows Scatterplots of the four different criteria used by SMAR Scan® and the AT-content with human MARs from SMART DB.

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Fig. 3 shows the distribution plots of MAR sequences by organism. MAR sequences from SMART DB of other organisms were retrieved and analyzed. The MAR sequences density distributions for the mouse, the chicken, the sorghum bicolor and the human are plotted jointly.

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Fig. 4 shows SMAR Scan® predictions on human chromosome 22 and on shuffled chromosome 22. Top plot : Average number of hits obtained by SMAR Scan® with five: rubbled, scrambled, shuffled within nonoverlapping windows of 10 bp, order 1 Markov chains model and with the native chromosome 22. Bottom plot: Average number of MARs predicted by SMAR Scan® in five: rubbled, scrambled, shuffled within non-overlapping windows of 10 bp, order 1 Markov chains model and with the native chromosome 22.

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Fig. 5 shows the dissection of the ability of the chicken lysozyme gene 5'-MAR to stimulate transgene expression in CHO-DG44 cells. Fragments B, K and F show the highest ability to stimulate transgene expression. The indicated relative strength of the elements was based on the number of high-expressor cells.

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Fig. 6 shows the effect of serial-deletions of the 5'-end (upper part) and the 3'-end (lower part) of the 5'-MAR on the loss of ability to stimulate transgene expression. The transition from increased to decreased activity coincide with B-, K- and F-fragments.

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Fig. 7 shows that portions of the F fragment significantly stimulate transgene expression. The F fragment regions indicated by the light grey arrow were multimerized, inserted in pGEGFP Control and transfected in CHO cells. The element that displays the highest activity is located in the central part of the element and corresponds to fragment FIII (black bar labelled minimal MAR). In addition, an enhancer activity is located in the 3'-flanking part of the FIII fragment (dark grey bar labelled MAR enhancer).

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Fig. 8 shows a map of locations for various DNA sequence motifs within the *cLysMAR*. Fig. 8 (B) represents a Map of locations for various DNA sequence motifs within the *cLysMAR*. Vertical lines represent the position of the computer-predicted sites or sequence motifs along the 3034 base pairs of the *cLysMAR* and its active regions, as presented in Fig. 5. The putative transcription factor sites, (MEF2 05, Oct-1, USF-02, GATA, NFAT) for activators and (CDP, SATB1, CTCF, ARBP/MeCP2) for repressors of transcription, were identified using MatInspector (Genomatix), and CpG islands were identified with CPGPLOT. Motifs previously associated with MAR elements are labelled

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in black and include CpG dinucleotides and CpG islands, unwinding motifs (AATATATT and AATATT), poly As and Ts, poly Gs and Cs, *Drosophila* topoisomerase II binding sites (GTNWAYATTNATTNATNNR) which had identity to the 6 bp core and High mobility group I (HMG-I/Y) protein binding sites. Other structural motifs include nucleosome-binding and nucleosome disfavoured sites and a motif thought to relieve the superhelical strain of DNA. Fig. 8(A) represents the comparison of the ability of portions of the cLysMAR to activate transcription with MAR prediction score profiles with MarFinder. The top diagram shows the MAR fragment activity as in Fig. 5, while the middle and bottom curves show MARFinder-predicted potential for MAR activity and for bent DNA structures respectively.

Fig. 9 shows the correlation of DNA physico-chemical properties with MAR activity. Fig. 9(A), represents the DNA melting temperature, double helix bending, major groove depth and minor groove width profiles of the 5'-MAR and were determined using the algorithms of Levitsky et al (Levitsky VG, Ponomarenko MP, Ponomarenko JV, Frolov AS, Kolchanov NA "Nucleosomal DNA property database", *Bioinformatics*, 15; 582592, 1999). The most active B, K and F fragments depicted at the top are as shown as in Figure 1. Fig. 9(B), represents the enlargement of the data presented in panel A to display the F fragment map aligned with the tracings corresponding to the melting temperature (top curve) and DNA bending (bottom curve). The position of the most active FIB fragment and protein binding site for specific transcription factors are as indicated.

Fig. 10 shows the distribution of putative transcription factor binding sites within the 5'-cLysMAR. Large arrows indicate the position of the CUE elements as identified with SMAR Scan®.

Fig. 11 shows the scheme of assembly of various portions of the MAR. The indicated portions of the cLysMAR were amplified by PCR, introducing BglII-BamHI linker elements at each extremity, and assembled to generate the depicted composite elements. For instance, the top construct consists of the assembly of all CUE and flanking sequences at their original location except that BglII-BamHI linker sequences separate each element.

Fig. 12 represents the plasmid maps.

Fig. 13 shows the effect of re-transfecting primary transfectants on GFP expression. Cells (CHO-DG44) were co-transfected with pSV40EGFP (left tube) or pMAR-SV40EGFP (central tube) and pSVneo as resistance plasmid. Cells transfected with pMAR-SV40EGFP were re-transfected 24 hours later with the same plasmid and a different selection plasmid, pSVpuro (right tube). After two weeks selection, the phenotype of the stably transfected cell population was analysed by FACS.

Fig. 14 shows the effect of multiple load of MAR-containing plasmid. The pMAR-SV40EGFP/ pMAR-SV40EGFP secondary transfectants were used in a third cycle of transfection at the end of the selection process. The tertiary transfection was accomplished with pMAR or pMAR-SV40EGFP to give tertiary transfectants. After 24 hours, cells were transfected again with either plasmid, resulting in the quaternary transfectants (see Table 4).

Fig. 15 shows comparative performance of SMAR prediction algorithms exemplified by region WP18A10A7. (A) SMAR Scan® analysis was performed with default settings. (B) SIDD analysis (top curve and left-hand side scale), and the attachment of several

DNA fragments to the nuclear matrix in vitro (bar-graph, right-hand side scale) was taken from Goetze et al (Goetze S, Gluch A, Benham C, Bode J, "Computational and in vitro analysis of destabilized DNA regions in the interferon gene cluster: potential of predicting functional gene domains." *Biochemistry*, 42:154-166, 2003).

Fig. 16 represents the results of a gene therapy-like protocol using MARs. The group of mice injected by MAR-network, induced from the beginning of the experiment, display a better induction of the hematocrit in comparison of mice injected by original network without MAR. After 2 months, hematocrits in "MAR-containing group" is still at values higher (65%) than normal hematocrit levels (45-55%).

Fig. 17 represents the scatterplot for the 1757 S/MAR sequences of the AT (top) and TA (bottom) dinucleotide percentages versus the predicted DNA bending as computed by SMAR Scan®.

Fig. 18 represents the dinucleotide percentage distribution plots over the 1757 non-S/MARs sequences.

Fig.19 shows the effect of various S/MAR elements on the production of recombinant green fluorescent protein (GFP). Populations of CHO cells transfected with a GFP expression vector containing or a MAR element, as indicated, were analyzed by a fluorescence-activated cell sorter (FACS®), and typical profiles are shown. The profiles display the cell number counts as a function of the GFP fluorescence levels.

Fig. 20 depicts the effect of the induction of hematocrit in mice injected by MAR-network.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to a purified and isolated DNA sequence having protein production increasing activity characterized in that said DNA sequence comprises at least one bent DNA element, and at least one binding site for a DNA binding protein.

Certain sequences of DNA are known to form a relatively "static curve", where the DNA follows a particular 3-dimensional path. Thus, instead of just being in the normal B-DNA conformation ("straight"), the piece of DNA can form a flat, planar curve also defined as bent DNA (Marini, *et al.*, 1982 "Bent helical structure in kinetoplast DNA", *Proc. Natl. Acad. Sci. USA*, 79: 7664-7664).

Surprisingly, Applicants have shown that the bent DNA element of a purified and isolated DNA sequence having protein production increasing activity of the present invention usually contains at least 10% of dinucleotide TA, and/or at least 12% of dinucleotide AT on a stretch of 100 contiguous base pairs. Preferably, the bent DNA element contains at least 33% of dinucleotide TA, and/or at least 33% of dinucleotide AT on a stretch of 100 contiguous base pairs. These data have been obtained by the method described further.

According to the present invention, the purified and isolated DNA sequence usually comprises a MAR nucleotide sequence selected from the group comprising the sequences SEQ ID Nos 1 to 27 or a cLysMAR element or a fragment thereof. Preferably, the purified and isolated DNA sequence is a MAR nucleotide sequence

selected from the group comprising the sequences SEQ ID Nos 1 to 27, more preferably the sequences SEQ ID Nos 24 to 27.

5 Encompassed by the present invention are as well complementary sequences of the above-mentioned sequences SEQ ID Nos 1 to 27 and the cLysMAR element or fragment, which can be produced by using PCR or other means.

10 An "element" is a conserved nucleotide sequences that bears common functional properties (i.e. binding sites for transcription factors) or structural (i.e. bent DNA sequence) features.

15 A part of sequences SEQ ID Nos 1 to 27 and the cLysMAR element or fragment refers to sequences sharing at least 70% nucleotides in length with the respective sequence of the SEQ ID Nos 1 to 27. These sequences can be used as long as they exhibit the same properties as the native sequence from which they derive. Preferably these sequences share more than 80%, in particular more than 90% nucleotides in length with the respective sequence of the SEQ ID Nos 1 to 27.

20 The present invention also includes variants of the aforementioned sequences SEQ ID Nos 1 to 27 and the cLysMAR element or fragment, that is nucleotide sequences that vary from the reference sequence by conservative nucleotide substitutions, whereby one or more nucleotides are substituted by another with same characteristics.

25 The sequences SEQ ID Nos 1 to 23 have been identified by scanning human chromosome 1 and 2 using SMAR Scan®, showing that the identification of novel MAR sequences is feasible using the tools reported thereafter whereas SEQ ID No 24 to 27 have been identified by scanning the complete human genome using the combined SMAR Scan® method.

30 In a first step, the complete chromosome 1 and 2 were screened to identify bent DNA element as region corresponding to the highest bent, major groove depth, minor groove width and lowest melting temperature as shown in figure 3. In a second step, this collection of sequence was scanned for binding sites of regulatory proteins such as SATB1, GATA, etc. as shown in the figure 8B) yielding sequences SEQ ID 1-23.
35 Furthermore, sequences 21-23 were further shown to be located next to known gene from the Human Genome Data Base.

40 With regard to SEQ ID No 24 to 27 these sequences have been yielded by scanning the human genome according to the combined method and were selected as examples among 1757 MAR elements so detected.

45 Molecular chimera of MAR sequences are also considered in the present invention. By molecular chimera is intended a nucleotide sequence that may include a functional portion of a MAR element and that will be obtained by molecular biology methods known by those skilled in the art.

50 Particular combinations of MAR elements or fragments or sub-portions thereof are also considered in the present invention. These fragments can be prepared by a variety of methods known in the art. These methods include, but are not limited to, digestion with restriction enzymes and recovery of the fragments, chemical synthesis or polymerase chain reactions (PCR).

Therefore, particular combinations of elements or fragments of the sequences SEQ ID

Nos 1 to 27 and cLysMAR elements or fragments are also envisioned in the present invention, depending on the functional results to be obtained. Elements of the cLysMAR are e.g. the B, K and F regions as described in WO 02/074969, the disclosure of which is hereby incorporated herein by reference, in its entirety. The preferred elements of the cLysMAR used in the present invention are the B, K and F regions. Only one element might be used or multiple copies of the same or distinct elements (multimerized elements) might be used (see Fig. 8 A)).

By fragment is intended a portion of the respective nucleotide sequence. Fragments of a MAR nucleotide sequence may retain biological activity and hence bind to purified nuclear matrices and/or alter the expression patterns of coding sequences operably linked to a promoter. Fragments of a MAR nucleotide sequence may range from at least about 100 to 1000 bp, preferably from about 200 to 700 bp, more preferably from about 300 to 500 bp nucleotides. Also envisioned are any combinations of fragments, which have the same number of nucleotides present in a synthetic MAR sequence consisting of natural MAR element and/or fragments. The fragments are preferably assembled by linker sequences. Preferred linkers are BglII-BamHI linker.

"Protein production increasing activity" refers to an activity of the purified and isolated DNA sequence defined as follows: after having been introduced under suitable conditions into a eukaryotic host cell, the sequence is capable of increasing protein production levels in cell culture as compared to a culture of cell transfected without said DNA sequence. Usually the increase is 1.5 to 10 fold, preferably 4 to 10 fold. This corresponds to a production rate or a specific cellular productivity of at least 10 pg per cell per day (see Example 11 and Fig. 13).

As used herein, the following definitions are supplied in order to facilitate the understanding of this invention.

"Chromatin" is the protein and nucleic acid material constituting the chromosomes of a eukaryotic cell, and refers to DNA, RNA and associated proteins.

A "chromatin element" means a nucleic acid sequence on a chromosome having the property to modify the chromatin structure when integrated into that chromosome.

"Cis" refers to the placement of two or more elements (such as chromatin elements) on the same nucleic acid molecule (such as the same vector, plasmid or chromosome).

"Trans" refers to the placement of two or more elements (such as chromatin elements) on two or more different nucleic acid molecules (such as on two vectors or two chromosomes).

Chromatin modifying elements that are potentially capable of overcoming position effects, and hence are of interest for the development of stable cell lines, include boundary elements (BEs), matrix attachment regions (MARs), locus control regions (LCRs), and universal chromatin opening elements (UCOE).

Boundary elements ("BEs"), or insulator elements, define boundaries in chromatin in many cases (Bell A and Felsenfeld G. 1999; "Stopped at the border: boundaries and insulators, *Curr Opin Genet Dev* 9, 191-198) and may play a role in defining a transcriptional domain in vivo. BEs lack intrinsic promoter/enhancer activity, but rather are thought to protect genes from the transcriptional influence of regulatory elements in the surrounding chromatin. The enhancer-block assay is commonly used to identify

insulator elements. In this assay, the chromatin element is placed between an enhancer and a promoter, and enhancer-activated transcription is measured. Boundary elements have been shown to be able to protect stably transfected reporter genes against position effects in *Drosophila*, yeast and in mammalian cells. They have also been shown to increase the proportion of transgenic mice with inducible transgene expression.

Locus control regions ("LCRs") are cis-regulatory elements required for the initial chromatin activation of a locus and subsequent gene transcription in their native locations (Grosveld, F. 1999, "Activation by locus control regions?" *Curr Opin Genet Dev* 9, 152-157). The activating function of LCRs also allows the expression of a coupled transgene in the appropriate tissue in transgenic mice, irrespective of the site of integration in the host genome. While LCRs generally confer tissue-specific levels of expression on linked genes, efficient expression in nearly all tissues in transgenic mice has been reported for a truncated human T-cell receptor LCR and a rat LAP LCR. The most extensively characterized LCR is that of the globin locus. Its use in vectors for the gene therapy of sickle cell disease and β -thalassemias is currently being evaluated.

"MARs", according to a well-accepted model, may mediate the anchorage of specific DNA sequence to the nuclear matrix, generating chromatin loop domains that extend outwards from the heterochromatin cores. While MARs do not contain any obvious consensus or recognizable sequence, their most consistent feature appears to be an overall high A/T content, and C bases predominating on one strand (Bode J, Schlake T, RiosRamirez M, Mielke C, Stengart M, Kay V and KlehrWirth D, "Scaffold/matrix-attached regions: structural properties creating transcriptionally active loci", *Structural and Functional Organization of the Nuclear Matrix: International Review of Cytology*, 162A:389-453, 1995). These regions have a propensity to form bent secondary structures that may be prone to strand separation. They are often referred to as base-unpairing regions (BURs), and they contain a core-unwinding element (CUE) that might represent the nucleation point of strand separation (Benham C and al., Stress induced duplex DNA destabilization in scaffold/matrix attachment regions, *J. Mol. Biol.*, 274:181-196, 1997). Several simple AT-rich sequence motifs have often been found within MAR sequences, but for the most part, their functional importance and potential mode of action remain unclear. These include the A-box (AATAAAYAAA), the T-box (TTWTWTTWTT), DNA unwinding motifs (AATATATT, AATATT), SATB1 binding sites (H-box, A/T/C25) and consensus Topoisomerase II sites for vertebrates (RNYNNCNGYNGKTNYNY) or *Drosophila* (GTNWAYATTNATNNR).

Ubiquitous chromatin opening elements ("UCOE", also known as "ubiquitously-acting chromatin opening elements") have been reported in WO 00/05393.

An "enhancer" is a nucleotide sequence that acts to potentiate the transcription of genes independent of the identity of the gene, the position of the sequence in relation to the gene, or the orientation of the sequence. The vectors of the present invention optionally include enhancers.

A "gene" is a deoxyribonucleotide (DNA) sequence coding for a given mature protein. As used herein, the term "gene" shall not include untranslated flanking regions such as RNA transcription initiation signals, polyadenylation addition sites, promoters or enhancers.

A "product gene" is a gene that encodes a protein product having desirable characteristics such as diagnostic or therapeutic utility. A product gene includes, e. g.,

structural genes and regulatory genes.

5 A "structural gene" refers to a gene that encodes a structural protein. Examples of structural genes include but are not limited to, cytoskeletal proteins, extracellular matrix proteins, enzymes, nuclear pore proteins and nuclear scaffold proteins, ion channels and transporters, contractile proteins, and chaperones. Preferred structural genes encode for antibodies or antibody fragments.

10 A "regulatory gene" refers to a gene that encodes a regulatory protein. Examples of regulatory proteins include, but are not limited to, transcription factors, hormones, growth factors, cytokines, signal transduction molecules, oncogenes, proto-oncogenes, transmembrane receptors, and protein kinases.

15 "Orientation" refers to the order of nucleotides in a given DNA sequence. For example, an inverted orientation of a DNA sequence is one in which the 5' to 3' order of the sequence in relation to another sequence is reversed when compared to a point of reference in the DNA from which the sequence was obtained. Such reference points can include the direction of transcription of other specified DNA sequences in the source DNA and/or the origin of replication of replicable vectors containing the
20 sequence.

"Eukaryotic cell" refers to any mammalian or non-mammalian cell from a eukaryotic organism. By way of non-limiting example, any eukaryotic cell that is capable of being maintained under cell culture conditions and subsequently transfected would be
25 included in this invention. Especially preferable cell types include, e. g., stem cells, embryonic stem cells, Chinese hamster ovary cells (CHO), COS, BHK21, NIH3T3, HeLa, C2C12, cancer cells, and primary differentiated or undifferentiated cells. Other suitable host cells are known to those skilled in the art.

30 The terms "host cell" and "recombinant host cell" are used interchangeably herein to indicate a eukaryotic cell into which one or more vectors of the invention have been introduced. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or
35 environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

40 The terms "introducing a purified DNA into a eukaryotic host cell" or "transfection" denote any process wherein an extracellular DNA, with or without accompanying material, enters a host cell. The term "cell transfected" or "transfected cell" means the cell into which the extracellular DNA has been introduced and thus harbours the extracellular DNA. The DNA might be introduced into the cell so that the nucleic acid is replicable either as a chromosomal integrant or as an extra chromosomal element.

45 "Promoter" as used herein refers to a nucleic acid sequence that regulates expression of a gene.

50 "Co-transfection" means the process of transfecting a eukaryotic cell with more than one exogenous gene, or vector, or plasmid, foreign to the cell, one of which may confer a selectable phenotype on the cell.

The purified and isolated DNA sequence having protein production increasing activity also comprises, besides one or more bent DNA element, at least one binding site for a DNA binding protein.

- 5 Usually the DNA binding protein is a transcription factor. Examples of transcription factors are the group comprising the polyQpolyP domain proteins.
Another example of a transcription factor is a transcription factor selected from the group comprising SATB1, NMP4, MEF2, S8, DLX1, FREAC7, BRN2, GATA 1/3, TATA, Bright, MSX, AP1, C/EBP, CREBP1, FOX, Freac7, HFH1, HNF3alpha, Nkx25,
10 POU3F2, Pit1, TTF1, XFD1, AR, C/EBPgamma, Cdc5, FOXD3, HFH3, HNF3 beta, MRF2, Oct1, POU6F1, SRF, V\$MTATA_B, XFD2, Bach2, CDP CR3, Cdx2, FOXJ2, HFL, HP1, Myc, PBX, Pax3, TEF, VBP, XFD3, Brn2, COMP1, Evf1, FOXP3, GATA4, HFN1, Lhx3, NKX3A, POU1F1, Pax6, TFIIA or a combination of two or more of these transcription factors are preferred. Most preferred are SATB1, NMP4, MEF2 and
15 polyQpolyP domain proteins.

- SATB1, NMP4 and MEF2, for example, are known to regulate the development and/or tissue-specific gene expression in mammals. These transcription factors have the capacity to alter DNA geometry, and reciprocally, binding to DNA as an allosteric ligand
20 modifies their structure. Recently, SATB1 was found to form a cage-like structure circumscribing heterochromatin (Cai S, Han HJ, and Kohwi-Shigematsu T, "Tissue-specific nuclear architecture and gene expression regulated by SATB1" *Nat Genet*, 2003, 34(1): p. 42-51).

- 25 Yet another object of the present invention is to provide a purified and isolated cLysMAR element and/or fragment, a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

- 30 More preferably, the cLysMAR element and/or fragment are consisting of at least one nucleotide sequence selected from the B, K and F regions.

- A further object of the present invention is to provide a synthetic MAR sequence comprising natural MAR element and/or fragments assembled between linker
35 sequences.

- Preferably, the synthetic MAR sequence comprises a cLysMAR element and/or fragment a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.
40 Also preferably, linker sequences are BglII-BamHI linker.

- An other aspect of the invention is to provide a method for identifying a MAR sequence using a Bioinformatic tool comprising the computing of values of one or more DNA sequence features corresponding to DNA bending, major groove depth and minor
45 groove width potentials and melting temperature. Preferably, the identification of one or more DNA sequence features further comprises a further DNA sequence feature corresponding to binding sites for DNA binding proteins, which is also computed with this method.

- 50 Preferably, profiles or weight-matrices of said bioinformatic tool are based on dinucleotide recognition.

The bioinformatic tool used for the present method is preferably, SMAR Scan®, which contains algorithms developed by Gene Express ([http://srs6.bionet.nsc.ru/srs6bin/cgi-bin/wgetz?-e+\[FEATURES-SitelD:'nR'\]](http://srs6.bionet.nsc.ru/srs6bin/cgi-bin/wgetz?-e+[FEATURES-SitelD:'nR'])) and based on Levitsky *et al.*, 1999. These algorithms recognise profiles, based on dinucleotides weight-matrices, to compute the theoretical values for conformational and physicochemical properties of DNA.

Preferably, SMAR Scan® uses the four theoretical criteria also designated as DNA sequence features corresponding to DNA bending, major groove depth and minor groove width potentials, melting temperature in all possible combination, using scanning windows of variable size (see Fig. 3). For each function used, a cut-off value has to be set. The program returns a hit every time the computed score of a given region is above the set cut-off value for all of the chosen criteria. Two data output modes are available to handle the hits, the first (called "profile-like") simply returns all hit positions on the query sequence and their corresponding values for the different criteria chosen. The second mode (called "contiguous hits") returns only the positions of several contiguous hits and their corresponding sequence. For this mode, the minimum number of contiguous hits is another cut-off value that can be set, again with a tunable window size. This second mode is the default mode of SMAR Scan®. Indeed, from a semantic point of view, a hit is considered as a core-unwinding element (CUE), and a cluster of CUEs accompanied by clusters of binding sites for relevant proteins is considered as a MAR. Thus, SMAR Scan® considers only several contiguous hits as a potential MAR.

To tune the default cut-off values for the four theoretical structural criteria, experimentally validated MARs from SMART DB (<http://transfac.gbf.de/>- SMART DB) were used. All the human MAR sequences from the database were retrieved and analyzed with SMAR Scan® using the "profile-like" mode with the four criteria and with no set cut-off value. This allowed the setting of each function for every position of the sequences. The distribution for each criterion was then computed according to these data (see Fig. 1 and 3).

The default cut-off values of SMAR Scan® for the bend, the major groove depth and the minor groove width were set at the average of the 75th quantile and the median. For the melting temperature, the default cut-off value should be set at the 75th quantile. The minimum length for the "contiguous-hits" mode should be set to 300 because it is assumed to be the minimum length of a MAR (see Fig. 8 and 9). However, one skilled in the art would be able to determine the cut-off values for the above-mentioned criteria for a given organism with minimal experimentation.

Preferably, DNA bending values are comprised between 3 to 5 ° (radial degree). Most preferably they are situated between 3.8 to 4.4 °, corresponding to the smallest peak of Fig. 1.

Preferably the major groove depth values are comprised between 8.9 to 9.3 Å (Angström) and minor groove width values between 5.2 to 5.8 Å. Most preferably the major groove depth values are comprised between 9.0 to 9.2 Å and minor groove width values between 5.4 to 5.7 Å.

Preferably the melting temperature is comprised between 55 to 75 ° C (Celsius degree). Most preferably, the melting temperature is comprised between 55 to 62 ° C.

The DNA binding protein of which values can be computed by the method is usually a transcription factor preferably a polyQpolyP domain or a transcription factor selected

from the group comprising SATB1, NMP4, MEF2, S8, DLX1, FREAC7, BRN2, GATA 1/3, TATA, Bright, MSX, AP1, C/EBP, CREBP1, FOX, Freac7, HFH1, HNF3alpha, Nkx25, POU3F2, Pit1, TTF1, XFD1, AR, C/EBPgamma, Cdc5, FOXD3, HFH3, HNF3 beta, MRF2, Oct1, POU6F1, SRF, V\$MTATA_B, XFD2, Bach2, CDP CR3, Cdx2, FOXJ2, HFL, HP1, Myc, PBX, Pax3, TEF, VBP, XFD3, Brn2, COMP1, Evil, FOXP3, GATA4, HFN1, Lhx3, NKX3A, POU1F1, Pax6, TFIIA or a combination of two or more of these transcription factors.

However, one skilled in the art would be able to determine other kinds of transcription factors in order to carry out the method according to the present invention.

In case SMAR Scan® is envisaged to perform, for example, large scale analysis, then, preferably, the above-mentioned method further comprises at least one filter predicting DNA binding sites for DNA transcription factors in order to reduce the computation.

The principle of this method combines SMAR Scan® to compute the structural features as described above and a filter, such as for example, the pfsearch, (from the pftools package as described in Bucher P, Karplus K, Moeri N, and Hofmann K, "A flexible search technique based on generalized profiles", *Computers and Chemistry*, 20:324, 1996) to predict the binding of some transcription factors.

Examples of filters comprise, but are not limited to, pfsearch, MatInspector, RMatch Professional and TRANSFAC Professional

This combined method uses the structural features of SMAR Scan® and the predicted binding of specific transcription factors of the filter that can be applied sequentially in any order to select MARs, therefore, depending on the filter is applied at the beginning or at the end of the method.

The first level selects sequences out of the primary input sequence and the second level, consisting in the filter, may be used to restrain among the selected sequences those which satisfy the criteria used by the filter.

In this combined method the filter detects clusters of DNA binding sites using profiles or weightmatrices from, for example, MatInspector (Quandt K, Frech K, Karas H, Wingender E, Werner T, "MatInd and MatInspector New fast and versatile tools for detection of consensus matches in nucleotide sequence data", *Nucleic Acids Research*, 23, 48784884, 1995.). The filter can also detect densities of clusters of DNA binding sites.

The combined method is actually a "wrapper" written in Perl for SMAR Scan® and, in case the pfsearch is used as a filter, from the pftools. The combined method performs a twolevel processing using at each level one of these tools (SMAR Scan® or filter) as a potential "filter", each filter being optional and possible to be used to compute the predicted features without doing any filtering.

If SMAR Scan® is used in the first level to filter subsequences, it has to be used with the "all the contiguous hits" mode in order to return sequences. If the pfsearch is used in the first level as first filter, it has to be used with only one profile and a distance in nucleotide needs to be provided. This distance is used to group together pfsearch hits that are located at a distance inferior to the distance provided in order to return sequences; The combined method launches pfsearch, parses its output and returns

sequences corresponding to pfsearch hits that are grouped together according to the distance provided. Then whatever the tool used in the first level, the length of the sub-sequences thus selected can be systematically extended at both ends according to a parameter called "hits extension".

The second and optional level can be used to filter out sequences (already filtered sequences or unfiltered input sequences) or to get the results of SMAR Scan® and/or pfsearch without doing any filtering on these sequences. If the second level of combined method is used to filter, for each criteria considered cutoff values (hit per nucleotide) need to be provided to filter out those sequences (see Fig. 20).

Another concern of the present invention is also to provide a method for identifying a MAR sequence comprising at least one filter detecting clusters of DNA binding sites using profiles or weightmatrices. Preferably, this method comprises two levels of filters and in this case, SMAR Scan® is totally absent from said method. Usually, the two levels consist in pfsearch.

Also embraced by the present invention is a purified and isolated MAR DNA sequence identifiable according to the method for identifying a MAR sequence using the described bioinformatic tool, the combined method or the method comprising at least one filter.

Analysis by the combined method of the whole human genome yielded a total of 1757 putative MARs representing a total of 1 065 305 base paires. In order to reduce the number of results, a dinucleotide analysis was performed on these 1757 MARs, computing each of the 16 possible dinucleotide percentage for each sequence considering both strands in the 5' to 3' direction.

Surprisingly, Applicants have shown that all of the "super" MARs detected with the combined method contain at least 10% of dinucleotide TA on a stretch of 100 contiguous base pairs. Preferably, these sequences contain at least 33% of dinucleotide TA on a stretch of 100 contiguous base pairs.

Applicants have also shown that these same sequences further contain at least 12% of dinucleotide AT on a stretch of 100 contiguous base pairs. Preferably, they contain at least 33% of dinucleotide AT on a stretch of 100 contiguous base pairs.

An other aspect of the invention is to provide a purified and isolated MAR DNA sequence of any of the preceding described MARs, comprising a sequence selected from the sequences SEQ ID Nos 1 to 27, a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

Preferably, said purified and isolated MAR DNA sequence comprises a sequence selected from the sequences SEQ ID Nos 24 to 27, a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants. These sequences 24 to 27 correspond to those detected by the combined method and show a higher protein production increasing activity over sequences 1 to 23.

The present invention also encompasses the use of a purified and isolated DNA sequence comprising a first isolated matrix attachment region (MAR) nucleotide sequence which is a MAR nucleotide sequence selected from the group comprising

- a purified and isolated DNA sequence having protein production increasing activity,
 - a purified and isolated MAR DNA sequence identifiable according to the method for identifying a MAR sequence using the described bioinformatic tool, the combined method or the method comprising at least one filter,
 - the sequences SEQ ID Nos 1 to 27,
 - a purified and isolated cLysMAR element and/or fragment,
 - a synthetic MAR sequence comprising natural MAR element and/or fragments assembled between linker sequences,
- a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants or a MAR nucleotide sequence of a cLysMAR element and/or fragment, a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants for increasing protein production activity in a eukaryotic host cell.

Said purified and isolated DNA sequence usually further comprises one or more regulatory sequences, as known in the art e.g. a promoter and/or an enhancer, polyadenylation sites and splice junctions usually employed for the expression of the protein or may optionally encode a selectable marker. Preferably said purified and isolated DNA sequence comprises a promoter which is operably linked to a gene of interest.

The DNA sequences of this invention can be isolated according to standard PCR protocols and methods well known in the art.

Promoters which can be used provided that such promoters are compatible with the host cell are, for example, promoters obtained from the genomes of viruses such as polyoma virus, adenovirus (such as Adenovirus 2), papilloma virus (such as bovine papilloma virus), avian sarcoma virus, cytomegalovirus (such as murine or human cytomegalovirus immediate early promoter), a retrovirus, hepatitis-B virus, and Simian Virus 40 (such as SV 40 early and late promoters) or promoters obtained from heterologous mammalian promoters, such as the actin promoter or an immunoglobulin promoter or heat shock promoters. Such regulatory sequences direct constitutive expression.

Furthermore, the purified and isolated DNA sequence might further comprise regulatory sequences which are capable of directing expression of the nucleic acid preferentially in a particular cell type (e. g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert, et al., 1987. *Genes Dev.* 1: 268-277), lymphoid-specific promoters (Calame and Eaton, 1988. *Adv. Immunol.* 43: 235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989. *EMBOJ.* 8: 729-733) and immunoglobulins (Banerji, et al., 1983. *Cell* 33: 729-740; Queen and Baltimore, 1983. *Cell* 33:741-748), neuron-specific promoters (e. g., the neurofilament promoter; Byrne and Ruddle, 1989. *Proc. Natl. Acad. Sci. USA* 86: 5473-5477), pancreas-specific promoters (Edlund, et al., 1985. *Science* 230: 912-916), and mammary gland-specific promoters (e. g., milk whey promoter; U. S. Pat. No. 4,873,316 and European Application No. 264,166).

Developmentally-regulated promoters are also encompassed. Examples of such promoters include, e.g., the murine hox promoters (Kessel and Gruss, 1990. *Science* 249: 374-379) and thea-fetoprotein promoter (Campes and Tilghman, 1989. *Genes*

Dev. 3: 537-546).

Regulatable gene expression promoters are well known in the art, and include, by way of non-limiting example, any promoter that modulates expression of a gene encoding a desired protein by binding an exogenous molecule, such as the CRE/LOX system, the TET system, the doxycycline system, the NFkappaB/UV light system, the Leu3p/isopropylmalate system, and the GLVPc/GAL4 system (See e. g., Sauer, 1998, Methods 14 (4): 381-92 ; Lewandoski, 2001, Nat. Rev. Genet 2 (10): 743-55; Legrand-Poels et al., 1998, J. Photochem. Photobiol. B. 45: 18; Guo et al., 1996, FEBS Lett. 390 (2): 191-5; Wang et al., PNAS USA, 1999, 96 (15): 84838). However, one skilled in the art would be able to determine other kinds of promoters that are suitable in carrying out the present invention.

Enhancers can be optionally included in the purified DNA sequence of the invention then belonging to the regulatory sequence, e.g. the promoter.

The "gene of interest" or "transgene" preferably encodes a protein (structural or regulatory protein). As used herein "protein" refers generally to peptides and polypeptides having more than about ten amino acids. The proteins may be "homologous" to the host (i.e., endogenous to the host cell being utilized), or "heterologous," (i.e., foreign to the host cell being utilized), such as a human protein produced by yeast. The protein may be produced as an insoluble aggregate or as a soluble protein in the periplasmic space or cytoplasm of the cell, or in the extracellular medium. Examples of proteins include hormones such as growth hormone or erythropoietin (EPO), growth factors such as epidermal growth factor, analgesic substances like enkephalin, enzymes like chymotrypsin, receptors to hormones or growth factors, antibodies and include as well proteins usually used as a visualizing marker e.g. green fluorescent protein.

Preferably the purified DNA sequence further comprises at least a second isolated matrix attachment region (MAR) nucleotide sequence selected from the group comprising

- a purified and isolated DNA sequence having protein production increasing activity,
- a purified and isolated MAR DNA sequence identifiable according to the method for identifying a MAR sequence using the described bioinformatic tool, the combined method or the method comprising at least one filter,
- the sequences SEQ ID Nos 1 to 27,
- a purified and isolated cLysMAR element and/or fragment,
- a synthetic MAR sequence comprising natural MAR element and/or fragments assembled between linker sequences,

a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants. The isolated matrix attachment region (MAR) nucleotide sequence might be identical or different. Alternatively, a first and a second identical MAR nucleotide sequence are used.

Preferably, the MAR nucleotide sequences are located at both the 5' and the 3' ends of the sequence containing the promoter and the gene of interest. But the invention also envisions the fact that said first and or at least second MAR nucleotide sequences are located on a sequence distinct from the one containing the promoter and the gene of interest.

Embraced by the scope of the present invention is also the purified and isolated DNA sequence comprising a first isolated matrix attachment region (MAR) nucleotide sequence which is a MAR nucleotide sequence selected from the group comprising

- a purified and isolated DNA sequence having protein production increasing activity,
- a purified and isolated MAR DNA sequence identifiable according to the method for identifying a MAR sequence using the described bioinformatic tool, the combined method or the method comprising at least one filter,
- the sequences SEQ ID Nos 1 to 27,
- a purified and isolated cLysMAR element and/or fragment,
- a synthetic MAR sequence comprising natural MAR element and/or fragments assembled between linker sequences,

a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants that can be used for increasing protein production activity in a eukaryotic host cell by introducing the purified and isolated DNA sequence into a eukaryotic host cell according to well known protocols. Usually applied methods for introducing DNA into eukaryotic host cells applied are e.g. direct introduction of cloned DNA by microinjection or microparticle bombardment; electrotransfer; use of viral vectors; encapsulation within a carrier system; and use of transfecting reagents such as calcium phosphate, diethylaminoethyl (DEAE) –dextran or commercial transfection systems like the Lipofect-AMINE 2000 (Invitrogen). Preferably, the transfection method used to introduce the purified DNA sequence into a eukaryotic host cell is the method for transfecting a eukaryotic cell as described below.

The purified and isolated DNA sequence can be used in the form of a circular vector. Preferably, the purified and isolated DNA sequence is used in the form of a linear DNA sequence as vector.

As used herein, "plasmid" and "vector" are used interchangeably, as the plasmid is the most commonly used vector form. However, the invention is intended to include such other forms of expression vectors, including, but not limited to, viral vectors (e. g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The present invention further encompasses a method for transfecting a eukaryotic host cell, said method comprising

- a) introducing into said eukaryotic host cell at least one purified DNA sequence comprising at least one DNA sequence of interest and/or at least one purified and isolated DNA sequence comprising a MAR nucleotide sequence or other chromatin modifying elements,
- b) subjecting within a defined time said transfected eukaryotic host cell to at least one additional transfection step with at least one purified DNA sequence comprising at least one DNA sequence of interest and/or with at least one purified and isolated DNA sequence comprising a MAR nucleotide sequence or other chromatin modifying elements
- c) selecting said transfected eukaryotic host cell.

Preferably at least two up to four transfecting steps are applied in step b).

In order to select the successful transfected cells, a gene that encodes a selectable marker (e. g., resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. The gene that encodes a selectable marker might be located

on the purified DNA sequence comprising at least one DNA sequence of interest and/or at least one purified and isolated DNA sequence consisting of a MAR nucleotide sequence or other chromatin modifying elements or might optionally be co-introduced in separate form e.g. on a plasmid. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. The amount of the drug can be adapted as desired in order to increase productivity

Usually, one or more selectable markers are used. Preferably, the selectable markers used in each distinct transfection steps are different. This allows selecting the transformed cells that are "multi-transformed" by using for example two different antibiotic selections.

Any eukaryotic host cell capable of protein production and lacking a cell wall can be used in the methods of the invention. Examples of useful mammalian host cell lines include human cells such as human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol 36, 59 (1977)), human cervical carcinoma cells (HELA, ATCC CCL 2), human lung cells (W138, ATCC CCL 75), human liver cells (Hep G2, HB 8065); rodent cells such as baby hamster kidney cells (BHK, ATCC CCL 10), Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, *Proc. Natl. Acad. Sci. USA*, 77, 4216 (1980)), mouse sertoli cells (TM4, Mather, *Biol. Reprod* 23, 243-251 (1980)), mouse mammary tumor (MMT 060562, ATCC CCL51); and cells from other mammals such as monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); myeloma (e.g. NS0) /hybridoma cells.

Preferably, the selected transfected eukaryotic host cells are high protein producer cells with a production rate of at least 10 pg per cell per day.

Most preferred for uses herein are mammalian cells, more preferred are CHO cells.

The DNA sequence of interest of the purified and isolated DNA sequence is usually a gene of interest preferably encoding a protein operably linked to a promoter as described above. The purified and isolated DNA sequence comprising at least one DNA sequence of interest might comprise additionally to the DNA sequence of interest MAR nucleotide sequence or other chromatin modifying elements.

Purified and isolated DNA sequence comprising a MAR nucleotide sequence are for example selected from the group comprising the sequences SEQ ID Nos 1 to 27 and/or particular elements of the cLysMAR e.g. the B, K and F regions as well as fragment and elements and combinations thereof as described above. Other chromatin modifying elements are for example boundary elements (BEs), locus control regions (LCRs), and universal chromatin opening elements (UCOE) (see Zahn-Zabal et al. already cited). An example of multiple transfections of host cells is shown in Example 12 (Table 3).

The first transfecting step (primary transfection) is carried out with the gene of interest (SV40EGFP) alone, with a MAR nucleotide sequence (MAR) alone or with the gene of interest and a MAR nucleotide sequence (MAR-SV40EGFP). The second transfecting step (secondary transfection) is carried out with the gene of interest (SV40EGFP) alone, with a MAR nucleotide sequence (MAR) alone or with the gene of interest and a MAR nucleotide sequence (MAR-SV40EGFP), in all possible combinations resulting from the first transfecting step.

Preferably the eukaryotic host cell is transfected by:

- a) introducing a purified DNA sequence comprising one DNA sequence of interest and additionally a MAR nucleotide sequence,
b) subjecting within a defined time said transfected eukaryotic host cell to at least one additional transfection step with the same purified DNA sequence comprising one DNA sequence of interest and additionally a MAR nucleotide sequence of step a).

Also preferably, the MAR nucleotide sequence of the of the purified and isolated DNA sequence is selected from the group comprising

- a purified and isolated DNA sequence having protein production increasing activity,
- a purified and isolated MAR DNA sequence identifiable according to the method for identifying a MAR sequence using the described bioinformatic tool, the combined method or the method comprising at least one filter,
- the sequences SEQ ID Nos 1 to 27,
- a purified and isolated cLysMAR element and/or fragment,
- a synthetic MAR sequence comprising natural MAR element and/or fragments assembled between linker sequences,

a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

Surprisingly, a synergy between the first and second transfection has been observed. A particular synergy has been observed when MAR elements are present at one or both of the transfection steps. Multiple transfections of the cells with pMAR alone or in combination with various expression plasmids, using the method described above have been carried out. For example, Table 3 shows that transfecting the cells twice with the pMAR-SV40EGFP plasmid gave the highest expression of GFP and the highest degree of enhancement of all conditions (4.3 fold). In contrast, transfecting twice the vector without MAR gave little or no enhancement, 2.8-fold, instead of the expected two-fold increase. This proves that the presence of MAR elements at each transfection step is of particular interest to achieve the maximal protein synthesis.

As a particular example of the transfection method, said purified DNA sequence comprising at least one DNA sequence of interest can be introduced in form of multiple unlinked plasmids, comprising a gene of interest operably linked to a promoter, a selectable marker gene, and/or protein production increasing elements such as MAR sequences.

The ratio of the first and subsequent DNA sequences may be adapted as required for the use of specific cell types, and is routine experimentation to one ordinary skilled in the art.

The defined time for additional transformations of the primary transformed cells is tightly dependent on the cell cycle and on its duration. Usually the defined time corresponds to intervals related to the cell division cycle.

Therefore this precise timing may be adapted as required for the use of specific cell types, and is routine experimentation to one ordinary skilled in the art.

Preferably the defined time is the moment the host cell just has entered into the same phase of a second or a further cell division cycle, preferably the second cycle.

This time is usually situated between 6h and 48 h, preferably between 20h and 24h after the previous transfecting event.

Also encompassed by the present invention is a method for transfecting a eukaryotic host cell, said method comprising co-transfecting into said eukaryotic host cell at least one first purified and isolated DNA sequence comprising at least one DNA sequence of

interest, and a second purified DNA comprising at least one MAR nucleotide selected from the group comprising:

- a purified and isolated DNA sequence having protein production increasing activity,
- 5 - a purified and isolated MAR DNA sequence identifiable according to the method for identifying a MAR sequence using the described bioinformatic tool, the combined method or the method comprising at least one filter,
- the sequences SEQ ID Nos 1 to 27,
- a purified and isolated cLysMAR element and/or fragment,
- 10 - a synthetic MAR sequence comprising natural MAR element and/or fragments assembled between linker sequences,

a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

Said first purified and isolated DNA sequence can also comprise at least one MAR nucleotide as described above.

Also envisioned is a process for the production of a protein wherein a eukaryotic host cell is transfected according to the transfection methods as defined in the present invention and is cultured in a culture medium under conditions suitable for expression of the protein. Said protein is finally recovered according to any recovering process known to the skilled in the art.

Given as an example, the following process for protein production might be used.

The eukaryotic host cell transfected with the transfection method of the present invention is used in a process for the production of a protein by culturing said cell under conditions suitable for expression of said protein and recovering said protein. Suitable culture conditions are those conventionally used for in vitro cultivation of eukaryotic cells as described e.g. in WO 96/39488. The protein can be isolated from the cell culture by conventional separation techniques such as e.g. fractionation on immunoaffinity or ion-exchange columns; precipitation; reverse phase HPLC; chromatography; chromatofocusing; SDS-PAGE; gel filtration. One skilled in the art will appreciate that purification methods suitable for the polypeptide of interest may require modification to account for changes in the character of the polypeptide upon expression in recombinant cell culture.

The proteins that are produced according to this invention can be tested for functionality by a variety of methods. For example, the presence of antigenic epitopes and ability of the proteins to bind ligands can be determined by Western blot assays, fluorescence cell sorting assays, immunoprecipitation, immunochemical assays and/or competitive binding assays, as well as any other assay which measures specific binding activity.

The proteins of this invention can be used in a number of practical applications including, but not limited to:

1. Immunization with recombinant host protein antigen as a viral/pathogen antagonist.
- 45 2. Production of membrane proteins for diagnostic or screening assays.
3. Production of membrane proteins for biochemical studies.
4. Production of membrane protein for structural studies.
5. Antigen production for generation of antibodies for immuno-histochemical mapping, including mapping of orphan receptors and ion channels.

Also provided by the present invention is a eukaryotic host cell transfected according to any of the preceding transfection methods. Preferably, the eukaryotic host cell is a mammalian host cell line.

As already described, example of useful mammalian host cell lines include human cells such as human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., *J. Gen Virol* 36, 59 (1977)), human cervical carcinoma cells (HELA, ATCC CCL 2), human lung cells (W138, ATCC CCL 75), human liver cells (Hep G2, HB 8065); rodent cells such as baby hamster kidney cells (BHK, ATCC CCL 10), Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, *Proc. Natl. Acad. Sci. USA*, 77, 4216 (1980)), mouse sertoli cells (TM4, Mather, *Biol. Reprod* 23, 243-251 (1980)), mouse mammary tumor (MMT 060562, ATCC CCL51); and cells from other mammals such as monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); monkey kidney cells (CV1 ATCC CCL 70); African green monkey kidney cells (VERO-76, ATCC CRL-1587); canine kidney cells (MDCK, ATCC CCL 34); buffalo rat liver cells (BRL 3A, ATCC CRL 1442); myeloma (e.g. NS0) /hybridoma cells.

Most preferred for uses herein are CHO cells.

The present invention also provides for a cell transfection mixture or Kit comprising at least one purified and isolated DNA sequence according to the invention.

The invention further comprises a transgenic organism wherein at least some of its cells have stably incorporated at least one DNA sequence of

- a purified and isolated DNA sequence having protein production increasing activity,
- a purified and isolated MAR DNA sequence identifiable according to the method for identifying a MAR sequence using the described bioinformatic tool, the combined method or the method comprising at least one filter,
- the sequences SEQ ID Nos 1 to 27,
- a purified and isolated cLysMAR element and/or fragment,
- a synthetic MAR sequence comprising natural MAR element and/or fragments assembled between linker sequences,

a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

Preferably, some of the cells of the transgenic organisms have been transfected according the methods described herein.

Also envisioned in the present invention is a transgenic organism wherein its genome has stably incorporated at least one DNA sequence of

- a purified and isolated DNA sequence having protein production increasing activity,
- a purified and isolated MAR DNA sequence identifiable according to the method for identifying a MAR sequence using the described bioinformatic tool, the combined method or the method comprising at least one filter,
- the sequences SEQ ID Nos 1 to 27,
- a purified and isolated cLysMAR element and/or fragment,
- a synthetic MAR sequence comprising natural MAR element and/or fragments assembled between linker sequences,

a sequence complementary thereof, a part thereof sharing at least 70% nucleotides in length, a molecular chimera thereof, a combination thereof and variants.

Transgenic eukaryotic organisms which can be useful for the present invention are for example selected from the group comprising mammals (mouse, human, monkey etc) and in particular laboratory animals such as rodents in general, insects (drosophila,

etc), fishes (zebra fish, etc.), amphibians (frogs, newt, etc..) and other simpler organisms such as c. elegans, yeast, etc....

- 5 Yet another object of the present invention is to provide a computer readable medium comprising computer-executable instructions for performing the method for identifying a MAR sequence as described in the present invention.

- 10 The foregoing description will be more fully understood with reference to the following Examples. Such Examples, are, however, exemplary of methods of practising the present invention and are not intended to limit the scope of the invention.

EXAMPLES

Example 1: SMAR Scan® and MAR sequences

A first rough evaluation of SMAR Scan® was done by analyzing experimentally defined human MARs and non-MAR sequences. As MAR sequences, the previous results from the analysis of human MARs from SMART Db were used to plot a density histogram for each criterion as shown in Fig. 1. Similarly, non-MAR sequences were also analyzed and plotted. As non-MAR sequences, all Ref-Seq-contigs from the chromosome 22 were used, considering that this latter was big enough to contain a negligible part of MAR sequences regarding the part of non-MAR sequences.

The density distributions shown in Fig. 1 are all skewed with a long tail. For the highest bend, the highest major groove depth and the highest minor groove width, the distributions are right skewed. For the lowest melting temperature, the distributions are left-skewed which is natural given the inverse correspondence of this criterion regarding the three others. For the MAR sequences, biphasic distributions with a second weak peak, are actually apparent. And between MAR and non-MAR sequences distributions, a clear shift is also visible in each plot.

Among all human MAR sequences used, in average only about 70% of them have a value greater than the 75th quantile of human MARs distribution, this for the four different criteria. Similarly concerning the second weak peak of each human MARs distribution, only 15% of the human MAR sequences are responsible of these outlying values. Among these 15% of human MAR sequences, most are very well documented MARs, used to insulate transgene from position effects, such as the interferon locus MAR, the beta-globin locus MAR (Ramezani A, Hawley TS, Hawley RG, "Performance- and safety-enhanced lentiviral vectors containing the human interferon-beta scaffold attachment region and the chicken beta-globin insulator", *Blood*, 101:4717-4724, 2003), or the apolipoprotein MAR (Namciu, S, Blochinger KB, Fournier REK, "Human matrix attachment regions insulate transgene expression from chromosomal position effects in *Drosophila melanogaster*", *Mol. Cell. Biol.*, 18:2382-2391, 1998).

Always with the same data, human MAR sequences were also used to determine the association between the four theoretical structural properties computed and the AT-content. Fig. 2 represents the scatterplot and the corresponding correlation coefficient r for every pair of criteria.

Example 2: Distribution plots of MAR sequences by organism

MAR sequences from SMART DB of other organisms were also retrieved and analyzed similarly as explained previously. The MAR sequences density distributions for the mouse, the chicken, the sorghum bicolor and the human are plotted jointly in Fig. 3.

Example 3: MAR prediction of the whole chromosome 22

All RefSeq contigs from the chromosome 22 were analyzed by SMAR Scan® using the default settings this time. The result is that SMAR Scan® predicted a total of 803 MARs, their average length being 446 bp, which means an average of one MAR predicted per 42 777 bp. The total length of the predicted MARs corresponds to 1% of the chromosome 22 length. The AT-content of the predicted regions ranged from

65,1% to 93.3%; the average AT-content of all these regions being 73.5%. Thus, predicted MARs were AT-rich, whereas chromosome 22 is not AT-rich (52.1% AT).

SMARTest was also used to analyze the whole chromosome 22 and obtained 1387 MAR candidates, their average length being 494 bp representing an average of one MAR predicted per 24 765 bp. The total length of the predicted MARs corresponds to 2% of the chromosome 22. Between all MARs predicted by the two softwares, 154 predicted MARs are found by both programs, which represents respectively 19% and 11% of SMAR Scan® and SMARTest predicted MARs. Given predicted MARs mean length for SMAR Scan® and SMARTest, the probability to have by chance an overlapping between SMAR Scan® and SMARTest predictions is 0.0027% per prediction.

To evaluate the specificity of SMAR Scan® predictions, SMAR Scan® analyses were performed on randomly shuffled sequences of the chromosome 22 (Fig. 4). Shuffled sequences were generated using 4 different methods: by a segmentation of the chromosome 22 into nonoverlapping windows of 10 bp and by separately shuffling the nucleotides in each window; by "scrambling" which means a permutation of all nucleotides of the chromosome; by "rubbling" which means a segmentation of the chromosome in fragments of 10 bp and a random assembling of these fragments and finally by order 1 Markov chains, the different states being the all the different DNA dinucleotides and the transition probabilities between these states being based on the chromosome 22 scan. For each shuffling method, five shuffled chromosome 22 were generated and analyzed by SMAR Scan® using the default settings. Concerning the number hits, an average of 3 519 170 hits (sd: 18 353) was found for the permuted chromosome 22 within nonoverlapping windows of 10 bp, 171 936,4 hits (sd: 2 859,04) for the scrambled sequences and 24 708,2 hits (sd: 1 191,59) for the rubbled chromosome 22 and 2 282 hits in average (sd: 334,7) for the chromosomes generated according to order 1 Markov chains models of the chromosome 22, which respectively represents 185% (sd: 0.5% of the mean), 9% (sd: 1.5%), 1% (sd: 5%) and 0.1% (sd: 15%) of the number of hits found with the native chromosome 22. For the number of MARs predicted, which thus means contiguous hits of length greater than 300, 1 997 MARs were predicted with the shuffled chromosome 22 within windows of 10 bp (sd: 31.2), only 2.4 MARs candidates were found in scrambled sequences (sd: 0.96) and none for the rubbled and for the sequences generated according to Markov chains model, which respectively represents 249% and less than 0.3% of the number of predicted MARs found with the native chromosome 22. These data provide indications that SMAR Scan® detects specific DNA elements which organization is lost when the DNA sequences are shuffled.

Example 4: Analysis of known matrix attachment regions in the Interferon locus with SMAR Scan®

The relevance of MAR prediction by SMAR Scan® was investigated by analyzing the recently published MAR regions of the human interferon gene cluster on the short arm of chromosome 9 (9p22). Goetze et al. (already cited) reported an exhaustive analysis of the WP18A10A7 locus to analyze the suspected correlation between BURs (termed in this case stress-induced duplex destabilization or SIDD) and *in vitro* binding to the nuclear matrix (Fig. 9, lower part). Three of the SIDD peaks were in agreement with the *in vitro* binding assay, while others did not match matrix attachment sites. Inspection of the interferon locus with SMAR Scan® (Fig. 9, top part) indicated that three majors peaks accompanied by clusters of SATB1, NMP4 and MEF2 regulators binding sites

correlated well with the active MARs. Therefore, we conclude that the occurrence of predicted CUEs and binding sites for these transcription factors is not restricted to the cLysMAR but may be a general property of all MARs. These results also imply that the SMAR Scan® program efficiently detects MAR elements from genomic sequences.

Example 5: Accuracy of SMAR Scan® prediction and comparison with other predictive tools

The accuracy of SMAR Scan® was evaluated using six genomic sequences for which experimentally determined MARs have been mapped. In order to perform a comparison with other predictive tools, the sequences analyzed are the same with the sequences previously used to compare MAR-Finder and SMARTest. These genomic sequences are three plant and three human sequences (Table 1) totalizing 310 151 bp and 37 experimentally defined MARs. The results for SMARTest and MAR-Finder in Table 1 come from a previous comparison (Frisch M, Frech K, Klingenhoff A, Cartharius K, Liebich I and Werner T, In silico pre-diction of scaffold/matrix attachment regions in large genomic sequences, *Genome Research*, 12:349-354, 2001.). MAR-Finder has been used with the default parameters excepted for the threshold that has been set to 0.4 and for the analysis of the protamine locus, the AT-richness rule has been excluded (to detect the non AT-rich MARs as was done for the protamine locus).

Sequence, description and reference	Length (kb)	Experimentally defined MARs positions (kb)	SMARTest prediction positions (kb)	MAR-Finder prediction positions (kb)	SMART Scan prediction positions (kb)
<i>Oryza Sativa</i> putative ADP-glucose pyro- phosphorylase subunit SH2 and putative NADPH dependant reductase A1 genes (U70541). [4]	30.034	0.0-1.2 5.4-7.4 17.3-18.5 20.0-23.1	- 6.5-7.0 15.2-15.7 16.2-16.6 17.6-18.3 19.6-20.1 20.7-21.3 23.6-23.9 25.0-25.4 27.5-27.9	- - 15.7-15.9 - 17.5-18.4 19.8-20.4 21.3-21.5 23.9-24.2 24.7-25.1 -	- - 15.6-16 - 17.6-18.2 21.6-22 - 23.4-23.8 - -
<i>Sorghum bicolor</i> ADP- glucose pyrophospho- rylase subunit SH2. NADPH-dependant reductase A1-b genes (AF010283). [4]	42.446	0.0-1.5 7.1-9.7 22.4-24.7 32.5-33.7 41.6-42.3	- - 21.3-21.9 22.9-24.0 - 27.3-27.6 -	- - - 23.2-24.2 - 26.9-27.5 -	- 7.4-7.7 21.5-21.8 22.9-23.2 23.6-24.0 27.3-27.6 33.4-33.9
<i>Sorghum bicolor</i> BAC clone 110K5 (AF124045). [37]	78.195	~0.9 ~5.8 ~6.3 ~9.3 ~15.0 ~18.5 ~21.9 ~23.3 ~25.6 ~29.1 ~34.6 ~44.1 ~48.5 ~57.9 ~62.9 ~67.1 ~69.3 ~73.7	- - - - 15.1-15.8 - 21.7-22.0 - - - - - 44.1-44.5 47.9-49.5 - - 63.1-63.7 - - 74.3-74.7	- - - - - - - - - - - - - 47.9-49.4 - - - - -	- - - - - - 21.4-21.9 - - - 29.2-29.5 - 39.0-40.0 - 48.1-48.6 48.8-49.3 - - - 74.3-74.6
Human alpha-1-antitry- sin and corticosteroid binding globulin intergenic region (AF156545). [35]	30.461	2.6-6.3 22.0-30.4	5.5-6.0 - 25.7-26.2 27.5-27.8 -	3.0-3.2 5.1-6.0 24.9-25.3 25.5-25.8 26.2-26.4 27.5-28.2	5.4-5.8 - 25.8-26.4 - -
Human protamine locus (U15422). [24]	53.060	8.8-9.7 32.6-33.6 37.2-39.4 51.8-53.0	- - - -	8.0-8.9 ^a 33.9-34.8 ^a 33.9-34.8 ^a -	- - - -
Human beta-globin locus (U01317). [21]	75.955	1.6-3.0 15.6-19.0 44.7-52.7 60.0-70.0	- 18.0-18.4 - 34.4-34.9 - 56.6-57.1 59.8-60.3 65.6-66.0	- 15.5-16.0 18.0-18.4 - 50.6-50.8 56.5-57.2 58.1-58.5 63.0-63.6	2.3-2.6 15.3-15.6 - - - - 62.8-63.1 -

			67.6-67.9 68.8-69.1	68.7-69.3 -	66.3-66.7 -
Sum(kb)	310.151	at least 56.1	14.5	13.8	9.5
Total numbers :		37	28	25	22
Average kb /predicted MAR			11.076	12.406	14.097
True positives [number of experimentally defined MAR found]			19[14]	20[12]	17[14]
False positives			9	5	5
False negatives			23	25	23
Specificity			19/28= 68%	20/25= 80%	17/22= 77%
Sensitivity			14/37= 38%	12/37= 32%	14/37= 38%

Table 1: Evaluation of SMAR Scan® accuracy

- 5 Six different genomic sequences, three plant and three human sequences, for which experimentally defined MARs are known, were analyzed with MAR-Finder, SMARTest and SMAR Scan®. True positive matches are printed in bold, minus (-) indicates false negative matches. Some of the longer experimentally defined MARs contained more than one in silico prediction, each of them was counted as true positive match.
- 10 Therefore, the number of true in silico predictions is higher than the number of experimentally defined MARs found. Specificity is defined as the ratio of true positive predictions, whereas sensitivity is defined as the ratio of experimentally defined MARs found. * AT-rich rule excluded using MAR-Finder.
- 15 SMARTest predicted 28 regions as MARs, 19 (true positives) of these correlate with experimentally defined MARs (specificity: 68%) whereas 9 (32%) are located in non-MARs (false positives). As some of the longest experimentally determined MARs contains more than one in silico prediction, the 19 true positives correspond actually to 14 different experimentally defined MARs (sensitivity: 38%). MARFinder
- 20 predicted 25 regions as MARs, 20 (specificity: 80%) of these correlate with experimentally defined MARs corresponding to 12 different experimentally defined MARs (sensitivity: 32%). SMAR Scan® predicted 22 regions, 17 being true positives (specificity: 77%) matching 14 different experimentally defined MARs (sensitivity: 38%).
- 25 As another example, the same analysis has been applied to human chromosomes 1 and 2 and lead to the determination of 23 MARs sequences (SEQ ID N° 1 to 23). These sequences are listed in Annex 1 in ST25 format.

Example 6: Analyses of the whole genome using the combined method (SMAR Scan®-pfsearch)

In order to test the potential correlation between the structural features computed by SMAR Scan® and the S/MAR functional activity, the whole human genome has been analyzed with the combined method with very stringent parameters, in order to get

35 sequences with the highest values for the theoretical structural features computed, which are called "super" S/MARs below. This was done with the hope to obtain predicted MAR elements with a very potential to increase transgene expression and recombinant protein production. The putative S/MARs hence harvested were first

40 analyzed from the bioinformatics perspective in an attempt to characterize and classify them.

6.1 S/MARs predicted from the analysis of the whole human genome

As whole human genome sequence, all human RefSeq (National Center for Biotechnology Information, The NCBI handbook [Internet]. Bethesda (MD): National Library of Medicine (US), Oct. Chapter 17, The Reference Sequence (RefSeq) Project, 2002 (Available from <http://www.ncbi.nih.gov/entrez/query.fcgi?db=Books>) contigs (release 5) were used and analyzed with the combined method, using SMAR Scan® as filter in the first level processing, employing default settings except for the highest bend cutoff value, whereas a stringent threshold of 4.0 degrees (instead of 3.202 degrees) has been used for the DNA bending criterion.

In the second level processing, predicted transcription factors binding have been sought in the sequences selected from the previous step without doing any filtering on these sequences.

The analysis by the combined method of the whole human genome came up with a total of 1757 putative "super" S/MARs representing a total of 1 065 305 bp (0.35% of the whole human genome). Table 2 shows for each chromosome: its size, its number of genes, its number of S/MARs predicted, its S/MARs density per gene and its kb per S/MAR. This table shows that there are very various gene densities per S/MAR predicted for the different chromosomes (standard deviation represents more than 50% of the mean of the density of genes per S/MAR predicted and the fold difference between the higher and the lower density of genes per S/MAR is 6,5). Table 2 also shows that the kb per S/MAR varies less than the density of genes per S/MAR (standard deviation represents 25% of the mean of kb per S/MAR and the fold difference between the higher and the lower kb per S/MAR is 3.2).

Chromosome	Number of genes per chromosome	Size of the chromosome (millions bp)	Number of S/MARs predicted	Density of genes per S/MAR	Kb per S/MAR
1	2544	230	85	29.9	2705
2	1772	241	143	12.3	1685
3	1406	198	101	13.9	1960
4	1036	190	118	8.7	1610
5	1233	180	116	10.6	1551
6	1247	170	94	13.2	1808
7	1383	160	179	7.7	1754
8	942	145	77	12.2	1883
9	1100	119	48	22.9	2479
10	1003	133	71	14.1	1873
11	1692	132	67	25.2	1970
12	1278	131	78	16.3	1679
13	506	97	70	7.2	1385
14	1168	88	36	32.4	2444
15	895	83	35	25.5	2371
16	1107	81	41	27	1975
17	1421	80	37	38.4	2162
18	396	75	51	7.7	1470
19	1621	56	36	45.02	1555
20	724	60	28	25.8	2142
21	355	34	18	19.7	1888
22	707	34	28	25.2	1214
X	1168	154	170	6.8	905
Y	251	25	30	8.3	833
Sum	26 955	3 050	1 757	457	433 12
Mean	1 123	127	73	19	1 804
Sd	510	72.8	45	10	462

Table 2: Number of S/MARs predicted per chromosome. The number of genes per chromosome

corresponds to the NCBI human genome statistics (Build 34 Version 3) (National Center for Biotechnology Information, The NCBI handbook [Internet]. Bethesda (MD): National Library of Medicine (US), Oct. Chapter 17, The Reference Sequence (RefSeq) Project, 2002 (Available from <http://www.ncbi.nih.gov/entrez/query.fcgi?db=Books>) based on GenBank annotations. Chromosome sizes are the sum of the corresponding human RefSeq (National Center for Biotechnology Information, The NCBI handbook [Internet]. Bethesda (MD): National Library of Medicine (US), Oct. Chapter 17, The Reference Sequence (RefSeq) Project, 2002 (Available from <http://www.ncbi.nih.gov/entrez/query.fcgi?db=Books>) (release 5) contig lengths

6.2 Bioinformatics analysis of "super" MARS for transcription factor binding sites

The 1757 predicted "super" S/MARs sequences obtained previously by SMAR Scan® were then analyzed for potential transcription factors binding sites. This has been achieved using RMatch™ Professional (Kel AE, Gossling E, Reuter I, Cheremushkin E, KelMargoulis OV, Wingender E, MATCH: A tool for searching transcription factor binding sites in DNA sequences, *Nucleic Acids Res.* 31(13):35769, 2003), a weight matrixbased tool based on TRANSFAC (Wingender E, Chen X, Fricke E, Geffers R, Hehl R, Liebich I, Krull M, Matys V, Michael H, Ohnhauser R, Pruss M, Schacherer F, Thiele S, Urbach S, The TRANSFAC system on gene expression regulation, *Nucleic Acids Research*, 29(1):2813, 2001). Match™ 2.0 Professional has been used with most of the default settings Match™ analysis was based on TRANSFAC Professional, release 8.2 (20040630). The sums of all transcription factors binding prediction on the 1757 sequences analyzed according to Match™ are in Table 3. Based on this table, only the transcription factors totalizing at least 20 hits over the 1757 sequences analyzed were considered for further analyses.

Hereafter are some of the human transcription factors that are the most often predicted to bind on the 1757 putative S/MAR sequences and their Match description: Cdc5 (cell division control protein 5) a transcriptional regulator/repressor, Nkx3A a homeodomain protein regulated by androgen, POU1F1 (pituitaryspecific positive transcription factor 1) which is specific to the pituitary and stimulates cells proliferation. Thus, in addition to SATB1, NMP4 and MEF2, other transcription factors can participate in the activity of MARS.

API	1	AR	2	Bach2	1	Brn2	1
C/EBP	20	C/EBPgamma	5	CDP CR3	1	COMP1	2
CREBP1	34	Cdc5	858	Cdx2	35	Evi1	472
FOX	78	FOXD3	79	FOXJ2	244	FOXP3	29
Freac7	272	GATA1	2	GATA3	142	GATA4	125
HFH1	12	HFH3	1	HLF	275	HNF1	337
HNF3alpha	23	IINF3beta	71	HP1	2	Lhx3	22
MEF2	114	MRF2	57	Myc	18	NKX3A	849
Nkx25	2	Oct1	191	PBX	5	POU1F1	483
POU3F2	11	POU6F1	29	Pax3	3	Pax6	20
Pit1	505	SRF	8	TEF	2852	TFIIA	14
TTF1	1	V\$MTATA_B	4	VBP	53	Vmw65	1
XFD1	65	XFD2	418	XFD3	2		

Table 3 is a summary of all transcription factors binding prediction (totalizing 20 hits or more) on the 1757 sequences analyzed.

5 6.3 Bioinformatics analysis of predicted "super" MARs for dinucleotide frequencies

10 Various computer analysis were performed in order to easily identify "super" S/MAR sequences using an explicit criterion that could be identified without computing. Among those, a di-nucleotide analysis was performed on the 1757 superMARs, computing each of the 16 possible dinucleotide percentage for each sequence considering both strands in the 5' > 3' direction.

15 A summary (min., max., median, mean, 25th percentile and 75th percentile) as well as the histograms of each dinucleotide percentage over the 1757 S/MAR sequences are respectively presented in Table 4. A similar analysis was performed on randomly selected sequences from the human genome, representing randomly selected non-S/MAR sequences (which might however contain some MARs). Table 5 represents respectively a summary of the dinucleotide content analysis for these sequences.

Table 4: Dinucleotide percentages over the 1757 S/MAR sequences

20

	AA %	AC %	AG %	AT %
Minimum	0.000	0.0000	0.0000	18.50
25th percentile	4.234	0.9372	0.1408	32.11
Median	7.843	2.2408	0.4777	34.68
Mean	7.184	3.2117	1.0865	34.32
75th percentile	10.110	4.7718	1.5096	36.94
Maximum	17.290	12.9479	8.1230	50.00
	CA %	CC %	CG %	CT %
Minimum	0.0000	0.00000	0.0000	0.0000
25th percentile	0.9695	0.00000	0.0000	0.1408
Median	1.9776	0.00000	0.0000	0.4777
Mean	2.6977	0.14123	0.2709	1.0865
75th percentile	3.7543	0.09422	0.1256	1.5096
Maximum	10.4061	4.24837	7.4410	8.1230
	GA %	GC %	GG %	GT %
Minimum	0.00000	0.0000	0.00000	0.0000
25th percentile	0.08696	0.0000	0.00000	0.9372
Median	0.32616	0.0000	0.00000	2.2408
Mean	0.63347	0.2104	0.14123	3.2117
75th percentile	0.83333	0.1914	0.09422	4.7718
Maximum	5.77889	9.8793	4.24837	12.9479
	TA %	TC %	TG %	TT %
Minimum	28.63	0.00000	0.0000	0.000
25th percentile	33.48	0.08696	0.9695	4.234
Median	35.22	0.32616	1.9776	7.843
Mean	35.29	0.63347	2.6977	7.184
75th percentile	37.14	0.83333	3.7543	10.110
Maximum	50.00	5.77889	10.4061	17.290

25 Considering the results of the predicted S/MAR elements and of the nonS/MAR sequences in the summary tables, noticeable differences can be noticed in the AT et TA dinucleotide contents between these two groups of sequences. AT and TA represent respectively at least 18,5 % and 28.6 % of the dinucleotide content of the predicted S/MAR sequences, whereas the minimum percentages for the same dinucleotides in

nonS/MAR sequences are respectively 0.3 % and 0%. Similarly, the maximum CC and GG content in S/MAR sequences is 4.2 %, whereas in nonS/MAR sequences the percentages for these two dinucleotides can amount up to 20.8 %.

- 5 The correlation between AT and TA dinucleotide percentages and the DNA highest bend as computed by SMAR Scan® is depicted in Fig. 17 for the predicted S/MAR sequences and in Fig.18 for the nonS/MAR sequences. The different scatterplots of these figures show that the TA percentage correlates well with the predicted DNA bend as predicted by SMAR Scan®.

10

Table 5: Dinucleotide percentages over the 1757 nonS/MAR sequences summary

	AA %	AC %	AG %	AT %
Minimum	0.000	1.735	1.512	0.3257
25th percentile	7.096	4.586	6.466	5.1033
Median	9.106	5.016	7.279	6.8695
Mean	8.976	5.054	7.184	7.0108
75th percentile	10.939	5.494	7.969	8.7913
Maximum	17.922	13.816	12.232	23.1788
	CA %	CC %	CG %	CT %
Minimum	3.571	0.8278	0.0000	1.512
25th percentile	6.765	4.1077	0.4727	6.466
Median	7.410	5.5556	0.8439	7.279
Mean	7.411	5.9088	1.2707	7.184
75th percentile	8.010	7.2460	1.5760	7.969
Maximum	15.714	20.8415	12.6074	12.232
	GA %	GC %	GG %	GT %
Minimum	1.319	0.4967	0.8278	1.735
25th percentile	5.495	3.2615	4.1077	4.586
Median	6.032	4.4092	5.5556	5.016
Mean	6.065	4.7468	5.9088	5.054
75th percentile	6.602	5.8824	7.2460	5.494
Maximum	10.423	16.0000	20.8415	13.816
	TA %	TC %	TG %	TT %
Minimum	0.000	1.319	3.571	0.000
25th percentile	3.876	5.495	6.765	7.096
Median	5.625	6.032	7.410	9.106
Mean	5.774	6.065	7.411	8.976
75th percentile	7.464	6.602	8.010	10.939
Maximum	24.338	10.423	15.714	17.922

- 15 Four of the novel super MARs were randomly picked and analyzed for AT and TA dinucleotide content, and compared with the previously known chicken lysMAR, considering windows of 100 base pairs (Table 6).

Surprisingly, Applicants have shown that all of the super MARs have AT dinucleotide frequencies greater than 12%, and TA dinucleotides greater than 10% of the total dinucleotides analysed in a window of 100base pairs of DNA. The most efficient MARs display values around 34% of the two dinucleotide pairs.

20

Table 6. Summary of %AT and TA dinucleotide frequencies of experimentally verified MARs

25

CLysMAR (average of CUEs)	AT% : 12.03	TA% : 10.29	SEQ ID No
P1_68	AT% : 33.78	TA% : 33.93	SEQ ID No
P1_6	AT% : 34.67	TA% : 34.38	SEQ ID No

P1 42	AT% : 35.65	TA% : 35.52	SEQ ID No
Mean value for all human "super"MARs	AT% : 34.32	TA% : 35.29	
Mean value for all human non-MARs	AT% : 7.01	TA% : 5.77	

6.4 Analysis of orthologous intergenic regions of human and mouse genomes

- 5 In order to get an insight on S/MAR evolution, orthologous intergenic regions of human and mouse genomes have been analysed with SMAR Scan®. The data set used is composed of 87 pairs of complete orthologous intergenic regions from the human and mouse genomes (Shabalina SA, Ogurtsov AY, Kondrashov VA, Kondrashov AS, Selective constraint in intergenic regions of human and mouse genomes, *Trends*
- 10 *Genet*, 17(7):3736, 2001) (average length ~12 000 bp) located on 12 human and on 12 mouse chromosomes, the synteny of these sequences was confirmed by pairwise sequence alignment and consideration of the annotations of the flanking genes (experimental or predicted).
- 15 Analysis of the 87 human and mouse orthologous intergenic sequences have been analysed with SMAR Scan® using its default settings. Analysis of the human sequences yielded a total of 12 S/MARs predicted (representing a total length of 4 750 bp), located on 5 different intergenic sequences.
- 20 Among the three human intergenic sequences predicted to contain a "super" S/MAR using SMAR Scan® stringent settings, one of the corresponding mouse orthologous intergenic sequence is also predicted to contain a S/MAR (human EMBL ID: Z96050, position 28 010 to 76 951 orthologous to mouse EMBL ID: AC015932, positions 59 884 to 89 963). When a local alignment of these two orthologous intergenic sequences is
- 25 performed, the best local alignment of these two big regions correspond to the regions predicted by SMAR Scan® to be S/MAR element. A manual search for the mouse orthologs of the two other human intergenic sequences predicted to contain a "super" S/MAR was performed using the Ensembl Genome Browser (<http://ensembl.org>). The mouse orthologous intergenic sequences of these two human sequences were
- 30 retrieved using Ensembl orthologue predictions (based on gene names), searching the orthologous mouse genes for the pairs of human genes flanking these intergenic regions.
- 35 Because SMAR Scan® has been tuned for human sequences and consequently yields little "super"MARs with mouse genomic sequences, its default cutoff values were slightly relaxed for the minimum size of contiguous hits to be considered as S/MAR (using 200 bp instead of 300 bp). Analysis by SMAR Scan® of these mouse sequences predicted several S/MARs having high values for the different computed structural features. This finding suggests that the human MAR elements are conserved across
- 40 species.

Example 7 : Dissection of the chicken lysozyme gene 5'- MAR

- 45 The 3000 base pair 5'-MAR was dissected into smaller fragments that were monitored for effect on transgene expression in Chinese hamster ovary (CHO) cells. To do so, seven fragments of ~400 bp were generated by polymerase chain reaction (PCR). These PCR-amplified fragments were contiguous and cover the entire MAR sequence when placed end-to-end. Four copies of each of these fragments were ligated in a head-to-tail orientation, to obtain a length corresponding to approximately half of that of

the natural MAR. The tetramers were inserted upstream of the SV40 promoter in pGEGFPControl, a modified version of the pGL3Control vector (Promega). The plasmid pGEGFPControl was created by exchanging the luciferase gene of pGL3Control for the EGFP gene from pEGFP-N1 (Clontech). The 5'-MAR-fragment-containing plasmids thus created were co-transfected with the resistance plasmid pSVneo in CHO-DG44 cells using LipofectAmine 2000 (Invitrogen) as transfection reagent, as performed previously (Zahn-Zabal, M., et al., "Development of stable cell lines for production or regulated expression using matrix attachment regions" *J Biotechnol*, 2001. 87(1): p. 29-42.). After selection of the antibiotic (G-418) resistant cells, polyclonal cell populations were analyzed by FACS for EGFP fluorescence.

Transgene expression was expressed at the percentile of high expressor cells, defined as the cells which fluorescence levels are at least 4 orders of magnitude higher than the average fluorescence of cells transfected with the pGEGFPControl vector without MAR. Fig. 5 shows that multimerized fragments B, K and F enhance transgene expression, despite their shorter size as compared to the original MAR sequence. In contrast, other fragments are poorly active or fully inactive.

Example 8 : Specificity of B, K and F regions in the MAR context

The 5'-MAR was serially deleted from the 5'-end (Fig.6, upper part) or the 3'-end (Fig.6, lower part), respectively. The effect of the truncated elements was monitored in an assay similar to that described in the previous section. Figure 6 shows that the loss of ability to stimulate transgene expression in CHO cells was not evenly distributed.

In this deletion study, the loss of MAR activity coincided with discrete regions of transition which overlap with the 5'-MAR B-, K- and F-fragment, respectively. In 5' deletions, activity was mostly lost when fragment K and F were removed. 3' deletions that removed the F and b elements had the most pronounced effects. In contrast, flanking regions A, D, E and G that have little or no ability to stimulate transgene expression on their own (Fig. 5), correspondingly did not contribute to the MAR activity in the 5'- and 3'-end deletion studies (Fig. 6).

Example 9:Structure of the F element

The 465 bp F fragment was further dissected into smaller sub-fragments of 234, 243, 213 bp and 122, 125 and 121 bp, respectively. Fragments of the former group were octamerized (8 copies) in a head-to-tail orientation, while those of the latter group were similarly hexa-decamerized (16 copies), to maintain a constant length of MAR sequence. These elements were cloned in pGEGFPControl vector and their effects were assayed in CHO cells as described previously. Interestingly, fragment FIII retained most of the activity of the full-length F fragment whereas fragment FII, which contains the right-hand side part of fragment FIII, lost all the ability to stimulate transgene expression (Fig. 7). This points to an active region comprised between nt 132 and nt 221 in the FIB fragment. Consistently, multiple copies of fragments FI and FIB, which encompass this region, displayed similar activity. FIIA on its own has no activity. However, when added to FIB, resulting in FIII, it enhances the activity of the former. Therefore FIIA appears to contain an auxiliary sequence that has little activity on its own, but that strengthens the activity of the minimal domain located in FIB.

Analysis of the distribution of individual motifs within the lysozyme gene 5'-MAR is shown in Fig. 8 A, along with some additional motifs that we added to the analysis. Most of these motifs were found to be dispersed throughout the MAR element, and not

specifically associated with the active portions. For instance, the binding sites of transcription factors and other motifs that have been associated with MARs were not preferentially localized in the active regions. It has also been proposed that active MAR sequences may consist of combination of distinct motifs. Several computer programs (MAR Finder, SMARTest, SIDD duplex stability) have been reported to identify MARs as regions of DNA that associate with the DNA matrix. They are usually based on algorithms that utilizes a predefined series of sequence-specific patterns that have previously been suggested as containing MAR activity, as exemplified by MAR Finder, now known as MAR Wiz. The output of these programs did not correlate well with the transcriptionally active portions of the *cLysMAR*. For instance, peaks of activity obtained with MAR Finder did not clearly match active MAR sub-portion, as for instance the B fragment is quite active in vivo but scores negative with MAR Finder (Fig. 8B, compare the top and middle panels). Bent DNA structures, as predicted by this program, did not correlate well either with activity (Fig. 8B, compare the top and bottom panels). Similar results were obtained with the other available programs (data not shown).

The motifs identified by available MAR prediction computer methods are therefore unlikely to be the main determinants of the ability of the *cLysMAR* to increase gene expression. Therefore, a number of other computer tools were tested. Surprisingly, predicted nucleosome binding sequences and nucleosome disfavoring sequences were found to be arranged in repetitively interspersed clusters over the MAR, with the nucleosome favouring sites overlapping the active B, K and F regions. Nucleosome positioning sequences were proposed to consist of DNA stretches that can easily wrap around the nucleosomal histones, and they had not been previously associated with MAR sequences.

Nucleosome-favouring sequences may be modelled by a collection of DNA features that include moderately repeated sequences and other physico-chemical parameters that may allow the correct phasing and orientation of the DNA over the curved histone surface. Identification of many of these DNA properties may be computerized, and up to 38 different such properties have been used to predict potential nucleosome positions. Therefore, we set up to determine if specific components of nucleosome prediction programs might correlate with MAR activity, with the objective to construct a tool allowing the identification of novel and possibly more potent MARs from genomic sequences.

To determine whether any aspects of DNA primary sequence might distinguish the active B, K and F regions from the surrounding MAR sequence, we analyzed the 5'-MAR with MAR Scan®. Of the 38 nucleosomal array prediction tools, three were found to correlate with the location of the active MAR sub-domains (Fig. 9A). Location of the MAR B, K and F regions coincides with maxima for DNA bending, major groove depth and minor groove width. A weaker correlation was also noted with minima of the DNA melting temperature, as determined by the GC content. Refined mapping over the MAR F fragment indicated that the melting temperature valley and DNA bending summit indeed correspond the FIB sub-fragment that contains the MAR minimal domain (Fig. 9B). Thus active MAR portions may correspond to regions predicted as curved DNA regions by this program, and we will refer to these regions as CUE-B, CUE-K and CUE-F in the text below. Nevertheless, whether these regions correspond to actual bent DNA and base-pair unwinding regions is unknown, as they do not correspond to bent DNA as predicted by MAR Wiz (Fig.9B).

Example 10 : Imprints of other regulatory elements in the F fragment

Nucleosome positioning features may be considered as one of the many specific chromatin codes contained in genomic DNA. Although this particular code may contribute to the activity of the F region, it is unlikely to determine MAR activity alone, as the 3' part of the F region enhanced activity of the minimal MAR domain contained in the FIB portion. Using the MatInspector program (Genomatix), we searched for transcription factor binding sites with scores higher than 0.92 and found DNA binding sequences for the NMP4 and MEF2 proteins in the 3' part of the F fragment (Fig. 8B). To determine whether any of these transcription factor-binding sites might localize close to the B and K active regions, the entire 5'-MAR sequence was analyzed for binding by NMP4 and MEF2 and proteins reported to bind to single-stranded or double-stranded form of BURs. Among those, SATB1 (special AT-rich binding protein 1) belongs to a class of DNA-binding transcription factor that can either activate or repress the expression of nearby genes. This study indicated that specific proteins such as SATB1, NMP4 (nuclear matrix protein 4) and MEF2 (myogenic enhancer factor 2), have a specific distribution and form a framework around the minimal MAR domains of *cLysMAR* (Fig. 10). The occurrence of several of these NMP4 and SATB1 binding sites has been confirmed experimentally by the EMSA analysis of purified recombinant proteins (data not shown).

Example 11 : Construction of artificial MARs by combining defined genetic elements

To further assess the relative roles of the various MAR components, the *cLysMAR* was deleted of all three CUE regions (Fig. 11, middle part), which resulted in the loss of part of its activity when compared to the complete MAR sequence similarly assembled from all of its components as a control (Fig. 11, top part). Consistently, one copy of each CUE alone, or one copy of each of the three CUEs assembled head-to-tail, had little activity in the absence of the flanking sequences. These results strengthen the conclusion that optimal transcriptional activity requires the combination of CUEs with of flanking sequences. Interestingly, the complete MAR sequence generated from each of its components, but containing also BglII-BamHI linker sequences (AGATCC) used to assemble each DNA fragment, displayed high transcriptional activity (6 fold activation) as compared to the 4.8 fold noted for the original MAR element in this series of assays (see Fig. 5).

We next investigated whether the potentially curved DNA regions may also be active in an environment different from that found in their natural MAR context. Therefore, we set up to swap the CUE-F, CUE-B and CUE-K elements, keeping the flanking sequences unchanged. The sequences flanking the CUE-F element were amplified by PCR and assembled to bracket the various CUEs, keeping their original orientation and distance, or without a CUE. These engineered ~1.8 kb MARs were then assayed for their ability to enhance transgene expression as above. All three CUE were active in this context, and therefore their action is not restricted to one given set of flanking sequences. Interestingly, the CUE-K element was even more active than CUE-F when inserted between the CUE-F flanking sequences, and the former composite construct exhibited an activity as high as that observed for the complete natural MAR (4.8 fold activation). What distinguishes the CUE-K element from CUE-F and CUE-B is the presence of overlapping binding sites for the MEF-2 and SatB1 proteins, in addition to its CUE feature. Therefore, fusing CUE-B with CUE-F-flanking domain results in a higher density of all three binding sites, which is likely explanation to the increased activity. These results indicate that assemblies of CUEs with sequences containing binding sites

for proteins such as NMP4, MEF-2, SatB1, and/or polyPpolyQ proteins constitute potent artificial MAR sequences.

Example 12 : Expression vectors

5 Three expression vectors according to the present invention are represented on Figure 12.

Plasmid pPAG01 is a 5640 bp pUC19 derivative. It contains a 2960 bp chicken DNA fragment cloned in *Bam*H1 and *Xba*I restriction sites. The insert comes from the border of the 5'-end of the chicken lysozyme locus and has a high A/T-content.

10

Plasmid pGEGFP (also named pSV40EGFP) control is a derivative of the pGL3-control vector (Promega) in which the luciferase gene sequence has been replaced by the EGFP gene sequence from the pEGFP-N1 vector (Clontech). The size of pGEGFP plasmid is 4334bp.

15

Plasmid pUbCEGFP control is a derivative of the pGL3 with an Ubiquitin promoter.

20

Plasmid pPAG01GFP (also named pMAR-SV40EGFP) is a derivative of pGEGFP with the 5'-Lys MAR element cloned in the MCS located just upstream of the SV40 promoter. The size of the pPAG01EGF plasmid is 7285bp.

Example 13 : Effect of the additional transfection of primary transfectant cells on transgene expression

25 One day before transfection, cells were plated in a 24-well plate, in growth medium at a density of 1.35×10^5 cells/well for CHO-DG44 cells. 16 hours post-inoculum, cells were transfected when they reached 30-40% confluence, using Lipofect-AMINE 2000 (hereinafter LF2000), according to the manufacturer's instructions (Invitrogen). Twenty-seven microliters of serum free medium (Opti-MEM; Invitrogen) containing 1.4 μ l of
30 LF2000 were mixed with 27 μ l of Opti-MEM containing 830 ng of linear plasmid DNA. The antibiotic selection plasmid (pSVneo) amounted to one tenth of the reporter plasmid bearing the GFP transgene. The mix was incubated at room temperature for 20 min, to allow the DNA-LF2000 complexes to form. The mixture was diluted with 300 μ l of Opti-MEM and poured into previously emptied cell-containing wells. Following 3
35 hours incubation of the cells with the DNA mix at 37°C in a CO₂ incubator, one ml of DMEM-based medium was added to each well. The cells were further incubated for 24 hours in a CO₂ incubator at 37°C. The cells were then transfected a second time according to the method described above, except that the resistance plasmid carried another resistance gene (pSVpuro). Twenty-four hours after the second transfection,
40 cells were passaged and expanded into a T-75 flask containing selection medium supplemented with 500 μ g/ml G-418 and 5 μ g/ml puromycin. After a two week selection period, stably transfected cells were cultured in 6-well plates. Alternatively, the cell population was transfected again using the same method, but pTKhygro (Clontech) and pSVdhfr as resistance plasmids. The expression of GFP was analysed with
45 Fluorescence-activated cell sorter (FACS) and with a Fluoroscanner.

50 Fig.13 shows that the phenotype of the twice-transfected cells (hereafter called secondary transfectants) not only was strongly coloured, such that special bulb and filter were not required to visualize the green color from the GFP protein, but also contained a majority of producing cells (bottom right-hand side FACS histogram) as compared to the parental population (central histogram). This level of fluorescence corresponds to specific cellular productivities of at least 10 pg per cell per day. Indeed,

cells transfected only one time (primary transfectants) that did not express the marker protein were almost totally absent from the cell population after re-transfection. Bars below 10^1 units of GFP fluorescence amounted 30% in the central histogram and less than 5% in the right histogram. This suggested that additional cells had been transfected and successfully expressed GFP.

Strikingly, the amount of fluorescence exhibited by re-transfected cells suggested that the subpopulation of cells having incorporated DNA twice expressed much more GFP than the expected two-fold increase. Indeed, the results shown in Table 2 indicate that the secondary transfectants exhibited, on average, more than the two-fold increase of GFP expected if two sets of sequences, one at each successive transfection, would have been integrated independently and with similar efficiencies. Interestingly, this was not dependent on the promoter sequence driving the reporter gene as both viral and cellular promoter-containing vectors gave a similar GFP enhancement (compare lane 1 and 2). However, the effect was particularly marked for the MAR-containing vector as compared to plasmids without MAR- (lane 3), where the two consecutive transfections resulted in a 5.3 and 4.6 fold increase in expression, in two distinct experiments.

Type of plasmids	Primary transfection	Secondary transfection	EGFP fluorescence Fold increase
pUbCEGFP	4'992	14'334	2.8
pSV40EGFP	4'324	12'237	2.8
pMAR-SV40EGFP	6'996	36'748	5.3

Type of plasmids	Primary transfection	Secondary transfection	EGFP fluorescence Fold increase
pUbCEGFP	6'452	15'794	2.5
pSV40EGFP	4'433	11'735	2.6
pMAR-SV40EGFP	8'116	37'475	4.6

Table 7. Effect of re-transfecting primary transfectants at 24 hours interval on GFP expression. Two independent experiments are shown. The resistance plasmid pSVneo was co-transfected with various GFP expression vectors. One day post-transfection, cells were re-transfected with the same plasmids with the difference that the resistance plasmid was changed for pSVpuro. Cells carrying both resistance genes were selected on 500 μ g/ml G-418 and 5 μ g/ml puromycin and the expression of the reporter gene marker was quantified by Fluoroscanner. The fold increases correspond to the ratio of fluorescence obtained from two consecutive transfections as compared to the sum of fluorescence obtained from the corresponding independent transfections. The fold increases that were judged significantly higher are shown in bold, and correspond to fluorescence values that are consistently over 2-fold higher than the addition of those obtained from the independent transfections.

The increase in the level of GFP expression in multiply transfected cells was not expected from current knowledge, and this effect had not been observed previously.

Taken together, the data presented here support the idea that the plasmid sequences that primarily integrated into the host genome would facilitate integration of other plasmids by homologous recombination with the second incoming set of plasmid molecules. Plasmid recombination events occur within a 1-h interval after the plasmid DNA has reached the nucleus and the frequency of homologous recombination

between co-injected plasmid molecules in cultured mammalian cells has been shown to be extremely high, approaching unity (Folger, K.R., K. Thomas, and M.R. Capecchi, Nonreciprocal exchanges of information between DNA duplexes coinjected into mammalian cell nuclei. *Mol Cell Biol*, 1985. 5(1): p. 59-69], explaining the integration of multiple plasmid copies. However, homologous recombination between newly introduced DNA and its chromosomal homolog normally occurs very rarely, at a frequency of 1 in 10^3 cells receiving DNA to the most [Thomas, K.R., K.R. Folger, and M.R. Capecchi, High frequency targeting of genes to specific sites in the mammalian genome. *Cell*, 1986. 44(3): p. 419-28.]. Thus, the results might indicate that the MAR element surprisingly acts to promote such recombination events. MARs would not only modify the organization of genes in vivo, and possibly also allow DNA replication in conjunction with viral DNA sequences, but they may also act as DNA recombination signals.

Example 14 : MARs mediate the unexpectedly high levels of expression in multiply transfected cells

If MAR-driven recombination events were to occur in the multiple transfections process, we expect that the synergy between the primary and secondary plasmid DNA would be affected by the presence of MAR elements at one or both of the transfection steps. We examined this possibility by multiply transfections of the cells with pMAR alone or in combination with various expression plasmids, using the method described previously. Table 3 shows that transfecting the cells twice with the pMAR-SV40EGFP plasmid gave the highest expression of GFP and the highest degree of enhancement of all conditions (4.3 fold). In contrast, transfecting twice the vector without MAR gave little or no enhancement, 2.8-fold, instead of the expected two-fold increase. We conclude that the presence of MAR elements at each transfection step is necessary to achieve the maximal protein synthesis.

Table 8

Primary transfection		Secondary transfection		
Type of plasmid	EGFP-fluorescence	Type of plasmid	EGFP-fluorescence	Fold increase
pMAR	0	pMAR	0	0
		pSV40EGFP	15'437	2.3-2.5
		pMAR-SV40EGFP	30'488	2.6-2.7
pMAR-SV40EGFP	11'278	pMAR-SV40EGFP	47'027	4.3-5.3
		pMAR	12'319	1.0-1.1
pSV40EGFP	6'114	pSV40EGFP	17'200	2.8
		pMAR	11'169	1.8-2.3

Interestingly, when cells were first transfected with pMAR alone, and then re-transfected with pSV40EGFP or pMAR-SV40EGFP, the GFP levels were more than doubled as compared to those resulting from the single transfection of the later plasmids (2.5 and 2.7 fold respectively, instead of the expected 1-fold). This indicates that the prior transfection of the MAR can increase the expression of the plasmid used in the second transfection procedure. Because MARs act only locally on chromatin structure and gene expression, this implies that the two types of DNA may have integrated at a similar chromosomal locus. In contrast, transfecting the GFP expression vectors alone, followed by the MAR element in the second step, yielded little or no improvement of the GFP levels. This indicates that the order of plasmid

transfection is important, and that the first transfection event should contain a MAR element to allow significantly higher levels of transgene expression.

If MAR elements favoured the homologous recombination of the plasmids remaining in episomal forms from the first and second transfection procedures, followed by their co-integration at one chromosomal locus, one would expect that the order of plasmid transfection would not affect GFP levels. However, the above findings indicate that it is more favourable to transfect the MAR element in the first rather than in the second transfection event. This suggests the following molecular mechanism: during the first transfection procedure, the MAR elements may concatemerize and integrate, at least in part, in the cellular chromosome. This integrated MAR DNA may in turn favour the further integration of more plasmids, during the second transfection procedure, at the same or at a nearby chromosomal locus.

Example 15 : MARs as long term DNA transfer facilitators

If integrated MARs mediated a persistent recombination-permissive chromosomal structure, one would expect high levels of expression even if the second transfection was performed long after the first one, at a time when most of the transiently introduced episomal DNA has been eliminated. To address this possibility, the cells from Table 3, selected for antibiotic resistance for three weeks, were transfected again once or twice and selected for the incorporation of additional DNA resistance markers. The tertiary, or the tertiary and quaternary transfection cycles, were performed with combinations of pMAR or pMAR-SV40EGFP, and analyzed for GFP expression as before.

Table 9

Tertiary transfection			Quaternary transfection		
Type of plasmid	EGFP-fluorescence	Fold increase	Type of plasmid	EGFP-fluorescence	Fold increase
pMAR	18368	2.2	pMAR pMAR-SV40EGFP	43'186 140'000	2.4 7.6
pMAR-SV40EGFP	16544	2.0	pMAR-SV40EGFP pMAR	91'000 33'814	5.5 2.0

Table 9. MARs act as facilitator of DNA integration.

The pMAR-SV40EGFP/ pMAR-SV40EGFP secondary transfectants were used in a third cycle of transfection at the end of the selection process. The tertiary transfection was accomplished with pMAR or pMAR-SV40EGFP, and pTKhygro as selection plasmid, to give tertiary transfectants. After 24 hours, cells were transfected again with either plasmid and pSVdhfr, resulting in the quaternary transfectants which were selected in growth medium containing 500 µg/ml G-418 and 5µg/ml puromycin, 300 µg/ml hygromycin B and 5µM methotrexate. The secondary transfectants initially exhibited a GFP fluorescence of 8300. The fold increases correspond to the ratio of fluorescence obtained from two consecutive transfections as compared to the sum of

fluorescence obtained from the corresponding independent transfections. The fold increases that were judged significantly higher are shown in bold, and correspond to fluorescence values that are 2-fold higher than the addition of those obtained from the independent transfections.

These results show that loading more copies of pMAR or pMAR-SV40EGFP resulted in similar 2-fold enhancements of total cell fluorescence. Loading even more of the MAR in the quaternary transfection further enhanced this activity by another 2.4-fold. This is consistent with our hypothesis that newly introduced MAR sequences may integrate at the chromosomal transgene locus by homologous recombination and thereby further increase transgene expression.

When the cells were transfected a third and fourth time with the pMAR-SV40EGFP plasmid, GFP activity further increased, once again to levels not expected from the addition of the fluorescence levels obtained from independent transfections. GFP expression reached levels that resulted in cells visibly glowing green in day light (Fig. 14). These results further indicate that the efficiency of the quaternary transfection was much higher than that expected from the efficacy of the third DNA transfer, indicating that proper timing between transfections is crucial to obtain the optimal gene expression increase, one day being preferred over a three weeks period.

We believe that MAR elements favour secondary integration events in increasing recombination frequency at their site of chromosomal integration by relaxing closed chromatin structure, as they mediate a local increase of histone acetylation (Yasui, D., et al., SATB1 targets chromatin remodelling to regulate genes over long distances. *Nature*, 2002. 419(6907): p. 641-5.]. Alternatively, or concomitantly, MARs potentially relocate nearby genes to subnuclear locations thought to be enriched in trans-acting factors, including proteins that can participate in recombination events such as topoisomerases. This can result in a locus in which the MAR sequences can bracket the pSV40EGFP repeats, efficiently shielding the transgenes from chromatin-mediated silencing effects.

Example 16 : Use of MARs identified with SMAR Scan® II to increase the expression of a recombinant protein.

Four MAR elements were randomly selected from the sequences obtained from the analysis of the complete human genome sequence with SMAR Scan® or the combined method. These are termed 1_6, 1_42, 1_68, (where the first number represents the chromosome from which the sequence originates, and the second number is specific to the predicted MAR along this chromosome) and X_S29, a "super" MAR identified on chromosome X. These predicted MARs were inserted into the pGEGFPControl vector upstream of the SV40 promoter and enhancer driving the expression of the green fluorescent protein and these plasmids were transfected into cultured CHO cells, as described previously (Zahn-Zabal, M., et al., *Development of stable cell lines for production or regulated expression using matrix attachment regions*. J Biotechnol, 2001. 87(1): p. 29-42). Expression of the transgene was then analyzed in the total population of stably transfected cells using a fluorescent cell sorter (FACS) machine. As can be seen from Fig. 19, all of these newly identified MARs increased the expression of the transgene significantly above the expression driven by the chicken lysosome MAR, the "super" MAR X_S29 being the most potent of all of the newly identified MARs.

Example 17: Effect on hematocrit of *in vivo* expression of mEpo by electrotransfer of Network system with and without Human MAR (1-68).

5 The therapeutic gene encodes EPO (erythropoietin), an hormone used for the treatment of anemia. The EPO gene is placed under the control of a doxycycline inducible promoter, in a gene switch system described previously called below the Network system (Imhof, M. O., Chatellard, P., and Mermod, N. (2000). A regulatory network for efficient control of transgene expression. *J. Gene. Med.* **2**, 107-116.). The
10 EPO and regulatory genes are then injected in the muscle of mice using an *in vivo* electroporation procedure termed the electrotransfer, so that the genes are transferred to the nuclei of the muscle fibers. When the doxycycline antibiotic is added to the drinking water of the mice, this compound is expected to induce the expression of EPO, which will lead to the elevation of the hematocrit level, due to the increase in red blood
15 cell counts mediated by the high levels of circulating EPO. Thus, if the MAR improved expression of EPO, higher levels of hematocrit would be expected.

In vivo experiments were carried out on 5 week-old C57BL6 female mice (Iffa Credo-Charles River, France). 30µg of plasmid DNA in normal saline solution was delivered by
20 trans-cutaneous injections in the tibialis anterior muscle. All injections were carried out under Ketaminol (75 mg/kg) and Narcoxyl (10 mg/kg) anesthesia. Following the intramuscular injection of DNA, an electrical field was applied to the muscle. A voltage of 200 V/cm was applied in 8 ms pulses at 1Hz (Bettan M, Darteil R, Caillaud JM, Soubrier F, Delaere P, Branelec D, Mahfoudi A, Duverger N, Scherman D. 2000. "High-level protein secretion into blood circulation after electric pulse-mediated gene transfer into skeletal muscle". *Mol Ther.* **2**: 204-10).

16 mice were injected by the Network system expressing EPO without the 1_68 MAR and 16 other mice were injected with the Network system incorporating the MAR in 5' of
30 the promoter/enhancer sequences driving the expression of the activator and EPO genes. In each group, half of the mice were submitted to doxycycline in drinking water from the beginning of the experiment (day 0 – the day of electrotransfer) and in the other half, doxycycline was put in drinking water starting at day 21.

35 Blood samples were collected using heparinated capillaries by retro-orbital puncture at different times after the injection of plasmids. Capillaries were centrifuged 10 minutes at 5000 rpm at room temperature and the volumetric fraction of blood cells is assessed in comparison to the total blood volume and expressed as a percentile, determining the hematocrit level.

40 As can be deduced from Fig. 16 The group of mice injected by MAR-network, induced from the beginning of the experiment, display a better induction of the hematocrit in comparison of mice injected by original network without MAR. After 2 months, haematocrits in "MAR-containing group" is still at values higher (65%) than normal
45 hematocrit levels (45-55%).

More importantly, late induction (day 21) is possible only in presence of MAR but not from mice where the Network was injected without the MAR. Thus the MAR likely protects the transgenes from silencing and allows induction of its expression even after
50 prolong period in non-inducing conditions.

Overall, the MAR element is able to increase the expression of the therapeutic gene as detected from its increased physiological effect on the hematocrit.

CLAIMS

1. A purified and isolated DNA sequence having protein production increasing activity, characterized in that said DNA sequence comprises a) at least one bent
5 DNA element, wherein the bent DNA element contains at least 33% of dinucleotide TA and/or at least 33% of dinucleotide AT on a stretch of 100 contiguous base pairs, b) at least one binding site for a DNA binding protein, c) and that it is a MAR nucleotide sequence with the sequence SEQ ID No 25, or a sequence complimentary thereof, or
10 a sequence having at least 90% identity with said sequence SEQ ID No 25.
2. The purified and isolated sequence of claims 1, characterized in that said DNA binding protein is a transcription factor.
- 15 3. The purified and isolated sequence of claim 2, characterized in that the transcription factor is selected from the group comprising the polyQpolyP domain proteins.
4. The purified and isolated sequence of claim 2, characterized in that the
20 transcription factor is selected from the group comprising SATB1, NMP4, MEF2, S8, DLX1, FREAC7, BRN2, GATA 1/3, TATA, Bright, MSX, AP1, C/EBP, CREBP1, FOX, Freac7, HFH1, HNF3alpha, Nkx25, POU3F2, Pit1, TTF1, XFD1, AR, C/EBPgamma, Cdc5, FOXD3, HFH3, HNF3 beta, MRF2, Oct1, POU6F1, SRF, V\$MTATA_B, XFD2, Bach2, CDP CR3, Cdx2, FOXJ2, HFL, HP1, Myc, PBX, Pax3,
25 TEF, VBP, XFD3, Brn2, COMP1, Evl, FOXP3, GATA4, HFN1, Lhx3, NKX3A, POU1F1, Pax6, TFIIA and Vmw65 or a combination of two or more of these transcription factors.
5. The use of a purified and isolated DNA sequence comprising a first isolated
30 matrix attachment region (MAR) nucleotide sequence which is a MAR nucleotide sequence selected from the group comprising:
 - a purified and isolated DNA sequence of any of claims 1 to 4,
 - the sequence SEQ ID No 25,

or a sequence complementary thereof, for increasing protein production activity in a eukaryotic host cell.

6. The use of the purified and isolated DNA sequence of claim 5, characterized in that said purified and isolated DNA sequence further comprises a promoter operably linked to a gene of interest.

7. The use of the purified and isolated DNA sequence of claims 5 or 6, characterized in that said purified and isolated DNA sequence further comprises at least a second isolated matrix attachment region (MAR) nucleotide sequence which is a MAR nucleotide sequence selected from the group comprising:

- a purified and isolated DNA sequence of any of claims 1 to 4,
- the sequence SEQ ID No 25,

or a sequence complementary thereof, for increasing protein production activity in a eukaryotic host cell.

8. The use of the purified and isolated DNA sequence of claim 7, characterized in that said first and at least second MAR sequences are located at both the 5' and the 3' ends of the sequence containing the promoter and the gene of interest.

9. The use of the purified and isolated DNA sequence of claim 7, characterized in that said first and/or at least second MAR sequences are located on a sequence distinct from the one containing the promoter and the gene of interest.

10. The use of the purified and isolated DNA sequence of any of claims 5 to 9, characterized in that said purified and isolated DNA sequence is in the form of a linear DNA sequence as vector.

11. A method for transfecting a eukaryotic host cell, said method comprising a) introducing into said eukaryotic host cell at least one purified DNA sequence comprising at least one purified and isolated DNA sequence consisting of a MAR nucleotide sequence of any of claims 1 to 4, b) subjecting within a defined time said transfected eukaryotic host cell to at least one additional transfection step with at least one purified DNA sequence comprising at least one DNA sequence of interest

and/or with at least one purified and isolated DNA sequence consisting of a MAR nucleotide sequence or other chromatin modifying elements, and c) selecting said transfected eukaryotic host cell.

5 12. The method of claim 11, characterized in that said DNA sequence of interest is a gene of interest coding for a protein operably linked to a promoter.

10 13. The method of claims 11 or 12, characterized in that the selected transfected eukaryotic host cells are high protein producer cells with a production rate of at least 10 pg per cell per day.

14. The method of any of claims 11 to 13, characterized in that the MAR nucleotide sequence is selected from the group comprising:
- a purified and isolated DNA sequence of any of claims 1 to 4,
15 - the sequence SEQ ID No 25,
or a sequence complementary thereof.

15. The method of any of claims 11 to 14, characterized in that the MAR nucleotide is a purified and isolated sequence according to any of claims 1 to 4, or
20 a sequence complementary thereof.

16. The method of any of claims 11 to 15, characterized in that the defined time corresponds to intervals related to the cell division cycle.

25 17. The method of claim 16, characterized in that the defined time is the moment the host cell just has entered into a second cell division cycle.

18. A method for transfecting a eukaryotic host cell, said method comprising co-transfecting into said eukaryotic host cell at least one first purified and isolated DNA
30 sequence comprising at least one DNA sequence of interest, and a second and isolated purified DNA comprising at least one MAR nucleotide selected from the group comprising:

- a purified and isolated DNA sequence of any of claims 1 to 4,
- the sequence SEQ ID No 25,

or a sequence complementary thereof.

- 5 19. A process for the production of a protein wherein a) a eukaryotic host cell transfected according to any of claims 11 to 18 is cultured in a culture medium under conditions suitable for expression of said protein and b) said protein is recovered.
- 10 20. A eukaryotic host cell transfected according to any one of claims 11 to 18.
21. A cell transfection mixture or kit comprising at least one DNA sequence according to any of claims 1 to 4.
- 15 22. A transgenic non-human organism characterized in that at least some of its cells have stably incorporated at least one DNA sequence of any of claims 1 to 4.
23. A transgenic non-human organism characterized in that its genome has stably incorporated at least one DNA sequence of any of claims 1 to 4.
- 20 24. The transgenic non-human organism of claims 22 or 23 characterized in that some of its cells have been transfected according to the method of any of claims 11 to 18.
- 25 25. A eukaryotic host cell transfected with at least one DNA sequence according to any of claims 1 to 4.

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SEQUENCE LISTING

<110> Selexis S.A.

<120> HIGH EFFICIENCY GENE TRANSFER AND EXPRESSION IN MAMMALIAN
CELLS BY A MULTIPLE TRANSFECTION PROCEDURE OF MAR SEQUENCES

<130> SEL PCT 012

<150> US 60/513,574

<151> 2003-10-24

<150> EP 04 002 722.9

<151> 2004-02-06

<160> 241

<170> PatentIn version 3.1

<210> 1

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<212> DNA

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<220>

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SEL PCT 012.ST25

<222> (1)..(320)

<223> MAR of human chromosome 1, nt from 36686 to 37008

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<222> (1)..(320)

<223> MAR of human chromosome 1, genomic contig; 36686 to 37008

<400> 1

ttatattatg ttgttatata tatttatatta tgttattaga ttataattatg ttgttatatt 60

atataataat attatattat atattatata ttatattata taatatataa taatattata 120

taattatata ttacattata taatatataa taatattata taattatata ttacattata 180

taatatataa taatattata taataatata taattatata atataata atattatata 240

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gtatataata ttatataata 320

<210> 2

<211> 709

<212> DNA

<213> Homo sapiens

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<222> (1)..(709)

<223> MAR of human chromosome 1, nt from 142276 to 142984

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(709)

<223> MAR of human chromosome 1, genomic contig; 142276 to 142984

<400> 2

tacaatatat ttctattat atatatttg tattatatat aatatacaat atattttcta 60

ttatatataa tataatttg attatatata ttacaatata ttgtgatta tataatatat 120

aatacaatat ataatatatt gtattatata ttatatata caatatatta tatattgtat 180

tatatattat atataaact atataatata ttgtattata tattatatat aatactatat 240

aatatatttt attatatatt atatataata caatatataa tatattgtat tataatacaa 300

tgattataa tgtattatat tgtattatat attatatata atacaatata taataatata 360

ttataatata taataataat ataataaat aataatatat attgtattat atattatata 420

atacaatata taataatttg tattatatat atttattac atataatata taatacatta 480

tataatatat ttgtattat atataatata ttattattg tattatagat aatatatttt 540

attatatatt atatataata caatatataa tataatttgg attgtatata atatataata 600

caatatataa tatattgtat tatatataat attaatatat ttgtattat atatttatat 660

tttatattat aattatgttt tgcattatat attcatatt atatatacc 709

<210> 3

<211> 409

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

SEL PCT 012.ST25

<222> (1)..(409)

<223> MAR of human chromosome 1, nt from 1368659 to 1369067

<220>

<221> misc_binding

<222> (1)..(409)

<223> MAR of human chromosome 1, genomic contig; 1368659 to 1369067

<400> 3

tacacataaa tacatatgca tatatatattat gtatatatac ataaatacat atgcatatac 60

attatgtata tatacataaa tacatatgca tatacattat gtatatatac ataaatacat 120

atgcatatac attatgtata tatacataaa tacatatgca tatacattat gtatatatac 180

ataaatacat atgcatatac attatgtata tatacataaa tacatatgca tatacattat 240

gtatatatac ataaatacat atgcatatac tatatacata aattatatta tatacataat 300

acataatacat atattatgtg tatatatata taaatacata tacatatatt atgtgtatat 360

atacatgata catatacata tattatgtat atatatacat aaatacata 409

<210> 4

<211> 394

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(394)

<223> MAR of human chromosome 1, genomic contig; 2839089 to 2839482

SEL PCT 012.ST25

<400> 4

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tatgtatata tacacacata tgtatatata cacacatacg tatatacgtata tatatgtata 60
tatacacaca tatgtatata cgtatatatg tatatatata cacatatgta tatacgtata 120
tatgtatata tacacacata tgtatatatg tatatatgta tatatacaca catatgtata 180
tatgtatata tacacacata tgtatatatg tatatatgta tatatacaca catgtgtata 240
tatatatata catatgtata tatgtatata tacacacata tgtatatatg tgtatgtata 300
tatacacaca tatgtatata tacacacata tatgtatata tacacacata cttatatata 360
cacatatata tgtatatata cacatatgta taca 394
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<210> 5

<211> 832

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(832)

<223> MAR of human chromosome 1, genomic contig; 1452269 to 1453100

<400> 5

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tatattacta tatatacaat atacatatta ctatatatac catgtattac tatatatatc 60
tactatatat attactatat atacaaaata tatattacta tatatacaat atacatatta 120
ctatatatac catatattac tatatatatc tactatatat attactatat atacaaaata 180
tatattacta tatatactat atattactgt atatacaata tatattacta tatatatatc 240
atatattact atatatacac tatatattac tatatatata caatatatat attactatat 300
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atacacaatg tatataacta tatatacaat atataattact atatatacta tatatattac 360

tatacatact atataattact ctatatatac aatatatata ttacaatata tactacatat 420

tactacatat actttatata ttactatata tactatatat tactgtatat acaatatata 480

ttactaaata tacacaatat atattactat atatacaaa tatatatatt actatatata 540

cacattatat atgactatat atacacacta tatatattac tatatatata caatatataa 600

ctatatatac acagtatata tattactata tatacacaa atatatatta ctatatatac 660

actatatatt actatatata cacaatatat attactctat gtatacacta tatatattac 720

tatatataca gaatatatat aactatatat acactattatt actatatata ctatatatta 780

ctatatgtac tatatatatt actatatata ctatatatta ctatatatac ac 832

<210> 6

<211> 350

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(350)

<223> MAR of human chromosome 1, genomic contig; 831495 to 831844

<400> 6

aatatataat atataaatat taatatgtat tatataaat atattaatat attatattat 60

attactatat aaataatatt aatatattat attaaaatat taataaatat atcatattaa 120

atattatatt aattaaatat taataaatat attatattaa tatatttata tattaaacct 180

ataacatatg catatactta ttatatata acaigcatgt acttatttat atatacaata 240

tatatttata tattatataa tatattatat gtatttatat attatatatc atattattata 300

SEL PCT 012.ST25

tgtatttata tattatata catataatat atatatattat attatatata 350

<210> 7

<211> 386

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(386)

<223> MAR of human chromosome 1, genomic contig; 1447225 to 1447610

<400> 7

acatttaatt taattatata ctgctatata taattaaatc tatatatcta tataacttat 60

aatttatatt aatttaatta tatatactat atagttatat atacatatat gtaattatat 120

atagtataat tatagtatat atgtatatat aatgtaagta aatatatagt atatatattat 180

atatactata tattatata tatgtcttta tatatactaa tatatatata catatgtaat 240

atgtacatat ggcatatatt ttatagtga tatatacata tatgtaatat atatagtaat 300

atgtaaatat ataglacata ttttaattata tggtaatatata tacacatatata tgtaatatgt 360

gtattatagt acatatatta tagtat 386

<210> 8

<211> 585

<212> DNA

<213> Homo sapiens

<220>

SEL PCT 012.ST25

<221> misc_binding

<222> (1)..(585)

<223> MAR of human chromosome 1, genomic contig; 4955365 to 4955949

<400> 8

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atacacacat atacacatat gtacgtatat atactatata tacacacata tacacatatg   60
tacgtatata tactatatat acacacatat acacatatgt acgtatatat actatatata   120
cacacatata cacatatgta cgtatatata ctatatatac acacatatat acatatgtac   180
gtatatatac tatatatata cacatatata catatgtacg tatatattat atatacacac   240
atatacacat atgtacgtat atatactata tatacacaca tatacacata tgtacgtata   300
tatactatat atacacacat atacacatat gtacgtatat atactatata tacacacata   360
tacacatatg tacgtatata tactatatat acacacatat acacatatgt acgtatatat   420
actatatata cacacatata cacatatgta cgtatatata ctatatatac acacatatat   480
acatatgtac gtatatatac tatatatata cacatatata catatgtacg tatatatat   540
atatataccc atacacatac gtatatacgt acatatatat acgta                      585

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<210> 9

<211> 772

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(772)

<223> MAR of human chromosome 1, genomic contig; 5971862 to 5972633

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<400> 9

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agtaaacata tatatagtaa atatatatag tgtatatata gtaaatatat atagtgcata   60
tatatagtc atatatatag tgtatatata gtaaatatat agtgtatata tatagtaa   120
atatatagtg tatatatagt aaatatatat agtaaata tatatactat atatagtaaa   180
tatatatata ctatatatag taaatatata tatagtatat atatagtaaa tatatatata   240
gtatatatat agtaaata tatatagtat atatatagta aatatatata tagtatatat   300
agtaaata tatagtatat atatagtaaa tatatatata gtatatatat agtaaata   360
tatatagtat atatatagta aatatatata tagtatatat atagtaata tatatagtat   420
atatatagta aatatatata gtatatatat agtaaata tatagtatat atatagtaaa   480
tatatatata ctgtatatat atagtaata tatatactat gtatatatat agtaaata   540
tatatactgt atatatatag taaatatata tacactgtat atatatagta aatatatata   600
cactgtatat acatagtaaa tatatatata ctgtatatat atagtaata tatatact   660
gtatatatat agtaaata tatatactgt atatatatag taaatatata tacagtgtat   720
atacatagta aatatatata cagtgtatat acatagtaaa tatatatata gt       772

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<210> 10

<211> 304

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(304)

<223> MAR of human chromosome 1, genomic config; 6221897 to 6222200

<400> 10

SEL PCT 012.ST25

atataaata tatataatta tattatatat aatatataat atataaatt atattatata 60
 ttatatataa tatattatat attatatata taatatatat tatatattaa atatatatta 120
 tatatataat atatatata tattaaatat atattatata tataatatat attatatata 180
 atatatataa tatatattat atatatatta tatattatat atatatatta tatatatata 240
 atatatataa tatatattat atataatata tattatatat atataatata tataatatat 300
 atta 304

<210> 11

<211> 311

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(311)

<223> MAR of human chromosome 1, genomic contig; 9418531 to 9418841

<400> 11

tatatataat atttatatat aatattcatg tatttatata taaatattta tatatttata 60
 tataaatatt tatatattta tatataaata ttatatatt tatatataat atttatatat 120
 tatatataat atttatatat tatatataat atttatatat aatatttata tatttatatat 180
 aatatttata tatttatatg tataatatat attttatata tgtatgtata atatatattt 240
 tatatatgia tgtataatat attttatata tgtatgtata atatatattt atatatataa 300
 tataatttat a 311

<210> 12

<211> 302

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(302)

<223> MAR of human chromosome 1, genomic contig; 15088789 to 15089090

<400> 12

atataatata tatattatat atataaatat atataaatat ataacatata tattatatat 60

aaatatatat aaatatataa catatatatt atatataaa atatataaa atatataaca 120

tatatattat atatataaat atatataaat atataacata tatattatat atataaatat 180

atattatata ttatatata taatatatat aaatatataa tatatattta tatatataat 240

atatataaat atataatata tatatttata tataatatat ataaatatat aatatataat 300

at 302

<210> 13

<211> 461

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(461)

<223> MAR of human chromosome 1, genomic contig; 6791827 to 6792287

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<400> 13

tatataatat atattatata tacacatata taatatatat tatatafaca catatataat 60
 atatattata tatacacata tataatatat attatatata cacatatata atatattatta 120
 tatatacaca tatataatat atattatata tacacatata taatatatat tatatatata 180
 catatataat atataattata tatacacata tataatatat attatatata cacatatata 240
 atatattatta tatatacaca tatgtaatat atattatata cacacatata atatattatta 300
 tatacacata tataatatat attatatata catatataat atataattata tatacacata 360
 tataatatat attatatata cacatatata atatattatta tatatacaca tataatatat 420
 aatatatata catatataat atatattatta tatatgcaca t 461

<210> 14

<211> 572

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(572)

<223> MAR of human chromosome 1, genomic contig; 163530 to 164101

<400> 14

atattataat tatatatatt atatataatt atataaaata tatattataa ttatatatat 60
 ttatatataat atatattatta taattaatat attatatata atatatatat tatatatataat 120
 atatattatta tatatattat atataatata tataatatat ataatatata atataatata 180
 tatattatat ataatatata atatatatata tatattataa tataatatat ataatatata 240
 atataatata tataatatat aatatataat ataatatata atatatatata tatataatat 300

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aatatataat atataataa tataatataa tatataatat atataatata ttataatata 360

atatatataa tatataatat aatatatata atataataa taatatataa tatataatat 420

atatttaata tatttattaa ttatttgta tatatttatt aatatataat atataatata 480

tttaatatat tataactata tatttatatta taattatata tatttatatat atacaattat 540

aattatatat tatatatact tataatatat at 572

<210> 15

<211> 357

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(357)

<223> MAR of human chromosome 1, genomic contig; 1842332 to 1842688

<400> 15

tatatctata tatatctata tatatataat atagataata tctatatata taatatagat 60

aatatttatct atataataa tagataatat tatctatata taatatagat aatatttatct 120

atatataaaa ttataftata tctatatata ttatatatat aaaattatat tatatctata 180

tataatatag ataatatcta tatataaata gataatatct atatatataa tatagatat 240

atctatatta tagatataga taataftatc tatatttatag atattatcta tatataatat 300

agataatat atctatatta tatatataat atatctatat tatctataat attatct 357

<210> 16

<211> 399

<212> DNA

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<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(399)

<223> MAR of human chromosome 1, genomic contig; 2309560 to 2309958

<400> 16

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attatatata atatatatta tatattatat atatcaagca gcagatataa tatataatat   60
atataatata tataatatat attgtatatt atataatata taatatatat aatatatatt  120
gtatattata taatatataa tatatataat atatattgta tattatataa tatataatat  180
atataatata tattgtatat tatataatat ataatatatg taatatatta tgtaatatat  240
tatataatat alattatata ttatatataa tatatattat atataatata tattacataa  300
tatattacat atattacgta atatatgta tatattacat ataatatata acatatatta  360
cgtaatatat gtaatatatt acatataata tatacatta                          399
    
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<210> 17

<211> 394

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(394)

<223> MAR of human chromosome 1, genomic contig; 2231759 to 2232152

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<400> 17
 atatatactt ataaattata tacttatata tacttataaa ttatatactt atatatactt 60
 ataaattata tacttatata tacttataaa ttatatactt atatatactt ataaattata 120
 tacttatata tacttataaa ttatatactt atatatactt ataaattata tacttatata 180
 tacttataaa ttatatactt atatataatt ataaattata tacttatata taattataaa 240
 ttatatactt atatataatt ataaattata tacttatata taattataaa ttatatactt 300
 atatataatt ataaattata tacatatata taattataaa ttatatacat atataattat 360
 aaattatata catatataat tataaattat atac 394

<210> 18
 <211> 387
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_binding
 <222> (1)..(387)
 <223> MAR of human chromosome 1, genomic contig; 7406524 to 7406910

<400> 18
 tatattatat ataatatata ttatatataa tataaataat atatattata tataatatat 60
 aaataatata taatatataa ataatatata atatataata tataaataat atataatata 120
 taacatatata ataatatata taatatataa ataatatata taatatataa ataatatata 180
 taatatataa aaatatataa tatataatac atatataaat aatatattat attatatatg 240
 atacataata tattatatat aatatattat atgatacata atatattata tagaatatat 300
 tatatgatac ataatatatt atatagaata tattatatga tacataatat attatatgat 360

acataatata ttatatataa tatatta

387

<210> 19

<211> 370

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(370)

<223> MAR of human chromosome 1, genomic contig; 9399572 to 9399941

<400> 19

catatataca tatatacaca tatatacaca tatatataca catacatatg tacacatata 60

tatacacata tgatacaca tatatacaca tatatacaca catatataca catatataca 120

cacatatata cacatatata cacatatata cacatatata catatataca catatataca 180

tatatacaca tatatataat atacacacat atatatacac atatatacac acatatatac 240

acatatatac acatatatat acacatatat acacatatat acatatatac acatatatat 300

acatatatac acatatatac atatatacac atatatacat atatacacac atatatacac 360

atacatatac

370

<210> 20

<211> 377

<212> DNA

<213> Homo sapiens

<220>

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<221> misc_binding

<222> (1)..(377)

<223> MAR of human chromosome 1, genomic contig; 12417411 to 12417787

<400> 20

attatatata ataatataa ttatatatt atatafaaat tataataaat acatataatt 60

atatatttat atataaatta tatataataa ataatataa ttacatatat ttataaatta 120

taataaaiaa atataaiaa atataaiaa atataaiaa atataaiaa atataaiaa 180

ttatatatat ttatatgtag attatatata aatatatata atttatatat ataataatat 240

atataattta tatatatataa tatatatata ataatatata ataatttata tatataatta 300

tatatataat aaatatataa taatatatat aatttatata tataattata tatataataa 360

atatatatataa ttatatat 377

<210> 21

<211> 1524

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1524)

<223> MAR of human chromosome 1, genomic contig; 1643307 to 1644830

<400> 21

tataaatata tataaatata taaatatata taaatatata aatatatata aatatatata 60

aatatatataa aatatataaa tatatatataa tatatatataa tatataaaaa cataaaaaata 120

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tatataaata tatataaata tataaaaata tataaatata taaatatata aaaatatata	180
aatatataaa tatatacata aatatatata aatatatata aatatataaa aatatatata	240
aatatataaa tatatataaa tatatataaa tatatataaa tatataaaaa tatatataaa	300
tatataaata tataaaaaata tatataaata tataaatata taaatatata taaatatata	360
aatatataaa taaatataag tatttatgaa tatatatgaa tatataaata tataaaaaaat	420
atatataaat atataaatat atataaatat ataaatatat acatatatac atafataaat	480
aaataaatat aagtatttat gaatatatat gaatatataa atafataaaa aatatatata	540
aatatataaa tatatataaa tataaatata taaaaatata taaaaatata tataaatata	600
taaatatata taaatatata aatatatata aatatatata aatatataaa tatatataaa	660
tatataaaa tatataaata tataaatata tataaatata tataaatata taaatatata	720
aatataaata tataaatata tataaatata tataaatata taaatatata taaatatata	780
taaatatata taaatatata taaatatata aatatatata aatatatata taaatatata	840
taaatatata aatatataaa tatataaaaa tatataacaa tatataaata tatataaaaa	900
tatataacaa tatataaata taaatatata taaaaatata taacaatata taaatatata	960
tatataaaa tatataaata taaatatata aaatatatat aaatatataa atatatataa	1020
atatataaat gtataaatat atataaaaaat atataacaat atataaatat ataaatatat	1080
aacaatatat aaatatataa aaatatataa caatatataa atataaatat atataaaaaat	1140
atataacaat atataaatat aaatatatat ataaatatat aaatatataa ataaaaaata	1200
tatataaata tataaatata tatataaata tatataaata tataaatgta taaatatata	1260
taaatatata aatatataaa aatatataaa tatatataaa tatatataaa tatataaata	1320
taaatatata aatatatata aatatataaa tataaatata taaacatata taaatatata	1380
taaataaaca tatataaaga tatataaaga tataaagata tataaatata taaatatata	1440
aagatatata aatatataaa gatatatataa tatataaaga tatataaata tataaagata	1500
tataaatata atafataaat atat	1524

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<211> 664

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(664)

<223> MAR of human chromosome 1, genomic contig; 1398763 to 1399426

<400> 22

acacatatat atataaaata tatatatata cacacatatata taaaaaatat atatatatat 60

acacatatat ataaaatata tatatacaca catatatata aaatatatat atacacacat 120

atatataaaa tatatatata cacacatatata taaaaaatat atatatacac acatatatat 180

aaaatatata tatacacaca tatatatataa atatatatat acacacatat atataaaata 240

tatatataca cacatatata taaaatatat atatacacac atatataataa aatatatata 300

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SEL PCT 012.ST25

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 ttttaagac tctgtctcaa aaaaaaagaa aaaaaaaaaa aatatatata tatatatata 4020
 tatacacgaa tttgggcca ggcacagtgg cttatgctg taatcccagc actttgggag 4080
 ggccgaggtg ggtggatcac aaggtcagga gttgagacc agcctggcca atatggtgaa 4140
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tgagccagga tcgcatcact gcactccagc ctgggtaaca gagcaagact ctgtctcaaa 4320
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<210> 27

<211> 3354

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(3354)

<223> MAR X_S29 of chromosome X

<400> 27

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 ctaaggcaaa aagctgaggt ttcaggagct tgaaggtaaa gaggaagaaa gaaatgggaa 180
 tgggaattgg aaagacaaat atcgttaaga gaaaattgct ttaggagag gggaaagaat 240
 ctatgtgtac ttaagactat ggaatcaatc ccatttaagc tgggaaacta gtttcatata 300
 taactaataa attttattta cagaatatct atttacctga tctaggcttc aagccaaagg 360
 gactgtgtga aaaaccatca gttctgtcat attcctaaaa aaaaattaaa aagttaaaaa 420

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taaataaata ataaaacttc ttttcttca aaataatcaa ggtgcttatt cacatccatt 480
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 aattcaagtt gatacatgtc actttaaga ggtcaactaa tatttgctag ttgagctaac 600
 catataggct ttaaatactt tcatagtaga aagaaaatga aaatcattag tgaactgtat 660
 aaaatagatc atacttttg aaagaatcag actgaagttt ccgaaaaaaa gaagtaagct 720
 tcaatgaaaa ggtaagtga ttagcatctt actcagcacc tactatggac ttaacaccta 780
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 atacacatat atatacgtat atatatatat gtatatatat acatatatat acatatatat 1920

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atatacgtat atatacgt atatacgtat caatgtaaat tatttgggaa atttggtatg 1980
 aatagtcttc cctgtgaaca cagatcataa aatcatatat caagcagaca aataagtagt 2040
 agtcacttat atgcttatac ttgtaactta aagtaaaaga attacaaaag catatgacaa 2100
 agactaattt taagatatcc taatttaaatt tgtttctaa aagtggtat accattttac 2160
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 acacagaaaa catacaaaac gtattttta gacaaataaa aacagaactt gtacctcaga 3120
 tgatactgga gattgtgtg acatattagc attatcactg tcttgctaaa acataaaaaat 3180
 aaaaagatgg aagatgaaat facaatacaa atgatgattt aaacatataa aaggaaaata 3240
 aaaattgttc tgaccaacta ctaaaggaag acctactaaa gatatgcat ccagcacatt 3300
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<211> 677

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(677)

<223> MAR of chromosome 1 genomic contig; 12803267..12803943

<400> 28

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tatacataat agtatatatt ataataaca taattgtata tatcatatag tatacattat   120
agtatatc atatagtata cattatagta tatatcatat agtatacatt atatagtata   180
tatcatatag tatacattat agtatatc atatagtata cattatagta tatatcatat   240
agtatacgtata atagtatata tcatatagta tacgtaatag tatatatcat atagtatacg   300
taatagtata tatcatatag tatacgtaat agtatatc atatagtata cgtaatagta   360
tatatcatat agtatacgtata atagtatata tcatatagta tacgtaatag tatatatcat   420
atagtatacg taatagtata tatcatatag tatacgtaat agtatatc atatagtata   480
tattatatag tatatatcat atagtatata ttatatagta tatatcatat agtatatatt   540
atatagtata tatcatatag tatatatat atagtatata tcatatagta tatataatag   600
tatatatcat atagtatata taatagtata tatcatatag tatatatact atactatatt   660
atatatagta tacataa                                     677

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<210> 29

<211> 332

<212> DNA

SEL PCT 012.ST25

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(332)

<223> MAR of chromosome 1 genomic contig; 13079684..13080015

<400> 29

ttaattatat tatatatatt atataattat atattaatat atattaatta tattatatat 60

attatataat tatatatataa tatatatataa ttatattata tatattatat aattatatat 120

taatatatat taattatat atatatatta tataattata tattaatata tattaattat 180

attatatata ttatatatta taattatata ttatataatt ataatatata tgttaatata 240

atatatatataa ttaatatata attaaaacta ttaattata tgtatattat atataatatg 300

tattatttaa ataataaata tattatttat at 332

<210> 30

<211> 479

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(479)

<223> MAR of chromosome 1 genomic contig; 15682296..15682774

<400> 30

SEL PCT 012.ST25

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acaagtacat atatatatagta tatatatata tacaagtaca tatatatagt atatatatat 120
acaagtacat atatatatagta tatatatata caagtacata tatatatagt atatatatat 180
acaagtacat atatatatagta tatatatata caagtacata tatatatagt atatatatat 240
acaagtacat atatatatagta tatatatata caagtacata tatatatagt atatatatat 300
acaagtacat atatatatag tatatatata tacaagtaca tatatatata gtatatatat 360
atacaagtac atatatatag tatatatata tatatacaag tacatatata tagtgtatat 420
atatatatac aagtacatat atatacttgt attagtatat atatatatat atacaagta 479

<210> 31

<211> 531

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(531)

<223> MAr of chromosome 1 genomic contig; 15694611..15695141

<400> 31

tataatatat ataatacata atagatatat tatattatat aatagatatata taattataaa 60
cataataata tataatgaat ataataataa ataaatataa taaaatatat aatatatcta 120
ttatgtatta tatattatat atgtttatat ataataaat tatatatgtt tatatatataat 180
ataattatat atgtttatat ataataaat tatatatatt atattataga tataatatat 240
aatatactat atattataga tataatatat aatatactat atattataga tataatatat 300
aatatactat atattataga tataatatat aatatactat atattataga tataatatat 360

SEL PCT 012.ST25

aatatactat atattataga tataatata atatatatt atatattata gatataatat 420

ataatatatt atatattata tctatatata atatattgta tattatatat aatatattgt 480

atattatata taatatattg tatattatat ataatatatt gtatattata t 531

<210> 32

<211> 378

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(378)

<223> MAR of chromosome 1 genomic contig; 886276..886653

<400> 32

ttatattata tatcttaccat aaattatata tatatattac ataaattata tacaatataa 60

attatataca atataattta tatataaaat ataaattata taaataattt atatataaaa 120

tataaattat ataaataatt tatatataaa atataaatta tgtataaaat ttatatataa 180

aatataaatt gtgtataaaa ttatatataa aatataaatt gtgtataaaa ttatatata 240

aaatataaat tatatataat ttatatatta taatataaat tatatataat atatatcata 300

aaatataaat tatatataat atatatcata agatataaat tatatataat atatatcata 360

agatataaaa tatataat 378

<210> 33

<211> 595

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(595)

<223> MAR of chromosome 1 genomic contig; 3326732..3327326

<400> 33

aaaatatata aatatatata aaaatatata aaaatatata aatatatata aaaatatata 60

aatatatata aatatatata aaaatatata aatatatata aatatatata aaaatatata 120

atatatataa aatatatata aatatatata aatatatata aaaatatataa tatatatataa 180

aatafaaata tatataaata tatataaaaa tataaatata tataaatata tataaatata 240

taaaatatata taaaatatata taaaatatata aatatatata aatatatata aatatatata 300

aatatataaa tatataaaaa tatatatataa tatataaata tatataaata tataaatata 360

taaaatatata tataaatata taaaatatata taaaatatata taaaatatata tataaatata 420

tataaatata tatatatata aatatatata aatatatata taaaatatata taaaatatata 480

tatatatata taaaatatata taaaatatata taaaatatata tataaatata tataaatata 540

tataaatata tatataaata tatataaata tatatatataa tatatatataa tatat 595

<210> 34

<211> 738

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(738)

SEL PCT 012.ST25

<223> MAR of chromosome 1 genomic contig; 4485716..4486453

<400> 34

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aatagata atatatta tatgatagat atataatata ttatataata tataatatat   60
tatatatcta tcatataata tatataatat ataatatatt atatatctat catataatat  120
aatatatata atatataata tatatcatat tatattgtat ataatatata tcatattata  180
ttgtatataa tatatatcat attatattgt atataatata tatcatatta tattgtatat  240
aatatatatc atattatatt gtatataata tatatcatat tatattgtat ataatatata  300
tcatattata ttgtatataa tatatatcat attatattgt atataatata tatcatatta  360
tattgtatat aatatataatc atattatatt gtatataata tatatcatat tatattgtat  420
aiaatatata tcatattata ttgtatataa tatatatcat attatattgt atataatata  480
tatcatatta tattgtatat aatatataatc atatattatc tattatattg tatataatat  540
atattatata ttatctatta tattgtatat aatatatatatt atatattatc tattatattg  600
tatataatat atattatata ttatctatta tattgtatat aatatataat aaatatagta  660
tatataatag ataatatata gtatatatga tatatttatat atactatata ttatatatca  720
tatatactat atactata                                     738

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<210> 35

<211> 386

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(386)

<223> MAR of chromosome 1 genomic contig; 5423067..5423452

SEL PCT 012.ST25

<400> 35

taaaatatata aaaatatata taaaaatata aaaatatata tataaatata taaaaatatt 60

tatataaata tataaatata taaatatata ttatatataa tatataaata tataaatata 120

taaaatatata ttatatataa tatataaata tatatttata taaatatata aatatatata 180

aaatatataa atatatattt atataaatat ataaatatat ataaaaatata taaatatata 240

tattttatat aaatatataa atatatataa aatatataaa tatatatatt ttatataaat 300

atataaatat atataaata tataaatata tatattttat atatttatat atataaatac 360

atatatttca tatatcacat atatga 386

<210> 36

<211> 584

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(584)

<223> MAR of chromosome 1 genomic contig; 5805559..5806142

<400> 36

taaaatattt taaaatatat atattttata atatatattt tatattataa tgtgtacata 60

atatatatata taalataata tatataaac tgtatattat attatatata ttataatata 120

tattattata tattatatata tatataaat aatatatatt ataatatatt atattatata 180

tattataatg tattataata tatattatat tatattttat aatatatatt atattatata 240

ttataatata tattatatata tatattataa tatattttat attatatatt atattatata 300

SEL PCT 012.ST25

atacatatta taatacatat tatataatat attataatat gtattataat acatattata 360
 taatatatta taatatatta tatataataa tatattataa tacatattat atataatata 420
 tattatgtat attatatata atatatatta caatgtatat tatgtatatt atatatatta 480
 tatatcatat aatatatatt atataataa tgatatataa tatatattat ataatatatt 540
 atatgatata tataatatgt attacatgta atatatatca taat 584

<210> 37

<211> 345

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(345)

<223> MAR of chromosome 1 genomic contig; 10802644..10802988

<400> 37

tgatatata tactatatat atactatata tatagtgtat atatatacta tatatatact 60
 atatatatag tgatatata tactatatat atagtatata gtatatatag taatatatat 120
 atatagtata tatatacact atatatagta tatatagtat atatatatgg tgtatatagt 180
 atatatatag tgatatata gtatatatat attgtatata tagtatatat attgtgtata 240
 tatagtatat atatagtata tatagtatat atagtatata tatagtatat atatactata 300
 tatatagtat atatatatgg tatatatata ctatatatat agtat 345

<210> 38

<211> 474

<212> DNA

SEL PCT 012.ST25

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(474)

<223> MAR of chromosome 1 genomic contig; 13496468..13496941

<400> 38

atattatata taatataatt ataictataa ttatatatta tatataatat aattatatat 60

ctataattat atattatata taatatatat tatatataat atataattat atataattta 120

tataatataa tatataatat ataattatat ataattatat aatataatat ataatatata 180

attatataata attatataa tataatatat aatatataat tatatatatt tatataatat 240

aattatatat aatatataat tatatataat ttatataata taattatata taatatataa 300

ttatatataa tttatataat ataattatat ataattatat attatataata attatataa 360

tataattata tataatatat aattatatat aatatataat tatatataat tatatataat 420

atataattat atataattta tataatataa ttatatatta tatatatatt atat 474

<210> 39

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(483)

<223> MAR of chromosome 1 genomic contig; 2509163..2509645

SEL PCT 012.ST25

<400> 39

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caaaatacat aatatataat agtattatat aatagtatgt atagttataa tatatagtat   60
aattacaata tatgatatgg ttatatatt atatatagta taatataata taacataata   120
ctattataat atataaacta tataatatat actattataa tatatgaact attataatat   180
ataaactata tataatatat aatatgtact attataatat ataaactatt ataataaat   240
atataaacta ttataataca taaactatta taatatatat aatactatgt atacatatat   300
tacattatgt acatactaca ttatgtatta tgtatgtata tatacacaaa atacataata   360
tataatagta ttatataata gtatatatag ttataatata tagtataatt acaatatata   420
atatgggtta tataattatat atagtataat acaatataac ataatactat tatatataaa   480
cta
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483

<210> 40

<211> 641

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(641)

<223> MAR of chromosome 1 genomic contig; 2776349..2776989

<400> 40

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tgttatatat atataacata gatattatat atacatgtta tatatataac atagatatta   60
tatatacatg ttatatatat aacatagata ttatatatat aacatagata ttatatatac   120
atgttatata taacatagat attatatata catgttatat ataacagata ttatatatac   180
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atgttatata taacatagat attatataat tatgttatata ataacataga tattatata 240
 gtttatataa tatataacat atgtttaaca tatataatat ataacatgtt tatataatat 300
 ataacataat tatatgttat atatgatata aaacatatat attatatacg ttatatgtaa 360
 tatataacat atattgtata cgttatatgt aatatataac atatattgta tacgttatat 420
 gtaatatata acalatattg tatacgttat atgtaatatata taacatatat tgcatacgtt 480
 atatgtaata tataacatat attgtatacg ttatatgtaa tatgtaacat atattgtata 540
 cgttatatgt aataigtaat atataatata tataacatgt atataataca tatatgtata 600
 taacatatat ataacatatata taacatatat gttatatatt a 641

<210> 41

<211> 745

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(745)

<223> MAR of chromosome 1 genomic contig; 2858703..2859447

<400> 41

atatttatat atgtaataat atataatata ttatatgta ttgtatatg taataatata 60
 tatataataa aatatgtaat aatatataat atatttatat ataaatatat tatattatat 120
 atatattatt atatttataa tataatatat atttatatta tatattataa atatattatta 180
 tataatatat attataaata tatattatat aatatatatt ataaatatat attatattat 240
 atattataaa tatattattat ataatatata ttataaatat atatttatata atatattatta 300
 taaatatata ttattttat aatatatatt ttgtatatatt atatattata tattataaat 360

SEL PCT 012.ST25

attattatat ttataatata ttatatatt tatataaat atagatata tattataaat 420
 atatcttata aatatatata ttatatata tatattataa atatataaat ataaatatat 480
 aatataatat aatataatat aataaatata atatataata tatataatat ataataaata 540
 taataaatat aaatatatca tataaatata aatataaata taaatatatc atataaatat 600
 atatatttat atgatataatt atagtatata taaatatatt tatatattat aaaatattta 660
 tataatatat aattataata ttttatata tataaattaa ctaatatata taaactaata 720
 taatatataa tgtaataata tagta 745

<210> 42

<211> 307

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(307)

<223> MAR of chromosome 1 genomic contig; 945522..945828

<400> 42

catatataat atatattacc tatgttatat aggtcatata taacataaat atattacata 60
 tatgtaatat atattaaata taaatatata acatatatgt gtaactatat atgtaaatat 120
 gtacatatac atatatgtaa atatataata tatatttaca ttatattata taatatatat 180
 ttacattata tatttatata tacattatat atatttacct tataaatatt tatataatat 240
 atatttacct tatattacct tatataaaat acaatatatt acattataat acattataac 300
 agataaaa 307

<210> 43

SEL PCT 012.ST25

<211> 357

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(357)

<223> MAR of chromosome 1 genomic contig; 3402743..3403099

<400> 43

aatattatat taaatataat atattaatat ttaatatatt taatataata ttaaataaat 60

atattataaa taaattataa tatataaata tatattatgt atttatgtat aatatataaa 120

aattatatat aatatatata tttttataaa tatataaata tataataaat aaatatatta 180

aataaataat aatataftaa atattaatat attaaatat attatattaaa tataatatgt 240

aatatgaaat atattaaata ttatatatta aatataatat ataattgtgaa atatattaaa 300

tattatatat taaatataat atataatatg aaatatatta aatattatat attaaat 357

<210> 44

<211> 323

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(323)

<223> MAR of chromosome 1 genomic contig; 3485830..3486152

SEL PCT 012.ST25

<400> 44
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 tagtatatt gtatactata ttttatata tttagtatat ttgtatacta tatatttata 120
 tattagaat attgtatac tatatattha tatatttagt atatttgtat actatatatt 180
 tagtatatt gtatactata ttttatata tttagtatat ttgtatacta tatatttata 240
 tatttagtat atttatatac tatatactta tatatttagt atatttatat actatafact 300
 tatatattha gtatattht ata 323

<210> 45

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(498)

<223> MAR of chromosome 1 genomic contig; 3548336..3548833

<400> 45

aattattact atattgttaa tataattatt atataatata atataattat atcaactatta 60
 ttatattata gtattaatat aatagtgtat aacattaata taatatagta ttaataaat 120
 agcgtataac attaatataa tatagtatta atataatagc gtataacatt aatataatat 180
 agtattaata taatagtgtat tattaatata atatagtatt aatatataat attaatataa 240
 tatalcaata taatagtata taatataata taatatatca atataatagt atataatata 300
 atataatata tcaatataat agtatataat ataataatata atalcaatat aatagtatat 360

SEL PCT 012.ST25

aatattaata taatataata tcaatataat agtatataat attaatatat taatataata 420
 gtatataata ttaatgtaat ataataattaa cataatgtat ataataatat aatagtatat 480
 aatactaata taatataa 498

<210> 46

<211> 400

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(400)

<223> MAr of chromosome 1 genomic contig; 4595109..4595508

<400> 46

aaataaatta tattatatat tatatattat tcaatataact ataatatata ttatatatgt 60
 ttaatacaat atataaatatt tacatatatt cccatttatt tatataacat atatttatatg 120
 atatttatata ttactccata taatataata tattatacat aatatattac tcagtataat 180
 acataaatata tataatatat tactcggtat aatatataat attatatgtt atgcaatata 240
 atatataata ttatatataa tacattattc aatataatat ataattattat atataataca 300
 ttattcaata taatatataa tacactattc aatataatat acaatattat atataataca 360
 ttattcaata taatatatat tatataatat atatatttat 400

<210> 47

<211> 403

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(403)

<223> MAr of chromosome 1 genomic contig; 7205509..7205911

<400> 47

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agtatatata tgtgtatata tatgagtata tatatgtgta tatatatgag tatatatatg   60
tgtatatata tgagtatata tatgtgtata tatatgagta tatatatgtg tatatatatg   120
agtatatata tgtgtatata tatgagtata tatatgtgta tatatatgag tatatatatg   180
tgtatatata tgagtatata tatgtgtata tatgagtata tatatgtgta tatatgagta   240
tatatatatg tgtatatatg tgagtatata tatgtgtata tatatgagta tatatgtgta   300
tatatatgag tatacatatg tgtatatata tgagcatata tgtgtatata tatgagtata   360
tatatgtgta tatatatgag tatatatgtg tatatatatg agt                       403

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<210> 48

<211> 309

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(309)

<223> MAR of chromosome 1 genomic contig; 7507280..7507588

<400> 48

SEL PCT 012.ST25

tataaaatat atattatfta tatattatat ataaaatata tattatatta tatattatag 60
 atataataaa taaataatat ataatatatt atataattat ttatacataa ttatatataa 120
 ttataigtaa ttgtacaatt atatataatt atatacaatt atacacataa ttatatataa 180
 ttatacaatt atatacataa ttatatatat aatatacata attatatatt aattatacaa 240
 ttatatatat aattatatat aattatacaa ttatatatat aattattatg tatattatat 300
 tatataata 309

<210> 49

<211> 516

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(516)

<223> MAR of chromosome 1 genomic contig; 3581085..3581600

<400> 49
 atatatatat atatatatat atttatatat atatatatta atatatatta tatataaaaa 60
 tatataaaat ttatatatat aatttatata tataaaaata tataaaaatt atatatataa 120
 ttatatata taaaaatata taaaatttat atatatata ttatatata aaaatatata 180
 aaatttatat atataattta tatatatataa aatatataaa atttatatat ataatttata 240
 tatataaaaa tatataaaat ttatatatat aatttatata tataaaaata tataaaaatt 300
 atatatataa ttatatata taaaatatat aaatttatata tataattata tatataatat 360
 aaaatttat atataattat atatatataa taaaattata tatataatta tatatataat 420
 ataaaattat atatatattg tatatatata aatatataaa aatttatata tataaaatat 480

aaaatataca taaaaataaa tatatataat ttatat 516

<210> 50

<211> 534

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(534)

<223> MAR of chromosome 1 genomic config; 3084851..3085384

<400> 50

atataatata tatgactata tttttatat tatattctat ttcaataaaaa tttttatatt 60

ttattatata ttataatata taattatata tgtaataata tataatatat aatatatatt 120

ttatattata ttttataatt atttttatat ttatattat attttattat atatattata 180

atatataatt atatatgcaa taatatatta tatattataa tatataatta tatatgcaat 240

aalatattat atattataat atataattat atatgcaata atatattata gattataata 300

tataattata tatgcaataa tatattatat attatatatt agataatata ttaatatata 360

ttataacata taatatataa catataatat ataatatatt atctaataa taatataaca 420

tataatatat aatatattat ataatatatt attacatata taatatattg taatatataa 480

tattacatat atcttcaaaa agagttaagt gtatataata catatatata ccat 534

<210> 51

<211> 583

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(583)

<223> MAR of chromosome 1 genomic contig; 160087..160669

<400> 51

tatttatata aaatatataa aatatattat atataaatat attatatata atatattat 60

atattatata atatattat atattatata taatatattt tatataatat acataatata 120

tttatatat tatatataat atattttata tataatgtac aatatattt atatattata 180

tataatatat ttatatata ctatacaata tattttatat attatatatt ttatatatat 240

tttcatgta acatatatat ttatatata atatatatat catataatat atatattata 300

tataatatat ataccatata taatatattt tatatataat atgtatatca tatatagtat 360

attttatata taataggtat accatatata atatatttta tatataatat gtataacata 420

tataatatat ttatatata atatgtatata catatataat atattttata tattatagat 480

accataigta atatacttta tatataatat agataccata tgaatatata ttatatata 540

atatagatac catatgtaat atactttata tataatatag ata 583

<210> 52

<211> 314

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(314)

SEL PCT 012.ST25

<223> MAR of chromosome 1 genomic contig; 4350424..4350737

<400> 52

```
tatgtgtata taaatatatg tatatatgtg tatataaata tatataaata tatgtatata    60
tgtatatata catatatatta tatataaata tatgcatata ttatatata aaatatatgc    120
atatatgtat atatatataaa tatatacata tatgtatata tataaaatat atacatatat    180
gtatatatat aaaatatata catatatgta tatatatata atatatatat atatatatat    240
atataaata tatacatata tgtatatata taaaatatat acatatattt atatatataa    300
aataccaagt ctta                                     314
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<210> 53

<211> 828

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(828)

<223> MAR of chromosome 1 genomic contig; 8443267..8444094

<400> 53

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tattatataa ttatatatac tatataatta tataatatat agttatatag tatatataat    60
atatataata tatactatag tatatataat atatatataa tatactatag tatatataat    120
atataattat atataatata tataatatag tatatattat atatatatta tatatatata    180
atatatatat aatatatata atatagtata tataatatat aattatatat aatatataat    240
atagtatata taatatataa tatatatata attatatact ataatatata taatatataa    300
```

SEL PCT 012.ST25

ttatataa taaactatag tatatattat tatataaat agatataata tatataatta 360
 ttatataa tagtatatat aatatataat tatataaat agatataata taatataatt 420
 atataata tagtatatat aatatataat tatattatat tatataaat atataaattat 480
 aatatataat tatattatat aatatatata atataaatt atattatata attatattat 540
 ataataata taatatataa ttatattata taatatatat aatatataat tatattatat 600
 aatatatata atataaatt atattatata atatatataa tatataatta tattatataa 660
 tatataaat atataattat atattatata taatatagta tatataaat gtaattatat 720
 atcatataat atataacatt gtatataata tataattaca tattatataa tgaatataat 780
 atataaatt atacattata taatatagta tataattata tattatgt 828

<210> 54

<211> 573

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(573)

<223> MAR of chromosome 1 genomic contig; 8703190..8703762

<400> 54

tatattatat ataaaatata catataatat acctataata tacatataat atataatata 60
 tattatgtac atataatata catataatat atataatata taatgtacat ata atataca 120
 tataatatat gttatatatt atataaaaa tataggatat atataatata gaatatatat 180
 actatattgt atataaaga tatataatat atagtatata tactatataa tatataatat 240
 atagtatata taatatataa tatagaatat atatacaata tataatatag aatataggat 300

SEL PCT 012.ST25

atatatagaa tatacatata taatatgtat atattatata ttatattata tattatataa 360
 aaatatataa tatataatat aaaaatatat tatatattat ataataaaa atatattata 420
 tattatataat tatataatat aaaaatatatt atatattata tattatataat aaaaatatatt 480
 atatattata tattatataat aaaaatatat tatatattat atattatata taaaaatata 540
 ttatataita tatataaaaa tatatattat tac 573

<210> 55

<211> 597

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(597)

<223> MAR of chromosome 1 genomic contig; 8819076..8819672

<400> 55

acatatctta tatataaaat atataaatat acacatatit tatatataat atatattata 60
 tatatgaaat atacacatat ttttatatat ataatatata tattatataat aatatatgca 120
 tatattatat ataaaaatata tatattatat ataaaatag catatattat atataatata 180
 tataatataa aatatataat atatattata tattatataat aatatatatt atatataata 240
 catatatata atatataata tatataaaat ataatatata tattatataa tatatatata 300
 aatatatata atataiatat aatatatata ttatatataa aatatatatt atagtataaa 360
 tatataatat atataatata tatattatat gtaaaatata tattatataat aaaaatatata 420
 atatataaaa tatatattat atataaaata tataatatat aaaaatatata atatataata 480
 aatatataat atatataaat atatattata tataaaatat ataatatata taaatatata 540

SEL PCT 012.ST25

ttatatataa aatatataat atatatataat atatatataa taaaaatat atattat 597

<210> 56

<211> 646

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(646)

<223> MAr of chromosome 1 genomic contig; 759619..760264

<400> 56

taatatatat aatatatat atataataat atataatata tattatatta taatatataa 60

tatattatat aataatatat attatataat atataataat atataataa catattatt 120

aataatatat aatatatat atataataat atataatata tattatataa taatatatat 180

tatattatat aatatataat atataataa tatattatat aatatatat aatatatat 240

atagaatgat atattagata ttatataatt atatatataa tattatatat tatataataa 300

tatataatat atattatata attatataa taattatata tattatataa ttatatataa 360

tatattatat aattatatat ataattatat atattatata attatataa atatatatta 420

tataattata tatataatac tatatattat ataattatat ataattatat atattatata 480

atttatataa ttatatatat tatatattat ataattatat atattatata ttatatataa 540

acatatatat tatatattat ataataacat atatatataa tattatataa tacatatata 600

ttatatatta tataatacat tattatataa tatataatat atatta 646

<210> 57

<211> 752

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(752)

<223> MAR of chromosome 1 genomic config; 1226710..1227461

<400> 57

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taaacatata tataaatata tataaatata tatataaata tatataaata tataaatata   60
taaatatata tgaatatata aatatatata aatatatatg aatatataaa tatatatata   120
aatatataa aatatatata taaatatata taaatatata taaatatata taaatatata   180
taaataaata tataaatata tataaatata taaatatata tataaatatg taaataaata   240
tatataaata tataaatata tataaatata tataaatata tatagaaata tatatagaaa   300
tatatataaa tatatataga aatatataga aatatatata gaaatatata taaatatata   360
taaatataga aatatatata aatatatata aatatatata gaaatatata atatatataa   420
atatatataa atatataaat atatatataa atatatatat aaatatatat aaatatatat   480
aaatatatat aaatatatat aaatatatat ataatatat aaatctatat taatatatat   540
taatatataa atctatatta atatatatta atatatatat taatatatat taatatataa   600
atatatatat taatatataa atatatataa atatatatgt aaatatatat ataaatatat   660
ataaatatat atataaafac atataaatat atatataaat atatataaat atatatataa   720
atatatataa atatatatat aaatatatat aa                                     752

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<210> 58

<211> 300

<212> DNA

SEL PCT 012.ST25

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(300)

<223> MAR of chromosome 1 genomic contig; 1119049..1119348

<400> 58

taataacat ttatataat atatgtaata tatatffat atatatgtaa tatatattt 60

atataatata tgtaatatat attttatata tatgtaatat atattttata taatatatgt 120

aatatatatt ttatataata tatgtaatat atattttata taatatatgt aatatatatt 180

ttatataata tatgtaatat atattttata taatatatgt aatatatatt ttatataata 240

tatgtaatat atattttata taatatatgt aatatatatt ttatatatat gtaatacata 300

<210> 59

<211> 617

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(617)

<223> MAR of chromosome 1 genomic contig; 3603613..3604229

<400> 59

aaaatataat atataataata tataatatat ataatatatt atatatataaa tatataatat 60

SEL PCT 012.ST25

ataatatata taataaaata tacataatat ataagtata ataaaatata cataatatat 120
aatatataat aaatatataa tatataatat ataataaaat atataatata taatatataa 180
taaaatatat aatatattat atataataaa atatataata tattatatat aataaaatat 240
ataatatatt atatataata aaatatataa tatattatat ataataaaat atataatata 300
ttatatataa taaaatatat aatatattat atataataaa atatataata tataatatat 360
aataatatat ataatatata atatataata taaaatatat ataatatata atatataata 420
taaaatatat aatatataat atatataata aaatatatat gatataaat atatataata 480
aaatatatga tatataatat atataataaa atatataata tataatataa tatataatat 540
atatactaaa aaatatataa tatataataa aaaatatata atatataata tatataatat 600
ataataaaat atatata 617

<210> 60

<211> 674

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(674)

<223> MAR of chromosome 1 genomic config; 2592460..2593133

<400> 60

taagcttata tatatatata agcttatata tatatatata agcttatata tatatagaaa 60
gcttatatat atatagaaag cttatatata taagaagctt atatataaaa gcttatgtat 120
aaatatatat aaatatattt atttatgctt atagatacat atataaatat atttatttat 180
atttatatat aaacatatat ttatatatat ttatataata ttattttatt atataataaa 240

SEL PCT 012.ST25

atatataata aataataaat atatataata tatttattgt attatttata taaatttatt 300
aatataatat aiaataaaat aataattata taaatatata aatatctata aatatatata 360
aatatatata atatctataa atatatatata atataaatat atataaatatc tataaaatata 420
gataaaatata aatatatata atatctataa atatatagataa atataaatat atataactat 480
alataaaat atataactat atataaatat atatataaat atataaact atatatataa 540
ctatatatat aaatatatat aactatatat ataaatatat atataaatat atataactat 600
alatataaat atataaact atatatataat atatatataa atatatataa ctatatatat 660
aaatatatat ataa 674

<210> 61

<211> 1694

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1694)

<223> MAR of chromosome 1 genomic config; 2891680..2893373

<400> 61

atatgtaata catatattat atagcatat atacatgcat atgtatatac atatattata 60
tatgcatata tacatgcata tgtatataca tatataaagt atgattatat ataatatata 120
catgtatatg tatatacatg tatatattat attatatatt attatacat attattatgt 180
ctatatataa tataatatat acatattaat aatataaac ataataaat ataatatatt 240
atataatata taatatataa taatatatta tataatacat aatataaat aatatattat 300
aigatacata atataatata atatattata tgatacataa tataatataa tacatatata 360

SEL PCT 012.ST25

taatatatta ttattattaa tataatatat acatatatt atacatacat atatattata	420
ttatatataa tatacatata atataatatg taatatatta tataatataa tacataatat	480
aatacatatt aataatatat tattaataag ataatatata tgtatctata atatatacat	540
atatgtatat gtatgtatat attatagata tacatgttta tacatgtata tattatagat	600
atatacatgt atatacatgt atatattata gatatacata tgtatatacg tatatattat	660
agatatatat gtatatatgt atatattata tagatataat atatacaaga atataagaat	720
atatataata taatatataa tacacataat acgtatatat tatatatata tgtatattat	780
atatgtacat atatacatgt atattatata tacatgtata ttatatatac atgcatatta	840
tatatatttt tatatatat atccatgtat attatgtata ttgtgtata ttatatatac	900
atgtatatta tatatacatg catattatat atatttttat atataatatc catatatatt	960
atgtatattt gtgtatatta tatatacata tatattatat atacatggat attatatata	1020
cacatatatt atatatacat atatattata tatacacata tattatatat acatgtatat	1080
tatatataca cgtatattat atatacacac gtatattata tatacacgta tattatatat	1140
acacacgtat attatatata cacgtatatt atatacacac acgtatatta tatatacacg	1200
tatattatat atacacacgt atattatata tacacgtata ttatatatac acacgtatat	1260
tatatataca cgtatattat atatacacac gtatattata tatacacgta tattatatat	1320
acacacgtat attatatata cacgtatatt atatacacac acgtatatta tatatacatg	1380
tatattatat atacatgtat attatatata cacatgtata ttatatatac atgtatatta	1440
tatatacata tgtatattat atatgcatgt atattatata tacacatgta tattatatat	1500
acacatgtat attatatata catatatatt atatatacat gtatattatg tatacatata	1560
tattatatat acatgtatat tatagataca tatattattaa atatacatgt atattatgta	1620
tacatatata ttaaataac atgtatattg tatatacata tatattatat acatgtatat	1680
tacatgtata cata	1694

<210> 62

<211> 587

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(587)

<223> MAR of chromosome 1 genomic contig; 3432560..3433146

<400> 62

gaattatata tatatagctg aattatatac atatataata tatacaatat atattatata 60

tttatatag atatatacaa tatatattac atattatata tacaatatat aatatataat 120

atataatatt atataattata tattgtatat aatatatatt atataacatt atataatata 180

taattatata tattatatat tgtatataat atatattata taacattata taatatatac 240

tattatatat tataatatat aatatataat aatatataat agtatatatt atatatatg 300

tatatattat atataaatat ataatatata atatatatta tataatatat attatataat 360

atataattatt atataattata tatttatata taatatatat tatatatatt atattttata 420

tataaatata taatatataa taatatataa tttaatatat ataatatata caatatataa 480

tatataatat attaatatat ataatatata caatatataa tatataatat ataatatata 540

atataaatta tiatatataa tatatattat atatagctga attatat 587

<210> 63

<211> 313

<212> DNA

<213> Homo sapiens

<220>

SEL PCT 012.ST25

<221> misc_binding

<222> (1)..(313)

<223> MAR of chromosome 1 genomic contig; 3805392..3805704

<400> 63

tatataatat gtatattatg taatatfita tatagcatat algtatatta tatataatct 60

tttatatata gtatataata tgtatattat atattatata attatataat tatgtattat 120

ataaaatata ttatataata tataattata tatfittiga aatatagatt atataataa 180

tatatggcag tgagctgaga tataatatat attatctata ctatataata tatattatat 240

atactctata ttatatatgt atatattata tataafatat acatatataa tgtgtatata 300

ttatatataa taa 313

<210> 64

<211> 349

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(349)

<223> MAR of chromosome 1 genomic contig; 4521378..4521726

<400> 64

ttatatacac tatataatat gtatttatat atacttatat acactatata tgtatttata 60

tataattata tacactatat aatatgtatt tatatataat tatatacact atataaatg 120

tatttatata taattatata cactatataa tatgtattta tatataattg tatacactat 180

SEL PCT 012.ST25

ataatgtata ttatatata attgtataca ctatataatg tatatttatg tataattgta 240

tacactatat aatgtatatt tatgtataat tgtatacact atataatgta tatttatgta 300

taattgtata taccatataa tgtatatatta tgtataattg tatatacca 349

<210> 65

<211> 500

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(500)

<223> MAR of chromosome 1 genomic contig; 3240166..3240665

<400> 65

ttatatata atatatatta tataattata tattaatata taatatatat ttatatataa 60

tatatattat atatttatat tacatatatt tataatgtaa tatatatttt atatatattat 120

atattttata tatttatata ttatatattt atatatata ttatatatt atatatattat 180

attatatatt tatatatatt atttatatat tatatatffa tatttatatat ttatatattg 240

tatatattata ttatatattt atatatgta ttatatatt atatatattat atactatata 300

tatttatata tatttatatat ttatatatta tatatatffa tatatatatt atatttatat 360

attatatata ttatatata ttatatattt atatatata tatatttata tatatttatat 420

atatttatat atatttatata ttatatata atatatatta tatattttat ctatatattt 480

atatattaat atatatatta 500

<210> 66

<211> 866

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(866)

<223> MAR of chromosome 1 genomic contig; 409429..410294

<400> 66

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atatatataa tatattatat atatttatata ttatatatat aatacatata ttatatatat   60
aatatataat acatatattta tatatattat atatttatata taatatataa tacatatatt   120
alatataata tataatatat aatafattat ataataaat tatataattta tataatataa   180
tataatatai aatatttatat aatttatataa tatatataat tatatttatat attataaata   240
ttatataata tatatattac aaatatatat tatatatatt ataaatatta tataacatat   300
atatttatata atatatataa tataiaatat atataaaaaat ataatatata agatatatat   360
aatatatgat atatatgata tataatatat gatatatatg atatatataa tatatgatat   420
atatgatata tatgatatat ataatatatg atatatatga tatatatgat atatgatata   480
tatgatatat gatatatatg atatatatga tatatgatat atatgatata tatgatatat   540
gatatatatg atatatatga tatatgatat gatatatata atatatgata tgatatatat   600
aatatatgat atatatgata tatgatatgt aatatatatg atatattata tataatatat   660
aatatataca taatatataa tatataatat ataatatata taatatgtga tatatataat   720
atatgatata tgatatatga tatatattat ataatatata taatatatat tatatataat   780
atatattata taatatatat aatatatatt atatataata tataagatat aagatataat   840
atatataata tataatatat ataata                                     866

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<210> 67

SEL PCT 012.ST25

<211> 335

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(335)

<223> MAR of chromosome 1 genomic contig; 614754..615088

<400> 67

acccaatata tgtgtatata tgtatgtata tatacatata catacataca tatatgtaca 60

tacatatata catacataca tatatatgta catacatata tacatacata catatatata 120

tataacatat atacacacat atatacagat atacatata acatacatat atacatataa 180

catatatata tacatatata catataaacac atacatacat acatatatac atacaacata 240

tatacataca tatatacata tgtatacata catatatgta tacatatatg tatacatata 300

tgtatacata tatgtatata tatattgta tatat 335

<210> 68

<211> 455

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(455)

<223> MAR of chromosome 1 genomic contig; 1299520..1299974

SEL PCT 012.ST25

<400> 68

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ggatatatat attattagtt gttatattat tatattatt atattattt atatataata 60
tattatatca tatatattat tatatataat atattataic atatatatta ttatataata 120
tattatatca tatatattat tatatataat atattattata tatattatta tatataatat 180
atattatata tattattatg tataatatat atattatata ttatttatat atatataaat 240
tatataataa tatataatta attatacata tatacalata taagtataca tataatatat 300
ttatatagta tatataaata tatatacaat atatttatat attatatatt atatataaat 360
atatacaata tatttatatc atatatttta tatatgatac atataatata tattatatat 420
gatataaat atatatcata tatgatatat aacat 455
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<210> 69

<211> 404

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(404)

<223> MAR of chromosome 1 genomic contig; 1970778..1971181

<400> 69

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atatataata tgtataatat ataatatata tcatatattg ttctatgtat attacatata 60
atatgcatta tatattatat attgcatata atatgcatta tatattatat attgcatata 120
atatgcatta tatattatat attgcatata atatgcatta tatattatat attgcatata 180
atatgcatta tatattatat attgcatata atatgcatta tatattatat attgcatata 240
```

SEL PCT 012.ST25

atatgcatta tatattatat aatatatata catataatat atataattta tatatattta 300

tatatattta catttattat atatttatta tatataaata ttttttata tttacttat 360

atattatata taatatatat aatatatata ttatatataa tata 404

<210> 70

<211> 605

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(605)

<223> MAR of chromosome 1 genomic contig; 3562918..3563522

<400> 70

tatatatata aaatcacatat atattatata tatttatatat aatcacatata ttatatatta 60

tatataatac acgtatataa tatataatat ataatacata taatatatat gatatatatat 120

acatataata tatatgatat ataatacata tataatatatat atgatatata atacatatatat 180

aatatatatt atatataata catatataat atatattata tataatacat atataatata 240

tatttatatat aatcacatata taatatatat tatatataat acatatataa tatatatttat 300

ataatacata tataatatatat attatataat acatgtatat aatatatatt atataataata 360

catatatatt atataatata tgiatataat atatattata tataatacat atatattata 420

tatttatatat taatatattt atataatagt aatatataat attaatatat tatatatatt 480

aatttatatat ataatacata tatttatatat aatataaata tatataatac atataataata 540

cacatatatt atataatata tatatttatatat ataatatata tatttatatat aatatatatg 600

taata 605

SEL PCT 012.ST25

<210> 71

<211> 317

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(317)

<223> MAR of chromosome 1 genomic contig; 189743..190059

<400> 71

tatttttat atttatatat tatatatatt ttatatgtta atatattata tataaaaatta 60

tataatttta ctacatatata tatataaaat tatataattt tactacatat aatatataaa 120

atttatataat ttactatat ataatatata aaattatata attttatata taatatatat 180

tataatatat atttatatgca atatataatta tatattatat tataatatat tgtatatatt 240

tgtatatataa atatataata tataatatat ttatagacaa taatatataa tataatatat 300

aaaattttat atataaa 317

<210> 72

<211> 522

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(522)

SEL PCT 012.ST25

<223> MAR of chromosome 1 genomic contig; 229111..229632

<400> 72

gatatatata ttatatata taaaagatat atattattta tatataaaga tatatattta 60
tatatatata agatatatat ttttatata tataaaagat atatatttat atatatgata 120
tatatttttt atatatatata aagatatata ttatatata tgatatatat ttttatata 180
taaaagatat atataaaaga tatatattat ttatatatat aaaagatata tatataaaag 240
atatatatta ttatatata taaatgatat atattattta tatataaaag atatatatta 300
ttatatata aaagatatat attatttata tatataaaag atatacatat aaaagatata 360
ttttatata taaaagatat atatatttat atataaaaga tacatafatt tatatatata 420
aaagatatat atatttttat atataaaata tatattatat atataaaaga tatatatata 480
tatatatatc ttatatatat aaaagatata tataaatata ta 522

<210> 73

<211> 1110

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1110)

<223> MAR of chromosome 1 genomic contig; 1138030..1139139

<400> 73

tatgtatgta tacataatat attatatatg tatattatgt atacataata tattatatat 60
gtatattatg tatacataat atattatata tgtatattat gtatacataa tatattatat 120

SEL PCT 012.ST25

attatatgta tattatgtat acataatata ttatatatta tatgtatatt atgtatacat	180
aatatattat atatttatatg tatattatgt atacataata tattatatat tatatgtata	240
ttatgtatac ataatatatt atatattata tgtatattat gtatacataa tatattatat	300
attatatgta tattatgtat acataatata ttatatatta tatgtatatt atgtatacat	360
aatatattat atatttatatg tatattatgt atacataata tattatatat tatatgtata	420
ttatgtatac ataatatatt atatattata tgtatattat gtatacataa tatattatat	480
attatatgta tattatgtat acataatatt tatatatatt atgtatatta tgtatacata	540
atatattata tatttatatgt atatttatgta tacataatat gtacacataa tatttatata	600
ttatatgtat attatgtata cataaatatt atatattata tgtatattat gtatacataa	660
tatttatata ttatatgtat attatgtata cataaatatt atatattata tgtatattat	720
gtatacataa tatttatata ttatatgtat attatgtata cataatatat tatataittat	780
atgtatatta tgtatacata atatattata tatttatatgt atattatgta tacataatat	840
attatatatt atatgtatat tatgtatata taatatattat atatttatatg tatattatgt	900
atacataata tatttatatat tatatgtata ttatgtatac ataatatatt atatattata	960
tgtatattat gtatacataa tatattatat attatatatg tatattatgt atacataata	1020
tatttatatat tatatatgta tattatgtat tatattatat attatgtata ttatagatta	1080
tgtatgcata cataatatgt attgtatatt	1110

<210> 74

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(521)

SEL PCT 012.ST25

<223> MAR of chromosome 1 genomic contig; 2863407..2863927

<400> 74

aatatatata aatatataaa tatatatataa tatatatataa tataaatata taaatatata 60

tatgtataa tatgtataa tatgtataa tatgtatatg tatatatatg taaatgtatg 120

taaatatata taaatatatg taaatatata taaatatatg taaatatata aatatatata 180

actatatata aatatatata aatatataa tataaatata tataaatata tataaatata 240

tataataata catataaata tataataaaa tacatatataa tatatatataa tatataaaaa 300

tatatataaa tatatatata aatatataaa catatatataa tatataaata tatataaata 360

tataaatata taaatatat aaatatatat aaatatataa atatatatata atatagataa 420

atatagataa atatataaat atatataaat atataaatat agataaatat ataaatatat 480

aaatatataat atataaaaat atatataaat atataaaaat a 521

<210> 75

<211> 560

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(560)

<223> MAR of chromosome 1 genomic contig; 5712303..5712869

<400> 75

atatataat atatataat tatatatat ataatatat attatatata atgtataat 60

atatatatata tataatatat ataatatat atattttta tataaatata ttatatatt 120

SEL PCT 012.ST25

atatattata tataaattta tatatatataa ttttatata ttatatatat ttatatatta 180
 tatattgtat atatttatat attacatatt gtatatattt atatattata fattatatat 240
 ttatatatta tatatttatat atttatatat tatatatattt atatatttat atatttatata 300
 taaatttatt atatataata tataaatata fattatataa tataaatttg tatatataat 360
 atatatttat atttatata aaatatttat atttatata aaatataata taaatatata 420
 catataatat atataattata fatttataat tatatatattt atataatata tataatatat 480
 aatatataat acatatatat catatatgaa atatatatca tatattatac atatttatata 540
 taacatatat atttatatc 560

<210> 76

<211> 479

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(479)

<223> MAR of chromosome 1 genomic contig; 8578812..8579290

<400> 76

tatgggtatc atatagtata tatggggtag atatatggta tatatatggg ttatatatat 60
 gatatatatt atatatgtat atgggtatata tatgggtat atattatata tgcatatggg 120
 aigtatatgg tatatatatg atatatatcat atgggtatata tatatgttat atatgatata 180
 tataagggtat atatatggta tatataagggt atatatagta tatatatggg atatataagg 240
 tatatatgtt atatatatgg tatatataag gtatatatat tgtatatatg gtatatatat 300
 ggtttatata taiggtgtgt atatatgggt ttatatatata cactttatat actatatatt 360

SEL PCT 012.ST25

atatacacac tatatataat atatattata tatagttaaa tatatggtat atgcaattag 420

atatatggta tatgtaatta tatatatggt atatagatgg tgtatatatg gtatatata 479

<210> 77

<211> 477

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(477)

<223> MAR of chromosome 1 genomic contig; 8579294..8579770

<400> 77

tatagtatat atacacacta taggtaatat actacatatt atatacacac tataaataaa 60

atatataata tataatattt tctatatagt atatattata tattgtatat actatatata 120

atatatacta tagacagtag atactttata tactatagac agtatatact atatactgta 180

tacactatag acagtatata ctatatactg tatacagtat atgtagtgta tatgtagtgt 240

atataatata tagtatatat tatctatact atatacagta tatatagtgt atacataata 300

tatattatat attatatata ctatatacag tatacatagt gtatatgtag tgtataatat 360

atataatgtg tatataaaat atatatacta tatataatat atattatata taatatatac 420

actatata ctatagatac actatafalt cactalatat actatatata ctatata 477

<210> 78

<211> 331

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(331)

<223> MAR of chromosome 1 genomic contig; 8580024..8580354

<400> 78

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actataatgtt atatacataa gatatagtat ataccatata ttatatacat tatatatagt   60
gtatactata tataatgtat ataatatata gtatatatac actatatata ctatgtatat   120
atacactata tatactatgt atatatcac tatatatact atgtatatat acactatata   180
tactatgtat atatacacta tatatactat gtatatatac actatatata ctatgtatat   240
atacactata tatactatgt atatatcac tatatatact atgtatatat agtgtatata   300
tactgtatat gttatagtg atatatagta t                                     331
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<210> 79

<211> 410

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(410)

<223> MAR of chromosome 1 genomic contig; 8580705..8581114

<400> 79

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tatagtctat attatataca gtctatataa tatatagtat atactatata tacttttcct   60
```

SEL PCT 012.ST25

cattctgact atatactata tatatactat atatagtata ttagtggtat atatacacca 120
 tatatactat atatagtata cataccatat atagtatact atacatacca tatatagtat 180
 acataccgta tatagtatac tatacttacc atatatagta tacatactat atataatata 240
 tctgggtgat atatacacta tatatactat atatactata tatagtatat gtacactatt 300
 tatagtattt atagtatata tactgtatat atagtatgta gtatatatac tatatattat 360
 gtgactata tataatatag actatgtgta gagtatatat actatatata 410

<210> 80

<211> 433

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(433)

<223> MAR of chromosome 1 genomic contig; 12979167..12979599

<400> 80

atatataata tatatatgtc ctatatafaa aatataatcat atatataaat atatatgata 60
 tatatttatat attaaatata taattatata taaatatata ttatataata aatatattat 120
 ttcaatatat ataaatatat ttaaatatat ttaaataagaa tattaaatat ataaatatat 180
 aattatattt aatatataaa tatatatata atatatatt atatttaata tatataaata 240
 tatattaaat atataattat atatttatat attattata tataaatata tatttgttct 300
 aaataaatat atattctaaa tatataatat ttatattat ataatatata atataaaata 360
 tataataaat atataatata taaataaata aatatttatt ataaaatata tataaatatt 420
 aaatatatat taa 433

SEL PCT 012.ST25

<210> 81

<211> 385

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(385)

<223> MAR of chromosome 1 genomic contig; 16336644..16337028

<400> 81

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tttatataaa tatctatata aataaatata taaatatata aatataaata tatataaata   60
tataaataaaa tatataaata tatataaata taaatatata tataactatg aatttatatt  120
tatataaata tatatctata tgaatataaa tatatattta tataaatata aatatatata  180
taaatatata tafttatata gatafaaata tatatataaa tatatatatt tatatagata  240
taaatatata tctatatatg aatatatafc tataggaata taaatatata tctatataaa  300
tataaatata tataagtata aatatatata aatatatafc tatataaata taaatatata  360
tataaatata aatatatata taaat                                     385

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<210> 82

<211> 363

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

SEL PCT 012.ST25

<222> (1)..(363)

<223> MAR of chromosome 1 genomic contig; 20624448..20624810

<400> 82

tatatatata gttatatata tatatatata tatagttata tatatatatt tatatagtta 60

tatatatagt tatatatata gttatatata tatagttata tatatagtta tatatatagt 120

tatatatata tagttatata tatagttata tatatagtta tatatatagt tatatatata 180

tagttatata tatagttata tatatatagt tatatatata gttatatata tatagttata 240

tatatagtta tatatatagt tatatatata gttatatata tagttatata tatatagtta 300

tatatatata gttatatata tatagttata tatatagtta tatatatata gttatatata 360

tag 363

<210> 83

<211> 310

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(310)

<223> MAR of chromosome 1 genomic contig; 566025..566334

<400> 83

tatatataat atatattgta tatattatat attgtatata taatatatat tgtatatatt 60

atatattgta tatataatat atattgtata tattatatat tgtatatata atatatatat 120

tgtatatatt atatattgta tatataatat atatattgta tatattatat attgtatata 180

SEL PCT 012.ST25

taatatatat attgtatata ttatatattg tatatataat atatattg tatatattat 240

atattgtata tataatatat atattgtata tattatatat agtatatatt atatatagta 300

tatataatat 310

<210> 84

<211> 1236

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1236)

<223> MAR of chromosome 1 genomic contig; 1171429..1172664

<400> 84

aaagtattat atgtattata tgtatatgta ttatatatta catatgtatt atatataata 60

tatattatat attattatat attatatatt atatattatt atttatataa tgtattatat 120

attatatagt atatatagta tatataatgt attatatatt atatagtata tatagtatat 180

ataatgtatt atatatagta tatataatgt attatatagt atatatacta tataatgtat 240

tacatattat gtatagtata tgtaatgtat tatataattat atagtatatg taatgtatta 300

tatgtattat atagtatata ttatatatga tgtattattt agtatatata atatatatga 360

tgtattatat aacatatata atatatatga tgtattatat agcatgtata gtatatatga 420

tgtattatat agcatgtata gtatatatga tgtattatat atagcatgta tagtatatat 480

gatgtattat atatagcatg tatagtatat atgatgtatt atatatagca tgtatagtat 540

atatgatgta ttatatatag catgtatagt atatatgatg tattatatat agcatgtata 600

gtatatatga tgtattatat atagcatgta tagtatatat gatgtattat atatagcatg 660

SEL PCT 012.ST25

tatagtatat atgatgtatt atatatagca tgtatagtat atatgatga ttatatatag 720
catgtatagt atatatgatg tattatalat agcatgtata gtatatatga tgtattatat 780
attatatatg gtatatatga tgtattatat attatatatg gtatatatga tgtattatat 840
attatatatg gtatatatga tgtattatat attatatata atatatatga tgtattatat 900
attatatata atatatatga tgtattatat atgatgtatt atatataata tatatgatgt 960
attatatata ttattatcta ttatatacga tgtattatat gcaagttatt atgtataata 1020
tataatgtat tatatattat ataatgtata atatataaat atataaatat ataattatgt 1080
ataaatatag aaatatatatac attatacatt atatacatta taatgtataa tatataaata 1140
tattatatat aaatgtatac attatatata aatatattat atacattata tataaaatat 1200
gtatatagtt attatacctt atatatacta aacagt 1236

<210> 85

<211> 309

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(309)

<223> MAR of chromosome 1 genomic contig; 1925173..1925481

<400> 85

atatatttat ataaatatat ttatatataa tatatattat ataattattat aatatatgtt 60
atattatata tattttatatac aatatataat atattattata tatattttat acaatatata 120
atatatatata tatatatttt atataatata taatatatat tatatatatt ttatacaata 180
tataatatat attatatatt atataafata tattatatat attttatata atatataata 240

SEL PCT 012.ST25

tatattttat acaatatata atgtatatca ttatattata taatgtatat catattatat 300

aatgtatat 309

<210> 86

<211> 312

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(312)

<223> MAR of chromosome 1 genomic contig; 4396756..4397067

<400> 86

cacagtgtat atatagtata tatactgtat atatactgtg tatatacact gtatatacac 60

agtgtatata cagtatatat actatatata cactgtgtat atatagtata tataaattct 120

aggaatatat atactatata tatactatat atataaattc taggaatata tacacactat 180

atatacacta tatafacaca tatatacact atatatatta tacacatata ttatatatat 240

acactatata tacacgagat atataacata tacactatat actatacata acatatatac 300

tatatatact at 312

<210> 87

<211> 398

<212> DNA

<213> Homo sapiens

<220>

SEL PCT 012.ST25

<221> misc_binding

<222> (1)..(398)

<223> MAR of chromosome 1 genomic contig; 56057..56454

<400> 87

atatafatta catattatat atataatata tattatataa tatatattat attatataat 60

atataatata aatataatat aaattatatt atataatata taatataaat ataataataa 120

ttatataaat ataatafata ttttattata taatataata tatattatat aaatataata 180

tataaattat ataataatata atatatata taatataata tattttatta tataaatata 240

tattatatta tataatatat attttattat ataatatata ttatatatt atagaatata 300

atatafatti tattatataa tatatattat ataatatata ttatattat atataacata 360

tattattata taaaatatgt ataatatata ttatataa 398

<210> 88

<211> 391

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(391)

<223> MAR of chromosome 1 genomic contig; 56984..57374

<400> 88

tactataata catattatat ataattattat atactatata ttactatatt attatattat 60

atataattaa actatattat agtatataat atataatata tactatatgt aatattacta 120

SEL PCT 012.ST25

tgatactgat attatattat atataattaa attatattat attaatatat aaattatata 180
 taatacataa tatataaatt atattatatt atttatatat aatgtatgcc atataattta 240
 tatataatgc atttatata atttatatat aatgcattaa atataaatta tatataatgc 300
 atttatata atttatata atgcattata tataatttat attaatata taaatttata 360
 tttaatatat ttatatatta tatataataa a 391

<210> 89

<211> 309

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(309)

<223> MAR of chromosome 1 genomic contig; 469547..469855

<400> 89

atatatatgt aatatatatg ttatatatgt aatatatatg ttatgttata tatgttatat 60
 atatgttata tataatatat atgttatata tacgttatat gttatatata tgttatatat 120
 aatatatggt atatatatgt tatatgttat atatgttata tataatatat gttatatata 180
 atatatgita tatatgttat atataatata tgttatatat atttatata atatatgtta 240
 tatatattat atataatata taatatatgt gatataaat ataaaatata tgtgatatat 300
 atttatatat 309

<210> 90

<211> 441

<212> DNA

SEL PCT 012.ST25

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(441)

<223> MAR of chromosome 1 genomic contig; 546190..546630

<400> 90

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atacacaaca tatgtgtata tatatagtat atatacaca catatgtgta tatatatagt   60
atatatacac aatatatgtg tatatatata gtatatatac acaatatatg tgtatatata  120
gtataaatat atactatata tagtatatat agtataaata tatactatat atagtatata  180
catagtataa atatatata tatatagtat atacatagta taaatatata ctatatatag  240
tatatacata gtataaatat atactatata tagtatatac atagtataaa tataactat  300
atatagtata tacatagtat aaatatatac tatatatagt atatacatag tataaatata  360
tactatatat agtatatata tagtataaat atatactata tatagtatat acatagtata  420
aatatatact atatatagta t                                     441

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<210> 91

<211> 1367

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1367)

<223> MAR of chromosome 1 genomic contig; 124643..126009

SEL PCT 012.ST25

<400> 91

atatttatat gatataaat atataata ttatatataa tattatatat gatataaac	60
attatataat attatatatg atatatatta tatatatatt atagatata taatatatat	120
aatattatat atgatattat atacatata taatatataa aatattatat atgatatata	180
atatatataa tattatatat attatatata ttatatatca tatataaat tctaaatata	240
taatatataa tgatatataa gattatatatc attatatata atataata ttatatatga	300
tatataaat tatatacaatt atataataa tataatgtat ataattatt atattatata	360
ttatatatt atacaatgta tataatatta tatatcatat atatttatat tatatacaat	420
gtatataata ttatatatca tatataaat tatatacaat gtatataata tatatttatat	480
atatttatat tatatacaat gtatataata tatatttatat atatttatat tatatacaat	540
gtatataata tatatttatat atatttatat tatatacaat gtatacaata ttatatatta	600
tatatttatat atttatatta tatacaatgt atatttatata tattatatat ttatatatta	660
tacaatgtat atatttatata ttatatattt atatttatata caatgtatat attatatatt	720
atatttatat attatatata atgtatatat tatatatatt atatttatat tatatacaat	780
gtatatatta tatatttatat atttatatta tatataatgt atgtaatt atatttatata	840
tatttatatt atataaatg tatgtaatat tatataatt atatttatat tatatataat	900
gtatgtaata ttatatatta tatatttata ttatatataa tgtatgtaat attatatatt	960
atatttatat attatatata atgtatgtaa tattatatat tatataatt tatttatatat	1020
aatgtatgta atatttatata ttatatattt atatttatata taatgtatgt aatatttatat	1080
attatatatt tatatttatat ataatgtatg taattattata tatttatatat ttatatatta	1140
tataatgtat gtaatttat atatttatata ttatatatt atataatgta tgtaattatta	1200
tatatttatat atttatatta tatataatgt atataatt atatttatata tatttatatt	1260
gtatataata ttatatatta tatatttata ttgtatataa tatataatt atatttatat	1320
tgatatataat attatatatt atatttatat attatatata atgtata	1367

SEL PCT 012.ST25

<210> 92

<211> 458

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(458)

<223> MAR of chromosome 1 genomic contig; 58908..59365

<400> 92

tatatgatataatgatataatgggatataatgatataatgatataatgggatata	60
atgatataatgatataatgatataatgggatataatgatataatgatataatgggatata	120
atgatataatgatataatgatataatgggatataatgatataatgatataatgggatata	180
tatatgatataatgatataatgatataatgggatataatgatataatgatataatgggatata	240
atgatataatgatataatgatataatgggatataatgatataatgatataatgggatata	300
atgatataatgatataatgggatataatgatataatgatataatgggatataatgggatata	360
atgatataatgatataatgggatataatgatataatgatataatgggatataatgggatata	420
tatatgatataatgatataatgggatataatgatataatgggatataatgggatata	458

<210> 93

<211> 330

<212> DNA

<213> Homo sapiens

<220>

SEL PCT 012.ST25

<221> misc_binding

<222> (1)..(330)

<223> MAR of chromosome 1 genomic contig; 306867..307196

<400> 93

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ataatatata aatatatag atatatatct atatatatca tatataaata tatatgatat   60
atatctatat atatcatata taaatatata tgatatataa atatatatga tatatatcta   120
tatatatcat atataaatat atatgatata taaatatata tgatatatat ctatatatat   180
catatataaa tatatatgat atatatctat atatcatata taaatatata tgatatatat   240
ctatatatat catatataaa tatatatgat atctatctat atatatcata tataaatata   300
tatgatatct atctatatat atcatatata                                     330

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<210> 94

<211> 353

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(353)

<223> MAR of chromosome 1 genomic contig; 636899..637251

<400> 94

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tatgtataca tatacacata tacgtatata tatacatata tacacatata cgtatatata   60
tacgtataca tacatatgta tatgtatacg tatacacaca tatgtatatg tatacgfata   120
cacacatata cgtatatatg tatacgfata cacacatata cgtatatgta tacatatata   180

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SEL PCT 012.ST25

tgtgtacata tacgtatata cgtatattgta tacatatata cgtttatgta tatatacgta 240
tatacgtata tatgtatatg tatacatata tacatatatg tgtatatatg tatatacgta 300
tatgtgtata tatacaatat acatacatgc acatatatgt gtatatgcac ata 353

<210> 95

<211> 345

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(345)

<223> MAR of chromosome 1 genomic contig; 1435510..1435854

<400> 95

atcatatata ttatatatca tatatatgat atataaaaat tatatatcat atatatgata 60
tataaaaaat atatatatca tatataatat atataatat ttatatatat aaattatata 120
taatatatat aaattatata tatcatatat atgatatata atttatatat catatatatg 180
aatatataa tatattattt atataataa tattatatat tatataatat gtaatatata 240
ttatatatta catattatat tatttataaa taatatttta taatatatat aatattatat 300
aatatagaat atttatattt atattattaca tattatataa tatat 345

<210> 96

<211> 521

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(521)

<223> MAR of chromosome 1 genomic contig; 39695..40215

<400> 96

tatatatata atagatatta tatatctatt atatatctat tatalatata atagatatta 60

tatatctatt atatatataa tagatattat atatctatta tatalataat agatattata 120

tatctattat atataatata tatctattat atattatata tctattatat ataatatata 180

tctattatat atattatata tctattatat atataataga tattatatat ctattatata 240

taatatatat ctattatata ttatatatct attatatata tgtatctatt atatatatta 300

tgtatctatt atatataata tatatctatt atatatatat tatatataat atattatata 360

tattattatat atctattata tataatatat atctattata tatattatat atctattata 420

tattattatat atctattata tataatatat atctattata tatattatat atctattata 480

tataatatat attatatata tattatatat tgtatatcta t 521

<210> 97

<211> 484

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(484)

<223> MAR of chromosome 1 genomic contig; 1286007..1286490

SEL PCT 012.ST25

<400> 97

atatcatata tattatatat catatatatg atatataaaa attatatatc atatatatga 60

tatatataaa ttatatatat catatataat atatataata tattatatat ataaattata 120

tataatatta tatataaatt atatatcaca tatatgacat ataaattata tatcacatat 180

atgatatata atttatatat cacatatatg atatataatt tatatatcat atatatgata 240

tataatttat atacatata tatgatatat aatttatata tcatatatat gatatatata 300

atataattat tatatatat atattatata ttatataata tgaatatat attatatatt 360

atataatag taatatatat tatatatatc atattatatt atttataaat aatattttat 420

aatatatata atattatata atatagaata ttatatatta tatattacat attatataat 480

atat 484

<210> 98

<211> 244

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(244)

<223> MAR of chromosome 1 genomic contig; 73556..73879

<400> 98

attatatatt atattatata atatataata atattatata attatatatt acattatata 60

atatataata atattatata ataatatata attatataat atataataat attatataat 120

attatataat attatataat atataaatat ataataatat atattatatt atataatagt 180

atatattata ttatataata tatgttatta tattatataa tataaactat tatataatat 240

SEL PCT 012.ST25

244

aata

<210> 99

<211> 463

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(463)

<223> MAR of chromosome 1 genomic contig; 179038..179500

<400> 99

tacaatatat ttctattat atatatttg tattatatat aatatacaat atattttcta 60

ttatatataa tatattttgt attatatata ttacaatata tttgtatta tataatatat 120

aatacaatat aatatattgt attatataat atataatact atataatata ttgtattata 180

tattatatat aatactatat aatatatttt attatatatt atatataata ctatataata 240

tattttatta tatattatat ataatacaat atataatata ttgtattata atacaatgta 300

ttataatgta ttatatataa tatataatac aatatataat attatatata ttatatata 360

tatatatttt gtattatata tttgtatta tatataattt gtattatata ttatatattt 420

atattataat tatgttttgc attatatatt tcatattata tat 463

<210> 100

<211> 390

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(390)

<223> MAR of chromosome 1 genomic contig; 55617..56006

<400> 100

tgtataatat atatacttta tatataatat atatacttta tatatatact atatactaata 60

atatataata tatactatat ataatatata ctaatatata taatatatac actatatata 120

atatatacta atatatatta tatatacttt atataatatata tactaatata tataatatat 180

atactttata tataatatat actaatatat ataattgtata tactttatat ataatatata 240

ctaatatata atatatatac ttatatata atatatata atatatatta tatatacttt 300

atatatatata tatatacttta tatattatat atgcttatat ataatatata cactaatata 360

taatatatat actttatata ttatatttta 390

<210> 101

<211> 582

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(582)

<223> MAR of chromosome 2 genomic contig; 1157405..1157986

<400> 101

tgtatatgta tatatacaca tacgcacata tatgtatatg tatatatata catacgcaca 60

SEL PCT 012.ST25

tatatgtata tgtatatata cacatacgcacatatatgta tatgtatatg tatatgtata 120
tatacacata tacacatatata tgtatatgtata tatatacacata tatacacata tatgtatatg 180
tatatatata cacatacacata tatatgtata tgtatatata cacatacacata tatatgtata 240
tgtatatgtata tatatacacata tacacatatata tgtatatgtata tatgtatatata tacacatatata 300
cacatatata cacatatatgta tacatatatg tgtatatata tacacatatata tatacacatatata 360
tgtatacacata tatgtgtata tatacacata tatatacacata tatacacatatata cacatatatg 420
tgtatgtata tatacacata tacatatata tgtatatgtg tatatatatt agacagatat 480
atatgtacat atacatatat atgta tatgt atagtatatat gtatatgtat atgtatatgt 540
atatgcatat ataatatata tatacacatatata tgtatatgtata ta 582

<210> 102

<211> 322

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(322)

<223> MAR of chromosome 2 genomic contig; 1858638..1858959

<400> 102

acacatatata tacacatatat atatacacat cacatatata ccatatatat acataccata 60
tatataccat atatatacat accatatata caccatatat atacatacca tatatatata 120
ccatatatat acataccata tatataccat atatatacat accatatata taccatatat 180
atacatacca tatatatata ccatatatat acataccata tatatacacc atatatatat 240
atacatatata tatacatatat atataccata tatatacacc atatatacac accatatata 300

ccatataat acaccatata ta

322

<210> 103

<211> 914

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(914)

<223> MAR of chromosome 2 genomic contig; 5712196..5713109

<400> 103

aaatataat tctatata gaaaatata attctatata tatagaatat atatagaata 60

tatattctat atatattcta tatatataga atatataat aaaacatata ttctatata 120

aaaatata ttctatata ataaaatata tattctatata tatagaatg tatataaaat 180

atatattcta tatatataga atgtatataa aatatatatt ctatatata agaattgata 240

taaaatata attctatata tatagaatgt atataaaata tatattctat atatataga 300

tatatataac atatataga aatatataa aaatatata aaatacatat ttctatata 360

aaatatata aaatacatat ttctatata aaatafatat caatacatat ttctatata 420

aaatatata aaatatata tcatatata aaaaatata aaatatata tcatatata 480

aaaatata tgaatatata ttctctatata ataaaatata tataatatata attatatata 540

taaaatata ataatatata ttatatata aaaaatata taatatata tcatatata 600

aaattatata taaatatata ttcatatata taatatata aaattattat ttcatatata 660

aaatatatt aaatatata ttctatatag aatatatatt ctatatataa aaatatata 720

taaatatatt ttctatatag aaatatata gaaatatata gaatatata aaatatata 780

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tatatatact atatatacaa tatataattat atataaaata tatatacaat atatattcta 840
 tatattaata tatagaatat atattaacat atatttcaat atattaatat atgaaatata 900
 tataaataatt tcat 914

<210> 104

<211> 370

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(370)

<223> MAR of chromosome 2 genomic contig; 5713613..5713982

<400> 104

tatttcatat ataatatata tataaaatat atatttcata tacataatat atataatata 60
 aataaaatat atatttcata tatataatat atataaatata tataaaacat atatttcata 120
 tataatatat ataaactata tatttcatat ataatatata taaactatat atttcatatata 180
 cataatatat ataatatata ttcatattat attatatata taatatatat tcatatatata 240
 taatalataa aatagatata aatatatata aatatatatt tcatatatata tatatatataa 300
 atatatatata atatatttt tatatatatat atatataatt catatatataa tataaaaaaa 360
 tatatatattc 370

<210> 105

<211> 442

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(442)

<223> MAR of chromosome 2 genomic contig; 7481647..7482088

<400> 105

atataaatta tataatatgt tatataatat ataaatatat tatataacat gttatataat 60

atataacatg ttatataata tataacatgt tatataatat ataacatgtt atataatata 120

taacatgta tataatatat tatgtaatat gttatataat atataatata ttatataaca 180

tggtatataa tatataacat gttatataat atgttatata atataaaat atattatatt 240

atatgttata taatatataa atattatata ttatatgta tataatatat aaatatatta 300

tattatatgt tatataatat ataaatatat tatattgtat gttatataat atataaatat 360

attatatgt atgttatata atataaaat atattatatt gtatgttata taatatataa 420

atatattata ttatatatgt ta 442

<210> 106

<211> 338

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(338)

<223> MAR of chromosome 2 genomic contig; 9594557..9594894

SEL PCT 012.ST25

<400> 106
 tatataaata tataccatat atataaatat atatattcca tatataaata tatatattcc 60
 atatataaa atatatatat tccatatata aatatatata ttccatatat ataaatatat 120
 atataaatat atatattcca tatatatataa tatatatata aatatatata ttccatatata 180
 aatatatata tattccatat ataaaaatat atatatttc catatatataa aatatatata 240
 tattccatat atataaatat atatatttc catatatata aatatatata tattccatat 300
 atataaatat atatatttc catatatata aatatata 338

<210> 107

<211> 364

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(364)

<223> MAR of chromosome 2 genomic contig; 10519720..10520083

<400> 107
 ttatatatat ttataaat atataaagc tatatatatt tatatatatat atattatata 60
 tattagctat atatatttat ataataatat attatatatt agctatatat atttatatat 120
 aataatatat ataagctata tatttatata tattatatat tagctatatata tatttatata 180
 taatatatta tatattagct atatatttat atataataaa taatatatat attagctata 240
 tatatttata tataataata tatataagct atatatttat atataatata ttatatatta 300
 gctatatata ttatatata ataatatatt atatatttagc tatatatatt tatatatatat 360
 atat 364

SEL PCT 012.ST25

<210> 108

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(342)

<223> MAR of chromosome 2 genomic contig; 11481943..11482284

<400> 108

tacatataat atataattat atataatata tattatatat tacatataat atatatatat 60

tacatatgta atatatatat tatatatgta atatatatta tatatgtaat atatatatta 120

tatatgtaat atatatatta tatatgtaat atatatatta tatatgtaat atatatatta 180

tatgtaatat atatatgtaa tatatatata atatatatgt aatatatata taatatatat 240

gtaatatata tataatatat atgtaatata tatattatat atatgtaata tatatcatat 300

atatgtaata tatatcatat atatgtaata tatatcatat at 342

<210> 109

<211> 415

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(415)

SEL PCT 012.ST25

<223> MAR of chromosome 2 genomic contig; 13499598..13500012

<400> 109

tatatatata tatatatata atataatata atatatatat aaatatatat aatataaatt 60

tatatatata tatttatata tacatatata aatatatatatt tatatttata tataaatata 120

tataaatata tataaatata tatttatata tacatatata aatatatatg ttcatataaa 180

tatatatgta tatatacata tataaatata tatttatatat gtatatatat aatataatat 240

ataataataa tataatatat attataataa tataatatat tatatatatat atatatataa 300

tataatatat aatatataat atataatata tatttatatat tatataatat ataaaatata 360

tatttatataa tatatatata taatatatat aaataaatat atataaagat ataaa 415

<210> 110

<211> 330

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(330)

<223> MAR of chromosome 2 genomic contig; 16370976..16371305

<400> 110

catttacata tgtatgtata agtatgtata ttacataact atacatacat acttataaat 60

atataagtat aatacatata tacttataaa tatataagta taatacatat atacttatat 120

atatataagt ataatacata cataactata catatataag tataatacat acatacttat 180

acatatataa gtataatata tacatactta tacatataag tataatacat acatacttat 240

SEL PCT 012.ST25

acatatataa gtataataca tacataactta tacatatata agtataatac ata cttatta 300

catatgtata taagtatatt acatacttat 330

<210> 111

<211> 702

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(702)

<223> MAR of chromosome 2 genomic contig; 626641..627342

<400> 111

tatatataca catatacata tataatatat atacatatac atatataatta tatataacata 60

tatattacat atatcatata tacatatata ttatatatac atatataatta tatatatcat 120

atafacatat atatattata tattatatat atcatatata catatatatt atatataatta 180

tatatatcat atatacatat atattatata tattatatat acatatatat tatatatatc 240

atalaaacat atatattata tatatcatat atacatatat attatatata ttatatatat 300

catatataca tatatatatt atatatcata tataatatat attatatata ttatatataa 360

tatatattat atatacatat atattatata tacatatata ttatatatac atatataatta 420

tatatacata tatattatat atacataat attatatata tacatatata ttatatatac 480

atatataatta tatatacata tattatatat acatatatat tatatataca tatattatat 540

atafacatat atattatata tacatatatt atatatatac atatataatta tatataacata 600

tattatatat atacatatat attatatata catatatatt atatacatat atattatata 660

tacatatata ttatatatat atataatata tatttatat at 702

SEL PCT 012.ST25

<210> 112

<211> 679

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(679)

<223> MAR of chromosome 2 genomic contig; 3196047..3196725

<400> 112

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atatattata tattcatata tcataaatat atatattata tattcatata ttatatatct   60
ataatattat atattcatat attatatatc tatatatatta tatattcata tattatatat  120
ctatttatat attcatatat tatatatcta tataatttat atattcgtat attatatatc   180
tatatattat atattcgtat attatatatc tatatatatt gtattcatat atatctatat  240
attatatata ttcatatata ttataaatta tattcatata gtatatatct attataaatg   300
tatattcata tagtatatat ctatatatta taaatataca tatattatat atttatatat  360
tatatatcca tatagatcta tatattatat atattcatat atgaatatat atatttatatg  420
tatatatatt ataaatatat ttatatagta tagatattat atagtatatg catatttata  480
ttataaataa ttacatagat atagtatat ttataaatta tatatatatta catattacat  540
gtatatattat atattataaa tacatattta catattataa atatatttat atattatgaa  600
tataatttat atattattac atatttacct atatgcatag ttatatatta taaatgca    660
ttatgtaaa tatatattt

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679

<210> 113

<211> 728

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(728)

<223> MAR of chromosome 2 genomic contig; 3196778..3197505

<400> 113

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tacataaata tatattaca atagttaa atctgatg taaatatgta ttataaat 60
ataaatatac atataatg taaatatata aatatacata tactatgtaa atatatgta 120
tatatacata tactatataa atatagaata tataaatata catatactat ataaatgt 180
aatatataaa tatatactat ataaatatac atatactata taaatgtatt tataatata 240
aaatatacat atactatata aatcatata tgaatatata atatataaat atatataata 300
tatgaatata tactcatata taaatatata tgaatatata ttataaat atagatataa 360
tatgaatata tattataat atagatat atattatg aatatatatt tataatata 420
agatatatac catatgaata tatattatac actatatgaa tatatattta taatatataa 480
atagatatat actatatgaa tatataat atatactcta tgaatatata atatatatac 540
tatatgaata tattatatac tgtatgaata tataatata agatglatac tatatgaata 600
tataatata agatatata actatatgaa tatatataat atagatat atactatg 660
aatatatatg atatatagat atatactata tgaatatata atatatagat atatattat 720
gatatatg
728

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<210> 114

<211> 413

<212> DNA

SEL PCT 012.ST25

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(413)

<223> MAR of chromosome 2 genomic contig; 2560638..2561050

<400> 114

atataaatat atatttatat attttatata aatatatata ttatatatt ttatatataa 60

tatatatatt tatatatatt tatataaata tatatattta tatatattta tataaatata 120

taaatatata tatttatata aatatataaa atatataaat atatttatat aaatatataa 180

aaatatataa tatatttata taaatatata aaatatataa atatatattat atataaatat 240

ataaaatata taaatatctt tatatatataa tatataaaat atataaatat ctttatatat 300

aaatatataa aatatataaa tatatttata tataaatata taaaatatat aaatatattt 360

atatacaaat atataaaata tataaatata ttatatata aatatataaa ata 413

<210> 115

<211> 361

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(361)

<223> MAR of chromosome 2 genomic contig; 4965309..4965669

SEL PCT 012.ST25

<400> 115

tatacgtata tatacatata tatacgtata tatatacata tatatacgtata tatatacata 60

tgatatatg tgtgtacatg tatatatata catatgtaca tatatatgta cacatatata 120

tatacatata tatgtacaca tatacatata tatgtacaca tatacatata catatatatg 180

tacacatata tatacatata tatgtacaca catatatata catatatatg tacacacata 240

tatacgtata tatgtacaca catatatatg tatatatatg tacacacata tatacgtata 300

tatatgtaca cacatatata tacgtatata tatgtacaca tatatatata cgtatatata 360

t 361

<210> 116

<211> 325

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(325)

<223> MAR of chromosome 2 genomic contig; 5258150..5258474

<400> 116

tacacacaca tatacatata tacatatata cgtgtatacgtata tatacgtata tacgtatata 60

tacatatatg tatacgtata cgtatatatg tatatatata tatatgtata cgtatacgtata 120

tatacgtata tatacatata tgtatacgtata tacgtatata cgtatatata catatatgta 180

tacgtatacgtata tatacgtata tatatacata catatgtata cgtatacgtata tatatgtata 240

tatacgtata tgtatacgtata tacatatata cgtatatata cgtatatgta tatgtatata 300

cgtatatgta tatatgtata tatac 325

SEL PCT 012.ST25

<210> 117

<211> 1508

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1508)

<223> MAR of chromosome 2 genomic contig; 6057499..6059006

<400> 117

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atataatata tataaattat ataatatata aaaattaata tataatatat ataaattata   60
taatatataa attaattata taatatatat aaattatata atatatataat taattatata   120
atatatataa attatataat acatatataat taattatata atatatataat tatataatat   180
atacaaatta tatactatat taattatata ttatataatt aattatataa tatatatataa   240
ttatatatta ttaaattaat tatataatat ataaattata taatatataa attaattata   300
taatatataa attatataat atataaatta attatataat atataaatta tataatatat   360
aaattaattg tataatatat aaattaatta tataatatat aatatataat taataaataa   420
ttatatatta attatataat taataaataa ataataaata tatataatta atatatata   480
tacaatcatat atatacata tagattatat aatagttata tattatataa taaattatat   540
ataatataia ataaacatat ataacatatg ttatatatta cataatatag tataatatat   600
aacatatgtt atatattaca taatatagta taatatataa catgttatat attacataat   660
atagtataat atataacata tgttatatat tacataatat agtataatat ataacatatg   720
ttatatatta cataatatag tataatatat aacatatgtt atatattaca taatatagta   780
taatatataa catatgttat atattacata atatagtata atatatataa tatgttatat   840

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SEL PCT 012.ST25

attacataat atagtataat atataacata tggatatat tacataatat agtataatat 900
 ataacatatg ttatatatta cataatatag tataatatat aacatatggt atatattaca 960
 taatatagta taatatataa catatggtat atattacata ataggtata atatataaca 1020
 tatgttatat attacataat atagtataat atataacata tggatatat tacataatat 1080
 agtataatat ataacatatg ttatatatta cataatatag tataatatat aacatatggt 1140
 atatattaca taatatagta taatatataa catgttatat attacataat atagtataat 1200
 atataacata tgctatatat tacataatat agtataatat ataggtata tattacataa 1260
 tatagtataa tatataacat atgttatata ttacatatta tagtataata tatatgttat 1320
 atattatata ataggtata atatataatg tatgttatat attatataat atagtataat 1380
 atataacatg ttatatatta tataatatag tataatatat atgttatata ttatatataa 1440
 tagtataata tataatatat gttatatatt atataatata gtataatata tatgttatat 1500
 attatata 1508

<210> 118

<211> 415

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(415)

<223> MAR of chromosome 2 genomic contig; 7996866..7997280

<400> 118

caattatata atatacatat tatataattg tataaattat acaatcatat aattatatta 60
 tatataatat acatataata taattatata taattatata attttataat ataattatat 120

SEL PCT 012.ST25

ataattatat aattatatat aatatatatt ataattatat atataatata tatattatat 180
 atattatata taatatataa ataatatata taatatatat ataattatat ataataatat 240
 atgtaatata tataatatat atataatata ttattataa ttatatatta tatatatatt 300
 ataatatata taattataaa taatatatat tataatatat ataataatat atatataatt 360
 atatataata atatatatta taattatata taataatata tataatttat ataatt 415

<210> 119

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(526)

<223> MAR of chromosome 2 genomic contig; 8300930..8301455

<400> 119

tatatcatat gatatttat acaatatatc atataatatg atatattata tgatatattg 60
 tacaatatat catatgatat atgatattat atacaatata tcatataagg tatatttat 120
 atcatatata atatatataa taatatatga tataatatat gatatatgat atataatata 180
 tgatatatga tatatgatat ataatatatg atatatgata tatgatatat aatatatgat 240
 atatgatata tgatatataa tatatgatat atgatatatg atatgatata tgatatatga 300
 tataatatat gatataatat atgatatata ttatatgata tataatatat gatataattt 360
 atatgataia taatatatga tatataatat ataatatatg atatgatata tattatatca 420
 tatataatat ataatatatt atatgatata tattatatat ttatatatat tatatatata 480
 aactatataa caatatataca tattatgtgt ataatatata ttacat 526

SEL PCT 012.ST25

<210> 120

<211> 402

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(402)

<223> MAR of chromosome 2 genomic contig; 8576553..8576954

<400> 120

atgtatatta tataacaatat agtatatcat atatatgtata tattatatag taatgtatta 60

tatataaigt ataagtata aatataaat atatactaca tactatacta ttatatatac 120

tatatattat atagtataca tatactatat aatagtctat atattatact atataatatg 180

ctatatatta tactatataa tatgctatat attatactat ataatatgct atatattata 240

ctatataata tgctatatat tatactatat aatatactat ataatatgct atatattata 300

ctatataata tactatatat tatactatat aatatactat ataacatact atatattata 360

tatgatacat atactatatt acatatataa tatafatata ta 402

<210> 121

<211> 477

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

SEL PCT 012.ST25

<222> (1)..(477)

<223> MAR of chromosome 2 genomic contig; 8785649..8786125

<400> 121

tatttatata tatatttata tatatattta tatatattta tatataiatl tatatatata 60

tttatatata tatttatata ttatatata tatattttta tatatttata tatatattta 120

tatatttata tatatttata ttatatata tatttatata tatttatata tatttatata 180

tatattttta tatatattta tatatatata ttatatata ttatatata ttatatata 240

tatttatata tatatttata tatatattca tatatattta tatatatatt catatatatt 300

tatatatata ttcatatata ttatatata tatttatata tatatttata tatatttata 360

tatatttata tatatattta tatatatatt tatatatata tatttatata tatatttata 420

tatatatatt tatatatata ttatatata tatatttata tatatattta tatatat 477

<210> 122

<211> 773

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(773)

<223> MAR of chromosome 2 genomic contig; 10064737..10065509

<400> 122

atatttatata tattacatat atatttatatt gtatataata tatatattat attgtatata 60

atatatatat tatattgtat ataatatata tatttatattg tatataatat atatattata 120

SEL PCT 012.ST25

ttgtatataa tatattatat tgtatatatt atattgtata tattatattg tataacaatat 180
 atattatatt gtatacaata tatattatat tgtatataat atattatatt gtatataata 240
 tattatattg tatatattat attgtatata atatattata ttgtatataa tatattatat 300
 tgtatatatt atattgtata taatatatta tatgtatata atatagtga tactatatta 360
 tataatatat attatataca atatataata tattgtatat catatatgat atattgtata 420
 taatatataa tatatgatat attgtatata atatattata tatgatatat tgtatattat 480
 atattatata tgatafattg tatattatat attatattat gatatattga tattatatat 540
 tatatattgt atataatatg ttatatattg tatataatat gttatatatt atatattgta 600
 tatatgttat atattatgta ttgtatataa tatgttatat attatattat gtatataatg 660
 tattatatat tataatattat atatattgta tataatgtat tatatattgt atattatata 720
 ttatatattg tatataatat attatataca ttatatata tattatatat tgt 773

<210> 123

<211> 1554

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1554)

<223> MAR of chromosome 2 genomic contig; 1039775..1041328

<400> 123

ataatatatt aaatgtatat ataatatatt aaatataaat atatttataa tatataaata 60
 ttatataaa tataaaatat atattaaata taaatatata faaaatatat attaaatata 120
 taaaatataa atatatatta aatatatatt aaatatataa aatataaata tatattaaat 180

SEL PCT 012.ST25

atatttlaaa tatataaaat ataaatatat attaaatata tttaaatat attaaatata	240
aatatatatt aaatatatt taaatatatt aaatataaat acatatatta aatatatt	300
atatatataa aatatataaa atataaatat atattaaata tatataaaat atatatgta	360
aatatafaaa agatatataa aatataaata tatattaaat atatatataaa tatatatata	420
ttaaatatat atattaaata taaatatata taaaatatata atatatgtat taaatatata	480
tattaaatat aaatatatgt attaaatata tattaaatat gaatatatgt attaaatata	540
tattaaatat aaatatatgt aitatatata tagaatataa atatatgtat taaatatagt	600
atattaaata taaatatata taaaatatat attaaatatg aatatatata aaatatat	660
attaaaaata tatataatat aaatatatat aaaatatata tattaaaaaat atatatata	720
taaatatata taaaatatat atattaaaaa tatatatataa atatatatat taaaatatata	780
tataaaatat atattatfaaa aatatatata aaatatatat attaaaaata tatattaaat	840
ataaatatat atattaaaaa tatattatfaa atataactat atattaaata tatattaaat	900
ataactatat attaaatata tattaaatat aactatatat taaatatata ttaaatatata	960
ctatatatta aatatattt aaatataact atattatfaa tatattatfaa atataactat	1020
atattaaata tatattfaaat ataactatat attaaatata tattaaatat aactatatat	1080
taaatatata tgaaatatata ctatatatta aatatattt aaatataact atagtatta	1140
aatataaata tatgtctfaa atatatatta aatataaata tatgtattfaa atatatatta	1200
aatataaata tgtgtattfaa atatatatta aatataaata tgtgtattfaa atatatatta	1260
aatataaata tgtgtattfaa atatatatta aatataaata tgtgtattfaa atactatat	1320
taaatataaa tatagtatt aaatatatat taaatatataa tatattatfaa atatatatat	1380
taaatataaa tatattatfaa atataaatat atattatfaa tatatatatt aaatataaat	1440
atatatataaa tatatatatt aaatataaat ataaatatata aatatattt aaatataaat	1500
acatatatta aatatatgta ttaaatatat atataaaata tatgtattfaa atat	1554

<210> 124

<211> 650

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(650)

<223> MAR of chromosome 2 genomic contig; 3944813..3945462

<400> 124

catgalatat tatgtataat atatattata gattacatat aaattatata tataatatat 60

aaattatata tatataatat tatataatat attatatata ttatacaatt atataatata 120

tataatatac aattatataa tatataatat acaattatat aatatataat acaatataat 180

atatatttaa tatattatat aatacatatt taatatatta tatattatat gttatatact 240

aaatatataa tatgtattta atatatacta ttatatatgt aatatattat ataatttatg 300

taacatatta tatattatat atgcaatata ttacatgltta catatatatt acatataata 360

tatgtaatat ataatafaca ctatattatt atagtatata atatactata ttatgtaatt 420

atataatata gtatattata cactatatta tattatcata taattatata ttatatata 480

tattacatat atattatgta atataatag caatatgtta catatataat atatatgtat 540

tatatagtat atatactata gtatatataa aatatatgct ataatatata ttttatatat 600

tataaatac atataatgta tcatatatta tatataatat atttataat 650

<210> 125

<211> 441

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(441)

<223> MAR of chromosome 2 genomic contig; 5314265..5314705

<400> 125

tataaatata tatgaaatat atataaatta tatataattt atatatacat atataaatta 60

tatataaatt atatataaat tatatatata tatataaatt atatattata tataaaaattg 120

tatatattta tatataaatt gtatatataa ttatatata aattgtatat ataatttata 180

tatacaatgt atatattaat ttatatatac aittgtatata taatttatat atacattgta 240

tatacaattt atatatacat tgtatatata atttatatat acattgtata tacaatttat 300

atataaatia tattatttat atatagtata tataaatata tatactatat ataaattata 360

tatttattta tatatttat taittatata taaattatat attatttata tatacattat 420

atataaatta tatattattt a 441

<210> 126

<211> 1169

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1169)

<223> MAR of chromosome 2 genomic contig; 5953971..5955139

<400> 126

SEL PCT 012.ST25

atgiattcat attatatt tatataaaa taatatat tcatattata tatttatata 60

taaataatat atattcatat tatatattta tatataaata tataatatat ttatgtataa 120

ataatatata tattcatatt atatatttct atataaataa tatatatatt catattatat 180

atttatatat aaatatataa tatatttata tataaatata taatatattt atatataata 240

tatatattca tatttatatat ttatatataa atatataata tatttatata taaataatat 300

atatattcat attatatt tatataaaa taatatatat tcatattata tatttatata 360

taaataatat atattcatat tatataclta tatataaata atatatttcc atatttatata 420

cttatatata aatatatat attcatatta tatatttata taaaaataat atatattcat 480

atttatatt tatatatatt atatatttcc atatttatata ttatatatt ctatatattc 540

atatttatata ttatatata aataatgiat attcatatta tatatttata tataaataat 600

gtatattcat atttatatt tatataaaa tatatattca tatttatatat ttatatataa 660

atatatttcc atatttatata ttatatata aatatattt catatttat atttatataa 720

aatatatata ttcatattat atttatatat aaatatatat attcatatat atatttatat 780

ataatatata tattcatatt atatatttat atataatata tatattcata ttatatattt 840

atatataaat aatatatata ttcatattat atatttatat ataaataatg tatattcata 900

ttatatattt atatataaat aatgtatatt catatttat atttatatat aaatatatat 960

attcatatta tatatttga tataaatata tattcatatt atatatttgt atatatttcc 1020

atatatttt atatataaat atataatatt catatttat ataaatatat atattcatat 1080

tatatattta tatatafaaa taatatatat tcatattatt tatatatata aatatatat 1140

attcatatta ttatatata taaataata 1169

<210> 127

<211> 653

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(653)

<223> MAR of chromosome 2 genomic contig; 6427669..6428321

<400> 127

tatatatgta tacatatatg tatatatgtg tatatatgta tacatatatg tatatatgtg	60
tatatatgta tacatatatg tatatatgtg tatatatgta tacatatatg tatatatgtg	120
tatatatgta tacatatatg tatatatgtg tatatatgta tacatatatg tatatatgtg	180
tatatatgta tacatatatg tatatatgtg tatatatgta tacatatatg tatacatgtg	240
tacatgtgta tacatatatg tatacatgtg tacatgtgta tacatatatg tatacatgtg	300
tacatgtgta tacatatatg tatatatgtg tatacatata tgtatatatg tgtatatatg	360
tatacatata tgtatataag tgtatatatg tgtatatgta tataagtgta tatatgtgta	420
tatgtatata agtgtatata tgtgtatatg tatataagtg tatatatgtg tatatatgta	480
tacatatatg tatatatgtg tatatatgtg tatatgtata taagtgata tatgtgtata	540
tatgtataca tatatatgtg tatatatgta tacatatatg tatatatgtg tatatatgta	600
tacatatatg taaataitg tatatatgtg tatatgtata taagtgata tat	653

<210> 128

<211> 414

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(414)

SEL PCT 012.ST25

<223> MAR of chromosome 2 genomic contig; 10890453..10890866

<400> 128

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tatattttgt aaatatatat atagtaaata tatgtaaata tatatatttt gtaaatatat   60
atatattttg taaatatatg taaatatata tattttgtaa atatatgtaa atatatatat   120
ttgtaaata taigtaaata tatatatttt gtaaatatat gtaaatatat atattttgta   180
aatatatgta aatatatata tttgtaaat ttatgtaaat atatatattt tgtaaatata   240
tgtaaatata tatatatttt gtaaatatat atacatatat attttgtaa tatataaaca   300
tatatatttt ataaatatat ttataaatat atatatgtta aatatattta taaatatatt   360
tataatatat atattgtaaa tatgtttata aatatatata ttgtatatat aaat       414
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<210> 129

<211> 496

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(496)

<223> MAR of chromosome 2 genomic contig; 13952568..13953063

<400> 129

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taatatatat attatatatt atatatgtta tatataatat acatatata tattatatat   60
tgtatatata atatacatat tatatattat atattgtata tataatatat atattatata   120
ttatatattg tatataatat atacatatata tatattatat attgtatata taatatatat   180
attatatatt atatatgtta tatataatat acatatata tattatatat tgtatatata   240
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SEL PCT 012.ST25

atatacatat tatatattat atattgtata tataatatac atattatata ttatatattg 300
 tatatataat atacatatta tatattataf attgtatafa taatatacat attatatatt 360
 atatatigta tatataatat acatattata tattatataf tgtatatata atatacatat 420
 tatatattat atattgtata tataatatac atattatata ttatatattg tatatataat 480
 atacatatta tatatt 496

<210> 130

<211> 317

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(317)

<223> MAR of chromosome 2 genomic contig; 16942865..16943181

<400> 130

tctcctagta gttatatata tatatatgtg tatatatata tctcctagta gatatatata 60
 tatatatatc cttagtagata tatatatata tatatcctag tagatatata tatatatata 120
 tcttagtagt tatatatata tatatatcct aacagttata tatatatata tcttagtagt 180
 tatatatata tatatcctag tagttatata tatatatata tcttagtagt tatatatata 240
 tatatcctag tagttatata tatatatatc cttagtagta tatatatata ttatatatta 300
 tataatatat atataat 317

<210> 131

<211> 464

<212> DNA

SEL PCT 012.ST25

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(464)

<223> MAR of chromosome 2 genomic contig; 17217049..17217512

<400> 131

acatactata tatatacaca tactatatat actatataca gtatatagta tacatatact 60
 atacatatac atatactata catatacata tacatatact aagtatacgt atatacagta 120
 catagtatat gtatactata tagtatgtat atatagcata tagtatgcgt atactctata 180
 tagcatatag tatgcatata cgctatatag catatagtat gcatatacta tatatagtat 240
 agagtaigcg tatactatat atatagtata gagtatgcgt atactatata tatagtatag 300
 agtatgcgta tactatatat atagtataga gtatgcgtat actatatata tagtatagag 360
 tatgcgtata ctatatatat agtatagagt atgcgtatac tatatatata gtatagagta 420
 tgcgtatact atatatatag tatagagtat gtatatatat agta 464

<210> 132

<211> 430

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(430)

<223> MAR of chromosome 2 genomic contig; 19647266..19647695

SEL PCT 012.ST25

<400> 132

tgtaaataata tgtaaataata taattatatt atatattata taaaaataata atatataata 60

tataatataat aaactatata ttaatafaat atatataaac tattatataa atacatatta 120

aatatattat attttaata ttatattatt aaatataata tafatttaatt atttatatat 180

taaatatata atatatttaa taattatata atatatagca taatttatat ttatattata 240

tataacattt tatatttata ttatattta tatatattta atttatatt atatttatatt 300

tatatttata ttatataata cataattata tatattttca taatttatat aataaagaaa 360

tgtatatttg ttatataata tatatattat ataatttatt atatattata taatatatat 420

tatataatat 430

<210> 133

<211> 2131

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(2131)

<223> MAR of chromosome 2 genomic contig; 20481223..20483353

<400> 133

tatatataaa tatatttata ttaatatat atttatataa atatatttt atataaatat 60

atatttaata taaataatctt tatatttaatt atatatttaa tataaatatc ttatattta 120

atatatattt atatataaat atatatttat atttaatat tataaatatt taatatatcgt 180

ttatatttaa tatatatttc tatataaata tatttatatt aacatatatt tatatataaa 240

SEL PCT 012.ST25

tatafftata ttaatatat ttacatatata atatattat atgtaatat ttacatatata	300
aatatattta tatttaatat atagcatat gtaatatat ttatatftaa taatatatt	360
atataaatat atttatatt aataatatt atatataaat atatttatat ttaatatata	420
ttaaatatat atttatatt aatatatt aataattat atatattat attaatata	480
tatttatat aaacatatat ttatatftaa tatattatt atataaacat atatttatat	540
ttaatatata ttatatataa acatatatt atatttaata tatatttata ttaatatat	600
tatatataaa catatatfta tatttaatat atatttatat taaatatata ttatatataa	660
acatatatt atatttaata tatatttata ttaatatat atttatatt aatatatata	720
tattaaatat atatttatat ttaatatata ttatatftaa atatattt atattaaata	780
tatttatatt taatatatat ttatatftaa tatattftaa atatttaata tatatttata	840
ttaatatat acatatatat ttatatftaa tatatacata tatatttata ttaatatat	900
acatatatat ttatatftaa tatatacata tatatttata ttaatatat aaatttatat	960
ttatatata taaaaatata tatttatatt taatatatat aaatatatat ttatatftaa	1020
tatatatt tatattgaat atatacataa atatattt atatttaata tataaacata	1080
tatttatatt tatattftaa atatattt atatttaata tataaatata tatttatatt	1140
taatatatt atatacata atatattt atttaatat ttatatata gatattfta	1200
tatttaatat atttatgtt attaatatat ttatatftaa tatatttata tattaatata	1260
ttatatatt atatttatat attaatatat ttatatfta tatttatatt ttatatatt	1320
atatattat atatttatat ttatatatat ttatatatat taataaatt atatttata	1380
tatttatata ttaataaatt tatatttatt acagtatat aaatatatt atatttata	1440
cagtatatata aataattfta tattttatag ttatatfaat atatttatat ttatacagt	1500
tatataaata tatttatatt ttatacagtt atataaatat atttatatt tatacagtt	1560
tataaatata ttatatatt atacagttat ataaatatat ttatatfta tacagttata	1620
taaatatatt tatatttatt acagtatat aaatatatt atatttata cagtatatata	1680
aatatattta tattttatag agttatatata atatattt attttatata gttatatata	1740

SEL PCT 012.ST25

tatatttatg tttatacat ttatataaat atatttatat ttataacatt tgtatttaaat 1800
 atatatttat atataaatat attttatatt taatataatt atataaaat atatattgat 1860
 atttaatatata tatttatata taaatatata ttgatattta atagtttat atataaatat 1920
 atatttatat ttaatatata tgtttatata tcaatatata ttatatatta atatatattt 1980
 acatataaat atatatattat attgatata tatttatatt tgatatatat ttatatata 2040
 ttaatatatt tacatttgat atatatatta tatatatata tatatttaca ttgatatat 2100
 attttatata tattaatat ttacatttg a 2131

<210> 134

<211> 842

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(842)

<223> MAR of chromosome 2 genomic contig; 20483478..20484319

<400> 134

tatatattta tgtttaatat atatttatag ataaatatat atttacgttt aatatatatt 60
 tatagataaa tatatatatta cgtttaatat atatttatct ataaatatat ttacgtttaa 120
 tatatatatta tatattaata tatttatggt taatatatat ttatatatat taatatattt 180
 atgtttaata tatatttata tattaatat ttatgttta atatatttat atatattaat 240
 atatttatgt ttaatatata ttatatggt aatatattta ggtatatata tatttatatg 300
 ttaatatata ttatatatta tatatttat ttatatataa aagtatatat aatatataaa 360
 tatttatata attatttat agtattttta tatatatatta tatataaatt ttatatattt 420

SEL PCT 012.ST25

tatatatata aatatatatt tatatatata tttatatat aaatatatat ttatatatac 480
 attatatata taaatatata tatttatatt ttatatataa atatatatat ttatatatac 540
 atttatatata tttatatat gtaaatatat atataaatt tatatatgti atatataatt 600
 ataaatttta tatatatatt tatatatata atatatatata tatatatataa tttatatat 660
 attatatata ttatatttt atatattata ttttatttta tatatattta tatgtatat 720
 atatttatat ttatatttt ttttatttta tatattttat atatataatt atatgtat 780
 attatatata ttatatatta taaatatat tataatatt atattatata tttattat 840
 at 842

<210> 135

<211> 645

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(645)

<223> MAR of chromosome 2 genomic contig; 20897566..20898210

<400> 135

gtatatttat attatatatt atataatata tattatatat taataaatta tatataatat 60
 aatatatatg tatatttata ttatgttat aatatacata taattatata tgtatgtata 120
 catgtatata tatacgtata tgtgtatatg tatacatata ggtatatgtg tacatgtata 180
 catataggta tatgtatatg tatacatgta tacatataat ataattacat atgtatgtat 240
 acatacatat gtaattatat tatatatgta tatgtatatt tatataatat ataatatgia 300
 ttatatatta tacatgcata ttatatgta tattatatat acacatatata tataattata 360

SEL PCT 012.ST25

tatgtatgta tatatacaca tatatatatta tattatataat gtatattata tacatatatt 420

tatattatat atgtatatat atttatcata ttatatgta atatgcatgt gtaataaata 480

atatacacat ttatatatgt atattatata catatatatta tattgtatat gtatatatat 540

ttatatatat ttgtatatca tatatttata tattgtatat ttatgtatat tatatatatta 600

tatattatat atgtattata taatatatat gtaaatatat attat 645

<210> 136

<211> 722

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(722)

<223> MAR of chromosome 2 genomic contig; 21664541..21665262

<400> 136

tataatatat attatattct atataaatg taaaatatat attatattct atataatgta 60

ttatatatag aatataatat attctatgta ttctataatc tatataaatc atattatata 120

ttatatagaa tattataaat aatatattct atattatata tagaatatat tctatatgtt 180

tatattctat atattatata tgaaatagta tataaaatat atataatata tataaaatat 240

gatatataat atatatataaa taatatataa tgtataatat ataaaataat atataatgta 300

taatatataa aataatatat aatgtataat atataaaata atatatatg tatattatat 360

aaaataatat ataatgtata ttatatataa aataatatat aatgtatatt atatatataaa 420

taatatataa tgatatataa ataatatata atatatata tataaaataa tatataatat 480

attatatata aaataatata tattatatat aaaataatat ataatatatt atatatataaa 540

SEL PCT 012.ST25

taatatatat tatatatataa ataatatata atattatata tataaataa tatatattat 600
 atataaaata atatatatta tatataaaat aatataatat atattatata taaaataata 660
 tataatatat tatataaaaa tataaatata ttatataaaa atataaaata taaaatatta 720
 ca 722

<210> 137

<211> 305

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(305)

<223> MAR of chromosome 2 genomic contig; 22834991..22835295

<400> 137

aatataaaat atatgatata taatacgtat tatatatgta taatacgtat tatatattaa 60
 tatataatat ataatacata ttatatatgt atataatata tactaatata tataatgtat 120
 acattatata ttacataat atataatata taatatagaa ttataattat atataatata 180
 taatatataa ttatatatat tattatatat gtatttatat tatatataat atattatata 240
 taatatatat tatataatta tataagtata taattatgtt atatacataa taatatataa 300
 tatat 305

<210> 138

<211> 352

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(352)

<223> MAR of chromosome 2 genomic contig; 25277762..25278113

<400> 138

taatatatat aatatattat atattatata taatatattt tataatatat aaaatatatt 60

atatataata tataatatat ttataatat atataatata ttatatataa tatataatat 120

attttataat atataataa tattaiatat attatatatt tatatttatt tatatatcca 180

taaatatata ttatatata atatatatta taatatatta tatataatat ataatatatt 240

ttataatata ttataatata taatatataa tatattttat aatatatata atataataa 300

tattatatat ttatatttat ttatatattc ataaatatat atatttatat ta 352

<210> 139

<211> 342

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(342)

<223> MAR of chromosome 2 genomic contig; 25378452..25378793

<400> 139

tatgtacata tatattttat atattatata taatatatat tatatgatat atataatata 60

SEL PCT 012.ST25

ttatataata taatatataa aatatatata atatatatta tattatataa attatattat 120
 atatatcata taataiatatt tatataattat ataatatata ttatattata tatattttat 180
 atattatatt atatatata tataicatat aatatatatt atattatata ttttatatat 240
 ta tataatat atattatata tttttatata ttatataata tatattatat attttatata 300
 ttatataata catatattat atataatata atatatatta ta 342

<210> 140

<211> 663

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(663)

<223> MAR of chromosome 2 genomic contig; 30209437..30210099

<400> 140

aatatataatt acataattgta tatatagtat atgtaatgta tataatatag tatattctat 60
 attgtataat agtaatatat agtatatgat atactatata ttacttatca tatatacaat 120
 atatatataa tegtatatatt tatattatat attgtatata tgtaatatat gatattgtaca 180
 tatgttatat atgtatataa tatactatat tatatatigt atattatata catatataac 240
 actattatag aatatataat atagcatatt atatacaata tagcatatag aatatataat 300
 atagcatatt atataataa tagtatatta tatacaatat ataatatagc atattatata 360
 taatatataa tagtatatta tatacaatat ataatatagc atatacaata tagtatataa 420
 tatataatat agcatataga atatagtata ttatatataa tatataatat agcatgtaca 480
 atatagtatg ttatatataa tatataatat agcatataga atatagtata ttatatataa 540

SEL PCT 012.ST25

tatataatat agcatatata atatattata ttatatacaa tatataatat agcatatata 600

atatagtata ttatatacaa tatataatac agcatatata atatagtata ttacatacag 660

tat 663

<210> 141

<211> 1200

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1200)

<223> MAR of chromosome 2 genomic contig; 31725089..31726288

<400> 141

tgtacttata tattataatg tatatataaa gtatatactt tatatatact tatataattat 60

aatgtatatt attgtatata agtatatatac ataatatata cttacatatg ctcacatata 120

ttataatgta tattgtatat attatataca tattatatat gtataatgta tatatacatt 180

atatatgtat aatgtatata tacattatat atgtataatg tatatataca ttatatatgt 240

ataatgtata taatatatac aatatatgta taatatataa tatatacaat atatgtataa 300

tatacaatat atgtataaia tacaatatat gtatagtata taatatatat tatatatgta 360

tagtatatta tatattatat atgtatagta tataatatgt ataagtata tattataata 420

tattatatat aatatctata acaatataat atattgtata tattatatat aatatatatt 480

tatataatat atattatata taatatatta tgtatttatt tatattatat ataataataa 540

tatatataat ataaataata ttattatat attaatataa atatttatat taatatatat 600

ttattatata taaataatat ctatgatata aataatatat aatatacatg tatatgttat 660

SEL PCT 012.ST25

aatatataca tataatatac atgtgtatat atactataca tgtatatata acatgtatat 720
 atatacatgt atatatatta tgtatacatg tatagtatat atacatgtat atatafacat 780
 atatactata caigtatata tacatgtata tatatacata tatactatac atgtatatat 840
 acatgtatat atacacatat atactataca tgtatatata catgtatata tatacatgta 900
 tgttatatac attattataa tatacatata tagtatacat tatatacatt atataatag 960
 cattattata atataatata cattattata atatacatta ttataatata atatacatta 1020
 ttataatata cattattata atatacatta taataatata cattattata atatacatta 1080
 taatatgaa gtatatatac tataatatat gtatatatta taatgtatat aatatacatt 1140
 attatatata agtatgtatt atataaagt atatattata atatatgtat atacatatat 1200

<210> 142

<211> 325

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(325)

<223> MAR of chromosome 2 genomic config; 32147252..32147576

<400> 142

aaatacaaat attatttat atataatata taatataata tattatttta tatataatat 60
 ataatttata attatatataa tatataatat atttatatat aatatataat ttattatat 120
 attaattata tatataataa atatatataa tatataattt tatttatatat taattatata 180
 tataataaat atatatataa tataataata ttatatatat tatatatataa tataaatatt 240
 tatataatat ataataaat atatttattt atatatataa atataatata taattatata 300

aatatataat atatttatat ataac

325

<210> 143

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(507)

<223> MAR of chromosome 2 genomic contig; 32312662..32313168

<400> 143

attatttata taaatattat atttatatta ttatataaaa tatttatatt atattattta 60

tataaatatt atatttatat tatttatata aatattatat ttatattatt tatataaata 120

ttatatttat attatttata taaatattat atttatatta ttatataaaa tatttatatt 180

atattattta tataaatatt atatttatat tatttatata aatattatat ttatattatt 240

tatataaata ttatatttat attatttata taaatattta ttatattat ttatataaat 300

attatattta tattatttat ataaatattt atttatatta ttatataaaa tatttatatta 360

tatttatata aataatatat aaataaatat ttataatga tataaatatt atttatatta 420

ttattttaa taaataatat aaattaatat aaatattaat attatttatt ttattataaa 480

taatatataat attatatatta tatttat

507

<210> 144

<211> 339

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(339)

<223> MAR of chromosome 2 genomic contig; 33651118..33651456

<400> 144

aaatataata tattatttat atataatata aatgatatat tatgtatata taaaatataa 60

ataatatatt atgtatatat aaaatataaa tattatttat atataaaata taaataatat 120

ttatatataa aatataaata ttatatatt tatatafaaa atataaataa tatattattt 180

atatataaaa taiaaataat atattattta tatataaata atatataaaa tataaatata 240

tattatatat aaataaaata tatatattat atatataaat ttatatataa tatataaat 300

ataatatata tatttaatat ttattatata atatataat 339

<210> 145

<211> 461

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(461)

<223> MAR of chromosome 2 genomic contig; 45073053..45073513

<400> 145

tggtatata tatatacgtg tacatatata tatatacatg tgtatatata tacgtgtaca 60

SEL PCT 012.ST25

tatacatata tacatgtgta tatatatgta catatacata tatacatgtg tatacatata 120
 tatatacatg facatatata tatatacatg tgtatacata catatatata tgtacatata 180
 catatatata tgtgtatact facatatata catgtacata facatatata catgtgtata 240
 tatacatata tacacgtaca tatatacatata facatgtaca tatatacatg tatacatata 300
 tacatgtaca tatgtacaia tatatacatgta facatatata catgtacata tgtacatata 360
 tacatgtata catatatata tgtacatatg facatatata catgtataca tatatacata 420
 tgtacatacg cacagataga catatatata tatgtacata c 461

<210> 146

<211> 1162

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1162)

<223> MAR of chromosome 2 genomic contig; 45487691..45488852

<400> 146

attatattat ctatatataat ctattatatac tattatatta tctatataat atctattata 60
 tatattatat tatctatata aatctattat atatattata ttatctatat aaatctatta 120
 tatatattat attatctata tatctattat atattatatt atattatatt atatafaata 180
 tctattatat atattatatt atattatatt atatafaata tctattatat atattatatt 240
 atctatataa tatctattat atattatata ttatattata tataatatct attatatata 300
 ttatattata ttatataaa tatctattat atctattata tatattatat atatctatta 360
 tatctattat atatattata tataatatct attatatcta ttatatatat tatatataat 420

SEL PCT 012.ST25

atctattata tctattatat tatattatat ataatatcta ttatatctat tatatatatt 480
 atatatact attatatcta ttatatatat tatatataat atctattata tctattatat 540
 atattatata taatatctat tatatctatt atatattata tatataatat ctattatata 600
 tattatatat tatatatata atatctatta tatctattat atctattata tatatatcta 660
 ttatatctat tatatatatt atatacataa tatctattat atctattata tatattatat 720
 atataatac tattatatct attatatata tactatctat tatatctatt atatatatta 780
 tatatgtact atctattata tctattatat ctattatata tatactatct attatatcta 840
 ttatatatat tatatatata ctatctatta tatctattat atatattata tatatactat 900
 ctattatata tctattatat atattatttt atattatata tagtatctat tacatatatt 960
 atattatatt atatataata tctattatat atattatat atattataaa taatatatat 1020
 aatatctglt atatataata gatattatat ataatatata atatataaa tagatattat 1080
 atatattata ttatataata tataatatat aatataatta atataaaaata tatataatat 1140
 ataattaata taatatgtaa ta 1162

<210> 147

<211> 562

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(562)

<223> MAR of chromosome 2 genomic contig; 45516233..45516794

<400> 147

acatattata tatattatat ataatatata ttatatatac atattatata tattatatat 60

SEL PCT 012.ST25

aatatatatt atatatacat attatatata ttatatatac atatatatat tgtatataat 120
 atatacatat tatatatatt atatatacat attatatatt atatataata tatacatatt 180
 atatattata tataaatatt atatattata tataaatatt atatatataa atattatata 240
 ttatatataa atattatata tcttatatat aaatataata tataatatat ataattatta 300
 tatattatat ataaatatta tatattattat ataattattat atataatata taaatatata 360
 tattatataa atattgtata tattatataa atattatata tattatatat aaatattata 420
 tatattatat aaatatatat aaatatataa aatatataaa tatgtaaaat ttattattat 480
 aaatatataa tataaatata taaatataaa tataaattat atataatata taatatatta 540
 tacataatat atactatata ta 562

<210> 148

<211> 801

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(801)

<223> MAR of chromosome 2 genomic contig; 45727251..45728051

<400> 148

atatatatat ataatatata catatataga atatatatat tatttatattc tatatataga 60
 atatatatat agaatatata tatatagaat atatatatag aatatatata tagaatatat 120
 atatagaata tatatataga atatatatat atagaatata tatatagaat atatatatat 180
 agaatatata tatatagaat atatatatat agaatatata tatatagaat atatatatag 240
 aatatatata tagaatatat atatatagaa tatatatata gaatatatat atatagaata 300

SEL PCT 012.ST25

tatatataga atatatatat atagaatata tatatagaat atatatatat agaatatata 360
 tatagaatat atatatatag aatatatata tagaatatat atatatagaa tatatatata 420
 gaatatatat atatagaata tatatataga atatatatat atagaatata tatatagaat 480
 atatatatat agaatafata tatagaatat atatatatag aatatatata tagaatatat 540
 atatatagaa tatatatata gaatatatat atatagaata tatatataga atatatatat 600
 atagaatata tatatagaat atatatatat agtatatata gaatatatat ataatgtata 660
 tatagaatat atatatatag aatatatata tagaatatat atatatagaa tatatatata 720
 gaatatatat atatagaata tatatataga atatatatat atatagaata tatatataga 780
 atatatatat atatatagaa t 801

<210> 149

<211> 346

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(346)

<223> MAR of chromosome 2 genomic contig; 50937238..50937583

<400> 149

taaaattata tatattatat ataatatata atatattata tataatatat attataatat 60
 atataatata tattatataa aatatattct atagaatata tattctatta tataatatat 120
 attctattat aatatatatt atatataata tatattctat tataatatat attatatata 180
 atatattcta ttatgatata tattatatat aataacatat attatatata atatatttc 240
 tattatataa aatatatatt atataaaaata tatattctat tatataaaat atatattata 300

SEL PCT 012.ST25

taaaatata attatattat ataaaatata tattatacta tatata 346

<210> 150

<211> 462

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(462)

<223> MAR of chromosome 2 genomic contig; 55672627..55673088

<400> 150

taaatata ttatatatta tattatata aatatattta tattatata tactataatt 60

tatatataat atatattata tatataatat atttataata tatatcatat aaataatata 120

tatttataat atatatcata taaataatat atatttataa tagatatcat ataaataata 180

tatatttata atagatatca tataaataat atatatttat aatagatatc atataaataa 240

tatatattta taatagatat catataaata atatatatft ataatatata tcataataat 300

aatatatatt tataatata atcatataaa taatatatat ttataatata tatcatataa 360

ataatatata ttataatag atatcatata aatatatat atttataata gatatcatat 420

aaataatata tatttataat agatatcata taaataatat at 462

<210> 151

<211> 401

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(401)

<223> MAR of chromosome 2 genomic contig; 56081352..56081752

<400> 151

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tatacatgta tgtattcgta tatgtatgtt atatatgtat atgtgttata tacatatata    60
tatatacatg tatatgtgtt atatacatat acatatatac atgtatatgt gttatatata    120
tatacatata tacatgtata tgtgttatat acatatatat atatacatgt atatgtgtta    180
tatacatgtg tatgtgtata tgttatatata catatatgtg tatgtgcatg tgtatatata    240
catataigta tatgtgtata tgttatatata catatatgta tatgtgtatg tgtatacgta    300
tatatacata tatgtgtatg tgtatgtgta tacgtatata tatacatata tgtgtatgtg    360
tatacgtaca tatacatata tgtgtatgtg tatacgtaca t                               401
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<210> 152

<211> 765

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(765)

<223> MAR of chromosome 2 genomic contig; 56404208..56404972

<400> 152

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tataattat aaagaatata tattatataa tatgtaaaga atatatatta tataatatgt    60
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SEL PCT 012.ST25

aaagaatata tattatata tatgtaaaga atatatatta tatataatat ataaagaata 120
 tatattatat aatatataaa gaatatatat tatatattat ataaagaata tatattatat 180
 ataatatata aagaatatat aatatataat atataaagaa tatatattat atataatata 240
 taaagaatat atattatata taatatataa agaatatata ttatatatta tataaagaat 300
 acatatatat aatatataaa gaatatatat tatatataat atataaagaa tatatattat 360
 atataatata taaagaatat atattatata taatatataa agaatatata ttatatataa 420
 tatataaaga atatatatta tatataatat ataaagaata tatattatat atattatata 480
 aagaatatta tatattatat aaagaatata taitatatat aatatataaa gaataaacat 540
 atatactata tataaagaat atacattata tatactatat ataaagaata tacattatat 600
 atactatata taaagaatat atataatata taaagaatat acattatata taatatataa 660
 agaatatatt atatatatta taaagaatac attataatat aaagaatata ttatatataa 720
 tataaagaat acattataat atataaagaa tatatataat atata 765

<210> 153

<211> 443

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(443)

<223> MAR of chromosome 2 genomic contig; 61953416..61953858

<400> 153

tttatatatt atagataaaa ttatatata ttacaigtaa tatataatat gtaaaatata 60
 ttatattaca tatataatat ataatatgta aaatatatta tattacatat ataatatata 120

SEL PCT 012.ST25

atatgtaaaa tatattatat tacatatata atataaaata ttacatatata tatattttac 180
 ataaatatat attatctatt acatatittat tatatgtaat aatatgtaca tatgtataaa 240
 tatgtatata ttaiacata tgtatatatt atatatatat atatatgtat atattatata 300
 tacatatata tgtatatatt atattatata tacatatata tgtatatatt atattatata 360
 tacatatata tgtatatatt atattatata tacatatata tgtatatata ttataaatat 420
 gtataataaa gatttatatg taa 443

<210> 154

<211> 372

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(372)

<223> MAR of chromosome 2 genomic contig; 62076211..62076582

<400> 154

tatatataat tatatatgta attatataac agtatatata attatataat attatcaata 60
 tatataatta tatataatta tcaatatata taattatcaa tagatatata taattatata 120
 tataattata tataattata tatcagtata tataattata taattatata tatgtatata 180
 taattatag tataaattat ctataagtat atataactat aatatataac aattatatat 240
 acttatgtat aattatatat actgatatat aattatatac aattatatat atcaattata 300
 tataaattat tataattata tatacatata tataattata tatataaatt atatgtaatt 360
 atataattac ac 372

<210> 155

SEL PCT 012.ST25

<211> 484

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(484)

<223> MAR of chromosome 2 genomic contig; 62158581..62159064

<400> 155

attatata atataaaat tacaatatt atttattat atattatata cataatata 60

atattcata tataatata attatata atataaaata tatattatgt ataattatata 120

ataaaatata ttatataatt atataaaca taaaatata ataataata attatata 180

atataaaata tatataaat ataaaatata tattatattgt aattataiat aatataaaat 240

atatatataa tataaaatata atattatata taattataat ataaaatata tattatata 300

tatatattat ataaaatata tattatata aattatata tatataaaat atattatata 360

tataattata taatataaaa tatatattgt atataattat atataatata aatatatata 420

aatatatgaa ataagatata tactatata aatatata attacatat aagatatata 480

tcatt 484

<210> 156

<211> 644

<212> DNA

<213> Homo sapiens

<220>

SEL PCT 012.ST25

<221> misc_binding

<222> (1)..(644)

<223> MAR of chromosome 2 genomic contig; 68145036..68145679

<400> 156

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tatatatg ctaatatg taatatat tatatatg ctaatatata tatgctaata 60
tataatat attatatata aatatataat atatatatat ataaatatat aatatattat 120
atataaatat ataataaaa tatataaat atatactata ttatatatta tgtataacat 180
ataatacata ttgttatat ataatatata tattatatgt tatatatat atattatata 240
taataataca atatatatta tatattatat gttatatatt atatatata tataatataa 300
cataatatat aatatatatt atattatata ttacatatat tagcaatat atatatataa 360
tatataaat atataaaaa tatataaaa aatataaaat atatatcaaa atataaacta 420
tataatatat aaaaatatat tatataaat atataaaaat ataaactata taatatataa 480
aaatatatta tatataaat ataaaaatat attatatatt atatatataa atatatata 540
tataatatat aaaaatatat ataaaatata aaaaatatat ataaaatata aaaaatatat 600
aaaataatat aaaatatata atatatata atataatata taat 644
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<210> 157

<211> 530

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(530)

<223> MAR of chromosome 2 genomic contig; 71257289..71257818

SEL PCT 012.ST25

<400> 157

atatctatta tatttatata ctttatataa attatatcta ttatatltat atactttata 60

taaatiatat ctatttatatt tatatacttt atataaatta tatctattat atttatatac 120

tttatataaa ttatatctat tatatttata tactttatat aaattatatac tatttatatt 180

atatacttta tataaafata taatttatatt tatatacttt atataaatat aattataaat 240

atatttatat actttatata aatataatta taaatataatt tatatacttt atataaatat 300

aattataaat atatttatat actttatata aatataatta taaatataatt tatatacttt 360

ataattatat gttatattta taatttatatt tatataattc ataattatat acattatgtt 420

tatagtata taatttataa ttatatacat tatatttata ttatataat ttataaattat 480

ataaattata taaattatat aaattatctt taatttatat tatataatct 530

<210> 158

<211> 337

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(337)

<223> MAR of chromosome 2 genomic contig; 73413615..73413951

<400> 158

acttatatta tatataacta tatttatgta tattaatata aattaatgat atataatata 60

tttaattatat attatttatat gtgatataaa atacttatat ttatactgta tatatgtata 120

tacacacata tatgtatata tgtatatata cacatatgta tatatgtata tgtatatatg 180

SEL PCT 012.ST25

tatactgtat atatgtatat acacacatat atgtatatat gtatatgtat atatgtatac 240

tgtatatatg tatatacata tatacatata tgatatatat cacatatatg tgatatataa 300

atatatttat ataaatataa tattaatatt tatatta 337

<210> 159

<211> 1340

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1340)

<223> MAR of chromosome 2 genomic contig; 77011049..77012388

<400> 159

atgtatttta tatagtatat attatgtatt atattgatat aattatataa caattatlla 60

tatataaaat aacaaataaa tatataaaat aataaatata tatttattat taaataataa 120

atatataatt attattaaat aataaatata taaagtaata aatatatatt tatatatata 180

ataattcata tatatttata tattaaataa ttcatatata tttaaataat taatacatat 240

ttaaataatt aatatatatt tatataatat atatttatat attaaataat taatatatat 300

ttatagatta aattaatata tttttatata tttaaataaa tttaatatat tatatatlla 360

tataatttaa attaataat ttatataatt taattlaatt taatataatt aaaatatatt 420

aaacattata taatatataa tatattlaatt atataatata tatttaatat ataatafatt 480

taatataata tatattlaatt atataatata tatttaatat ataatatatt taatatataa 540

tatatllaatt atataatata tatttaatat ataatatatt taatatataa tatatatlla 600

atatataata tatttaatat ataatatata tttaatatat aatatattta atatataata 660

SEL PCT 012.ST25

tatattlaa gtataatata ttaatatat aatatataa taatgtataa tatattlaa 720
 atataatata tatttgatgt ataatatatt taatatatat ttgatgtata atatatataa 780
 tatataatat atatttgatg tataatatat ttaatatata atatatattt gatgtataat 840
 atattlaata tataatatat atttgatgta taatatattt aatatataat atatatattga 900
 tgtataatat attlaatat taatatatat ttgatgtata atatatataa tatataatat 960
 atatttgatg tataatatat ttaatatata atatatattt gatgtataat atattlaata 1020
 tataatatat atttgatata taatatattt aatatataat atatatattga tatatatata 1080
 atatatataa tatatttgat atataatat ttaatatat aatatataa ttgatataa 1140
 tatattlaa atataatat tatttgatgt ataatatatt taatatataa tatatatattg 1200
 atatatataa tattlaatat ataatatata ttgatatat aatatattta atatatataa 1260
 tatattgat atataatat ttttctatt aattattat atataatat taaatatata 1320
 ttaattlaa atatatataa 1340

<210> 160

<211> 937

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(937)

<223> MAR of chromosome 2 genomic contig; 78226855..78227791

<400> 160

tgtgtatata tacatatatg tgtatctatg tgtatatata catatgtgta tatatacata 60

tatgtgtata tatacatatg tgtatatatg tgtatatatg tgtatatata catatatgig 120

SEL PCT 012.ST25

tatatatgtg tatatatgtg tatatataca tatatgtgta tatatgtgta tatatacata 180
 tgggtatata tgggtatata tacatatatg tgggtatatg tgggtatata catatatgtg 240
 tatatatgtg tatatataca tatatgtgta tatatgtgta tatatgtgta tatatacata 300
 tatgtgtata tatgtgtata tatacatata tgggtatata tgggtatata tacatatatg 360
 tgggtatatg tgggtatgtg tgggtatata catatatgtg tatatacata catatatgtg 420
 tatatatgtg tatatataca tatatgtata tatacatata tgggtatata tgggtatata 480
 tacatatatg tgggtatatg tgggtatata catatatgtg tatacataca tatatgtgta 540
 tatatgtgta tatatacata tatgtgtata catacatata tgggtatata tgggtatata 600
 tacatatatg tgggtatata catatatgtg tgggtatgtg tatacataca tatatgtgtg 660
 tatatatgtg tatacatatg tgggtatatg tgggtatata catatatgtg tgggtatatg 720
 tgggtatata catatatgtg tgggtatatg tgggtatata catatatgtg tgggtatatg 780
 tgggtatata catatatgtg tgggtatatg tgggtatata catatatgtg tgggtatatg 840
 tgggtatata catatatgtg tgggtatatg tgggtatata catatatgtg tgggtatatg 900
 tgggtatata catatatgtg tgggtatatg tgggtat 937

<210> 161

<211> 1350

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1350)

<223> MAR of chromosome 2 genomic contig; 79287748..79289097

<400> 161

SEL PCT 012.ST25

tatatatait atatataag taactgttct attatatata tattatatat attctgttc	60
tattatatat tatatatatt atattatata ttatatgtaa tatattatat atattataag	120
taatataita tatatattat atgtaataata ttatatatat tatatgtaat atattatata	180
tattatatgc aatatgttat atatattata tgcaatatgt tatatatatt atagcaata	240
tattatatat attatatgca atatattata tataatatat gtaatatatt atattatata	300
ttatatgtaa tatcttatat attatatgta atatattata tatattatat gtaatatctt	360
atatataita tatgtaatat attatatatt atagtaata tattatctta tatatattat	420
atgtaataia ttatatata tattatatgt aatatatait atagtaata tattacatat	480
tatatgtaat atatattata tgtaatatat tacatattat atgtaataata tattatatgt	540
aatatattac atattatatg taatatatta catattatat gtaatatatt atagtatta	600
tatgtaatat attatatgta ttatatgtaa tatattatat gtattatatg tattatatgt	660
aatatattat atgtattata tgtaatatat tatatattat atgtaattat attatatgta	720
atatattata ttatatatta tatatattat atgtaataata ttatatata tattatatat	780
attatatgta atatattata ttatatatta tatatattat atgtaataata ttatatata	840
tattatatat attatatgta atatattata ttatatatta tatatattat atgtaataata	900
ttatatata tattatatat attatatgta atatattata ttatatatta tatatattat	960
atgtaataata ttatatata tattatatat attatatgta atatattata ttatatatta	1020
tatatattat atgtaataata ttatatata tattatatat attatatgta atatattata	1080
ttatatatta tatatattat atgtaataata ttatatata tattatatat attatatgta	1140
atatattata ttatatatta tatatattat atgtaataata ttatatatta tatatattat	1200
attatatatt atagtaata tattatatata ttattatat attatatatt atagtaata	1260
tattatatata ttattatat atattatat attattata tataatatat tatattatat	1320
atattatatatt atatataatt ctgttcta	1350

<210> 162

<211> 332

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_difference

<222> (1)..(332)

<223> MAR of chromosome 2 genomic contig; 81142998..81143329

<400> 162

ctatgtatat aactatatat aactattata taacttaata agatatataa ctattatata 60

acttaataag ttatatataa ctattatata taacttaata agttatatat aactattata 120

taacttaata agttatatat aactattata taacttatta agttatatat aactatatat 180

aacttaataa gttatatata actattatat aacttaataa gttatatata actattatat 240

aacttaataa gttatatata actattatat aacttaataa gttatatata actatata 300

acttatatac aacttattaa gctatatata ta 332

<210> 163

<211> 327

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(327)

<223> MAR of chromosome 2 genomic contig; 84019536..84019862

SEL PCT 012.ST25

<400> 163

actgacagta tacatactgt atatataac agtatgtata catatacagt atgtatacta 60

tatacagtat gtatactgta tatatatata cagtatgtat actgtatata tatacagtat 120

gtatacgtat gtatactgta tatatgtatt atagtgtata tatgtattat agtgtatata 180

tgtattatat atattatagt gtatgtatta tatgtgtata tacatataat atattataca 240

tatacatatg cacaatatgt atatgtatta tatgtattca tatacatata tgtatatgta 300

taatatatgt atacatataa tacacat 327

<210> 164

<211> 407

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(407)

<223> MAR of chromosome 2 genomic contig; 1448030..1448436

<400> 164

tatataatat atattacata tatattatat ctatattatt tatattacat atgtaata 60

tattatattt atattattta tataatatat tatatatatt atattattta tatgtaatat 120

atttatattg ttatatata ttatatatt attatttata tataatacat atttatatt 180

tattatttat atataatata tataataaat atataatata tataaaaaata tatatatatta 240

atataatcat aatatatatt atatatatta tatataatat atataattgt acatatattt 300

atttatata ttatatatat aatatatatt ataaafataa tatataaata tttttataaa 360

tatatataaa tatttatattt atacattata ttatatata tattata 407

SEL PCT 012.ST25

<210> 165

<211> 1959

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1959)

<223> MAR of chromosome 2 genomic contig; 2117630..2119588

<400> 165

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tatacatgtt atagtgata tagtatacta atatataatg tatgtatgtg tatacatata    60
cacatataat atacacatat ataatatata tagtatataa taatgtataa tatataatat    120
ataatataaa aigtatagta tactacatat ttatatatag tatatagtat gcatagtaca    180
tatatactat atatgtagta tactatagtg tatatatagt acaccatata tagtataaat    240
atactatata gtatgtgtac tatatatata ctatatagta tatacagtat acatatatag    300
tataacctata ctatatagta tatatagtgt gcgtatacta tatagtatat atagtgtgcg    360
tatactatat agtatatata gtgtgcgtat actatatagt atatatagtg tgcgtatact    420
atatagtata tatagtgtgc gtatactata tagtatatat agtatacata tatagtgtgc    480
gtatactata tagtatatat agtatacata tatagtatgc gtatactata tatagtatac    540
atatatagta tatctagagt atatgtagta tgtatagtat atatagtcta catactgtat    600
atacagtata tatatactct atagtatact atacagtata gtatactata tagtatataa    660
tatatgtata ctatagaaac aactatata tagtatacta tatatactat atactatata    720
ctatatatag tatactatat atactacata ctatatatag tgtatgtata gtatatataa    780
actatatata gtgtatatag tatatatatt atatataata tatattatat tatattatac    840
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SEL PCT 012.ST25

tatatattat atglatatta tagtatatta tactattata tattatatat tatattatat 900
 attatataat ataataaat tatatattat aaaatatata ttttatatt atatatattt 960
 aaatatitta taatatatat ttataaat atatatata attatttat atataatata 1020
 aaatataata aatatattat aatatatatt ttataaatat aatatattata tattataaaa 1080
 atataaatat ataataatatt atatatata tatagtataa tatataatat gttatatagt 1140
 atcttatact attatactat atatatata tagtgtatat atagtatact atatatagtg 1200
 tatatagtggt atactatagt gtatatagtg tatactatag tgtatatagt gtatactata 1260
 tacactgtat atagttagtg atactatata cactgtatat agtagtgtat actatataca 1320
 ctgtatatag tagtgtatac tatatacact gtatatagta gtgtatacta tatacactgt 1380
 atatagtagt gtatactata tacactgtat atagttagtg atactatata cactgtatat 1440
 agtagtgtat actatataca ctgtatatag tagtgtatac tatatacact gtatatagta 1500
 gtgtatacta tatacactgt atatatagta tattatatat actatatatg tatatatagt 1560
 atacatatat attatatata cagtatatat agtatatata ctatgtagta tatatagtat 1620
 atatactata tagtatgtat agtatactat atagtatata tagtatatta tatagtatat 1680
 atactatata gtatatatag tataatgtat atatagtata tatactatat agtatatata 1740
 gtatatgtta tatatagtat atgtatatata tagtatacat agtatgtata tatagtatat 1800
 atagtataca tatatagtat gtacacagta tatatagtcct atagtatac tacatatagt 1860
 atacatgtat actatactac atatagtata catgtatact atactacata tagtatacat 1920
 gtatagtata ctacatatat tatacatgta tagaatact 1959

<210> 166

<211> 520

<212> DNA

<213> Homo sapiens

<220>

SEL PCT 012.ST25

<221> misc_binding

<222> (1)..(520)

<223> MAR of chromosome 2 genomic contig; 2119984..2120503

<400> 166

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tatgtatgca tcgtatacat atatagtata tatatgtatg catcgtatac atatatacag   60
tatatatagt atgcacgta tacatacagt atactatata tacagtatat acagtatact   120
atatatacag tatatacagt atactatata tacagtatat acagtatact gtatatacag   180
tatatacagt atatatagta tactatatat acagtatata tactatgtat tctatatata   240
gtatagtgtg catagtatac atatagtata cactatacta tatatagfat actatatata   300
cctatatag tatatatagt atactatata tagtatatat gtatactata tatagtgtat   360
atatatacta tatatagtg atatatatac tatatatagt atatatatac actatatatt   420
gtatagtata gtgtatatat agtatagfat atgtatatat acacatgfat acatgtatat   480
atgtatacta atatatacta atatatgtat aaatatatat                          520
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<210> 167

<211> 954

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(954)

<223> MAR of chromosome 2 genomic contig; 2578285..2579238

<400> 167

SEL PCT 012.ST25

tattatatat aactttataa tatataatat atattatata taactttata atatataata 60
 tatattatat ataactttat aatatataat atatattata tataacttta taatatataa 120
 tatatattat atataacttt ataatatata atatatatta tatataactt tataatatat 180
 aatatatatt atatataact ttataatata taatatatat tatatataac ttataatat 240
 ataatatata ttatatataa ctttataata tataatatat attatatata actttataat 300
 atataatata tattatatat aactttataa tatataatat atattatata taactttata 360
 atatataata tatattatat actatatata atatataact ttataatata taatatatat 420
 tatatactat atataacttt ataatatata atatatatta tatattatat ataactttat 480
 aatatataat atatattata tataacttta taatatataa tgtatattat atattatata 540
 ttatatatta tatataactt tataatatat aatgtatatt atatattata tataacttta 600
 taatatataa tatataatat aatatataac ttataatat atatacata tattatatat 660
 aactttataa tatatatcat atattatata taactataat atatatatca tatattatat 720
 ataactataa tatatatatc atataattata tataacttta taatatatat atcatatatt 780
 atatataact ttataatata tatcatatat tatatataac ttataatat atatcatata 840
 ttatatataa ctttataata tatattatat ataactttat aatatatatc atatattata 900
 tataacttta taatatatat catatattat atataacttt ataatatata tcat 954

<210> 168

<211> 452

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(452)

<223> MAR of chromosome 2 genomic contig; 3836217..3836668

SEL PCT 012.ST25

<400> 168

tttatatata aatatataac ttatatatat ttatatataa tacatatata tcttatatat 60

ataaaatata tatacatatt tatatatataa atacatatgt attatatata ttatatata 120

atacatatgt attatatata attatataat acatatgtat tatatacaat tatataatac 180

atatttataa atatatatat ttatatattat atatatattat atataaataa atatatattt 240

atagatttat ttatatataat atatatattat ataaatatat attatatat atttatataa 300

atataattt atatatattt ctatatatat atataaatat atgtataaat atatatattt 360

atacatatat tcatataaat atatatattt atacatatgt ttatatgaat atatatattat 420

acatgtaatt atatatatat atatttatat at 452

<210> 169

<211> 417

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(417)

<223> MAR of chromosome 2 genomic contig; 3837666..3838082

<400> 169

gatatatata ttatatataa tatatatata aagagatata ttatatatt tatttatata 60

aatatatttc ttatatataa gatatatgta aatatattta ttatatataa tatatttata 120

tatgtaaata tatatttata tatttatata ttatatatt tatttatata aatatatata 180

ttatatatt tatttatata tataaaaaata tataaatata aatatatata aatatatata 240

SEL PCT 012.ST25

attataaata tagaaataaa talaaatata aatatataaa tatatatataa tataaatata 300
 tataaatata aatatatata aatataaata tataaatgta taaatatata aatataaata 360
 tatataaata tgtataaata tataaatata taaatatata aaaatatata taaatac 417

<210> 170

<211> 1197

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1197)

<223> MAR of chromosome 2 genomic contig; 6294846..6296042

<400> 170

tatatactaa tatgtatata taaatatata aatatatata cacgtgtata tataaatata 60
 tatgtatata taaatatata tacatatatg tatataaaaa tatatacgta tatacgata 120
 tacgtatata tagatatata cgtatatatg tatatacgta tatatagata tatacgata 180
 tacgtatata tagatatata cgtatatatg tatatacgta tacatgtgta tatacgata 240
 tacacatata cgtatatatg tgtatatatg tatatgtata cattatatat acgtatatat 300
 acatatatgt atacatgtat atataaatat atacatatat gtatatatta tacatatatg 360
 tatatatat atatatatta tatataatata atatatata tataatatat atatatata 420
 taatatatata attatatata atatatata tattatatat aatatatata tatataatata 480
 attatatatg tacatatgta cataatgtat atagtatat atataatata tatgcacatg 540
 tatatatat atagtatat tatatatata tatgtatata tgtacatat atatatatg 600
 atagtacat attatatata catatgtata tatgtacata ttatatatac atagtatat 660

SEL PCT 012.ST25

atgtacatat tatatatata tatgtatata tgtacatat atatatatat atgtatatat 720
 gtgcatgcat atataatata taatatatta tagattataa tattatatac atatcatata 780
 ttatatactt atatatatat gtatatatta tatacatatt atatatata tacatataat 840
 atatgtatat aatatatata tatattatat attatatata atacattatg ttatatatta 900
 tgttatataa tatataattat ataatatata tatattatat ataatatata catatataat 960
 aaataatata taattatata tataatatat gcatataaat atgtaatata ttttatatta 1020
 tatatgatca tatataatat gacatattat atatgattat atatatgata tattatatat 1080
 gattatatat attatatata aatatatgat tatatataat catatatata aatatatgat 1140
 tatatgatta tatataaata tatatatatg attatatgat tatatataat tgattat 1197

<210> 171

<211> 362

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(362)

<223> MAR of chromosome 2 genomic contig; 6506971..6507332

<400> 171

tatatatagt gtatactata tatagctat atgcacacat aaactatata tacagtatat 60
 aatatgcgta tactatatac acagtatata ctacatgat actatatata gtatataaga 120
 tatatactat gtatataata tatatactag gtatatatat ccatatatat actatatact 180
 atagtatata catatatatg tacgtatata tgtatatgta catatatatg tagtatgtat 240
 atatatatat atatacacac tatagtatat acatatatat actatatata ccctatatag 300

SEL PCT 012.ST25

agtatattat atacagtata ctatatatac tatatatacc ctatatagag catgtctaig 360

ct 362

<210> 172

<211> 2578

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(2578)

<223> MAR of chromosome 2 genomic contig; 6507395..6509972

<400> 172

ggtatactat atatactata gagtatactt tatagtatat atacctatat tatatatata 60

tacatacact gtagtagtata tatgggtatat atactatata tggcatatat agtttatata 120

tatactatat atgggtatata tagtttatat atatactata tatgggtatat atagtttatata 180

tataccatat atgggtatata tagtttatat agtacatata gtatatatac aactgtata 240

gtatatatta ttagtagtatat atactatata tactgtatat atagtataaa tactatatat 300

agtatacact atatactata cactatatat actatatact atatactata tatagtatac 360

tatataglat atagtatact ctatatgtac tatagagtat actatatata ctatacataa 420

aataatttta tatatagtagc agcgtatact atatactata tatagtatac tctatatgta 480

ctatagagtg tagtatatac tatacagtat actctatata tactatacag tacactatat 540

atactatata tagtatattt tatatatagt acagtatata cagtatatat attatactat 600

atgtagtaca tatatagttt agtatatata gtatatatac tatactatat gtactacata 660

tataatagta tatataglat atatactata ctatatgtag tacatatata gtttagtata 720

SEL PCT 012.ST25

tatactagta tatagatata tagttatata gatataaat agtatatata gtatatatag 780
catatatagt atatatgcta tatatactat atagcatata ctatatacta tatatacagt 840
atatatagca tatatagcat atataatata tatacttttg atatacatac tatatacagt 900
atatatagta tatatactgt ataaatafac tatatatacc gtatatgcac actatatgct 960
atatatactia tatacactat atacagtata tatagtacac tatactatat aaagtatata 1020
tagtatacag tacactatac tatatacatt atatatagta tataattac atagtatata 1080
gtatataaai agtatatata gtatatacag tatatatata gcatacttta tatagtatac 1140
acagtatata gatactatat atgctatata tagtatctat atactgtata ttatatatac 1200
taatatagta tatatgtata tatatactgt atataaata tatacatata tagtatatat 1260
actatacata cacactatac atatgtatat atactataca tactatatac tatataicct 1320
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atatatactia tatagtatat tatatatact atataccata tatactatat atactgtata 1440
gtatactata tatactatat agtatactgt atatactata tagtatactg tatatactat 1500
atagtatact gtatatactia tatagtatac tgtatatact atatagtata ctgtatatac 1560
tatatagtat actgtatata ctatatatac tatatagtat actgtatata ctatatagta 1620
tactatatat actatatacc atatatacta tgtatatact atatatagta tatactatgt 1680
atagtctata tatagtatat atagtatata tgctatatat agtatatata gtatatatgc 1740
tatatataca gtctatatat agtatatata ctatatagac tatatatata gcatatatac 1800
tatatatact atataaata tatatggat atacatagta tctatatgta gtatctatat 1860
atagtaacca tatatactat atataggtac tatatatagt atataactt tatatagata 1920
ctatatatag tatatact ttatatagta tatatagtat atgtagcata tatagtatat 1980
atagtatata tagtatatag tatgtatagt atatafatat tatattgtat atacagtata 2040
tatactgtat atactatata aatagtlacat acagtatata cagtatatat gtactatata 2100
tagtatatac agtatatata gtatatatgt accatatata gtatatacag tatatacagt 2160
atatatgcac tatatggtat atacagtata tacagtatat atgtactata taaatagaat 2220

SEL PCT 012.ST25

atactctata tacagtatat atgtactata taaatata cactatgtac agtatatatg 2280
 tactatataa atagtatata cactatatac agtatatatg tactatatag tgtatacagt 2340
 atatacagta tataggtaact atatatggta tatacagtat atatgcacta tatggatatat 2400
 acagtatata tgcactatat atggatatata cagtatatat gtactatata tggatatatac 2460
 agtatatatg tactatatat ggtataatata gtatatatgt actatatatg gtatatatacag 2520
 ttatatacagt atatatgcac tatatatggg atatacagta tacatgtact atatatgg 2578

<210> 173

<211> 598

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(598)

<223> MAR of chromosome 2 genomic config; 7770400..7770997

<400> 173

gtgtattgta tatacatata cgtatctacg tatatacata tatgtattgt atatacatat 60
 atgtattgta tatacatata tgtatatacgt tatatacata tatgtattgt atatacatat 120
 atgtatatac gtatatatac atagtatat acgtatatag atatacatat atagtattg 180
 tatatacata tatgtatata catatatata tatatatga tatacatata tatgtattgt 240
 atatacatat acaatatatg tatatatata tatacatata caatatatgt atatacatat 300
 atagtattg tatatacata tatatgtatt gtatatatac atattgatat acatatatgt 360
 atatatatac atatgcatac atgtatatat acatatatgc atatatgtat atatacatat 420
 atacatatgt acatatatac atatatatac atagtatat atacatatat acatatgtac 480

SEL PCT 012.ST25

atatatacat atatacatat gtacataiat acatatatac atatgtacat atatacatat 540

atagatatat atacacatat atagatatatac ttatatgtat atatacatatac atacatat 598

<210> 174

<211> 1048

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1048)

<223> MAR of chromosome 2 genomic contig; 8332422..8333469

<400> 174

cattatatat aatatataat atattattat atataatata tataacatta tatatagtat 60

atattacata tataacatat attatatata acatatataa aatataacat attatatata 120

acatatataa aatataacat atattatata taacatatat aaaatataac atattattata 180

tataacatgt ataaaatata acatatatta tatataacat gtataaaata taacatatat 240

tatataacat gtataaaata taacatatat tatatatataa atattattata ttttatatat 300

tataaataaa atattattata ttttatatat tataacatat tatataaata atattataa 360

tataacatat attatatataa taatatataa catattattat ataaataata tataacataa 420

catattattat ataacatatata acatatataa tatattatat ataacatatata acatatataa 480

tattattatat ataacatatata acatatataa tatattatat ataacatatata acatatatta 540

tattatatat aacatatataa atattattata ttatatataa catataacat atattattatt 600

atatataaata tataacatat attattattat atataacata taacatatat tatattatat 660

ataatatata acatatatat tatatatata atataacata taacatatat tatatatata 720

SEL PCT 012.ST25

ataatatata acatatatta tatataatat aatatataac atatattata tataatataa 780
 tatataacat atattatata taatataata tataacatat attatataata atataatata 840
 taacatatat tatatataat ataatatata acatatatta tatataatat aatatataac 900
 atatattata tataatataa tatataacat atataatata taacatatag catatataat 960
 atataacata taacatatat tatatataac atataacata tattatatat aacatataac 1020
 atatataata tgtaacatta tatataac 1048

<210> 175

<211> 375

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(375)

<223> MAR of chromosome 2 genomic contig; 8909678..8910052

<400> 175

tatatacaca tatatacgta tgaatatata tacacatata cgtatgaata tatataccca 60
 tatacgtatg aatatacaca tatatafacg tacgtatata tatacacata tatacgtacg 120
 tatatatata cacatatata cgtacgtata tatatacaca tatatacgta cgaatatata 180
 tacacatata tacgtacgaa tatatatata catatatacg tacgaatata tatacacata 240
 tatacgtacg aatatatata cacatatata cgtacgaata tatatacaca tatatacgta 300
 cgaatatata tacacatata tacgtacgaa tatatatata catatatacg tacgaatata 360
 tatacacata tatak 375

<210> 176

SEL PCT 012.ST25

<211> 563

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(563)

<223> MAR of chromosome 2 genomic contig; 10572503..10573065

<400> 176

atttataata tataatgtata aatatatgta tatatttata tttaaataa tgtatatata 60

tttatattta aatatatgta tatatatgta tatttaaata tacgtgtata tatttatatt 120

taaataatagc tgtatatatt tatattttaa tataacgtgta tatatttata tttaaataa 180

cgtgtatata ttatatatta aatatatgta tatatatgta tatttaaata tacgtgtata 240

tatttatatt taaataatagc tgtatatatt tatattttaa tataacgtgta tatttatatt 300

taaataatagc tgtatatatta tatttaaata tatgtatgta tttaaataa tatattttaa 360

gtatatattt ataaatgtat acatgtatat ataaatatat atattttaa tatatatgta 420

tatatatatt tatatatgta tataagtata tatatatgta aatatatgta tatatttata 480

tatttatata agtatatata tttaaataa tgtatatatt tataatatat attttaaata 540

tatatttata tatttatatt ata 563

<210> 177

<211> 595

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(595)

<223> MAR of chromosome 2 genomic contig; 11609694..11610288

<400> 177

tataaatact atatatagta tatataatat tatatatact atatataaat atatgtagta 60

taaataatat ataataiaga tatataatat aatataatat gttataaata taaatatatt 120

tatataattt aatttataat atataatata taatatataa tttaatttta taatatataa 180

tatataattt aattttataa tatataatat ataatatgta aattatatat aatttaatat 240

atctaaatta tataatttaa atataaatat aatataaata tatctaacat aatatacata 300

acataaatat atatatgata tatagtacat ataaatatat atagtacata tagtatatat 360

aaatatatag tatatataaa tatagtatat ataaatatat agtatatata tagtatatat 420

aaatatatag tatatataaa tatatatagt atatataaat aatatatagt atataaataa 480

tatatattat faaatataat aataatttat tatatatact atattattt atgtattata 540

ttatatatat tattttatat ttaatatata ttattttata tatttatatt aatat 595

<210> 178

<211> 662

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(662)

<223> MAR of chromosome 2 genomic contig; 12699804..12700465

SEL PCT 012.ST25

<400> 178

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gtatatatat atatatatat atgggtgtata tatatatata tatatatggt gtatatatat   60
atatatatat atgggtgtata tatatatata tgggtgtatat atatatatgc tgtatatata   120
tatgggtatat atatatggia tatatatatt tgctatatat atagcagatc tgctatatat   180
atatatttgc tatatatata gcagatctgc tatatatatt tgctatatat atgctatata   240
tatgctacat atatgctata tatatgctat atatatgcta tatatatgct atatatatgc   300
tatatataig ctacatatat gctatatata tgctacatat atgctatata tatgctatat   360
atatatgcta tatatatgct atatatatat gctatatata tgctatatat atatgctata   420
tatatgctat atatatatgc tatatatatg ctatatatat gctatatata tagcatatat   480
atatagctat atatatgcta tatatatagc ttatatatat gctatatatg ctatatatat   540
gctatatata tagctatata tatgctatat atagctatat atatgctaca tatatgctat   600
atafatgccca tatglatgct atatatatgc tatatatata tgctatatat atgctatata   660
ta

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662

<210> 179

<211> 649

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(649)

<223> MAR of chromosome 2 genomic contig; 12821904..12822552

<400> 179

SEL PCT 012.ST25

tatgtaatat tatatatata aattatatat tatacatatg taatattata tatatatataa 60
 ttatatatta tacatatgta atattatata tatataaatt atatattata catatgtaat 120
 attatata tataaattat atattatata tatgtaatat tatatatata taaattatat 180
 attatacata tgtattatat atataaatta tatattatac atatataata tatatatataa 240
 ttatatatta tacatgata atatataata attatatatt atacatatat aatatatata 300
 aattatatat tatacatata taatatatat aaattatata ttatacatat ataatatata 360
 taaattatat attatacata tataatatat ataaattata tattatacat atataatata 420
 tataaattat atattatata tatataatat atataaatta tatattatac atatataata 480
 tatataaatt atatattata catatataat atatataaat tatatattat acatatataa 540
 tatatatataa ttatatatta tacatatata atatataata attatatatt atacatatat 600
 aatatatata aattatatat tatacatata taatatatat aaattatat 649

<210> 180

<211> 3191

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(3191)

<223> MAR of chromosome 2 genomic contig; 15356889..15360079

<400> 180

tacaattata tataactata aatataatat aatatatatt atctatatta catattaata 60
 tataatatat attacctatt aatatataat ataatatata taatatatat tacctattaa 120
 tatataatat aatatatata atatataatta cctatttaata tataataaaa tatatataat 180

SEL PCT 012.ST25

atataffaca tattattata taatatatat tatataacat atataacata tactatatat	240
tatataacat atataattgt atagtatta tatatattat atatactat acataatata	300
taaataatta aatatatgtt ataaatataa caaatatata acatatataa catatataac	360
atatatataa ttacataaaa tatataatac ataatatata ttatgcaaca tattatataa	420
tatataacat ataattgata ttatattata tcatatataa tacataatat ataatatatg	480
atataatata atataffata tatgatataa tataatatat tatatatgtt ataataaat	540
atatattata tataggatat attataacat attacataig atataataaa tttatctta	600
tatataggat atattataat atatacaca tagcatatat taaaatatat tacatatagt	660
atattatata tactatatgt atatafacat atagtatatt atagtatatt atacagtata	720
tattatatat actatatata gtagtataca gtatatatta tatatactat atatagtagt	780
atacagtata tattatacag tatatattat atacactata ttatatatta tgtataatat	840
atactatata tagtatatta tgtagtatat attaaacata atagatatat agtatatact	900
atagataata gatattatat agtatatagt atataffata tataatatat ataatatata	960
ttataacat atagtatata tgatatatta tatataatat atataatata taatatatgt	1020
aatataatac atattatata taatatatgt aatataatat aatatataat atagtataa	1080
taataatata tattatataa tataacatat ataaatataa taatatatat tatatgatat	1140
aacatacata aatataataa catatataat atataffata tattatattg tatatatgat	1200
atactatata ttacacatta tacattattt ataatatata attaatatat aacatatatt	1260
agataacata taattatatt tgtaacatat ataagatata attacatatata taacatatat	1320
aattatatat atatttatot aattatatat gaaattatat atgacatatata aaattatata	1380
ttatatatgt tatatgtatt atataffata tatgttatat atgttatata taacatatat	1440
aacatatata acacacacat ataacatatata taacatatat tacatatata acatatataa	1500
cacatatata attatctaac atagataata tatataatat ataataataac atatatatta	1560
tatattatac actotattat attatatata ttatacataa tatataatat atagtatata	1620
atataatata ttgtatatat gatataatat atattgtaca tagtataata facatatata	1680

SEL PCT 012.ST25

gtatattatg tataacataa tatatagtat attatgtata acataatata tagtatatta 1740
 tgtataacat aatatatagt atattatgta taacataata tatagtatat tatgtataac 1800
 ataatatata gtatattatg tataacataa tatatagtat attatgtata acataatata 1860
 tagtatatta tgtataacat aatatatagt atattatgta taacataata tatagtatat 1920
 tatgtataac ataatatata gtatattatg tataacataa tatatagtat attatgtata 1980
 tataatatat atattatata gtatattatg tatatataat atacatatta tatagtatat 2040
 tatgtatata taatatatcat attatatagt atattatgta tatataatat acatattata 2100
 tagtatatta tgtatatata atatacatat tatatagtat attatgtata tataatatat 2160
 atattatata gtatattatg tatatataat atacatatta tatagtatat tatgtatata 2220
 taatatatcat attatatagt atattatgta tatataatat acatattata tagtatatta 2280
 tgtatatata atatacatat tatatagtat attatgtata tataatatat atattatata 2340
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 gttatgtagt atattatgta tatataatat acatgttatg tagtatatta tgtatatata 2460
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 tgtatatata atagtatat tatatataat atatatatt tatatacat atgtatctat 2640
 ataatatata ttatgtatat attaggatc tatataatat atattatgta tatatattat 2700
 gtatctatat aatatatata ttatgtatat atattatgta tctatatat atatatatta 2760
 tatgtatatt atgtatctat ataatatata taatgtatat agatatatta tatattatgt 2820
 atatatatta tgtatctatt ttatatataa tgtatataga tatacaatat atattatgta 2880
 tatattatgt atctatatata tatatattat ttatatagat atatatatta tgtatatata 2940
 cataatatat tacatattat gtatatatat ataatatata atatatatg tatatatata 3000
 taatatataa tatattatatt attacatata ttatatataa tatattatatt tatgtatata 3060
 tattatgtat atataatgta tatataatat ataaagtga tatatattgt gtatatataa 3120
 tgtatatata ttacatatat tatgtatata tatattatcat ataatatata tactacatta 3180

SEL PCT 012.ST25
3191

tacataatat g

<210> 181

<211> 314

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(314)

<223> MAR of chromosome 2 genomic contig; 728676..728989

<400> 181

tgtgtatata tgtatatata atatataatta tataatatgc atagtataa aatatgtata 60

ttatatatgt atattttata tatatgtata tattatatgt atattttata tatgtatatt 120

ttatatatat gtatatatta tatatgtata ttttatatat atgtatatat tatatgtata 180

ttttatatat atgtatatat tatatatgta tttttatat atagtatat attatatatg 240

tatatattat atatatgtat attttatata tatgtatatc atatatatgt atatattata 300

tatatgtata tcctt 314

<210> 182

<211> 423

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

SEL PCT 012.ST25

<222> (1)..(423)

<223> MAR of chromosome 2 genomic contig; 737493..737915

<400> 182

ataatatata gtgiccttta tattatctaa tatgtaatat aatgtatttt atattatgta 60

ttttatatta tataatatat aatataatgt attttatatt atagtgtata taatatatag 120

tgcattatat attatgttat attatatata ttttattat ataaattata tattatatgt 180

tattttatat atattatata acatataata taacaatgca ttatatatta taaaatatat 240

aatacattac atattatata taatatataa tacattacat atattatata atatatata 300

cattatcata tattacaaat attacattag tataatagta attataatat aatatattat 360

atattacata tattatatta atgtaatagt aattataata taatatatat tatattttat 420

att 423

<210> 183

<211> 724

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(724)

<223> MAR of chromosome 2 genomic contig; 1069556..1070279

<400> 183

tattataata tattatatac atttatattgt atatatacta tatatggtat atatagtata 60

cataatataa aatgiataatt gtaatatata ttatatatat acatagtgtta cattatataa 120

SEL PCT 012.ST25

tataatataa tgtatattat aatatacatt ataataaat agtgtactat gtatatagta 180
 tatataatgt atattataat gtattatata gtataatata atataatata cattatatag 240
 tattgcatta tataatgctat ataatatata atattattatg tatatatata ttatatatac 300
 tatattatat agtacatata atgtatatata tatagtatat ataataaat acattatata 360
 tacaatatat aatgtatatt atagtagtg tataatgtaa tacattatac atagtacata 420
 aagtatatata taatatatta taatatataa tacaattat atattataat gtatatataa 480
 tattgtatat atactatata taatgtatat acaattatat ataattgtat atatacatgt 540
 atagtatat gtatatatac atgtatatgt atgtgtatat atacatatat gtatatgtat 600
 gtgtatatat gtatatgtat atagtatat gtatacgtat atagtatat acaatgtata 660
 tataatgtat ataaaaatat ataatatata caatatgtat ataatgtata taattatata 720
 atat 724

<210> 184

<211> 383

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(383)

<223> MAR of chromosome 2 genomic contig; 2719918..2720300

<400> 184

atattatat ttatatatt attatatat aaatatatat ttatatatta tatattatt 60

atatataaat atatattat atttatata ttattatat ataaatatat atttatatt 120

tatatattat ttatatataa atatatatt atatttata tattattat atataaatat 180

SEL PCT 012.ST25

atatttatat ttatatatt atttatatat aaatatatat ttatatatta tatattatt 240

atatataaat atatatttat atttatata ttatatatt atatattata tatattata 300

ttaattgtg tataatatat attataaat ataataaata tattatttt tatatatatt 360

ataaaaaatat ataatatata aaa 383

<210> 185

<211> 309

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(309)

<223> MAR of chromosome 2 genomic contig; 4994249..4994557

<400> 185

tataatatat aattgttata acattataac aattatatat tatatataat acaattatat 60

aatatatatt atataattgt aatatataat ataattatat aatatatatt atataatata 120

atatataata tatcatatat gttatatatt ttattatata atatataita tatataatat 180

tatatataat atatattata tataatatta tatataatat atattatata taatatatt 240

atatatatta tatataatat atattatata ttaaattatta tatatataat atatataaca 300

ttattgtta 309

<210> 186

<211> 740

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(740)

<223> MAR of chromosome 2 genomic contig; 5034916..5035655

<400> 186

tttatatata aaatattata tataatatta tatataatat ttctatata aaatgtgtat 60

ataattatat ataattatat aaaaatataat atagaatatc taataatgta taatatataa 120

catataaaaa taatattatt taatatataa tattttatat ataatatatt tatatatataat 180

ataatatata ttttatatat aattattaat tatataatta atatataata tatattttat 240

acataattat taattatata taattaatat ataatatatc ttatacataa ttatcaatta 300

tatataatta atatataata tatattttat acataattat taattatata taattaatat 360

ataatatatc ttatacataa tatatatataa tatattatat ataatatata ttatatataa 420

tatttatatat aatatatatt atatatatata aatttatata taatattata tataatatta 480

tatattttat atacaatatg atatataata taatttatat attatatata ttatatata 540

attattatat aaatttatata aatataaatt atatatttat atataattat tatataaatc 600

attatataat tattataatt ataatatata atataatata atattatata taatatatag 660

tattctatat aaataatata acatatattt tatatagaat attatatata atataatata 720

tattttatat agaattatat 740

<210> 187

<211> 847

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(847)

<223> MAR of chromosome 2 genomic contig; 6074678..6075524

<400> 187

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aatatagaca taaatata tgcataaata tatatatgca taaatatata taaaaatata   60
tataaatata tacataaata tatataaata tatacaaaaa tatatataaa tatataaaaa   120
aatatataaa tatatataca catatataaa tatatataca tacatatata aacatatata   180
cataaatata tatgtataaa tatatataca cataaatata tgtatgaata tatatacata   240
aatatatatg tataaatata tatacataaa tatataaaga tatatacata aatatatata   300
aatatatata cataaatata tataaatata tataaataga tatataaata tatatataaa   360
tatataaata tatatataaa tatataaata tataaaaaata gatatatataa tatatatata   420
aatatataaa tatatatata aatatatata aatatataaa tatatatata aatatatata   480
aatatataaa tatatataaa tatataaata tatatataaa tatatataaa tatataaata   540
tatataaata tatataaata tataaatata tatataaata tatataaata tataaatata   600
tatataaata tataaatata taaatatata tataaatata taaatatata taaatatata   660
taaatatata aatatatata aatatatata aatatataaa tatatataaa tatatataaa   720
tatatataaa tatataaata tatataaata tatataaata tatataaata tatataaata   780
tataaatata tatataaata taaatatata taaatatata aatatatata taaatatata   840
taaatat

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847

<210> 188

<211> 784

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(784)

<223> MAR of chromosome 2 genomic contig; 6108986..6109769

<400> 188

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atttatttat atatttaata tataaaatat atatttaata tataaaatgt atatatatac   60
atatattata tataatacaa tatatattat atataatata tattatatat aatattatat   120
attatattat aatataatat atatttatata taatataata tatattatat attattatat   180
ataatataat atattattata tattattata taataataaa tatatattat atattattat   240
atataatata atatatatta tataattata tatataatat aatatatatt atatatatat   300
tttatatata taatatataa tatatatatt atatatatat ttatatata taatatataa   360
tatatatatt atatatatat ttatatata taatatataa tatatatatt atatatatat   420
tttatatgta taatatataa tatatatatt atatatatat tatatatata taatatgtaa   480
tatatatatt atatatatat tatatatata atatatatta tacataaaat atattattata   540
tataatatat ataatatata ttatatataa aatatatttt atgtataata tatattatat   600
ataatatata atgtatattt atatatataaa tatatatatta tatacaatgt atatttatat   660
ataaaatata tatttatata caatgtatat ttatatataat atgtgtttaa tatatgaaat   720
atatatttat atataatata tatttaattct ataaaatata tattaaatat atatttatat   780
ttaa

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784

<210> 189

<211> 381

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(381)

<223> MAR of chromosome 2 genomic contig; 10389032..10389412

<400> 189

tatacacata tagagtatat agagtatata tagagtatat ctatagagta tatatgtata 60

tagagtatat aatacagcct accatatata tagtatacat atatatatac tctatatact 120

atatatatag tgtgtatata tatagtatag accctaccat atatatatat aggagtatat 180

aatatatac actcctacta tatatagtat gtatatagag agtatataga gtatatatac 240

agtatatata cacagtatat atatgccata tatagtatct atatacttat atatagtatg 300

tatctatata cttatatata gtatgtatct atatactata tatagtatgt atctatatac 360

tatatagagt atatatgtat a 381

<210> 190

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> misc_difference

<222> (1)..(507)

<223> MAR of chromosome 2 genomic contig; 11097807..11098313

<400> 190

SEL PCT 012.ST25

aattatatat aattattat atataattt atatttataa tattttata tacatattt 60
atatatcttt ataattatat attacatata taatattata taatatatai aatatatata 120
atatatatta tatattatat aatatatatt atatatttta tatataatat atataatata 180
tataatatat ataatatata taatatataa tataiattat ataatatata ttatatataa 240
tatatattat atataatata tattatatat aatatataaf atataataa tatataacat 300
ataataatat attacatata atttatatat aattttata taattatata tatttatata 360
ttttatata attatatata ttatatatt ttatatataat tatatatatt tatatatitt 420
tatataatta tatatatataa ttatatataa atatatataa ttatatataa ttatatataa 480
ttataaata tataattata tataatt 507

<210> 191

<211> 329

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(329)

<223> MAR of chromosome 2 genomic contig; 11234628..11234956

<400> 191

ttatagttaa atatataaat ataaaatata cagttttata cagtatatat aaaatatata 60
atatataata cataatacat tagttatata tactatatat actatatata ctacacgtat 120
agtatatata tgaaactata tatatactat acgtgtagta tatatatgaa actatatata 180
tactatacgt gtagtatata tatgaaacta tatactatac gtatagtata tatatgaaac 240
tatatatact atatataact aactataatt gtatatagtt aaaaatataa atataaata 300

tacagttaaa tatattaata tataatagt

329

<210> 192

<211> 584

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(584)

<223> MAR of chromosome 2 genomic contig; 797844..798427

<400> 192

tattatttta tgtataaat agataaaaat atatactaata atatatgtac ttatatatac 60

atcaafatat aatgtattat ttatactaa cgtatattat atatactagt atataatcta 120

tattatttta tatgttataa atataataa aaatatataa atattttatg catatatataa 180

tatataatat atactaacat gctaatttat atatacttat atataattta tatagtatat 240

aatatataaa tgtatataat acataattta tatatttata tattaatagt ttatatatta 300

gtatatatac taattttata tactaataaa taaatttat aatatataaa ttatatatta 360

tagtacataa tatatattat atagttaaat aactatgtaa ctataatata taactatata 420

tgatatacag ttatatataa tataaaattt acatacagta tataaaattat atactatata 480

tttatatata tatggatat aaattatata ctatacaattt atatacatat ggtatataaa 540

ttgtatacta tataatgtgt attagtatat atactaatat atac 584

<210> 193

<211> 363

<212> DNA

SEL PCT 012.ST25

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(363)

<223> MAR of chromosome 2 genomic contig; 1093824..1094186

<400> 193

tatacacaca catatatata cacatatata tacacatata tatatacaca tatatatata 60

catatatata cacgtatatata tgtatacaca tatatatgta tatatatata catatatata 120

cacatatata cgtgtatatata cgtatatatcg tacatatata cgtgtatatata cgtatatgcg 180

tacatatata cgtgtatatata cgtatatgcg tacatatata cgtgtatatata cgtatatgcg 240

tacatatata cgtgtatatata cgtatatgcg tacatatata cgtgtatatata cgtatatgcg 300

tacatatata cgtgtatatata cgtatatgcg tacatatata cgtgtatatata cgtatatgcg 360

tac 363

<210> 194

<211> 545

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(545)

<223> MAR of chromosome 2 genomic contig; 3456187..3456731

SEL PCT 012.ST25

<400> 194
tattataata tatatttata tattataata tatattatat tatatattta tatattataa 60
tatatattat attatatatt tatatattat aatatatatt atattataat atatatattat 120
attataatat attatattat aatatatatt atattattat atattataat ataatatata 180
ttataatata tattatattta taatttatat attatatata ttataatata tattatatta 240
tatatatatt tatattataa tatatattat tatatattat atattataat ttatattata 300
ttacaatata tattataaat atatatattta tattataaat atatatittt atattacaat 360
atatattata aatatatatt ttatattaca atatatattta taaatatata tattatatta 420
caatatatat tataaatata tattatatta caatatatat tatattataa tatatattta 480
tatatgatat attatattta atatatattta taacataata tataatatai aatatattaa 540
tataa 545

<210> 195

<211> 356

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(356)

<223> MAR of chromosome 2 genomic contig; 5001567..5001922

<400> 195

tataaaatat atgttatata tataatatat attatataat atataatata tataatatat 60
aaaatatata aaatatataa tatataatat aatatataat atatatata tataaaatat 120
atataatata aaatatatat aatatataat atatatata tataatacat ataatatata 180

SEL PCT 012.ST25

atatataata tataatata ataatatata atatataata tataatata ataatatata 240
 atatataata tatataatat ataatatata atatataata tataaatata taaatata 300
 tacacacata cacacacata tatgcatata tatacatata catgtgtaca tagata 356

<210> 196

<211> 321

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(321)

<223> MAR of chromosome 2 genomic contig; 5457330..5457650

<400> 196

tatacaatat attataaatt atatataatt tatatataat atatattata tataaattat 60
 atataattta tataatata aaattatata taatataaat tatatataat ttatataata 120
 tataaattat atattatata aattaaatat aatttatatt atatataaat tatatttaatt 180
 ttatataata tataaattat atttaattta tatataatat aaatttatatt ttatatatt 240
 atgtataatt tatatattta facatatata cattataata tattgtatag tatatataat 300
 atatagtata tataaagcat a 321

<210> 197

<211> 361

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(361)

<223> MAR of chromosome 2 genomic contig; 8124469..8124829

<400> 197

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tatatataat atattata tatattatat aaattatata taatatgtaa tataaatttt 60
gtaatatata ttatatatat aaattatata taatatatat taatatatat aatatataatt 120
aatatatata atatatatt atatatatt tatatgatat atataaatat atattatata 180
taaattatat atatacataa ttatatatca tataaattat atataatata cattatgtac 240
ataatatatg atatatata tataatatata attatatata attatatata tataattata 300
taatatatat aaattataat atataatata tataaattat aatatataat atatatataat 360
t                                     361
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<210> 198

<211> 418

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(418)

<223> MAR of chromosome 2 genomic contig; 11151485..11151902

<400> 198

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atgtaactat atatatagta tatatagtat atatatata tatagtgtgt atatatagta 60
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tatataact atagtggtg tatatatagt atatatatag tttatatatc gtatatcac 120
 tatatactat atagtggtata tatagtatat gtagtatata tagtatatat agtatagtat 180
 atatagtata tatagtggtat atatacigta tatataggtg acatagtata ctatatagia 240
 tacatatagt acactgtata gtatatatag tatagtatat atagtataca tagtatacta 300
 tatatagtat agtatacata gtatactata tagtatatag agtatatata cagtatacta 360
 tatagtatat agagtatata tacagtatac tatatcgtgt gtatagagta tatataca 418

<210> 199

<211> 394

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(394)

<223> MAR of chromosome 2 genomic contig; 13591477..13591870

<400> 199

ttatatatat ttatatata ttatatatat ttatatata ttatatatat attatatata 60
 tattatatat aattatatat aatatatatt atatatatta tatataatta tatataatat 120
 atattatata tattatatat ataatatata tataatatat atatttata tatgtattat 180
 atatatatta tatatatatt atatatatta tatatatatt atatatatta tattttatat 240
 atataatata acatatataa tatataatta tatattatat atatatatta ttatatataa 300
 tatatatatt atataatata atataaatt atatatatta tatattttat atattttat 360
 aaaaattatt ttatatatt ttatatataa atat 394

<210> 200

SEL PCT 012.ST25

<211> 1194

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1194)

<223> MAR of chromosome 2 genomic contig; 14996824..14998017

<400> 200

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taatatttat atatacatat aaaatttata tataatatat aatatttata tatacatata    60
aaatttatat atatatataa tatttatata tacatatataa atttatatat aatatataat    120
atttatatat acatatataaa ttatatata atatatataa ttatatata catataaaat    180
ttatatataa taaalattta tatatacata taaaatttat atataattta tatataacat    240
ataatattta tatataaaat ttatatataa catatatatta tatataattt atatatataca    300
tataatattt atatatataa tatatttatt tatacaattt atatatataa tataataact    360
atatatacat acataattta tatgatatat atttatata taatttatat gatatatataat    420
atatctaata tatatttat atatttatata tatttatatat aatttatata atatatatta    480
tatatatata ttatatataa tatatatatt atatatataat tatataatat atatatata    540
tatataattt atataatata tatttatatat ataatttata taatatatat tatatatata    600
atttatataa tatatatatt atataattta tatataacat attttatata catatatataat    660
ttatatataa tatatatatta catatacata tataattttt atataatata aaatatattct    720
atatacatat ataattttta tataatataa aatatttcta tatacatata taatttttat    780
ataatatata ttctatata catgtctaatt ttatatataa tatatatattc tatatacata    840
tataattttt atataatata taatattttt atatacataa tttttatata atatatattt    900

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acatatacat atataatttt tatataatat atatttatat atacatatat aatttttaca 960
 taatataat tatatatata tatataattt atatacaaca tataatatat acatatataa 1020
 ttatatata acatataata ttatgtata catatataat gtatacaca tatataatat 1080
 ttatatatac atataaatt tatatgtaat atatacatat ataatttata tgtaatatat 1140
 atacatgta aatttatatg tagtatatat acatgtataa ttatatgta gta 1194

<210> 201

<211> 487

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(487)

<223> MAR of chromosome 2 genomic contig; 14998429..14998915

<400> 201

tagtatatac ttacacatac atgtataatt atatgtaata tataatattt acatatataa 60
 ttatagataa tatatatitfa catatatac tataattata tataatatat aatgtttaca 120
 tatacatata taattatata taatatatat ttaaatac atatacaatt atataata 180
 tatatttaca tatgcatata taattataga taatatatat ttacatatatac atataaatt 240
 atataata tataatgttt acatatacat atataattat atataatata tatttaaata 300
 tacatatata attatatata atatafattt acatagcat atataattat agataatata 360
 tatttatata tacatatata attatatata atataataa ttacatatata catatataat 420
 gtatatataa tatataatat ttacatatatac atataaatt tatatatata atataattata 480
 tatatta 487

SEL PCT 012.ST25

<210> 202

<211> 421

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(421)

<223> MAR of chromosome 2 genomic contig; 16562490..16562910

<400> 202

tatatgaata tatatatgaa tatatacgta tataatgaata tatacatgta tgtatatatg 60

aatatatgta tatatatgaa tatatatgta tatatgaata tatgtatata tatgaatata 120

tatgtatata tgtatatata tgaatatata tgtatatatg tatatatatg aatatatatg 180

tatatatgta tatatgtata tataatgaata tataatgata tatgaatata tatgaatata 240

tatgtatata tatgaatata tatgaatata tgtgtatata tatgaatata tatgtatata 300

tatgaatata tgtatatata tatgaatata tatgtatata tgtatatatg aatatatatg 360

tgtatatgaa tatatatatg aatatatatg tgtatatgaa tatatatgaa tatatatgtg 420

t 421

<210> 203

<211> 479

<212> DNA

<213> Homo sapiens

<220>

SEL PCT 012.ST25

<221> misc_binding

<222> (1)..(479)

<223> MAR of chromosome 2 genomic contig; 21592301..21592779

<400> 203

tatatgtata cgtatataat atattatata ttatatacgt gtacgtatat atgtaatata 60
 taatgtatat gtacacgtat ataatatata atatattata tacgtatacg tatacattat 120
 atattacata tatacgtata tacgtatata aaatatatgt atatattata tatacgtata 180
 taatatatat tatataatat ataatatata cgtatacata taatatatta tatatacata 240
 ttatatatta tataattaaa ttatatatta tatcatatat aatatatgtg atataatata 300
 taatatatat atattacata atatattatta tatacatata catatataat atataatata 360
 ttatatatat atacatatat aatatataat atattatata catatacata tataatatat 420
 aatatattat atacatatat atatataata tataatatat tatatatata tattatata 479

<210> 204

<211> 870

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(870)

<223> MAR of chromosome 2 genomic contig; 22557584..22558453

<400> 204

tataatatat aatatacata atatgtatat ttatatacata atataaataa tatataataac 60

SEL PCT 012.ST25

atataatgtat attttatata tgtatatattt atatatattt tatatatattt atatatatgt 120
 atattttata tataatata atattgtata taataatata taatatatta tattatata 180
 aatatatata atatatatat aaatatatat tatatataat atgtataata tataatattt 240
 tatatataat atgtataata tatattttat atataataat atgtacaata tatattttat 300
 atataataat atgtacaata tatattttat atataataat atgtacaata tatattttat 360
 gtataaatgt tataatata attttatgt taatatatat ttatgtata atatatattt 420
 tacgtatat ttatatataa tatataatat ttatatata atataaaca ttatatatat 480
 aatatataat attatatata ttatatattt tatatataat atataaata atatatattt 540
 tatatataat atattttata tataatata ataaatatat atattatata taatatattt 600
 tatatataat atattttata tataatata aatatattt atattatata tataatata 660
 tatatatat atataatata ttatatataa tatataatat ataatatatt atataaata 720
 tataatata aatatattat atataatata taatatataa tatataatat attatatata 780
 atataaata tgaatatat aatatattt atataatata taatatata tataatattt 840
 tatatataat atataatata taatatataa 870

<210> 205

<211> 1086

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1086)

<223> MAR of chromosome 2 genomic contig; 30591960..30593045

<400> 205

SEL PCT 012.ST25

gtatataaa tatatattat attatgttat atattatgta gactatgtat taaatataatg 60
tatatattat atataaatat ataatatata ttataaattt ataattataa atatatattat 120
aatatatitt tctaaataatt tatatattat atattatatac taatgatata taataaatat 180
atttctaata tattttatat ttataaatat ttatatata ttatatattt tatatatact 240
atatattata tattatatat ttatatata ctatatatta tatagtatat attttatata 300
tactatatat tatatattat atattttata tatactatat attatatatt atatatttta 360
tatatactat atactattta ttatatattt tatatatact atatactatt tattatatat 420
tttatatata ctatatacta ttatttatat attttatata tactatatat tatatattat 480
atattttata tataatatat atttattata tattttatat attatatata ttatatatta 540
tatatttata tattatataa tatatattat atatagaata tafaatatat attatatata 600
atataatata atatatatta tataaaaat atataatata taaaatatat aatatatgat 660
atatataata tatattctat atttatatat atatatttta tattatatta atafataatt 720
atatattatc atatgtaata atagatatata tatgtaatat ataaattata attatatatt 780
aatattatat attatttaatt atgtatatatt acacatatat taattattaa atatatatat 840
ttaatatatt aaatattatg tattaaatat atataatata ttataaata ttttatatat 900
aatatataca tatatttaaca tatatgtata tatgtatata ttatatataa cattatatat 960
attatgttac atatactata ttttatatgt tacatatact atatatata tgttacatat 1020
aatatatata acatatatta taatatgtaa catattatat ataacatata atatatagta 1080
tatata 1086

<210> 206

<211> 406

<212> DNA

<213> Homo sapiens

<220>

SEL PCT 012.ST25

<221> misc_binding

<222> (1)..(406)

<223> MAR of chromosome 2 genomic contig; 36233909..36234314

<400> 206

attataaata tatattatag atattagata ttatagatat aatatatata atatatatta 60

tagatattat agatatagat ataatagata ttatagatat tatagatata atatatatta 120

tagatattat agatataata tatattatag atattataga tataatatat attatagata 180

ttatagatat aatatatatt atagatatata tatatattat agatattata gatatagata 240

ttatagatat tatatatatt atagatatata tatatattat agatattata gatatagata 300

ttatagatat aatatatatt atagatatata tagatataat atatatattata gatattatag 360

atataatata tattatagat ataagatat ttatagatat tacaga 406

<210> 207

<211> 797

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(797)

<223> MAR of chromosome 2 genomic contig; 36271745..36272541

<400> 207

atataaacat atacgtatat acacatatat acaaatacat atatacatat attatatata 60

tgatatata ttatattata catatattat atatatatta tattatacat atatacatat 120

SEL PCT 012.ST25

acacataaac atattacata catatacaaa ttatacacat atacatatat acatatatgt 180
 atatacatat attatatata aatatatgta tataaaatgt acattatata tacatatata 240
 ttatgtataa ataatatata aaataaacat aatatatatt tatagatatg atatatataa 300
 tatatatgta tacatatata calatatgta tatataatgt acattataca tacataaaca 360
 tcatatataa atgttatata tataatataa atatatataa tatataatat atactttata 420
 tactatatat aatatatata atatgatata acatatataa tatataatat atataatata 480
 tactatatat actgtatata atatatataa taatatatac tatatatat aaatataata 540
 tacataatat aatatatac atatatataa tataatatat aatatagtat atatactata 600
 tataataatt acatattata tattatacat tatatatatt ataattatta tatataatta 660
 tatattacat actttgtata taatgtaaat atacattaga atataaatg tatatatatg 720
 tacatatata atgtatatat gtatacatta tataaactat atataaacat tatattatat 780
 aaacattata tataaac 797

<210> 208

<211> 423

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(423)

<223> MAR of chromosome 2 genomic contig; 36498521..36498943

<400> 208

tattatatta tataattaat attatatatt taatatatta tatatttaat attatatatt 60

taatatatta tatatttaat attatatatt taatatatta tatatttaat attatatata 120

SEL PCT 012.ST25

taatatatta tatatttaaat attatatata taatatatta tatataatat tatatatatta 180

atattatata tataatatta tatatataat atattatata tttagtatta tgtatttaaat 240

atattatata tttagtatta tgtatttaaat atattatatta tttagtatta tatatttaaat 300

atattatatta tttagtatta tatatttaaat atattatata tttaatatat tatatatatta 360

ttatatattg tatatttaaat atattatata ttattatat attatatata attatatatt 420

taa 423

<210> 209

<211> 304

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(304)

<223> MAR of chromosome 2 genomic contig; 37179891..37180194

<400> 209

gtgtatatat atcatatata ttatatcata tatatgtgta tatatatcat atattatattc 60

atatatatgt gtatatatat catatatata tcatatatgt gtatatatca tatatattat 120

atatcatata tgggtatata tatcatatat tatatatcat atatatgtgt atatatcata 180

tatattatat atatttcata tgggtatata tatcatatat aatatatatg tttatatattc 240

atatatcata tataacatat atattgtgtat atatatata tataacatat atcatatatg 300

tgta 304

<210> 210

<211> 693

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(693)

<223> MAR of chromosome 2 genomic contig; 38440448..38441140

<400> 210

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tatatattct ttatatatt atataaata tatattcttt tatatattat ataatagata   60
tattctttta tatattatat atagtatata ttcttttata tattatatat agtatatatt  120
cttttatata ttatatatag tatatatctt ttatatatt atatatagta tatattcttt  180
tatatattat ataatagata tattctttta tatattatat atataatata tattctttta  240
tatatcatat ataatatata ttcttttata tattatatat aatatatatt cttttatata  300
ttatatatca tgtatatata atatacaaaa tatatataga ttttatatat agattattac  360
ataatagaat atattatata ttatatataa tatatacata atataaata ttatatatga  420
tataatatat atcatatata tcatataata tatattatat atcatatatt atataaata  480
atatatagat tatatataat tatatatata atatatataa ttatatatat tatctatata  540
tagataatat atataattat atataatata ttatatagat tatatataat tatattatat  600
acaaaatcta tatataatat atattatatt atataaata tacataacta tataaaaaat  660
ataatatata atatatataa tatataatat ata                                     693
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<210> 211

<211> 471

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(471)

<223> MAR of chromosome 2 genomic contig; 38887582..38888052

<400> 211

aacatatata ctatatatat tatatactat attatatatt atatataaa acatatatac 60

tatatataat atataaacat attatattat acatgatata gataaacata tatattatat 120

ataatataga taaaatatgt tatatataat ataagtata gacatatatt atatatacat 180

atatctaca tatattatat atatattcta cacatatatt attatatata catatattct 240

acatatatta tatatacata tattctacat atattatata facatatatt ctacatatac 300

atatatacat atattatata facatatatt atagatatat aatatataaa catatataat 360

attattatat ataatatata taataatatt atataatata taataatatt atacttata 420

tataaataat atatataatt tatatatata atattatata tatataatat a 471

<210> 212

<211> 1221

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1221)

<223> MAR of chromosome 2 genomic contig; 43885944..43887164

SEL PCT 012.ST25

<400> 212

catataaaca tatattatat gtaacatata aacatattat atgtaacata taatatataa 60
 tatataaaca tatattttat atatttatg ttacatataa tatataatat ataaacatat 120
 attatatatt atatgtaaca tataatatat aatatataaa catatatttt atatatataa 180
 tataaacata ttttatatat aatatataaa catattttat atataatata taaacatata 240
 ttttatatat aatatataaa catattttat atataatata taaacatata ttttatataa 300
 tatataaaca tataatatat ataatatata aaagtatata atataaatat atataatata 360
 aacatatata atataaatat atataaaata taaacatatg taatatataa acatatatta 420
 tatataatat ataaacatat attatagcta caatatataa acatatattg tacgtacaat 480
 atataaacat atatttatagc tacaatatat aaacatatat tatagctaca atatatataac 540
 atatatata cgtacaatat ataaacatat attatagcta caatatataa acatatatta 600
 tacgtacaat atataaacat atatttatagc tacaatatat aaacatatat tatagctaca 660
 atatatataac atatatata cgtacaatat ataaacatat attatagcta caataaacat 720
 atatttatagc tacaatatat aaacatatat tatagctaca atatatataac atatatata 780
 cgtacaatat ataaacatat atgtagcta caatatataa acatatatta tatgtataat 840
 atataaacat ataatatata atatatatta tatatatgtt tattatatat gtttatatat 900
 tatatatatac atatatatt atatttatata tgtttatata ttatatatta tataatatat 960
 atgtttatat attatatatt atataatata tatgtttata tattatatat tatataatat 1020
 atatgtttat atatttatata ttatatataa tatatgttta tatattatat attatatata 1080
 atatatgttt atatatataa tattatatataa tatatatgtt tatatatatt atatttatata 1140
 atatatatgt ttatatatta tatattatat aatatatatg ttatatatt atataaataa 1200
 taaacttaca tattttatta a 1221

<210> 213

<211> 543

<212> DNA

SEL PCT 012.ST25

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(543)

<223> MAR of chromosome 2 genomic contig; 45818200..45818742

<400> 213

tatgtatata tacatatata ttatacatg tatatatgta tatatacata tatatttata 60

catgtatata tatacatata tatttataca tgtatatata tacatatata ttatacatg 120

tatatatata catatatatt tatacatgta tgtatatata catatatatt tatacatgta 180

tgtatatata catatatatt tatacatgta tgtatatata catatatatt tatacatgta 240

tgtatatata catatatatt tatacatgta tgtatatata catatatatt tatacatgta 300

tgtatatata catatatatt tatacatgta tgtatatata catatatatt tatacatgta 360

tgtatatata catatatatt tatacatgta tgtatatata catatatatt tatacatgta 420

tgtatatata catgtatatt tatacatgta tgtatatata catgtatatt tatacatgta 480

tgtatatata catgtatatt tatacatgta tgtatatata catgtatatt tatacatgta 540

tac 543

<210> 214

<211> 463

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

SEL PCT 012.ST25

<222> (1)..(463)

<223> MAR of chromosome 2 genomic contig; 47055478..47055940

<400> 214

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atacacat atatacat atacacat atacataaa tacacacata ttacatata   60
tacacacata tatacatata tacatatata cacatatata catgcataca catatataca   120
tatatacaca catatacaca catatataca tatatacaca tatatacaca tatacacata   180
tatacacaca tatacatata tacacatata tacatatata catatataca cacatatata   240
catatataca tatacacata tatacacata tacatatata cacatatata cacatatata   300
catatataca catatataca tatatacaca tatatacaca catatacaca tatatacata   360
tatacatatg tatacacata tatacatatg tatacacata tatacacata tacatatata   420
catacacata tatacgtata tatgtgtata tatacacata tac                               463
    
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<210> 215

<211> 2482

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(2482)

<223> MAR of chromosome 2 genomic contig; 47492696..47495177

<400> 215

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aatatatata aaatatatta tattctatgt aatatataga atatataaaa tatattctat   60
atattatata gaatatatat ttataatat atattattta tatattttta tatatttata   120
    
```

SEL PCT 012.ST25

ttatttat atttatata aatttatata atttatatat ataatttata tataatttat	180
ataaattata tatataaatt atataaatt tatatataat ttatataaatt tatatatata	240
atttatatat aatttatatg atttttatat ataatttata tataatttat ataatttta	300
tataaatt atataaatt tatataaatt ttatatataa ttatataat atatatatat	360
aatttatata taatttatat aatttatata tataatttat atataattta tataatttat	420
atataaatt tatatatata ttatataatt tatatatata atttatatat aatttatata	480
atttatatat ataatttata cataatttat ataatttata tatataatt atataattta	540
tatatataat ttatatatat aatttatata atttatatat atgatttata taatttatat	600
atataattta tataatttat atatatataat tatatatata atttttatat aatttatata	660
ttataaatt atataatttat ataatttata tatttataat ttatatatt atataattta	720
tataattata atttatatat ttatataatt tatatatata tatttatata ttatataat	780
ttatatataa ttatttatat atttatatat aatttatata ttatatata atttatatat	840
aattatttat atatttatat atttatatat aatttatata tatttatata taatttatata	900
ataaaatata taatatataa tatataatat tataatagat aaaatatata ctatatatta	960
tataatttat atttatatta atatttatatg tataatttta tatatatatat aatatatatg	1020
atatatataa ttatatata tatataatat ataggtata tataatttta tatatatatat	1080
aatatatatg gtatatataa ttatatata tatataatat atgatatata atttatatat	1140
atataatat tatttatatat aatttatatat ctatatatta tatatttat atacaattt	1200
atatatatat ataatatata ttatatatat aatttatatat ctatatata tatatttat	1260
ataatttat atttatata aaatgtatat tatatatatat ttatatatat atataaaatg	1320
tatttatatat ataatttat ttatatata aaatgtatat tatatatatat ttattttat	1380
atataaaatg tatatttat ataattttat ttatatata aaatgtatat tatatatatat	1440
ttattttat atataaaatg tatatttat ataattttat ttatatata aaatgtatat	1500
tatatataat ttatatatat atataatatg tatatttat ataattttat atttatata	1560
atatgtatat tatatatatat ttatatatat atataatatg tatatttat ataattttat	1620

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attatatata atagtatat tatatatataa ttgtattat atataatatg tatattatat 1680
 ataattttat attatatata atagtatat tatatatataa ttatattat atataatatg 1740
 tatattatat ataattttat attatatata atagtatat tatatatataa ttatattat 1800
 atataatatg tatattatat ataattttat attatatata aaagtatat tatatatata 1860
 ttatattat atataatatg tatattatat ataattttat attatatata atagtatat 1920
 tatatatataa ttatattat atataaaatg tatattatat ataattttat attatatata 1980
 aaagtatat tatatatatt atataaaaa tgtatattat atatattata tataaaatgt 2040
 atattatata tattatatata aaagtatata ttatatatat tatatatataa atgtatatta 2100
 tgtatattat atataatgta tattatgtat attatatata atgtatatta tatataatat 2160
 atattatata taagtatat tatataatat atattatata ttataatata taatatacat 2220
 tatatattac atattatata taatataatta tatattatat attacatatt atataataa 2280
 tattatatata tatattaaat atafatttta tatattatat attatatatt atataaaata 2340
 tatatattat atattatata aaatatatat atattatatt atatattata ttaaatatat 2400
 atttatata taatatatat aatatataat atataaaata tatattatat attatatata 2460
 aattatatat attatatata aa 2482

<210> 216

<211> 539

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(539)

<223> MAR of chromosome 2 genomic contig; 47561069..47561607

SEL PCT 012.ST25

<400> 216

aacagtaata tatcactaat atataataat atataacagt aatatatcat taatatataa 60

tatatcatta gtatataata ttaatatata ttaatatata atatatcata tacaatatta 120

atatatatta atataataa atatattatt aatgtataat agtaataata tatattatca 180

atatatatta ctaatatata ataatatatc gtaatatat aatagatcat taatatataa 240

tgtaataata ttatgaatag ataatatatc agtatataat attaatatat taatatatta 300

tatattattt aataatatat aatatattaa taaataatia tatattaata tagcaatata 360

ttaatatatg actgtattat attattaata tataacaata tattatatat tatataataa 420

tttattatat aatatataat aatatattat atattatata acatattaat aatacataat 480

aacattaata atataataa atgttaatat attattatat tatatattaa tatataata 539

<210> 217

<211> 336

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(336)

<223> MAR of chromosome 2 genomic config; 52853648..52853983

<400> 217

tatatataa aaatatatat attttatata tatacataat atatatatgt atattttatg 60

tatatatcta taatatatat aatataataa aatatacata tatattttat atatatataa 120

tatacatata aaatatatat acataaaata tacatgtata ttttatgtat atataatata 180

tatataaaat atacatgtat attttatata tataatatatc atgtataatt aatatacatg 240

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tatgttatat atattacatg tatattatat ataatafaca tataaatfitt aaatttagtg 300

tataftacat gtatattata tataatatat gtatat 336

<210> 218

<211> 406

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(406)

<223> MAR of chromosome 2 genomic contig; 54866263..54866668

<400> 218

tacgtatata aaaatgtata ttacatata taaaataaat attttatata cgtatatataa 60

atatatattt attttatata cgtatatataa atattttatt tatatatgta tataaaaatat 120

ttattttata tacatgtata taaatatat atttatatat gtatatataa atatataffa 180

tatacatgta tataaaaatat atattatata tgtatatataa aatatatatg tatataaaat 240

atatataffa tatagatata taaaatatat attatataga tatataaaat atatataffa 300

tatagatata taaaatatat atattatata gatatatataa atatatatat tatatagata 360

tataaaaatat atatattata tagatatata aaatatatat attata 406

<210> 219

<211> 1452

<212> DNA

<213> Homo sapiens

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<220>

<221> misc_binding

<222> (1)..(1452)

<223> MAR of chromosome 2 genomic contig; 55113305..55114756

<400> 219

ataatatata atatatattg tatattatat tattatatat tatatattat taaatatata 60
tattatatta tatattatat aatatatatt atataataa atatagaata tataattata 120
tattatatta tatattatat aatatatatt atataataa atatagaata tataattata 180
tattatacta tatattatat aatatatatt atataataa atatagaata tataattata 240
tattatataa tatgtgaata atgtaataa taattatatt attacatat tatataatat 300
ataattatat tatataatat ataattatat tattgtata ttatatataa catatacatt 360
ataitatata taatataatt atataaatt aattataaat taattatata taattatata 420
atataatata taatatacat aatatataat atataatata taatatacat aatataatat 480
atattatata taatataata tatataatat aatataatat aatgtataat ataattatat 540
attatatata atataaattg ttatatatt atattatatt atataattaa ttatatgtaa 600
ttaatataat ataattatta tatataattt ttatatatt ataatatata attatataat 660
ataatataat tatattatat tatataatat atatatatta tataatataa tataattata 720
ttatatatt atataatata atataattat atattatatt atataataaa tataattata 780
taataataa tgattatata atatatattg tatattatat attatatatt gtattatgta 840
tattatatat tatatattat gtattatata tattatgtat attatatatt atgtatatta 900
tatattatat attatattat gtataatata ttatgtatgt tatatataat ataaattata 960
ttatatatta tgtatattat atataaatta tattatatat tatgtatatt atataataa 1020
taaagtatat attatgtata ttatatataa tataaagtat atattatgta tattatatat 1080
aatataaagt atatatattg tatattatat ataatataaa gtatatatta tgtatattat 1140

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atataatata aagtatatat tatgtatatatt atataataa taaagtatat attatgtata 1200
 ttatatataa tataaagtat atattatgta tattatatat aatataaagt atatatatg 1260
 tatattatat ataataataa gtatatatta tgtatatatt atataatata aagtatatat 1320
 tatgtatatatt atataataa taaagtatat attatgtata ttatatataa tataaagtat 1380
 atattatgta tattatatat aatataaagt atatatata tgtataaat tatatatattgt 1440
 tatatatattat at 1452

<210> 220

<211> 502

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(502)

<223> MAR of chromosome 2 genomic contig; 56350637..56351138

<400> 220

atatattata gaaatataaa tatatagata tatctatata ttatagaaat ataatatat 60
 agatatatct atatattata gaaatataaa tatatagata tatctatata ttatagaaat 120
 ataatatat agatatacct atatattata gaaatataaa tatatagata tacctatata 180
 ttatagaaat ataatatat agatatacct atatattata gaaatataaa tatatagata 240
 tatctatata ttatagaaat ataatatat agatatatct atatattata gaaatataaa 300
 tatatagata tatctatata ttatagaaat ataatatat agatatatct atatattata 360
 gaaatataaa tatatagata tatctatata ttatagaaat ataatatat agatatatct 420
 aacatatatg ttacatatta tatattatat atctatatat ctatataaca ttatatatct 480

atatactat ataacatata ta

502

<210> 221

<211> 794

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(794)

<223> MAR of chromosome 2 genomic contig; 57051633..57052426

<400> 221

aactatata actatattat atagttatac tatataact atattatata gttatataac 60

tattatataa ctgtattata tagttatata actattatata aactgtatta tatagttata 120

taactattat ataactgtat tatatagtta tataactata ttatataact gtgttatata 180

gttatataat atataactat attatataac tgtattatata agttatata tatataacta 240

tattatataa ctgtattata tagttatata ttatataact atattatata actgtattat 300

atagttatata attatataac tgtattatata agttataaaa ctatattata taactgtatt 360

atatagttat aaaactacta tataactgta ttatataatt ataaaattat actatataac 420

tgtattatata agttataaaa ctatactata taactgtatt atatagttat aaaactatac 480

tatataactg tattatataag ttataaagct atactatata actgtattat atagttatata 540

aactatacta tataactgta ttatataagtt ataaaactat actatataac tgtattatata 600

agttataaaa ttatattata taactgtatt atatagttat ataactatata tatataactg 660

tattatataag ttatataact atattatata agtgtattat atagttatata aactatatta 720

tataactgta ttatacagtt atataactat attatataac tgtattatata acttatataa 780

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794

ctatattata taac

<210> 222

<211> 300

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(300)

<223> MAR of chromosome 2 genomic contig; 57069272..57069571

<400> 222

acacatacat atatgtatat atgcacacac atatatatgt atatatacac atacatatat 60

gtatatatac atatatgtat atacgcacat acatatatgt atatatacac gtacatatat 120

gtctctatat atacacatac acatatgtat atacatatat gtgtatatat acacaatcat 180

atatgtatat acatatatac acatatatac aaacatatat gtatatatac atatgtatat 240

acatatatac acatatatac aaacatatat gtatatatac atatgtatat acatacacia 300

<210> 223

<211> 370

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(370)

SEL PCT 012.ST25

<223> MAR of chromosome 2 genomic contig; 57235143..57235512

<400> 223

tatttttata tataactata tatattttat atataaatta tatatatgat catatatata 60

atcatatata taatcatata tgattatata tgatcatata tatatttata tatataatta 120

tatatactta tatataatta tatatatatt tatatatata attatgtata cttatatata 180

tttatatata taattatata tacaatttat atatataatt atatataatt tatatataat 240

tatatatata aatttatatat aagtatatat aatttatatat atgtttatat ataattatat 300

atataaatga tatgtataat atataactat atataattat atataaatat atatatagat 360

tttatatata 370

<210> 224

<211> 306

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(306)

<223> MAR of chromosome 2 genomic contig; 57693125..57693430

<400> 224

tacgtatata cacgtataaaa tataaatata tacatgtata tacgtatata catgtataaaa 60

tataaatata tatatgtata tacgtatata catgtataaaa tatatatatg tatatacgta 120

tatacatgta taaatatata tatatgtata tacgtatata catgtataaaa tatatataca 180

tgtatatacg fatgttgtgt atacatacaa atctgtacat atatacatat atgttgtgtg 240

SEL PCT 012.ST25

tatatataca tctatacatg tgtatgcgta tatatgtata tgtatatata gtatatataa 300

tacatg 306

<210> 225

<211> 500

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(500)

<223> MAR of chromosome 2 genomic contig; 59810331..59810830

<400> 225

ttattatat gtaatatata ttgtattatt atatataata tatataatat atattgtatt 60

attatatata ttatatataa tatatatgtt attattatat atattatata taatatatat 120

tgtattatta tatatattat atataatata tattgtatat tatatatatt atatattata 180

ttattatata ttatatatat tatattatta tatattatat attatatata ttatattata 240

tattatatat tatattatat atattatatt atatattata tattatatta tatatattat 300

attatatatt atatattata ttatatatat tatattatat atattatata ttatatatta 360

tatatattat atattatata ttatatatat tatatattat atataatata tattatatta 420

ttatataata ttatatatta tatatattat atattatata taatatatat tatattatta 480

tataatatta tatattatat 500

<210> 226

<211> 565

<212> DNA

SEL PCT 012.ST25

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(565)

<223> MAR of chromosome 2 genomic contig; 59974589..59975153

<400> 226

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atatatgtat aatatgtata tatgtatata ttatgtatat gttatatatg taatatatgt   60
atgtatatat tatatatcat atataatata taatgtgtat atatgtatat atgtaigtat   120
acatgtatat acctatgtata tattgtatat attatatatg tatatataca tatacatata   180
taatatatac atatattata tacaatatat acatgtatat tatatacgat atatacatat   240
atattatata caatatatac atagtatata aatgtatata tacatacata tatacatatt   300
atatatgtat atatgtatac ataaatgtat atataatata tatacatata taaatgtata   360
catacgtaca tatacgtata tglatatgca tatatgtata tatgtgcata catatatatg   420
tatatacata tatgtacata tgtacatata cgtatatatg tacatatgta catatacgta   480
tatatgtaca tatgtacata tacgtatata tgtacatatg tacatatacg tatatatgta   540
catatgtaca tatatacata tatat                                     565

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<210> 227

<211> 427

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

SEL PCT 012.ST25

<222> (1)..(427)

<223> MAR of chromosome 2 genomic contig; 60605573..60605999

<400> 227

tatataatgt atataatgga tatagatata gatagata tatattttat ataatatata 60

ttatatatta tatataatat atgttatata tattatatat ttatatatat atatatttta 120

taiaaattat atatataata tatataatat atatattata tatattttat ataatatata 180

ttatatatta ttatatatat attttatata atatatttt tatataatat ataatatata 240

atatatttt tacataatat ataatatata atacgtatta tatataatat ataatacgta 300

tttatataa tatataatac gtattatata taatacgta tatattttat ataatatata 360

atacgatta tataatatac gtaattatat ttattataa tacgtattat atattatata 420

atatata 427

<210> 228

<211> 1199

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1199)

<223> MAR of chromosome 2 genomic contig; 61229949..61231147

<400> 228

gtatacatat ataaagtga tatataatgt atatacatat atacatatat aaagtatata 60

tataatatat acatatataa agtatatata taatatatac atatafaaag tatatatatat 120

SEL PCT 012.ST25

atatacatat ataaagtata tataatatat acatatataa agtatatata tcatatatac 180
 atataaaag tatatatata atatatatat atatacatat ataaagtata tataacatat 240
 atacatatat aaagtatata taacatatat acatatataa agtatatata taatatatac 300
 atatatatat atataaagta tatataacat atatacatat atacagtata tataacatat 360
 atacatatat acagtatata taacatatat acatatatac agtatatata acatatatac 420
 atatatatag tatatataac atatatatat atatacatga agtatatata acatatatac 480
 atatatatat gaagtatata taacatatat acatatatac atgaagtata tataacatat 540
 atacatatat acatgaagta tatataacat atatacatat atacatatat aaagtatata 600
 taacatatat atatatatat atataaagta taacatatat atatatatat atataaagta 660
 tatataatat ataacatatata catatatataa gtatatataa tatataacat atacatatat 720
 aaagtatata taatatataa catatatata tataaagtat atataatatata tacatatata 780
 catatatataa gtatatataa tatatatata catatatataa gtatatataa tatatatata 840
 tatatatata tataaagtat atataatatata tatatatata taaagtatat ataatatata 900
 tacatatata catatatataa gtatatataa tatatatata tatatatata tataaagtat 960
 atataatatata tatatatata tacatatata aagtatatat aatatatatata catatatata 1020
 tatataaagt atatatataa tatatatata tatatatata taaagtatat ataatatata 1080
 tacatatata catatatataa gtatatataa tatatatata tatatatata tataaagtat 1140
 atataatatg tatatatata tacatatata aagtatatat ataatatgta tacatatat 1199

<210> 229

<211> 454

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

SEL PCT 012.ST25

<222> (1)..(454)

<223> MAR of chromosome 2 genomic contig; 62181058..62181511

<400> 229

tatatatcat atattatata tgatatatat tatgtatata atacatatta tatataataa 60

atatttatta tataatgatat atattatgta tataatacat attatatata ataaatatat 120

attatattat atataataaa tatatattat attatatata atatatattt atatataaat 180

atattatata taaatataata ttatatataa aatatttata tattatatat aaatatatat 240

tatatataaa tatttatata ttatatataa atatttatat attatatata aatatttata 300

tatttatatat aaaatatatt atatatatta tatatattat atatttatata taatatattt 360

aatatataat atataaacat atattatata taatatataa acatatataa atatatattat 420

atataataga taaaaatata tataatatat ataa 454

<210> 230

<211> 658

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(658)

<223> MAR of chromosome 2 genomic contig; 62190919..62191576

<400> 230

tatatacaca actatatata taactatata tataacaacta tatatacaac tatatatata 60

actatatata taactatata taactatata tataactata tataactata tatataacta 120

SEL PCT 012.ST25

tatatataac tatataataac tatatatata actatatata actatatata actatatata 180
 taactatata tataactata tatataacta tatatataac tatatatact atatatafaa 240
 ctatatatat ataactatat atataactat atatatafaa ctatatataa ctatatatat 300
 ataactatat atataactat atatatafaa ctatatatat aactatatat atataactat 360
 atatataact atatatatat aactatatat aactatatat atataactat atatataact 420
 atatatatat aactatatat ataactatat atatataact atatatafaa ctatatatat 480
 ataactatat atataactat atatataact atatatafaa ctatatatat ataactatat 540
 atataactat atatatafaa ctatatatat aactatatat ataactatat atataactat 600
 atatatafaa ctatatatat aactatatat atataactat atatataact atatatat 658

<210> 231

<211> 1486

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(1486)

<223> MAR of chromosome 2 genomic contig; 62384127..62385612

<400> 231

attatatata atctattata tattatatct aatacatatt atatctaact tattgtatat 60
 tatatctaatt atataatata ttatatataa tatattatat attatatatt atatacaata 120
 tattatatat tatataatatt ataatatatt atatataata tattatatct aatatattac 180
 atattataic taatctatta tagatataat atgtaatata ttatatatta tatctaattag 240
 atattagata taatatataa tatattatta atataatata ttagatataa tatataatat 300

SEL PCT 012.ST25

aataatataat aatatatatt atggtaata tataatataat aattaataat atattatata	360
tataattatt atgaataata tatcatatat aatatctagt atattatata ttaataacat	420
ataaatatta tattaataat aaataacata ttaattattat atgaataata tataatatac	480
taattattata ttaataatata ataatatact aatatatata taataatata taatatacta	540
atattatatt aataatataat aataatactaa tattatatta ataatatata atatactaata	600
attatattaa taatatataa tataataata tattaagaat atataatata ctaatatatt	660
aagaatataat aataatactaa tattatatta ataatatata ttatattaa taatatatta	720
attattatta ataatattatt aataattata taattatgat tatattaata ttatcaattt	780
aataatattg attatataat atattatata tattatataat tatattattat atattatata	840
ttatattatta ataatatata ttatatataa tataatataat taataatata taagatatata	900
tataatataat taataatata tattagatat aatatataat atgaataata tatattagat	960
ataatataat atattaataa tatattatag ataatatata atattatatt aatatatatt	1020
agattgaata taatatatta ataatatata ttatatgtaa tataatataat taataatata	1080
tattagattg aatatataat atgaataata tatattagat gtaatatatt atattaataa	1140
tatatattag atgaatata atattatatt aatatatatt agattgaata taatatatta	1200
ataatataat ttatatgtaa tataatataat taatatataat tagattgaat ataatatatt	1260
aataatataat attagatatata ataatatata ttaataatata attagatatata ataatatata	1320
ttatatataat ataagatatata ataatatata ttaataatata ataagatatata ataatatata	1380
ttatatataat ataagatatata ataatatata ttaataatata atattagatat tataatataat	1440
taataatata tattagatat ctaatatcta ttatatatct aataga	1486

<210> 232

<211> 333

<212> DNA

<213> Homo sapiens

SEL PCT 012.ST25

<220>

<221> misc_binding

<222> (1)..(333)

<223> MAR of chromosome 2 genomic contig; 62538649..62538981

<400> 232

ttatatatat tatatatata tttttatat atatattata tatatatatt atatatatat 60

tatatatata ttttatatat atattatata tatattttat atatatatta tatatatatt 120

ttatatatat tatatatata ttttatatat attatatata tttttatat atatattata 180

tatatatttt atatatatat tatatatata ttttatatat atattatata tatattttat 240

atatatatta tatatatatt ttatatatat attatatata tttttatat atatattata 300

tatatatttt atatatatat tatatatata ttt 333

<210> 233

<211> 480

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(480)

<223> MAR of chromosome 2 genomic contig; 63240325..63240804

<400> 233

tatatataaa atatatatatt tttaaataata aaatataat atatittaat attaatatat 60

atatatttta atatataata tatataattat atattttata tataaaatat atatattata 120

SEL PCT 012.ST25

tattttatat ataaaatata tatattatat attttatata ttaaaatata tattttatat 180
 attttaatta ttaaaatata tatattatat attttaata taaaatatat atattatata 240
 tttaatatata taaaatatat atattatata tttaatatata taaaatatat atattttata 300
 ttatatata taaatatata tatttatatat tttaatatata aaaatatata tatttatatat 360
 tttaatatata aaaatatata tatttatatat tttaatatata aaaatatata tatttatatat 420
 tttaatatata ataaaatata tatattatat attttatata tattaaatat atattttata 480

<210> 234

<211> 302

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(302)

<223> MAR of chromosome 2 genomic contig; 63935480..63935781

<400> 234

atatatataa atatatatat aattatatat agatatatat aattatatat agatatatat 60
 attctatatt ctatatatat ataatatata atatataaat tatatataga atatatatta 120
 tatataatat attatatata ttatatataa tatatatatt atatatatta tatataatat 180
 atatatatta tatattatat ataatttata tatattatat atagaatatata tatttatatat 240
 agaatataga atatatataa tatatataga atacagaata tatatagaat atagaatatata 300
 ta 302

<210> 235

<211> 407

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(407)

<223> MAR of chromosome 2 genomic contig; 63935888..63936294

<400> 235

tataatatat taatataata tatagacagt atataatata atatacagac agtatataat 60

atacagacag tatataatat ataataattat atataatatt atataataa ttatataata 120

tattatatta tatatattat ataataatatt atattatata taatatatgt aafattatat 180

attatattat acataatata ttatatataa tatattatat ataataattat atatattata 240

tataatatat ataataataa tattataata tataatatat aatagtacag tatatattat 300

atatataatt ctatatataa tatatagaat tctatctatt tataatatat atagaattct 360

atatataata tataatatac agaattctat atatattata tatagaa 407

<210> 236

<211> 302

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(302)

<223> MAR of chromosome 2 genomic contig; 66958350..66958651

SEL PCT 012.ST25

<400> 236

tattatatat attgtatata tatgtatatt atatatattg tatatataat gtatattata 60

tatattatat atataatgtat attatatata ttgtatatat atgtatatia tatatatgt 120

atataatgtat atgtatatat gtatgtgtat atatatatac atatacacat atatgtgtat 180

gtatatatat gtgtgtatat acgtatatat acatatatac aattttgta tatatacata 240

tatacacata tatatgtgta tgtgtatatata tatacacata tatgtgtgtg tatatacaca 300

ta 302

<210> 237

<211> 651

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(651)

<223> MAR of chromosome 2 genomic contig; 68307125..68307775

<400> 237

gataattatat attgtatata ttatatatgt atataatata ctattatata ttatatatgt 60

atataatttt attaatatat atattatatt atattatata ttatattata ttatattata 120

tatataatat taatattata tattattata tattatatta tattaatatt atatatatat 180

aatatatata atatatataa tagtattata tataatatat ataatagtat tatatattat 240

atatatataa tactattata tatattatat ataatagtat tatatatatt atatatataa 300

tactattata tataatatat actattatat aatatatata atactattat atattattata 360

SEL PCT 012.ST25

tataatacta ttatatataa tatatataat actattatat ataatatata taatactatt 420
 atatataata tatataatac tattatatat aatatatata atactattat atataatata 480
 tataatacta ttatatataa tatatatatt atatataaft atattaatat ataatagtat 540
 catatataat aatagtatat ataatatata atatatatat tatatatatt ataatagtat 600
 atataacata taatatagta tatatattat atattatata taaaatattt a 651

<210> 238

<211> 367

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(367)

<223> MAR of chromosome 2 genomic config; 68308243..68308609

<400> 238

atatatatat atgagtcacac catacacata tatatatata atgtttatat atataatgta 60
 tatatatat gtttatatat aatgtatata tataatgttt atatataaa tglatatata 120
 taatgtttat atatataatg tatatatata atgtttatat atataatgtg tatatatat 180
 gtttatatat ataatgtgta tatataatgt ttatatataa tgtgtatata taatgtttat 240
 atatataatg tgtatatata atgtttatat atataatgtg tatatatat gtttatatat 300
 ataatgtgta tatatatat gtttatatat ataatgtgta tatatatat gtttatatat 360
 ataatgt 367

<210> 239

<211> 499

SEL PCT 012.ST25

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(499)

<223> MAR of chromosome 2 genomic contig; 410241..410739

<400> 239

ataatatgta tatatattat attatatatt atattacata ttatatatta tattacatat 60

tatatattta tatattacat attatatatt atattttata ttatatatta tatcatatat 120

atgttatgca ttatataata cataatatat tatatatgat ataatatata ttatatatta 180

ttatatataa tataattaat atattatgta ttatataata tatattatgt tataatatat 240

aatatatatt atataattat ataatatatt atgtattata taatatatat tatgttataa 300

tatattatat tatatatatt atatatatat tatatatata atgtatatta tatataaac 360

ataatatatt atatattata tattatttta tataatatat tatataatgt gatatatatt 420

ataatatatt atataacata gtaattata taatatatta tataatgtaa tatattatat 480

attatataat atattgtat 499

<210> 240

<211> 402

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

SEL PCT 012.ST25

<222> (1)..(402)

<223> MAR of chromosome 2 genomic contig; 31531..31932

<400> 240

cacattatat atataaacat tatatatata cacattatat atataaacat tatatatata 60

cacattatat atataaacat tatatatata cattatatat ataaacatta tatatacaca 120

ttatatatat aaacattata tatacaaatt atatatataa acattatatata tacaattat 180

atatataaac attatatata tacattatat atataaacat tatatatata cattatatat 240

ataaacatta tatatatata ttatatatat aaacattata tatatacatt atatatataa 300

acattatatata tatacattat atatatataaac gttatatata tacattatat atataaacat 360

tatatgtata cattatatat ataaacatta tatatatatg tg 402

<210> 241

<211> 421

<212> DNA

<213> Homo sapiens

<220>

<221> misc_binding

<222> (1)..(421)

<223> MAR of chromosome 2 genomic contig; 32415..32835

<400> 241

ataaatattt tatatatata atataatata tatactatat tataatgttat atatactatt 60

ataatatata taatatatat attatatatt atatatata ttattatatata tgatactatt 120

atatattaat ataattatat ataatatata tattatatata tatactatta tatattatat 180

SEL PCT 012.ST25

ataatagtat attatataat atatatatta tatataatag tattatatat actattatat 240
 attatatata ttatatatat ataaaatata atataatata tataatatat aatattaata 300
 ttatatatat aatataatat aatatataat ataataat atatatatta ataaaattat 360
 attaatatat aatatataat agtatattat atacatatat aatatataca atatataata 420

t

421