

DISEASE MARKER

Field of the Invention

- 5 The invention relates to disease processes.

Background of the Invention

- Muscular atrophy (MD) is a group of muscle diseases that typically results in increasing weakening and breakdown of skeletal muscles over time. The disorders differ in which muscles are primarily affected, the degree of weakness, how fast they worsen, and when symptoms begin. Many people will eventually
10 become unable to walk. Some types are also associated with problems in other organs.

Summary of the Invention

- The inventors have identified chromosome conformation signatures relevant to muscular atrophy. Accordingly the invention provides a method of detecting the muscular atrophy status in an individual, comprising determining the presence or absence of one or more chromosome interactions represented
15 by the probes shown in Table 1, to thereby detect muscular atrophy in the individual.

- Preferably the method is carried out to select an individual for receiving therapy or a treatment for muscular atrophy. The method may be carried out on individual that has been preselected based on a physical characteristic, risk factor or the presence of a symptom. The method is typically carried out to diagnose muscular atrophy or to determine prognosis for muscular atrophy, and preferably to
20 determine severity of muscular atrophy.

Brief Description of the Drawings

Figure 1 shows a description of the spinal and bulbar muscular atrophy (SBMA) samples used in the experimental work.

- Figure 2 shows the PCA of all SBMA arrays. PCA of more than 900k EpiSwitch CCSs. Sample SBMA0007
25 shows an issue. Squares show pHC and circles shows SMBA in all the figures.

Figure 3 shows the PCA of all SBMA arrays with SBMA0007 removed. The data then separates out disease and control samples.

Figure 4 shows a PCA with the samples labelled up by the FRS scope. There are no obvious clusters due to FRS score.

Figure 5 shows a PCA with samples labelled up by the CAG repeat. There are no obvious clusters by CAG repeat.

Figure 6 shows a PCA with samples labelled up by disease duration. There are no obvious clusters due to disease duration.

- 5 Figure 7 shows top significant chromosome interactions (also termed 'CCS', chromosome conformation signature) which are present and absent in SBMA. The top 200 interactions for each set were below ≤ 0.05 FDR identified. The two tables show the top 40 interactions per cohort, ranked by interaction frequency.

- Figure 8 shows genetic location mapping for SBMA present interactions. Although the drawing is not included here, but PD-L1 expression and PD-1 checkpoint pathways in cancer were looked at and interactions associated with them were identified as present in SBMA patients.
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Figures 9 and 10 show a pathway analysis of the top SBMA present interaction associated genes.

Figure 11 shows RET signalling associated pathways.

Figure 12 shows genetic location mapping for SBMA absent interactions.

- 15 Figure 13 shows a pathway analysis of top absent SBMA interaction associated genes.

Figure 14 shows disease analysis of top SBMA absent interaction associated genes, going from the left box to the right box. The figure shows disease enrichment analysis of the genes associated to the top CCSs absent in SBMA.

Figure 15 shows a preferred method for carrying out the marker detection step of the invention.

20 **Detailed Description of the Invention**

Terms Used Herein

The method of the invention may be referred to as the 'process' of the invention herein.

- The chromosome interactions which are typed may be referred to as 'markers', 'CCS', 'chromosome conformation signature' or 'epigenetic interaction' herein. Such interactions are recognised in the art as regions of the chromosome coming together in a stable manner and this represents a distinct mode of regulation. A chromosome interaction can also be referred to as a 'juxtaposition' of chromosomes, chromosome 'folding' or 'chromatin interaction'. Such interactions can be detected, for example, using the 3C (chromosome conformation capture) method.
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The word 'type' will be interpreted as per the context, but will usually refer to detection of whether a specific chromosome interaction is present or absent.

The chromosome interactions which are typed in the method of the invention are defined in Table 1.

They are defined by means of the probe sequences which detect the ligated product made by an

- 5 EpiSwitch method (see Figure 15). They are also defined by the position numbers of the interaction which are included within the probe name and they are also defined by the primer sequences which allow detection of the ligated sequence. The chromosome interaction can be defined by the 'probe location' given in the tables with reference to the chromosome number and the 'Start' and 'End' positions given for the chromosome regions which come together to form the interaction.

10 *Aspects of the Invention*

The invention relates to determining different aspects of muscular atrophy, including in respect to the presence or stage of muscular atrophy. This determining is by typing any of the relevant markers disclosed herein, for example in Table 1, or preferred combinations of markers, or markers in defined specific regions disclosed herein.

- 15 Specific number of markers may be chosen from any group of markers which is specifically disclosed herein. Preferred numbers of markers are at least 3, 5, 8, 10, 15 and at least 20. Preferred groups of markers are those shown in each table, or each part of a table (for example "Table 1A (part 1a)"), or all the markers associated with a distinct characteristic of muscular atrophy.

The invention includes a process of typing a patient to identify whether they have muscular atrophy

- 20 and/or the stage of muscular atrophy. The invention includes diagnosis of an individual for any condition or stage of disease as defined herein (i.e. prognosis), which can be thought of as determining the subgroup they belong to.

The invention also concerns a panel of epigenetic markers which relates to muscular atrophy. The panel may have been optimised in some way, for example by GLMNET analysis.

- 25 The invention therefore allows personalised therapy to be given to the patient which accurately reflects the patient's needs.

Any therapy, for example drug, which is mentioned herein may be administered to an individual based on the result of the process.

Marker sets are disclosed in the Tables and Figures. In one embodiment at least 10 markers from any disclosed marker set are used in the invention. In another embodiment at least 20% of the markers from any disclosed marker set are used in the invention.

The Epigenetic Interactions Relevant to the Invention

- 5 The chromosome interactions which are typed in the invention are typically interactions between distal regions of a chromosome, said interactions being dynamic and altering, forming or breaking depending upon the state of the region of the chromosome. That state will reflect different aspects of muscular atrophy and therefore the invention can be carried out to the presence, type, severity or stage of muscular atrophy.
- 10 The chromosome interaction may, for example, reflect if it is being transcribed or repressed. Chromosome interactions which are specific to muscular atrophy subgroups as defined herein have been found to be stable, thus providing a reliable means of measuring the differences between the two subgroups (for example a muscular atrophy group and a healthy group that does not have muscular atrophy).
- 15 Chromosome interactions specific to muscular atrophy will normally occur early in the disease process, for example compared to other epigenetic markers such as methylation or changes to binding of histone proteins. Thus the process of the invention is able to detect disease at an early stage. This allows early intervention (for example treatment) which as a consequence will be more effective. Chromosome interactions also reflect the current state of the individual and therefore can be used to assess changes
- 20 to disease status. Furthermore there is little variation in the relevant chromosome interactions between individuals within the same subgroup. Detecting chromosome interactions is highly informative with up to 50 different possible interactions per gene, and so processes of the invention can for example interrogate 500,000 possible different interactions.

- Chromosomal interactions may overlap and include the regions of chromosomes shown to encode
- 25 relevant or undescribed genes, but equally may be in intergenic regions. It should further be noted that the inventors have discovered that chromosome interactions in all regions are equally important in determining the status of a chromosomal locus.

- The chromosome interactions which are detected in the invention could be impacted by changes to the underlying DNA sequence, by environmental factors, DNA methylation, non-coding antisense RNA
- 30 transcripts, non-mutagenic carcinogens, histone modifications, chromatin remodelling and specific local DNA interactions. However it must be borne in mind that chromosome interactions as defined herein

are a regulatory modality in their own right and do not have a one to one correspondence with any genetic marker (DNA sequence change) or any other epigenetic marker.

The changes which lead to the chromosome interactions may be impacted by changes to the underlying nucleic acid sequence which themselves do not directly affect a gene product or the mode of gene expression. Such changes may be for example, SNPs within and/or outside of the genes, gene fusions and/or deletions of intergenic DNA, microRNA, and non-coding RNA. For example, it is known that roughly 20% of SNPs are in non-coding regions, and therefore the process as described is also informative in non-coding situation. In one aspect the regions of the chromosome which come together to form the interaction are less than 5 kb, 3 kb, 1 kb, 500 base pairs or 200 base pairs apart on the same chromosome.

The chromosome interaction which is detected may be within a gene, such as any gene mentioned herein. However it may also be upstream or downstream of the gene, for example up to 50,000, up to 30,000, up to 20,000, up to 10,000 or up to 5000 bases upstream or downstream from the gene or from the coding sequence.

The Process of the Invention

The process of the invention comprises a typing system for detecting chromosome interactions relevant to muscular atrophy. Any suitable typing method can be used, for example a method in which the proximity of the chromosomes in the interaction is detected. The typing method may be performed using the *EpiSwitch*[™] system mentioned herein which for example may be carried out by a method comprising the following steps (for example on a sample from the subject):

- (i) cross-linking regions of chromosome which have come together in a chromosome interaction,
- (ii) optionally isolating the cross-linked DNA from said chromosomal locus
- (iii) subjecting the cross-linked DNA to cleavage, and
- (iv) ligating the nucleic acids present in the cross-linked entity to derive a ligated nucleic acid with sequence from both the regions which formed a chromosomal interaction.

Detection of this ligated nucleic acid allows determination of the presence or absence of a particular chromosome interaction. The ligated nucleic acid therefore acts as a marker for the presence of the chromosome interaction. Preferably the ligated nucleic acid is detected by PCR or a probe based method, including a qPCR method.

In the method the chromosomes can be cross-linked by any suitable means, for example by a cross-linking agent, which is typically a chemical compound. In a preferred aspect, the interactions are cross-

linked using formaldehyde, but may also be cross-linked by any aldehyde, or D-Biotinoyl-e-aminocaproic acid-N-hydroxysuccinimide ester or Digoxigenin-3-O-methylcarbonyl-e-aminocaproic acid-N-hydroxysuccinimide ester. Para-formaldehyde can cross link DNA chains which are 4 Angstroms apart. Preferably the chromosome interactions are on the same chromosome. Typically the chromosome
5 interactions are 2 to 10 Angstroms apart.

The cross-linking is preferably *in vitro*. The cleaving is preferably by restriction digestion with an enzyme, such as TaqI. The ligating may form DNA loops.

Where PCR (polymerase chain reaction) is used to detect or identify the ligated nucleic acid, the size of the PCR product produced may be indicative of the specific chromosome interaction which is present,
10 and may therefore be used to identify the status of the locus. In preferred aspects the primers shown in any table herein are used, for example the primer pairs shown in Table 1 are used (corresponding to the chromosome interaction which is being detected). Homologues of such primers or primer pairs may also be used, which can have at least 70% identity to the original sequence.

Where a probe is used to detect or identify the ligated nucleic acid, this is generally by Watson-Crick
15 based base-pairing between the probe and ligated nucleic acid. Probe sequences as shown in any table herein may be used, for example the probe sequences shown in Table 1 (corresponding to the chromosome interaction which is being detected). Homologues of such probe sequences may also be used, which can have at least 70% identity to the original sequence.

Typing according to the process of the invention may be carried out at multiple time points, for example
20 to monitor the progression of the disease. This may be at one or more defined time points, for example at at least 1, 2, 5, 8 or 10 different time points. The durations between at least 1, 2, 5 or 8 of the time points may be at least 5, 10, 20, 50, 80 or 100 days. Typically there are 3 time points at least 50 days apart.

Subgroups and Personalised Treatment

25 As used herein, a “subgroup” preferably refers to a population subgroup, more preferably a subgroup in the population of a particular animal such as a particular eukaryote, or mammal. Most preferably, a “subgroup” refers to a subgroup in the human population. Therefore the process of the invention is preferably carried out to detect the presence of muscular atrophy in a human. The process of the invention may be carried out for diagnostic or prognostic purposes.

30 The invention includes detecting and treating particular subgroups in a population. The inventors have discovered that chromosome interactions differ between subsets (for example at least two subsets) in

the relevant population. Identifying these differences will allow physicians to categorize their patients as a part of one subset of the population. The invention therefore provides physicians with a process of personalizing medicine for the patient based on their epigenetic chromosome interactions. Such testing may be used to select how to subsequently treat the patient, for example the type of drug and/or its
 5 dose and/or its frequency of administration.

The individual that is tested in the process of the invention may have been selected in some way. The individual may be susceptible to any condition mentioned herein and/or may be in need of any therapy mentioned in. The individual may be receiving any therapy mentioned herein. In particular, the individual may have, or be suspected of having, muscular atrophy. Thus the invention includes a process
 10 of typing a patient to diagnose muscular atrophy, which is equivalent to determining the subgroup they belong to. The muscular atrophy may be any of the following conditions: spinal bulbar muscle atrophy (SBMA), a polyglutamine disease, dentatorubral-pallidoluysian atrophy, spinocerebellar ataxia, sarcopenia or cachexia. Therefore the process of the invention may comprise detecting (or diagnosing) any of these conditions. The process of the invention may comprise determining prognosis of any of
 15 these conditions, such as determining the severity.

The individual may be receiving any of the following or may have received any of these in the previous 365 days: physiotherapy, rehabilitation, therapeutic agents against tremor and muscle cramps, hormone therapy, surgical treatment of gynecomastia, tube feeding or ventilatory support. The individual may have cancer. The individual may be a human male of age 30 to 60, for example of age 40 to 50. The
 20 individual may have gynecomastia, testicular atrophy, reduced fertility or androgen insensitivity. The individual may have reduced fertility due to androgen insensitivity.

Tables Provided Herein

Table 1 shows 400 specific markers which can be used to detect muscular atrophy, i.e. their presence or absence can be used in such a detection (i.e. they are 'disseminating' markers). Table 1A shows 200
 25 markers which are only present in muscular atrophy. Table 1B shows 200 markers which are present only healthy controls, i.e. they are absent in muscular atrophy. The process of the invention can therefore be carried out using markers from Table 1A or from Table 1B, or from a selection of markers from both Table 1A and Table 1B.

The markers are defined using probe sequences (which detect a ligated product as defined herein). The
 30 first two sets of Start-End positions show probe positions, and the second two sets of Start-End positions show the relevant 4kb region.

The following information is provided in the probe data table:

RP - Rsum the Rank Product statistics evaluated per each chromosome interaction.

FC - Interaction frequency (positive or negative).

5 Pfp - estimated percentage of false positive predictions (pfp), both considering positive and negative chromosome interactions.

Pval - estimated pvalues per each CCSs being positive and negative.

Adj.P.value(FDR) - False discovery rate adjusted p.value.

Loop Detected - which state the loop is found in.

10 Simple permutation-based estimation is used to determine how likely a given RP value or better is observed in a random experiment. This has the following steps:

1. Generate p permutations of k rank lists of length n.
2. Calculate the rank products of the n CCS in the p permutations.
3. Count (c) how many times the rank products of the CCS in the permutations are smaller or equal to
15 the observed rank product. Set c to this value.
4. Calculate the average expected value for the rank product by: $Erp(g)=c/p$.
5. Calculate the percentage of false positives as: $pfp(g)=Erp(g)/rank(g)$ where rank(g) is the rank of CCS g in a list of all n CCSs sorted by increasing RP.

The rank product statistic ranks chromosome interactions according to intensities within each
20 microarray and calculates the product of these ranks across multiple microarrays. This technique can identify chromosome interactions that are consistently detected among the most differential chromosome interactions in a number of replicated microarrays. Where the p-value is 0 this indicates that there is very little variation in the Rank Product of the CCS across the samples, this is a good example of the signal to noise and effect size of CCS. Where p value is 0 and pfp is 0 this means that
25 permuted Rank Product doesn't differ from the actual observed Rank Product. These methods are described Breitling R and Herzyk P (2005) Rank-based methods as a non-parametric alternative of the t-test for the analysis of biological microarray data. J Bioinf Comp Biol 3, 1171–1189.

The FC indicates prevalence of marker in each comparison, 2 means twice over average test, 1.5 means 1.5 over the average test, etc., and so FC indicates the weight of a marker to phenotype/group. The FC
30 value can be used to give an indication of how many markers are needed for a highly effective test. Typically 5 to 10 markers will give a highly effective test, though even smaller numbers of markers will give a functional test for detection of muscular atrophy.

The probes are designed to be 30bp away from the Taq1 site. In case of PCR, PCR primers are typically designed to detect ligated product but their locations from the Taq1 site vary. Probe locations:

Start 1 - 30 bases upstream of TaqI site on fragment 1

End 1 - TaqI restriction site on fragment 1

Start 2 - TaqI restriction site on fragment 2

End 2 - 30 bases downstream of TaqI site on fragment 2

5 4kb Sequence Location:

Start 1 - 4000 bases upstream of TaqI site on fragment 1

End 1 - TaqI restriction site on fragment 1

Start 2 - TaqI restriction site on fragment 2

End 2 - 4000 bases downstream of TaqI site on fragment 2

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Preferred Marker Sets

The invention relates to detecting the presence of muscular atrophy by typing chromosome interaction markers, such as any of the specific markers disclosed herein, for example in Table 1, or preferred combinations of markers, or markers in defined specific regions disclosed herein. Markers present in genes and regions mentioned in the tables may be typed. Specific markers are defined herein by location or by probe and/or primer sequences. Therefore preferred markers are those which are represented by the probes and/or primer pairs disclosed in tables herein.

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Combinations of markers can be defined in different ways, such as:

- by ranking by any parameter defined herein, or

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- by any 'part' of Table 1,

- by reference to the 'number' of the marker which is listed in the left hand column of Table 1.

In a preferred aspect at least 10 markers are typed from the top 40 markers for any parameter mentioned in Table 1, such as FC.

In one aspect one or more markers are typed which:

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(i) are present in any one of the regions listed in Table 1; and/or

(ii) corresponds to any one of the chromosome interactions represented by any probe shown in Table 1; and/or

(iii) is present in a 4,000 base region which comprises or which flanks (i) or (ii).

In a preferred aspect:

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- at least 5 chromosome interactions are typed from Table 1A, and/or

- at least 5 chromosome interactions are typed from Table 1B.

In another preferred aspect at least 5 chromosome interactions are typed selected from:

- interaction numbers 1 to 40 from Table 1A, or

- interaction numbers 1 to 40 from Table 1B.

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Preferred Numbers of Markers to be Typed

Typing a very low number of the markers disclosed herein will result in an effective test due to the nature of regulation by chromosome interaction, including their network-like properties. The different numbers and combination of markers give rise to different performance properties. Further as will be appreciated the markers can be selected from Table 1 as a whole or from the parts of the table defined by Table 1A and Table 1B, or from parts defined by a number and letter (reflecting certain marker numbers).

In one aspect the process comprising typing at least 3, 5, 8, 10, 15 or 20 of the chromosome interactions represented by the probes in Table 1. In one embodiment at least 10 chromosome interactions represented by the probes in Table 1 are typed.

In one aspect the process comprising typing at least 50, 80, 100, 150, 200, 250, 300, 350 or all of the chromosome interactions represented by the probes in Table 1.

In one aspect the process comprising typing at least 3, 5, 8, 10, 15 or 20 of the chromosome interactions represented by the probes in Table 1A. In one embodiment at least 10 chromosome interactions represented by the probes in Table 1A are typed.

In one aspect the process comprising typing at least 30, 50, 80, 100, 150 or all of the chromosome interactions represented by the probes in Table 1A.

In one aspect the process comprising typing at least 3, 5, 8, 10, 15 or 20 of the chromosome interactions represented by the probes in Table 1B. In one embodiment at least 10 chromosome interactions represented by the probes in Table 1B are typed.

In one aspect the process comprising typing at least 30, 50, 80, 100, 150 or all of the chromosome interactions represented by the probes in Table 1B.

In one aspect at least 3, 5, 8, 10, 15 or 20 chromosome interactions are typed from the markers listed as numbers 1 to 40 in Table 1A and/or at least 3, 5, 8, 10, 15 or 20 chromosome interactions are typed from the markers listed as numbers 1 to 40 in Table 1B.

In one aspect at least 10 chromosome interactions are typed from the markers listed as numbers 1 to 40 in Table 1A and/or at least 10 chromosome interactions are typed from the markers listed as numbers 1 to 40 in Table 1B.

Types of Chromosome Interaction

In one aspect the locus (including the gene and/or place where the chromosome interaction is detected) may comprise a CTCF binding site. This is any sequence capable of binding transcription repressor CTCF. That sequence may consist of or comprise the sequence CCCTC which may be present in 1, 2 or 3 copies at the locus. The CTCF binding site sequence may comprise the sequence CCGCGNGGNGGCAG (in IUPAC notation). The CTCF binding site may be within at least 100, 500, 1000 or 4000 bases of the chromosome interaction or within any of the chromosome regions shown Table 1.

When detection is performed using a probe, typically sequence from both regions of the probe (i.e. from both sites of the chromosome interaction) could be detected. In preferred aspects probes are used in the process which comprise or consist of the same or complementary sequence to a probe shown in any table. In some aspects probes are used which comprise sequence which is homologous to any of the probe sequences shown in the tables.

The Approach Taken to Identify Markers and Panels of Markers

The invention described herein relates to chromosome conformation profile and 3D architecture as a regulatory modality in its own right, closely linked to the phenotype. The discovery of biomarkers was based on annotations through pattern recognition and screening on representative cohorts of clinical samples representing the differences in phenotypes. We annotated and screened significant parts of the genome, across coding and non-coding parts and over large sways of non-coding 5' and 3' of known genes for identification of statistically disseminating consistent conditional disseminating chromosome conformations, which for example anchor in the non-coding sites within (intronic) or outside of open reading frames.

In selection of the best markers we are driven by statistical data and p values for the marker leads. Selected and validated chromosome conformations within the signature are disseminating stratifying entities in their own right, irrespective of the expression profiles of the genes used in the reference. Further work may be done on relevant regulatory modalities, such as SNPs at the anchoring sites, changes in gene transcription profiles, changes at the level of H3K27ac.

We are taking the question of clinical phenotype differences and their stratification from the basis of fundamental biology and epigenetic controls over phenotype - including for example from the framework of network of regulation. As such, to assist stratification, one can capture changes in the network and it is preferably done through signatures of several biomarkers, for example through following a machine learning algorithm for marker reduction which includes evaluating the optimal number of markers to stratify the testing cohort with minimal noise. This may end with 3-20 markers.

Selection of markers for panels may be done by cross-validation statistical performance (and not for example by the functional relevance of the neighbouring genes, used for the reference name).

A panel of markers (with names of adjacent genes) is a product of clustered selection from the screening across significant parts of the genome, in non-biased way analysing statistical disseminating powers over 14,000-60,000 annotated EpiSwitch sites across significant parts of the genome. It should not be perceived as a tailored capture of a chromosome conformation on the gene of know functional value for the question of stratification. The total number of sites for chromosome interaction are 1.2 million, and so the potential number of combinations is 1.2 million to the power 1.2 million. The approach that we have followed nevertheless allows the identifying of the relevant chromosome interactions.

The specific markers that are provided by this application have passed selection, being statistically (significantly) associated with the condition or subgroup. This is what the data in the relevant table demonstrates. Each marker can be seen as representing an event of biological epigenetic as part of network deregulation that is manifested in the relevant condition. In practical terms it means that these markers are prevalent across groups of patients when compared to controls. On average, as an example, an individual marker may typically be present in 80% of patients tested and in 10% of controls tested.

Simple addition of all markers would not directly represent the network interrelationships between some of the deregulations. This is where the standard multivariate biomarker analysis GLMNET (R package) can be brought in. GLMNET package helps to identify interdependence between some of the markers, that reflect their joint role in achieving deregulations leading to disease phenotype. Modelling and then testing markers with highest GLMNET scores offers not only identify the minimal number of markers that accurately identifies the patient cohort, but also the minimal number that offers the least false positive results in the control group of patients, due to background statistical noise of low prevalence in the control group. Typically a group (combination) of selected markers (such as 3 to 10) offers the best balance between both sensitivity and specificity of detection, emerging in the context of multivariate analysis from individual properties of all the selected statistical significant markers for the condition.

The tables herein show the reference names for the array probes (60-mer) for array analysis that overlaps the juncture between the long range interaction sites, the chromosome number and the start and end of two chromosomal fragments that come into juxtaposition.

Samples and Sample Treatment

The process of the invention will normally be carried out on a sample. The sample may be obtained at a defined time point, for example at any time point defined herein. The sample will normally contain DNA from the individual. It will normally contain cells. In one aspect a sample is obtained by minimally invasive means, and may for example be a blood sample. DNA may be extracted and cut up with a standard restriction enzyme. This can pre-determine which chromosome conformations are retained and will be detected with the EpiSwitch™ platforms. Due to the synchronisation of chromosome interactions between tissues and blood, including horizontal transfer, a blood sample can be used to detect the chromosome interactions in tissues, such as tissues relevant to disease.

Preferred Aspects for Sample Preparation and Chromosome Interaction Detection

Methods of preparing samples and detecting chromosome conformations are described herein. Optimised (non-conventional) versions of these processes can be used, for example as described in this section.

Typically the sample will contain at least 2×10^5 cells. The sample may contain up to 5×10^5 cells. In one aspect, the sample will contain 2×10^5 to 5.5×10^5 cells

Crosslinking of epigenetic chromosomal interactions present at the chromosomal locus is described herein. This may be performed before cell lysis takes place. Cell lysis may be performed for 3 to 7 minutes, such as 4 to 6 or about 5 minutes. In some aspects, cell lysis is performed for at least 5 minutes and for less than 10 minutes.

Digesting DNA with a restriction enzyme is described herein. Typically, DNA restriction is performed at about 55°C to about 70°C, such as for about 65°C, for a period of about 10 to 30 minutes, such as about 20 minutes.

Preferably a frequent cutter restriction enzyme is used which results in fragments of ligated DNA with an average fragment size up to 4000 base pair. Optionally the restriction enzyme results in fragments of ligated DNA have an average fragment size of about 200 to 300 base pairs, such as about 256 base pairs. In one aspect, the typical fragment size is from 200 base pairs to 4,000 base pairs, such as 400 to 2,000 or 500 to 1,000 base pairs.

In one aspect of the EpiSwitch process a DNA precipitation step is not performed between the DNA restriction digest step and the DNA ligation step.

DNA ligation is described herein. Typically the DNA ligation is performed for 5 to 30 minutes, such as about 10 minutes.

The protein in the sample may be digested enzymatically, for example using a proteinase, optionally Proteinase K. The protein may be enzymatically digested for a period of about 30 minutes to 1 hour, for example for about 45 minutes. In one aspect after digestion of the protein, for example Proteinase K digestion, there is no cross-link reversal or phenol DNA extraction step.

- 5 In one aspect PCR detection is capable of detecting a single copy of the ligated nucleic acid, preferably with a binary read-out for presence/absence of the ligated nucleic acid.

Figure 15 shows a preferred process of detecting chromosome interactions.

Processes and Uses of the Invention

- The process of the invention can be described in different ways. It can be described as a process of
- 10 making a ligated nucleic acid comprising (i) *in vitro* cross-linking of chromosome regions which have come together in a chromosome interaction; (ii) subjecting said cross-linked DNA to cutting or restriction digestion cleavage; and (iii) ligating said cross-linked cleaved DNA ends to form a ligated nucleic acid, wherein detection of the ligated nucleic acid may be used to determine the chromosome state at a locus, and wherein preferably:
- 15 - the locus may be any of the loci or regions mentioned in Table 1, and/or
- wherein the chromosomal interaction may be any of the chromosome interactions mentioned herein or corresponding to any of the probes disclosed in Table 1, and/or
- wherein the ligated product may have or comprise (i) sequence which is the same as or homologous to any of the probe sequences disclosed in Table 1; or (ii) sequence which is complementary to (ii).
- 20 The process of the invention can be described as a process for detecting chromosome states which represent different subgroups in a population comprising determining whether a chromosome interaction is present or absent within a defined epigenetically active region of the genome, wherein preferably:
- the subgroup is defined by presence or stage of muscular atrophy, and/or
- 25 the chromosome state may be at any locus or region mentioned in Table 1; and/or
- the chromosome interaction may be any of those mentioned in Table 1 or corresponding to any of the probes disclosed in those tables.

Use of the Process of the Invention to Identify New Treatments

Knowledge of chromosome interactions can be used to identify new treatments for conditions. The invention provides processes and uses of chromosome interactions defined herein to identify or design new therapeutic agents, for example relating to therapy of muscular atrophy or related sub-conditions.

Homologues

- 5 Homologues of polynucleotide / nucleic acid (e.g. DNA) sequences are referred to herein. Such homologues typically have at least 70% homology, preferably at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 98% or at least 99% homology, for example over a region of at least 10, 15, 20, 30, 100 or more contiguous nucleotides, or across the portion of the nucleic acid which is from the region of the chromosome involved in the chromosome interaction. The homology may be
10 calculated on the basis of nucleotide identity (sometimes referred to as "hard homology").

- Therefore, in a particular aspect, homologues of polynucleotide / nucleic acid (e.g. DNA) sequences are referred to herein by reference to percentage sequence identity. Typically such homologues have at least 70% sequence identity, preferably at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity, for example over a region of at least 10, 15, 20, 30,
15 100 or more contiguous nucleotides, or across the portion of the nucleic acid which is from the region of the chromosome involved in the chromosome interaction. The homologues may have at least 70% sequence identity, preferably at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 98% or at least 99% sequence identity across the entire probe, primer or primer pair.

- For example the UWGCG Package provides the BESTFIT program which can be used to calculate
20 homology and/or % sequence identity (for example used on its default settings) (Devereux *et al* (1984) Nucleic Acids Research 12, p387-395). The PILEUP and BLAST algorithms can be used to calculate homology and/or % sequence identity and/or line up sequences (such as identifying equivalent or corresponding sequences (typically on their default settings)), for example as described in Altschul S. F. (1993) J Mol Evol 36:290-300; Altschul, S, F *et al* (1990) J Mol Biol 215:403-10.

- 25 Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pair (HSPs) by identifying short words of length W in the query sequence that either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighbourhood word score threshold (Altschul *et al*, supra). These initial
30 neighbourhood word hits act as seeds for initiating searches to find HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Extensions for the word hits in each direction are halted when: the cumulative alignment

score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W , T and X determine the sensitivity and speed of the alignment. The BLAST program uses as defaults a word length (W) of 11, the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1992) Proc. Natl. Acad. Sci. USA 89: 10915-10919) alignments (B) of 50, expectation (E) of 10, $M=5$, $N=4$, and a comparison of both strands.

The BLAST algorithm performs a statistical analysis of the similarity between two sequences; see e.g., Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90: 5873-5787. One measure of similarity provided by the BLAST algorithm is the smallest sum probability ($P(N)$), which provides an indication of the probability by which a match between two polynucleotide sequences would occur by chance. For example, a sequence is considered similar to another sequence if the smallest sum probability in comparison of the first sequence to the second sequence is less than about 1, preferably less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

The homologous sequence typically differs by 1, 2, 3, 4 or more bases, such as less than 10, 15 or 20 bases (which may be substitutions, deletions or insertions of nucleotides). These changes may be measured across any of the regions mentioned above in relation to calculating homology and/or % percentage sequence identity.

Homology of a 'pair of primers' can be calculated, for example, by considering the two sequences as a single sequence (as if the two sequences are joined together) for the purpose of then comparing against the another primer pair which again is considered as a single sequence.

EpiSwitch™ Technology

The EpiSwitch™ Technology also relates to the use of microarray EpiSwitch™ marker data in the detection of epigenetic chromosome conformation signatures specific for phenotypes. Aspects such as EpiSwitch™ which utilise ligated nucleic acids in the manner described herein have several advantages. They have a low level of stochastic noise, for example because the nucleic acid sequences from the first set of nucleic acids of the present invention either hybridise or fail to hybridise with the second set of nucleic acids. This provides a binary result permitting a relatively simple way to measure a complex mechanism at the epigenetic level. EpiSwitch™ technology also has fast processing time and low cost. In one aspect the processing time is 3 hours to 6 hours.

Arrays

All nucleic acids disclosed herein may be bound to an array, and in one aspect there are at least 15,000, 45,000, 100,000 or 250,000 different nucleic acids bound to the array, which preferably represent at least 300, 900, 2000 or 5000 loci. In one aspect one, or more, or all of the different populations of nucleic acids are bound to more than one distinct region of the array, in effect repeated on the array allowing for error detection. The array may be based on an Agilent SurePrint G3 Custom CGH microarray platform. Detection of binding of first nucleic acids to the array may be performed by a dual colour system.

The Threshold of Detection

The markers which are disclosed herein have been found to be 'disseminating markers' capable of determining muscular atrophy status or subgroup. In practical terms it means that these markers are prevalent across groups of patients when compared to controls (as is shown by the FC value, for example). On average, as an example, an individual marker may typically be present in 80% of patients tested and in 10% of controls tested. Thus in one aspect of the method an individual is deemed to be part of the relevant muscular atrophy subgroup if least 80% of the markers that are tested for that subgroup are present in the individual and/or if at least 80% of the markers that are tested which are related to the control (non-muscular atrophy group) are absent from the individual. Typically presence/absence of at least 8 markers out of 10 compared to the 'ideal' result shown in the table can be used to assign the individual to a subgroup.

20 Therapeutic Agents and Treatments

This section is relevant both to:

- therapeutic agents which are given to individuals selected by the process of the invention, and
- therapeutic agents which are selected based on the results of the process of the invention.

The invention provides therapeutic agents for use in preventing or treating a disease condition in certain individuals, for example those identified by a process of the invention. This may comprise administering to an individual in need a therapeutically effective amount of the agent. The invention provides use of the agent in the manufacture of a medicament to prevent or treat a condition in certain individuals. The disease or condition may be muscular atrophy, any type of muscular atrophy sub-condition or a stage of muscular atrophy.

The formulation of the agent will depend upon the nature of the agent. The agent will be provided in the form of a pharmaceutical composition containing the agent and a pharmaceutically acceptable carrier or diluent. Suitable carriers and diluents include isotonic saline solutions, for example phosphate-buffered saline. Typical oral dosage compositions include tablets, capsules, liquid solutions and liquid suspensions. The agent may be formulated for parenteral, intravenous, intramuscular, subcutaneous, transdermal or oral administration.

The dose of an agent may be determined according to various parameters, especially according to the substance used; the age, weight and condition of the individual to be treated; the route of administration; and the required regimen. A physician will be able to determine the required route of administration and dosage for any particular agent. A suitable dose may however be from 0.1 to 100 mg/kg body weight such as 1 to 40 mg/kg body weight, for example, to be taken from 1 to 3 times daily.

The therapeutic agent may be any such agent disclosed herein, or may target any 'target' disclosed herein, including any protein or gene disclosed herein in any table. It is understood that any agent that is disclosed in a combination should be seen as also disclosed for administration individually.

Therapeutic agents and treatments which can be used in the invention include physiotherapy, rehabilitation, agents that treat muscle tremors, agents that treat muscle cramps, hormone therapy, anti-testosterone leuprorelin.

Properties of Nucleic Acids of the Invention

The invention relates to certain nucleic acids, such as the ligated nucleic acids which are described herein as being used or generated in the process of the invention. These may be the same as, or have any of the properties of, the first and second nucleic acids mentioned herein. The nucleic acids of the invention typically comprise two portions each comprising sequence from one of the two regions of the chromosome which come together in the chromosome interaction. Typically each portion is at least 8, 10, 15, 20, 30 or 40 nucleotides in length, for example 10 to 40 nucleotides in length. Preferred nucleic acids comprise sequence from any of the genes mentioned in any of the tables. Typically preferred nucleic acids comprise the specific probe sequences mentioned in Table 1; or fragments and/or homologues of such sequences.

Preferably the nucleic acids are DNA. It is understood that where a specific sequence is provided the invention may use the complementary sequence as required in the particular aspect. Preferably the nucleic acids are DNA. It is understood that where a specific sequence is provided the invention may use the complementary sequence as required in the particular aspect.

The primers shown in Table 1 may also be used in the invention as mentioned herein. In one aspect primers are used which comprise any of: the sequences shown in Table 1; or fragments and/or homologues of any sequence shown in Table 1.

Screening to Identify Relevant Chromosome Interactions

- 5 In one aspect one or more of the chromosome interactions which are typed have been identified by a process of determining which chromosomal interactions are relevant to a chromosome state corresponding to a muscular atrophy subgroup of the population, comprising contacting a first set of nucleic acids from subgroups with different states of the chromosome with a second set of index nucleic acids, and allowing complementary sequences to hybridise, wherein the nucleic acids in the first and
10 second sets of nucleic acids represent a ligated product comprising sequences from both the chromosome regions that have come together in chromosomal interactions, and wherein the pattern of hybridisation between the first and second set of nucleic acids allows a determination of which chromosomal interactions are specific to the subgroup.

- The second set of nucleic acid sequences has the function of being a set of index sequences, and is
15 essentially a set of nucleic acid sequences which are suitable for identifying subgroup specific sequence. They can represent the 'background' chromosomal interactions and might be selected in some way or be unselected. They are in general a subset of all possible chromosomal interactions.

- The second set of nucleic acids may be derived by any suitable process. They can be derived computationally or they may be based on chromosome interaction in individuals. They typically
20 represent a larger population group than the first set of nucleic acids. In one particular aspect, the second set of nucleic acids represents all possible epigenetic chromosomal interactions in a specific set of genes. In another particular aspect, the second set of nucleic acids represents a large proportion of all possible epigenetic chromosomal interactions present in a population described herein. In one particular aspect, the second set of nucleic acids represents at least 50% or at least 80% of epigenetic
25 chromosomal interactions in at least 20, 50, 100 or 500 genes, for example in 20 to 100 or 50 to 500 genes.

- The second set of nucleic acids typically represents at least 100 possible epigenetic chromosome interactions which modify, regulate or in any way mediate a phenotype in population. The second set of nucleic acids may represent chromosome interactions that affect a disease state (typically relevant to
30 diagnosis or prognosis) in a species. The second set of nucleic acids typically comprises sequences representing epigenetic interactions both relevant and not relevant to a prognosis subgroup.

In one particular aspect the second set of nucleic acids derive at least partially from naturally occurring sequences in a population, and are typically obtained by *in silico* processes. Said nucleic acids may further comprise single or multiple mutations in comparison to a corresponding portion of nucleic acids present in the naturally occurring nucleic acids. Mutations include deletions, substitutions and/or
5 additions of one or more nucleotide base pairs. In one particular aspect, the second set of nucleic acids may comprise sequence representing a homologue and/or orthologue with at least 70% sequence identity to the corresponding portion of nucleic acids present in the naturally occurring species. In another particular aspect, at least 80% sequence identity or at least 90% sequence identity to the corresponding portion of nucleic acids present in the naturally occurring species is provided.

10 *Properties of the Second Set of Nucleic Acids*

In one particular aspect, there are at least 100 different nucleic acid sequences in the second set of nucleic acids, preferably at least 1000, 2000 or 5000 different nucleic acids sequences, with up to 100,000, 1,000,000 or 10,000,000 different nucleic acid sequences. A typical number would be 100 to 1,000,000, such as 1,000 to 100,000 different nucleic acids sequences. All or at least 90% or at least 50%
15 or these would correspond to different chromosomal interactions.

In one particular aspect, the second set of nucleic acids represent chromosome interactions in at least 20 different loci or genes, preferably at least 40 different loci or genes, and more preferably at least 100, at least 500, at least 1000 or at least 5000 different loci or genes, such as 100 to 10,000 different loci or genes. The lengths of the second set of nucleic acids are suitable for them to specifically hybridise
20 according to Watson Crick base pairing to the first set of nucleic acids to allow identification of chromosome interactions specific to subgroups. Typically the second set of nucleic acids will comprise two portions corresponding in sequence to the two chromosome regions which come together in the chromosome interaction. The second set of nucleic acids typically comprise nucleic acid sequences which are at least 10, preferably 20, and preferably still 30 bases (nucleotides) in length. In another
25 aspect, the nucleic acid sequences may be at the most 500, preferably at most 100, and preferably still at most 50 base pairs in length. In a preferred aspect, the second set of nucleic acids comprises nucleic acid sequences of between 17 and 25 base pairs. In one aspect at least 100, 80% or 50% of the second set of nucleic acid sequences have lengths as described above. Preferably the different nucleic acids do not have any overlapping sequences, for example at least 100%, 90%, 80% or 50% of the nucleic acids
30 do not have the same sequence over at least 5 contiguous nucleotides.

Given that the second set of nucleic acids acts as an 'index' then the same set of second nucleic acids may be used with different sets of first nucleic acids which represent subgroups for different

characteristics, i.e. the second set of nucleic acids may represent a 'universal' collection of nucleic acids which can be used to identify chromosome interactions relevant to different characteristics.

The First Set of Nucleic Acids (Screening for Relevant Chromosome Interactions)

- 5 The first set of nucleic acids are typically from subgroups relevant to muscular atrophy. The first nucleic acids may have any of the characteristics and properties of the second set of nucleic acids mentioned herein. The first set of nucleic acids is normally derived from samples from the individuals which have undergone treatment and processing as described herein, particularly the EpiSwitch™ cross-linking and cleaving steps. Typically the first set of nucleic acids represents all or at least 80% or 50% of the chromosome interactions present in the samples taken from the individuals.
- 10 Typically, the first set of nucleic acids represents a smaller population of chromosome interactions across the loci or genes represented by the second set of nucleic acids in comparison to the chromosome interactions represented by second set of nucleic acids, i.e. the second set of nucleic acids is representing a background or index set of interactions in a defined set of loci or genes.

Library of Nucleic Acids

- 15 Any of the types of nucleic acid populations mentioned herein may be present in the form of a library comprising at least 200, at least 500, at least 1000, at least 5000 or at least 10000 different nucleic acids of that type, such as 'first' or 'second' nucleic acids. Such a library may be in the form of being bound to an array. The library may comprise some or all of the probes or primer pairs shown in Table 1A or 1B. The library may comprise all of the probe sequence from any of the tables disclosed herein.

20 *Hybridisation*

- The invention typically requires a means for allowing wholly or partially complementary nucleic acid sequences to hybridise, for example in the method of the invention or between the first set of nucleic acids and the second set of nucleic acids to hybridise. In one aspect all of the first set of nucleic acids is contacted with all of the second set of nucleic acids in a single assay, i.e. in a single hybridisation step.
- 25 However any suitable assay can be used.

Labelled Nucleic Acids and Pattern of Hybridisation

- The nucleic acids mentioned herein may be labelled, preferably using an independent label such as a fluorophore (fluorescent molecule) or radioactive label which assists detection of successful hybridisation. Certain labels can be detected under UV light. The pattern of hybridisation, for example
- 30 on an array described herein, represents differences in epigenetic chromosome interactions between

the two subgroups, and thus provides a process of comparing epigenetic chromosome interactions and determination of which epigenetic chromosome interactions are specific to a subgroup in the population of the present invention.

The term 'pattern of hybridisation' broadly covers the presence and absence of hybridisation, for example between the first and second set of nucleic acids, i.e. which specific nucleic acids from the first set hybridise to which specific nucleic acids from the second set, and so it not limited to any particular assay or technique, or the need to have a surface or array on which a 'pattern' can be detected.

Forms of the Substance Mentioned Herein

Any of the substances, such as nucleic acids or therapeutic agents, mentioned herein may be in purified or isolated form. They may be in a form which is different from that found in nature, for example they may be present in combination with other substance with which they do not occur in nature. The nucleic acids (including portions of sequences defined herein) may have sequences which are different to those found in nature, for example having at least 1, 2, 3, 4 or more nucleotide changes in the sequence as described in the section on homology. The nucleic acids may have heterologous sequence at the 5' or 3' end. The nucleic acids may be chemically different from those found in nature, for example they may be modified in some way, but preferably are still capable of Watson-Crick base pairing. Where appropriate the nucleic acids will be provided in double stranded or single stranded form. The invention provides all of the specific nucleic acid sequences mentioned herein in single or double stranded form, and thus includes the complementary strand to any sequence which is disclosed.

The invention provides a kit for carrying out any process of the invention, including detection of a chromosomal interaction relating to prognosis. Such a kit can include a specific binding agent capable of detecting the relevant chromosomal interaction, such as agents capable of detecting a ligated nucleic acid generated by processes of the invention. Preferred agents present in the kit include probes capable of hybridising to the ligated nucleic acid or primer pairs, for example as described herein, capable of amplifying the ligated nucleic acid in a PCR reaction. A kit of the invention may comprise means to detect a panel of markers, such as any number of combination of markers disclosed herein.

The invention provides use of a reagent for preparing kit for carrying out the process of the invention. Such a reagent may be any suitable substance mentioned herein, such as the agents which are capable of detection of products of detection processes, including reagents which are any of the probes or primers mentioned herein. The invention provides use of the reagent in the process of the invention. The invention provides use of the reagent in the preparing of a means for carrying out the invention.

The invention provides a device that is capable of detecting the relevant chromosome interactions. The device preferably comprises any specific binding agents, probe or primer pair capable of detecting the chromosome interaction, such as any such agent, probe or primer pair described herein.

5 The invention provides use of detection of chromosome interactions as defined herein (for example by number or specific combination) to detect muscular atrophy or any characteristic of muscular atrophy, for example as defined herein. The invention provides use of a reagent (for example a probe, primer, label, device or array) in any method of the invention.

Detection Process

10 In one aspect quantitative detection of the ligated sequence which is relevant to a chromosome interaction is carried out using a probe which is detectable upon activation during a PCR reaction, wherein said ligated sequence comprises sequences from two chromosome regions that come together in an epigenetic chromosome interaction, wherein said process comprises contacting the ligated sequence with the probe during a PCR reaction, and detecting the extent of activation of the probe, and wherein said probe binds the ligation site. The process typically allows particular interactions to be
15 detected in a MIQE compliant manner using a dual labelled fluorescent hydrolysis probe.

The probe is generally labelled with a detectable label which has an inactive and active state, so that it is only detected when activated. The extent of activation will be related to the extent of template (ligation product) present in the PCR reaction. Detection may be carried out during all or some of the PCR, for example for at least 50% or 80% of the cycles of the PCR.

20 The probe can comprise a fluorophore covalently attached to one end of the oligonucleotide, and a quencher attached to the other end of the nucleotide, so that the fluorescence of the fluorophore is quenched by the quencher. In one aspect the fluorophore is attached to the 5' end of the oligonucleotide, and the quencher is covalently attached to the 3' end of the oligonucleotide.

25 Fluorophores that can be used in the process of the invention include FAM, TET, JOE, Yakima Yellow, HEX, Cyanine3, ATTO 550, TAMRA, ROX, Texas Red, Cyanine 3.5, LC610, LC 640, ATTO 647N, Cyanine 5, Cyanine 5.5 and ATTO 680. Quenchers that can be used with the appropriate fluorophore include TAM, BHQ1, DAB, Eclip, BHQ2 and BBQ650, optionally wherein said fluorophore is selected from HEX, Texas Red and FAM. Preferred combinations of fluorophore and quencher include FAM with BHQ1 and Texas Red with BHQ2.

30

Use of the Probe in a qPCR Assay

Hydrolysis probes of the invention are typically temperature gradient optimised with concentration matched negative controls. Preferably single-step PCR reactions are optimized. More preferably a standard curve is calculated. An advantage of using a specific probe that binds across the junction of the ligated sequence is that specificity for the ligated sequence can be achieved without using a nested PCR approach. The processes described herein allow accurate and precise quantification of low copy number targets. The target ligated sequence can be purified, for example gel-purified, prior to temperature gradient optimization. The target ligated sequence can be sequenced. Preferably PCR reactions are performed using about 10ng, or 5 to 15 ng, or 10 to 20ng, or 10 to 50ng, or 10 to 200ng template DNA.

Forward and reverse primers are designed such that one primer binds to the sequence of one of the chromosome regions represented in the ligated DNA sequence, and the other primer binds to other chromosome region represented in the ligated DNA sequence, for example, by being complementary to the sequence.

Choice of Ligated DNA Target

The invention includes selecting primers and a probe for use in a PCR process as defined herein comprising selecting primers based on their ability to bind and amplify the ligated sequence and selecting the probe sequence based properties of the target sequence to which it will bind, in particular the curvature of the target sequence.

Probes are typically designed/chosen to bind to ligated sequences which are juxtaposed restriction fragments spanning the restriction site. In one aspect of the invention, the predicted curvature of possible ligated sequences relevant to a particular chromosome interaction is calculated, for example using a specific algorithm referenced herein. The curvature can be expressed as degrees per helical turn, e.g. 10.5° per helical turn. Ligated sequences are selected for targeting where the ligated sequence has a curvature propensity peak score of at least 5° per helical turn, typically at least 10°, 15° or 20° per helical turn, for example 5° to 20° per helical turn. Preferably the curvature propensity score per helical turn is calculated for at least 20, 50, 100, 200 or 400 bases, such as for 20 to 400 bases upstream and/or downstream of the ligation site. Thus in one aspect the target sequence in the ligated product has any of these levels of curvature. Target sequences can also be chosen based on lowest thermodynamic structure free energy.

30

Particular Aspects

In one aspect only intrachromosomal interactions are typed/detected, and no extrachromosomal interactions (between different chromosomes) are typed/detected.

5 In particular aspects certain chromosome interactions are not typed, for example any specific interaction mentioned herein (for example as defined by any probe or primer pair mentioned herein). In some aspects chromosome interactions are not typed in any of the genes relevant to chromosome interactions mentioned herein.

10 The data provided herein shows that the markers are 'disseminating' ones able to differentiate cases and non-cases for the relevant disease situation. Therefore when carrying out the invention the skilled person will be able to determine by detection of the interactions which subgroup the individual is in. In one embodiment a threshold value of detection of at least 70% of the tested markers in the form they are associated with the relevant disease situation (either by absence or presence) may be used to determine whether the individual is in the relevant subgroup.

15 In one embodiment the process of the invention does not detect the presence of Huntington's disease, and is not carried out for the purpose of detection of Huntington's disease. In one embodiment the process of the invention is not carried out on an individual who is suspected of having Huntington's disease or who has symptoms of Huntington's disease.

Use of a Classifier

20 The method of the invention may include analysis of the chromosome interactions identified in the individual, for example using a classifier, which may increase performance, such as sensitivity or specificity. The classifier is typically one that has been 'trained' on samples from the population and such training may assist the classifier to detect any subgroup mentioned herein.

Screening process

25 The invention provides a process of determining which chromosomal interactions are relevant to a chromosome state corresponding to an prognosis subgroup of the population, comprising contacting a first set of nucleic acids from subgroups with different states of the chromosome with a second set of index nucleic acids, and allowing complementary sequences to hybridise, wherein the nucleic acids in the first and second sets of nucleic acids represent a ligated product comprising sequences from both the chromosome regions that have come together in chromosomal interactions, and wherein the
30 pattern of hybridisation between the first and second set of nucleic acids allows a determination of

which chromosomal interactions are specific to an prognosis subgroup. The subgroup may be any of the specific subgroups defined herein, for example with reference to particular conditions or therapies.

Publications

The contents of all publications mentioned herein are incorporated by reference into the present specification and may be used to further define the features relevant to the invention. The contents of the priority document, UK Patent Application No. 2016176.6 filed 12 October 2021, is also incorporated herein by reference.

Techniques Used to Identify the Specific Relevant Chromosome Interactions

The EpiSwitch™ platform technology detects epigenetic regulatory signatures of regulatory changes between normal and abnormal conditions at loci. The EpiSwitch™ platform identifies and monitors the fundamental epigenetic level of gene regulation associated with regulatory high order structures of human chromosomes also known as chromosome conformation signatures. Chromosome signatures are a distinct primary step in a cascade of gene deregulation. They are high order biomarkers with a unique set of advantages against biomarker platforms that utilize late epigenetic and gene expression biomarkers, such as DNA methylation and RNA profiling.

EpiSwitch™ Array Assay

The custom EpiSwitch™ array-screening platforms come in 4 densities of, 15K, 45K, 100K, and 250K unique chromosome conformations, each chimeric fragment is repeated on the arrays 4 times, making the effective densities 60K, 180K, 400K and 1 Million respectively.

Custom Designed EpiSwitch™ Arrays

The 15K EpiSwitch™ array can screen the whole genome including around 300 loci interrogated with the EpiSwitch™ Biomarker discovery technology. The EpiSwitch™ array is built on the Agilent SurePrint G3 Custom CGH microarray platform; this technology offers 4 densities, 60K, 180K, 400K and 1 Million probes. The density per array is reduced to 15K, 45K, 100K and 250K as each EpiSwitch™ probe is presented as a quadruplicate, thus allowing for statistical evaluation of the reproducibility. The average number of potential EpiSwitch™ markers interrogated per genetic loci is 50, as such the numbers of loci that can be investigated are 300, 900, 2000, and 5000.

EpiSwitch™ Custom Array Pipeline

The EpiSwitch™ array is a dual colour system with one set of samples, after EpiSwitch™ library generation, labelled in Cy5 and the other of sample (controls) to be compared/ analyzed labelled in Cy3.

The arrays are scanned using the Agilent SureScan Scanner and the resultant features extracted using the Agilent Feature Extraction software. The data is then processed using the EpiSwitch™ array processing scripts in R. The arrays are processed using standard dual colour packages in Bioconductor in R: Limma*. The normalisation of the arrays is done using the normalisedWithinArrays function in

5 Limma* and this is done to the on chip Agilent positive controls and EpiSwitch™ positive controls. The data is filtered based on the Agilent Flag calls, the Agilent control probes are removed and the technical replicate probes are averaged, in order for them to be analysed using Limma*. The probes are modelled based on their difference between the 2 scenarios being compared and then corrected by using False Discovery Rate. Probes with Coefficient of Variation (CV) $\leq 30\%$ that are ≤ -1.1 or ≥ 1.1 and pass the

10 $p \leq 0.1$ FDR p-value are used for further screening. To reduce the probe set further Multiple Factor Analysis is performed using the FactorMineR package in R.

* Note: LIMMA is Linear Models and Empirical Bayes Processes for Assessing Differential Expression in Microarray Experiments. Limma is an R package for the analysis of gene expression data arising from microarray or RNA-Seq.

15 The pool of probes is initially selected based on adjusted p-value, FC and CV $< 30\%$ (arbitrary cut off point) parameters for final picking. Further analyses and the final list are drawn based only on the first two parameters (adj. p-value; FC).

Statistical Pipeline

EpiSwitch™ screening arrays are processed using the EpiSwitch™ Analytical Package in R in order to

20 select high value EpiSwitch™ markers for translation on to the EpiSwitch™ PCR platform.

Step 1

Probes are selected based on their corrected p-value (False Discovery Rate, FDR), which is the product of a modified linear regression model. Probes below p-value ≤ 0.1 are selected and then further reduced by their Epigenetic ratio (ER), probes ER have to be ≤ -1.1 or ≥ 1.1 in order to be selected for further

25 analysis. The last filter is a coefficient of variation (CV), probes have to be below ≤ 0.3 .

Step 2

The top 40 markers from the statistical lists are selected based on their ER for selection as markers for PCR translation. The top 20 markers with the highest negative ER load and the top 20 markers with the highest positive ER load form the list.

30 *Step 3*

The resultant markers from step 1, the statistically significant probes form the bases of enrichment analysis using hypergeometric enrichment (HE). This analysis enables marker reduction from the significant probe list, and along with the markers from step 2 forms the list of probes translated on to the EpiSwitch™ PCR platform.

- 5 The statistical probes are processed by HE to determine which genetic locations have an enrichment of statistically significant probes, indicating which genetic locations are hubs of epigenetic difference.

The most significant enriched loci based on a corrected p-value are selected for probe list generation.

Genetic locations below p-value of 0.3 or 0.2 are selected. The statistical probes mapping to these genetic locations, with the markers from step 2, form the high value markers for EpiSwitch™ PCR

- 10 translation.

Array design and processing

Array Design

Genetic loci are processed using the SII software (currently v3.2) to:

- Pull out the sequence of the genome at these specific genetic loci (gene sequence with 50kb upstream and 20kb downstream)
- Define the probability that a sequence within this region is involved in CCs
- Cut the sequence using a specific RE
- Determine which restriction fragments are likely to interact in a certain orientation
- Rank the likelihood of different CCs interacting together.
- 20 - Determine array size and therefore number of probe positions available (x)
- Pull out x/4 interactions.
- For each interaction define sequence of 30bp to restriction site from part 1 and 30bp to restriction site of part 2. Check those regions aren't repeats, if so exclude and take next interaction down on the list. Join both 30bp to define probe.
- 25 - Create list of x/4 probes plus defined control probes and replicate 4 times to create list to be created on array
- Upload list of probes onto Agilent Sure design website for custom CGH array.

- Use probe group to design Agilent custom CGH array.

Array Processing

- Process samples using EpiSwitch™ Standard Operating Procedure (SOP) for template production.
 - Clean up with ethanol precipitation by array processing laboratory.
- 5 - Process samples as per Agilent SureTag complete DNA labelling kit - Agilent Oligonucleotide Array-based CGH for Genomic DNA Analysis Enzymatic labelling for Blood, Cells or Tissues
- Scan using Agilent C Scanner using Agilent feature extraction software.

- EpiSwitch™* biomarker signatures demonstrate high robustness, sensitivity and specificity in the stratification of complex disease phenotypes. This technology takes advantage of the latest
- 10 breakthroughs in the science of epigenetics, monitoring and evaluation of chromosome conformation signatures as a highly informative class of epigenetic biomarkers. Current research methods deployed in academic environment require from 3 to 7 days for biochemical processing of cellular material in order to detect CCSs. Those procedures have limited sensitivity, and reproducibility; and furthermore, do not have the benefit of the targeted insight provided by the *EpiSwitch™ Analytical Package* at the design
- 15 stage.

EpiSwitch™ Array in silico marker identification

- CCS sites across the genome are directly evaluated by the *EpiSwitch™* Array on clinical samples from testing cohorts for identification of all relevant stratifying lead biomarkers. The *EpiSwitch™* Array platform is used for marker identification due to its high-throughput capacity, and its ability to screen
- 20 large numbers of loci rapidly. The array used was the Agilent custom-CGH array, which allows markers identified through the *in silico* software to be interrogated.

EpiSwitch™ PCR

- Potential markers identified by *EpiSwitch™* Array are then validated either by *EpiSwitch™* PCR or DNA sequencers (i.e. Roche 454, Nanopore MinION, etc.). The top PCR markers which are statistically
- 25 significant and display the best reproducibility are selected for further reduction into the final *EpiSwitch™* Signature Set, and validated on an independent cohort of samples. *EpiSwitch™* PCR can be performed by a trained technician following a standardised operating procedure protocol established. All protocols and manufacture of reagents are performed under ISO 13485 and 9001 accreditation to ensure the quality of the work and the ability to transfer the protocols. *EpiSwitch™* PCR and *EpiSwitch™*

Array biomarker platforms are compatible with analysis of both whole blood and cell lines. The tests are sensitive enough to detect abnormalities in very low copy numbers using small volumes of blood.

The invention is illustrated by the following:

Example 1

5 Spinal and bulbar muscular atrophy (SBMA) is an exemplifying model muscle atrophy disease that can be used to identify the chromosome interactions relevant to muscle atrophy. SBMA is a rare disease with predominant manifestation in males (2.6:100,000) associated with genetic mutations in androgen receptor (AR) gene and inherited in X-linked recessive manner. Modulation of endocrine, neurological and muscular regulatory networks associated with impairment of AR gene lead to significant
10 pathophysiology and extreme disability. Interestingly, in homozygous females with AR impairment the symptoms are very mild, indicating the significance of the regulatory context in compensating the defect. As part of its pathophysiology, SBMA leads to muscle atrophy, largely due to lower motor neuron degeneration and lack of adequate stimulation. The disease has no treatment and there are limited prognostic insights.

15 Spinal muscular atrophy is a recognized model disease for the better understanding of spinal sarcopenia, motor neuron loss in sarcopenia, muscle atrophy, muscle wasting phenomenon as a result of ageing (sarcopenia) and as a result of underlying pathological signalling (cachexia, as particularly often observed in cancer) and for understanding shared mechanisms of muscle wasting with cancer.

Here we have analysed chromosome interactions of SBMA patients in comparison to healthy cohorts.

20 We have done whole genome screening across over 900,000 chromosome conformations covering all annotated genes and ncRNA across the genome.

A whole blood sample was provided from a United Kingdom cohort consisting of 12 SBMA patients and 7 age matched controls. The 12 SBMA patients were split between early and late disease onset patients, and are described in the table below.

25

Code	YOB	CAG size	Age 1st medical encounter	Disease duration	SBMAFRS
UCH0206	1939	40	66	21	32
UCH0081	1943	37	64	13	43
UCH0307	1950		57	13	26
UCH0213	1950	39	60	10	43
UCH0190	1951	45	63	6	47
UCH0210	1955		59	6	42
UCH0309	1956		52	12	
UCH0292	1958		57	5	40
UCH0189	1967	45	42	11	34
UCH0179	1969	46	46	5	50
UCH0312	1969		48	3	50
UCH0169	1974	49	35	11	36

In case of bulbar and spinal muscular atrophy genetic confirmation of CAG repeats in AR gene acts a accepted diagnostic readout. One challenge is to have a readout that confirms the severity of disease manifestation, especially as genetic disorder in many patients is compensated by epigenetic network.

- 5 That is why the present work is based on samples representing both early and late stages of muscular atrophy allowing prognosis to be determined, in particular in respect of severity in clinical manifestation of the disease, as well as a general diagnosis.

We have identified top 200 disseminating SBMA-specific CCS, with a False Discovery Rate FDR<0.05.

- Analysing genetic loci affected by conditional CCS, we performed pathway analysis and demonstrated
10 heavy involvement in SBMA specific profiling of Keratinization (24 genetic loci affected) and Olfactory

Transduction (31 genetic loci affected). Importantly, the same analysis demonstrated heavy involvement of T Cell Receptor Signalling Pathway (12 genes affected) and L1CAM Interactions (8 genes affected, L1CAM is a neuronal cell adhesion molecule with a strong implication in cell migration, adhesion, neurite outgrowth, myelination and neuronal differentiation). Most importantly, this analysis reveals an overlap
5 between sites implicated in SBMA regulation and PD-1 checkpoint network implicated in cancer immuno-therapy. This is a first molecular evidence for SBMA and cancer overlap, in the context of muscular atrophy being observed under both conditions. The results of the work are shown in the Figures and tables herein. The identified markers are suitable for detection on nested PCR platform.

Tables 1A and Table 1B show the markers that were identified by this work. They represent part of the
10 3D genomic regulatory control. There were distinct CCSs in the early phenotype compared to the late showing the CCSs change as the disease progresses and varies between phenotypes. The CCSs can be linked to each clinically defined subgroup to be used as a biomarker tool to predict outcome and progression in patients. The present work therefore provides both diagnostic and prognostic markers.

No.	Probe	RP/Rsum	Rprank	FC:(class1/class2)
1	Hg38_2_151357305_151361853_151612320_151619007_RF	87.63840883	1	2.283
2	Hg38_13_41466343_41476518_41555919_41561354_RF	288.7780393	2	2.007
3	Hg38_20_23380285_23385557_23532159_23546814_RR	534.5889718	4	1.878
4	Hg38_1_84316044_84322127_84529225_84540074_RF	663.6694959	10	1.87
5	Hg38_1_209333922_209340142_209404224_209420680_FF	446.7372857	3	1.87
6	Hg38_5_177834278_177839098_178009945_178017869_FR	662.5483965	9	1.832
7	Hg38_11_77781318_77787851_77893153_77899469_FR	732.8885954	12	1.798
8	Hg38_8_48489316_48497835_48710460_48716484_RR	755.6786775	13	1.794
9	Hg38_8_33042243_33047675_33243637_33249598_FR	930.5017332	18	1.788
10	Hg38_11_7823466_7827013_7890344_7893739_FR	1064.533822	22	1.776
11	Hg38_2_242078290_242088090_242115056_242117195_RR	626.2882701	6	1.776
12	Hg38_4_64204635_64210880_64341978_64349763_RF	1183.854495	27	1.771
13	Hg38_9_4737518_4739216_4871409_4877222_FF	855.3083509	15	1.767
14	Hg38_6_144636121_144641243_144691336_144697440_RF	578.9188967	5	1.767
15	Hg38_22_47207724_47217624_47356169_47358600_FF	665.6838613	11	1.765
16	Hg38_16_31853018_31860663_31871565_31877473_FR	836.8314653	14	1.764
17	Hg38_10_6735455_6749237_6766912_6769302_RF	648.2374782	8	1.764
18	Hg38_14_26681688_26687550_26802034_26810557_FR	1342.435576	33	1.76
19	Hg38_11_63024617_63034264_63124362_63131307_RR	639.5975048	7	1.758
20	Hg38_11_55823665_55829626_55865366_55868750_FR	866.3041714	17	1.726
21	Hg38_2_20791146_20796987_20975471_20980938_RR	857.2109811	16	1.716
22	Hg38_1_114264796_114271415_114388190_114393574_FF	1043.317342	20	1.702
23	Hg38_3_150148357_150152202_150276483_150282205_RF	1018.4725	19	1.692
24	Hg38_3_3070802_3073954_3162690_3172869_FF	2146.093548	53	1.684
25	Hg38_2_228849719_228856896_228936338_228946445_RR	2144.540397	52	1.682
26	Hg38_X_126618971_126632078_126813931_126821389_RR	1596.946758	38	1.682
27	Hg38_17_3298600_3300356_3435567_3441497_RF	1286.046191	32	1.682
28	Hg38_6_141949457_141959891_142112622_142115111_FF	1073.365868	23	1.681
29	Hg38_2_221629362_221633765_221703220_221711044_FF	1177.041857	26	1.679
30	Hg38_18_8164110_8169146_8228637_8240170_RF	1187.605744	28	1.675
31	Hg38_X_83389647_83396643_83505067_83507528_RR	1123.648127	25	1.67
32	Hg38_2_38740614_38746415_38982199_38993639_FF	1062.516677	21	1.666
33	Hg38_2_169562452_169564303_169638099_169647209_FF	1122.728889	24	1.664
34	Hg38_X_51609399_51612166_51861901_51874841_RF	1207.025498	29	1.658
35	Hg38_1_96786343_96792340_96953170_96960029_RR	1260.746357	30	1.657
36	Hg38_13_76879860_76881474_77089881_77098142_FF	1281.56965	31	1.653
37	Hg38_12_10235418_10237590_10417499_10425564_RF	1635.909028	39	1.647
38	Hg38_3_151888504_151893566_151931687_151943298_RR	1384.989976	35	1.643
39	Hg38_8_81036889_81041061_81244260_81253029_RF	2113.213401	50	1.641
40	Hg38_21_25447238_25454612_25514175_25521235_RF	2472.139306	68	1.639
41	Hg38_12_39724269_39737447_39830409_39841867_RF	2034.859484	48	1.637
42	Hg38_2_2911175_2916426_3008403_3014033_FR	1376.720339	34	1.635
43	Hg38_5_39037737_39046956_39197630_39209276_FR	2497.876062	69	1.63
44	Hg38_2_127388555_127395831_127412534_127416129_RR	3444.281703	126	1.623
45	Hg38_21_14583254_14600479_14842273_14847749_RF	1987.875145	45	1.622
46	Hg38_22_32455270_32461039_32549159_32556587_FR	1392.694528	36	1.621
47	Hg38_13_77416226_77433379_77635636_77642621_RR	2244.157946	57	1.617
48	Hg38_X_66017310_66021076_66266598_66279138_RR	1554.424806	37	1.616
49	Hg38_9_119814503_119824066_119942887_119944563_RR	2152.405439	54	1.61
50	Hg38_15_96378302_96385292_96582969_96587891_FR	1671.300538	40	1.607

Table 1A (part 1a)

				Probe sequence
No.	pfp	P.value	Type	60 mer
1	0	0	SBMA	AATGTTGATAAGTATTAGACGACTGGTTTCGATTTTCTTTAATCACTGCTAAATCTGCA
2	0	0	SBMA	TACTTACACTCAACAGGAGGGATATATTCGAATCATTTTGGGGGCATAAACATAAAACC
3	0	0	SBMA	GTAAGAGAAACTGTTCTTTCTGTCAGCTTCGAACTACATTGAAAATCTCTGTTTGTGTA
4	0	0	SBMA	TTTGCATTATTTGATATATCCATTCTCGACCATTTTTCAATTGAGTTATTAGTTTT
5	0	0	SBMA	CAAACATGTCTAACTCATGCAATTTTCTTCGAGTCTCCATTTGAAAAAGAGGTTTTTG
6	0	0	SBMA	GACTGAAAAAGTTAAGAAAACTTTCTACTCGATTAAACACCTATTTTATTGTGCTGCATT
7	0	0	SBMA	CTTCAGAACAGTAAAAAAGGTTTCGACTCCTATTTCTTCATCAAGCTTTCCATT
8	0	0	SBMA	GCTGACTTGATTTTGTCTGGATAAGCTTTTCGACTTCCTTATACTAGTAAGAGACTTAAGC
9	0	0	SBMA	CAGAGAGGGACATTATATAATGAAATAGTCGAGGTCTGATAGCAACCATTTACCAAATT
10	0	0	SBMA	GCTTCAAAAGGTCCTAGAAATAATCCACTCGAATCCTTGGCTTTTATTTTCTTCAGGGA
11	0	0	SBMA	AGGAAAGAAACATAAGAATTATTATTTCGAAAGTCATTGAAGATTACAGCAGGAGACA
12	0	0	SBMA	CCAGGCCTTGAAGAGATAATACAGGAATTCGAACCAATGTACATGTTACACATATTGATT
13	0	0	SBMA	ACAATCTCTGTTCTTTCTTTCTTTTTCGAGAATCATGGCTTTAAAGACACAGAGATG
14	0	0	SBMA	AAATTTAAAGTTTCTTCTTACAAAGCATTGCAAGTGAAGCCGTCATGATTGTTTCATA
15	0	0	SBMA	AGTACTGAAATATTGTATTGCTACTATTTTCGACACACACTTGATTGAATAAAAGGCGTA
16	0	0	SBMA	GTCTTTTAGAGATGAACAAAAATAAATTCGATCTGTCTGGTCAACATTCTGGGACAATG
17	0	0	SBMA	AAGTGTAGAGAAAGAAGATTAAGCAATTCGACATTCACCAATAAGGTATAAGTATTT
18	0	0	SBMA	TCAAGTCACTGGCAGGAAGAACAAGCTCTCGAAAAATACAGTGACATCTTTATTGTCT
19	0	0	SBMA	TATCCATTCCAGAAATTTTCATTATCTCGATGTATGGATTAAGTGTGTGATATTAACA
20	0	0	SBMA	ATATTGGGATTACTATGCAGATTACATTTTCGAGTGTTTAGGAAGTCATATAATGAACAA
21	0	0	SBMA	ATAAAATGGAGTAGAAATCAGTGAAATTCGAATCATTGATGAAAGGAAAATCTGAGAAG
22	0	0	SBMA	GTGTCTGTTACTGATCCTTATAGCTTCTTCGAAGAAACAAAATATCTTCAAAAATAAGT
23	0	0	SBMA	AGTTTGGTAAAGTTTCAGGATAAAAAATCGAATTAGGAGTCTTGAATTCATGTTTCAT
24	0	0	SBMA	TGTATTGGCATAAAGATAGACAAAATAGATCGAGAAGAACAGGATTTTGAATTGAGATAG
25	0	0	SBMA	TGTGAAACAAAGCCGCTATTACAGTCTCGACTTTGTTTCAGAGTTCAGAATCAATATCT
26	0	0	SBMA	CAAATCTTTCCAAAGTTAAAGTCCAAGTCGAACACAGCTACTACATTAAATATAACAAT
27	0	0	SBMA	CTCATCAGAATTGTTATAATAAAAAAGATCGAACAAGACTCTCTTCTCTAGTAAGTCCT
28	0	0	SBMA	AGAAATAAAGAAGGAGTCAAATACCTTCGATTTGAGCAGAAAGTCTGAAGGCACACA
29	0	0	SBMA	GATTGTATTACTTCAAATAAACTTGATCGAAGAAGTACAAGTCAAAGGCAGACAGCAC
30	0	0	SBMA	GAAAAAGAGAGAAACAACTATTACTTATCGAGTTTATGATTCTAAAATGTTGTTAGTA
31	0	0	SBMA	AATCAAATGATAGAAACATAGACCAAAGTCGAGTTTAAGGCAAAATGCAGTCTATGAAAA
32	0	0	SBMA	TAATCTTTTACATTCTGCTTTAAGCACATCGATTTTAAAGATTCTCTCAGTTGGAAGAAA
33	0	0	SBMA	TTGAACACAGACAAGGTACTAGGTAATATCGATTTTAGCTTTTTTTGACTTTTTCTCCA
34	0	0	SBMA	TTCTTGGTATGCCTGGTTTTTTTAAATTCGATTTTAGCCCTAATCCCATTGTGCTGTAA
35	0	0	SBMA	TGACTTCTGCTAGGATACACCAGAAAAATTCGAGTATGACAAAGAGCTTAAGCCAAGGTAG
36	0	0	SBMA	TACATGGCTTTATTGAAATAACATTCATCGAGTTTTCTTTCAAAGGAGATGGATCCAA
37	0	0	SBMA	CGTGACTGTATATCATGTCTTTGTTAATCGAGACTGGTTAATTTAAAAAGAAAAGAGGT
38	0	0	SBMA	TAGAAACAAAAGTTACAGAAATAATCCCTCGATAACATTGTTTTAATTTTCTGAGAAAAA
39	0	0	SBMA	CAAGCAAAACAATGGCTTAAATTGTTTCTCGAACAGCTGAAATCCCTGATGTATGCAAAAG
40	0	0	SBMA	TCCTACAAGAAATGCTAAAGAGAGTTATTCGATGAATTAATACATGCATTTTGAAATTGA
41	0	0	SBMA	TCTTAGGTTTGCAACAGACCAAGTAAGTCGATATTGGTTGGGAAGTGGTTAGTAATTAA
42	0	0	SBMA	CTAAAAGAAAACATAGGGGAAAAAGTCTCGATTTTCATAACATTTATCTTAGCCTCAAA
43	0	0	SBMA	TTACCTTTAAGTCAATGCCTCAAAAGTTCGAAAAGTGCCTTGATAATACCAGTGTCTT
44	0	0	SBMA	AATGTACACAACCAAGTCATAACCAAGTATCGACTTTTCTCTCCCAAGGGAGAGTTTACT
45	0	0	SBMA	TATAAACTGGAACCTTCAAATTTTCATGCTCGATTACTTAAGGCATGCTATTATAAATAAA
46	0	0	SBMA	TTGTGTACTAGTAACTGCAGGCATCCATCGAATGCTTTCAGTCAAGAGAAGGCAATGA
47	0	0	SBMA	TAAACACGAGCTTCTCAGCTGTGCTGCTCGAGATTTTTTAATTAATAGGATAGATGGAT
48	0	0	SBMA	CATGGTCACCAAAATATGGCATGACAGAATCGACAGAGAAAGCTACGACGAATAGGAGGT
49	0	0	SBMA	ATATTATCTTTTGATTTTCCAACATTCGACGCTGTCCAGTGAAAAATATAACACGAGC
50	0	0	SBMA	ATCTGTGAGATTTGCAGCTCTTTTGTCTCGAATTGAGTTATTTCAAAGATATTGATAA

Table 1A (part 1b)

No.	Probe Location				
	Chr	Start1	End1	Start2	End2
1	2	151357307	151357336	151618976	151619005
2	13	41466345	41466374	41561323	41561352
3	20	23380287	23380316	23532161	23532190
4	1	84316046	84316075	84540043	84540072
5	1	209340111	209340140	209420649	209420678
6	5	177839067	177839096	178009947	178009976
7	11	77787820	77787849	77893155	77893184
8	8	48489318	48489347	48710462	48710491
9	8	33047644	33047673	33243639	33243668
10	11	7826982	7827011	7890346	7890375
11	2	242078292	242078321	242115058	242115087
12	4	64204637	64204666	64349732	64349761
13	9	4739185	4739214	4877191	4877220
14	6	144636123	144636152	144697409	144697438
15	22	47217593	47217622	47358569	47358598
16	16	31860632	31860661	31871567	31871596
17	10	6735457	6735486	6769271	6769300
18	14	26687519	26687548	26802036	26802065
19	11	63024619	63024648	63124364	63124393
20	11	55829595	55829624	55865368	55865397
21	2	20791148	20791177	20975473	20975502
22	1	114271384	114271413	114393543	114393572
23	3	150148359	150148388	150282174	150282203
24	3	3073923	3073952	3172838	3172867
25	2	228849721	228849750	228936340	228936369
26	X	126618973	126619002	126813933	126813962
27	17	3298602	3298631	3441466	3441495
28	6	141959860	141959889	142115080	142115109
29	2	221633734	221633763	221711013	221711042
30	18	8164112	8164141	8240139	8240168
31	X	83389649	83389678	83505069	83505098
32	2	38746384	38746413	38993608	38993637
33	2	169564272	169564301	169647178	169647207
34	X	51609401	51609430	51874810	51874839
35	1	96786345	96786374	96953172	96953201
36	13	76881443	76881472	77098111	77098140
37	12	10235420	10235449	10425533	10425562
38	3	151888506	151888535	151931689	151931718
39	8	81036891	81036920	81252998	81253027
40	21	25447240	25447269	25521204	25521233
41	12	39724271	39724300	39841836	39841865
42	2	2916395	2916424	3008405	3008434
43	5	39046925	39046954	39197632	39197661
44	2	127388557	127388586	127412536	127412565
45	21	14583256	14583285	14847718	14847747

46	22	32461008	32461037	32549161	32549190
47	13	77416228	77416257	77635638	77635667
48	X	66017312	66017341	66266600	66266629
49	9	119814505	119814534	119942889	119942918
50	15	96385261	96385290	96582971	96583000

Table 1A (part 1c)

No.	4 kb Sequence Location				
	Chr	Start1	End1	Start2	End2
1	2	151357307	151361306	151615006	151619005
2	13	41466345	41470344	41557353	41561352
3	20	23380287	23384286	23532161	23536160
4	1	84316046	84320045	84536073	84540072
5	1	209336141	209340140	209416679	209420678
6	5	177835097	177839096	178009947	178013946
7	11	77783850	77787849	77893155	77897154
8	8	48489318	48493317	48710462	48714461
9	8	33043674	33047673	33243639	33247638
10	11	7823012	7827011	7890346	7894345
11	2	242078292	242082291	242115058	242119057
12	4	64204637	64208636	64345762	64349761
13	9	4735215	4739214	4873221	4877220
14	6	144636123	144640122	144693439	144697438
15	22	47213623	47217622	47354599	47358598
16	16	31856662	31860661	31871567	31875566
17	10	6735457	6739456	6765301	6769300
18	14	26683549	26687548	26802036	26806035
19	11	63024619	63028618	63124364	63128363
20	11	55825625	55829624	55865368	55869367
21	2	20791148	20795147	20975473	20979472
22	1	114267414	114271413	114389573	114393572
23	3	150148359	150152358	150278204	150282203
24	3	3069953	3073952	3168868	3172867
25	2	228849721	228853720	228936340	228940339
26	X	126618973	126622972	126813933	126817932
27	17	3298602	3302601	3437496	3441495
28	6	141955890	141959889	142111110	142115109
29	2	221629764	221633763	221707043	221711042
30	18	8164112	8168111	8236169	8240168
31	X	83389649	83393648	83505069	83509068
32	2	38742414	38746413	38989638	38993637
33	2	169560302	169564301	169643208	169647207
34	X	51609401	51613400	51870840	51874839
35	1	96786345	96790344	96953172	96957171
36	13	76877473	76881472	77094141	77098140
37	12	10235420	10239419	10421563	10425562
38	3	151888506	151892505	151931689	151935688
39	8	81036891	81040890	81249028	81253027
40	21	25447240	25451239	25517234	25521233
41	12	39724271	39728270	39837866	39841865
42	2	2912425	2916424	3008405	3012404

43	5	39042955	39046954	39197632	39201631
44	2	127388557	127392556	127412536	127416535
45	21	14583256	14587255	14843748	14847747
46	22	32457038	32461037	32549161	32553160
47	13	77416228	77420227	77635638	77639637
48	X	66017312	66021311	66266600	66270599
49	9	119814505	119818504	119942889	119946888
50	15	96381291	96385290	96582971	96586970

Table 1A (part 1d)

No.	probe	Primer ID
1	Hg38_2_151357305_151361853_151612320_151619007_RF	OBD160.001
2	Hg38_13_41466343_41476518_41555919_41561354_RF	OBD160.005
3	Hg38_20_23380285_23385557_23532159_23546814_RR	OBD160.009
4	Hg38_1_84316044_84322127_84529225_84540074_RF	OBD160.013
5	Hg38_1_209333922_209340142_209404224_209420680_FF	OBD160.017
6	Hg38_5_177834278_177839098_178009945_178017869_FR	OBD160.021
7	Hg38_11_77781318_77787851_77893153_77899469_FR	OBD160.025
8	Hg38_8_48489316_48497835_48710460_48716484_RR	OBD160.029
9	Hg38_8_33042243_33047675_33243637_33249598_FR	OBD160.033
10	Hg38_11_7823466_7827013_7890344_7893739_FR	OBD160.037
11	Hg38_2_242078290_242088090_242115056_242117195_RR	OBD160.041
12	Hg38_4_64204635_64210880_64341978_64349763_RF	OBD160.045
13	Hg38_9_4737518_4739216_4871409_4877222_FF	OBD160.049
14	Hg38_6_144636121_144641243_144691336_144697440_RF	OBD160.053
15	Hg38_22_47207724_47217624_47356169_47358600_FF	OBD160.057
16	Hg38_16_31853018_31860663_31871565_31877473_FR	OBD160.061
17	Hg38_10_6735455_6749237_6766912_6769302_RF	OBD160.065
18	Hg38_14_26681688_26687550_26802034_26810557_FR	OBD160.069
19	Hg38_11_63024617_63034264_63124362_63131307_RR	OBD160.073
20	Hg38_11_55823665_55829626_55865366_55868750_FR	OBD160.077
21	Hg38_2_20791146_20796987_20975471_20980938_RR	OBD160.081
22	Hg38_1_114264796_114271415_114388190_114393574_FF	OBD160.085
23	Hg38_3_150148357_150152202_150276483_150282205_RF	OBD160.089
24	Hg38_3_3070802_3073954_3162690_3172869_FF	OBD160.093
25	Hg38_2_228849719_228856896_228936338_228946445_RR	OBD160.097
26	Hg38_X_126618971_126632078_126813931_126821389_RR	OBD160.101
27	Hg38_17_3298600_3300356_3435567_3441497_RF	OBD160.105
28	Hg38_6_141949457_141959891_142112622_142115111_FF	OBD160.109
29	Hg38_2_221629362_221633765_221703220_221711044_FF	OBD160.113
30	Hg38_18_8164110_8169146_8228637_8240170_RF	OBD160.117
31	Hg38_X_83389647_83396643_83505067_83507528_RR	OBD160.121
32	Hg38_2_38740614_38746415_38982199_38993639_FF	OBD160.125
33	Hg38_2_169562452_169564303_169638099_169647209_FF	OBD160.129
34	Hg38_X_51609399_51612166_51861901_51874841_RF	OBD160.133
35	Hg38_1_96786343_96792340_96953170_96960029_RR	OBD160.137
36	Hg38_13_76879860_76881474_77089881_77098142_FF	OBD160.141
37	Hg38_12_10235418_10237590_10417499_10425564_RF	OBD160.145
38	Hg38_3_151888504_151893566_151931687_151943298_RR	OBD160.149
39	Hg38_8_81036889_81041061_81244260_81253029_RF	OBD160.153
40	Hg38_21_25447238_25454612_25514175_25521235_RF	OBD160.157

41	Hg38_12_39724269_39737447_39830409_39841867_RF	OBD160.161
42	Hg38_2_2911175_2916426_3008403_3014033_FR	OBD160.165
43	Hg38_5_39037737_39046956_39197630_39209276_FR	OBD160.169
44	Hg38_2_127388555_127395831_127412534_127416129_RR	OBD160.173
45	Hg38_21_14583254_14600479_14842273_14847749_RF	OBD160.177
46	Hg38_22_32455270_32461039_32549159_32556587_FR	OBD160.181
47	Hg38_13_77416226_77433379_77635636_77642621_RR	OBD160.185
48	Hg38_X_66017310_66021076_66266598_66279138_RR	OBD160.189
49	Hg38_9_119814503_119824066_119942887_119944563_RR	OBD160.193
50	Hg38_15_96378302_96385292_96582969_96587891_FR	OBD160.197

Table 1A (part 1e)

No.	Sequence	Primer ID	Sequence
1	CACACTGAGACTGATGGTGCCTGAGT	OBD160.003	CAGTGTCTGAAGCAAATCCTCTGAC
2	AAACTTCTTAGTGAGGAGGCTC	OBD160.007	AGCCTGGGTGACAGAGTGAGACT
3	AGTGTCTGGAGTTGGAAGAGCAG	OBD160.011	ACAGCAAGTTATCCCGAAGATGC
4	CACCTCCTGTGGTTTCTGCTTATGTGT	OBD160.015	GCTTCAAGACATTAGTTTTGGCAATAGT
5	CCCTGTGAGATAGGTGAAGTGGGTGT	OBD160.019	ATGGCTGAGTCTGAAAATGGAATGGG
6	GCAAAAGCAATAGCCAGCACCATAGA	OBD160.023	ACCAACCTCTCTTCTCTCAGCCTG
7	GAGCCACAAAGCCTAAAATACG	OBD160.027	GCCACACTGTTCTTACACTTGC
8	TGCGTATGTTGAACCACTTGC	OBD160.031	GCCTGGAAATGAGGAACCCTGGT
9	GATAATGCCATCGTCAGGTTGAAATC	OBD160.035	GCCAAAGCGGAACCAAGTAACTA
10	GCCCTCCTCCATACCAACTCGCT	OBD160.039	CCCTTGGCCACCACAGACTTCAG
11	AGGCAATGTGGATGCTGTAGTCAACT	OBD160.043	CTTCCCCTGCTGCCATCTAACATCCT
12	CCCTGAGTGAAAATCCAAAATCCTTG	OBD160.047	CATTTGCCAGGATGGTCGGTGGTA
13	ACCCCAACCAGTAGCAGTATCTG	OBD160.051	GTTGGCTATCCACTTTTCTCATCT
14	CTAAAGGAGTGAAGTGAAGCAGC	OBD160.055	GTTTGCTGAGAATGATGGTTTCCAG
15	CGTTCAGACTTTTCATCAATGTAACA	OBD160.059	GCTGTGGTTTACCTCTCTGCTATCTT
16	GGGCTGGAAGAAAATGAAGAGTGACTAC	OBD160.063	GCTATTTGCCAAGACCACAGTCAGACCA
17	CATAACTGACTTTACTTTTGGGATGATG	OBD160.067	GTAGACAGCATCCAGATTCTCTGAGTGT
18	TTGATGCCAGGTGCTTGTTGATGC	OBD160.071	GCTGAGAGCATTGTGGAAGAATCT
19	GCAGCCCTTAGGTAGCAAGATGC	OBD160.075	GAAGTTATCAAGTTCAACCTCCTATC
20	TGACATCAGGAAGAGACTCAGTGTAT	OBD160.079	CTGACTGATGTATCCTACCAATAAGC
21	ACACAGTTGGTAAGTGGCAAAGCC	OBD160.083	AACTATTCTAAGGGTCTTGGAAT
22	TCTGTGATTTTCTTCTCAAGTTGTG	OBD160.087	CATTTTGGTGCCTTCCCACATAAA
23	GCCAAATAGGACAGACCCACAGC	OBD160.091	GTCAATTCGTTCCCAAGTCACCTGCTTCA
24	AACACAATCTCACCCAAATCCCAGC	OBD160.095	CTTACCCATCTGACTGTGTTCTTAGC
25	CTACTCTCAATGTGACGACTGGAAGG	OBD160.099	GTAGGGAGGCAGAAATGGTGTGTTTG
26	TATGAGTCCCCAGAGGATAGAAGAAT	OBD160.103	TGGCACTACATAAAATCACCCATTGT
27	CAGCAAGATGCCTGAACAGACTTTAC	OBD160.107	TATCCACAACGAGGTGAGGACTCTCC
28	CCAGAAAAGCAGCAGTTACACCTACAGG	OBD160.111	CTTGAGAGTAAAGGTGGTAACATAACAC
29	ATGAAGGGCACCAAAAGATGCTACCT	OBD160.115	TGGCAGCAAACCTCTACCTTCTGGAG
30	CGGGAGGCTCAAAAGAGGGAGAAAGA	OBD160.119	TTGGCTAACACAGTCTCATCCAGTGA
31	GAGGTGTTTCAGTGAGAGTAGAGAGG	OBD160.123	AGAGCCACATTCAATAGACGACCCGT
32	TGTAGTCACCAATACCGTAAAACCCC	OBD160.127	CAAAGACTACTGGGTAACTACAGACG
33	TTTCTTATCTTGGTGCTGTTACATAGC	OBD160.131	GGCTTTTCTGTGATGCTCTGGTTGGCAA
34	TTTCTCCTCAAGATGGGTCTTATTTT	OBD160.135	CTGCCACCTCCTCTGTATGGTTCTTA
35	GACACACACAGAGGTAGTAGAGATTC	OBD160.139	GCTCTCTCAGCCAGGTGCTTAGTTT
36	CGAAGGATTGACTCTGATAGGCTTAC	OBD160.143	TGCTTGGCTGGCTCTAAAGGCTTGA

37	ACTTTTATTCCACTGGCAGCAAGGTAAT	OBD160.147	GAAGACAGATGACAGAAGACAGGTGGCT
38	AAGGAGTTGTTCTCAAGGTATGTTAC	OBD160.151	CTGACTGATTGCTCTATTGGTAAAT
39	CAGCCCAAAGCGAGGGTGGAACAT	OBD160.155	GTGAACTACTCTTTCTTGCTGCTTCC
40	ACCTGTCCTACAAGAAATGCT	OBD160.159	ACATGCATTTTGAAATTGATAGTT
41	CAGTAACTAATCTTCTCTGGTGACAA	OBD160.163	ACTCTACAGATTTCCAGGACCTACTG
42	CAAGACCACCAAATACAGAATGGAG	OBD160.167	GAGAAACGATTCTTAACCCCTACCAT
43	CCTTTCTCTCAGGTTTCTCTTTTCCC	OBD160.171	GAAGCCAAGCGAAGGCATCTGACTCA
44	GAGGAGCGAAAGAAAGGGTTTAGACTC	OBD160.175	CACTAAAAGTCCTAAAGAAGAAGCCAAA
45	GGAATCAGAAGAAGTGTGTGACCCA	OBD160.179	CAGTGAGAGAGAGCAATGGAGGAAGC
46	GTTGGTAGAATGAATCAATGGTAGAATG	OBD160.183	GCCTGGGTGACAGAGGGGAGACTC
47	GCTTCAAACAGACAAAGGTATTTCCT	OBD160.187	GCCCAGAGACTATGCTTTGAGAAT
48	CCACCAGCAGCAAAAGCAGCAG	OBD160.191	CCTTCTGCTTCTCCACCACCCAT
49	CCCTGTAGTTGGAAAGCAGCCGAGCC	OBD160.195	AATGTAGCCAGTGTACAGGCAGAAGTG
50	GTGCCTCTCTTACACTCATCTCTCA	OBD160.199	GCGAAAGACTCTGTAAGTGTGTTGGC

Table 1A (part 1f)

No.	Probe	Marker
1	Hg38_2_151357305_151361853_151612320_151619007_RF	OBD160.001.003
2	Hg38_13_41466343_41476518_41555919_41561354_RF	OBD160.005.009
3	Hg38_20_23380285_23385557_23532159_23546814_RR	OBD160.011.013
4	Hg38_1_84316044_84322127_84529225_84540074_RF	OBD160.015.017
5	Hg38_1_209333922_209340142_209404224_209420680_FF	OBD160.019.021
6	Hg38_5_177834278_177839098_178009945_178017869_FR	OBD160.023.025
7	Hg38_11_77781318_77787851_77893153_77899469_FR	OBD160.025.027
8	Hg38_8_48489316_48497835_48710460_48716484_RR	OBD160.029.031
9	Hg38_8_33042243_33047675_33243637_33249598_FR	OBD160.033.035
10	Hg38_11_7823466_7827013_7890344_7893739_FR	OBD160.037.039
11	Hg38_2_242078290_242088090_242115056_242117195_RR	OBD160.041.043
12	Hg38_4_64204635_64210880_64341978_64349763_RF	OBD160.045.047
13	Hg38_9_4737518_4739216_4871409_4877222_FF	OBD160.049.051
14	Hg38_6_144636121_144641243_144691336_144697440_RF	OBD160.053.055
15	Hg38_22_47207724_47217624_47356169_47358600_FF	OBD160.057.059
16	Hg38_16_31853018_31860663_31871565_31877473_FR	OBD160.061.063
17	Hg38_10_6735455_6749237_6766912_6769302_RF	OBD160.065.067
18	Hg38_14_26681688_26687550_26802034_26810557_FR	OBD160.069.071
19	Hg38_11_63024617_63034264_63124362_63131307_RR	OBD160.073.075
20	Hg38_11_55823665_55829626_55865366_55868750_FR	OBD160.077.079
21	Hg38_2_20791146_20796987_20975471_20980938_RR	OBD160.081.083
22	Hg38_1_114264796_114271415_114388190_114393574_FF	OBD160.085.087
23	Hg38_3_150148357_150152202_150276483_150282205_RF	OBD160.089.091
24	Hg38_3_3070802_3073954_3162690_3172869_FF	OBD160.093.095
25	Hg38_2_228849719_228856896_228936338_228946445_RR	OBD160.097.099
26	Hg38_X_126618971_126632078_126813931_126821389_RR	OBD160.101.103
27	Hg38_17_3298600_3300356_3435567_3441497_RF	OBD160.105.107
28	Hg38_6_141949457_141959891_142112622_142115111_FF	OBD160.109.111
29	Hg38_2_221629362_221633765_221703220_221711044_FF	OBD160.113.115
30	Hg38_18_8164110_8169146_8228637_8240170_RF	OBD160.117.119
31	Hg38_X_83389647_83396643_83505067_83507528_RR	OBD160.121.123
32	Hg38_2_38740614_38746415_38982199_38993639_FF	OBD160.125.127

33	Hg38_2_169562452_169564303_169638099_169647209_FF	OBD160.129.131
34	Hg38_X_51609399_51612166_51861901_51874841_RF	OBD160.133.135
35	Hg38_1_96786343_96792340_96953170_96960029_RR	OBD160.137.139
36	Hg38_13_76879860_76881474_77089881_77098142_FF	OBD160.141.143
37	Hg38_12_10235418_10237590_10417499_10425564_RF	OBD160.145.147
38	Hg38_3_151888504_151893566_151931687_151943298_RR	OBD160.149.151
39	Hg38_8_81036889_81041061_81244260_81253029_RF	OBD160.153.155
40	Hg38_21_25447238_25454612_25514175_25521235_RF	OBD160.157.159
41	Hg38_12_39724269_39737447_39830409_39841867_RF	OBD160.161.163
42	Hg38_2_2911175_2916426_3008403_3014033_FR	OBD160.165.167
43	Hg38_5_39037737_39046956_39197630_39209276_FR	OBD160.169.171
44	Hg38_2_127388555_127395831_127412534_127416129_RR	OBD160.173.175
45	Hg38_21_14583254_14600479_14842273_14847749_RF	OBD160.177.179
46	Hg38_22_32455270_32461039_32549159_32556587_FR	OBD160.181.183
47	Hg38_13_77416226_77433379_77635636_77642621_RR	OBD160.185.187
48	Hg38_X_66017310_66021076_66266598_66279138_RR	OBD160.189.191
49	Hg38_9_119814503_119824066_119942887_119944563_RR	OBD160.193.195
50	Hg38_15_96378302_96385292_96582969_96587891_FR	OBD160.197.199

Table 1A (part 1g)

No.	probe	RP/Rsum	Rprank	FC:(class1/class2)
51	Hg38_4_37200238_37206260_37300406_37312473_FF	2932.387886	93	1.603
52	Hg38_3_98352533_98365728_98383505_98386616_FR	1732.032487	41	1.602
53	Hg38_21_16639172_16644423_16670368_16680104_FF	3320.296898	119	1.601
54	Hg38_2_42656271_42661181_42695432_42702668_RF	2433.098065	66	1.599
55	Hg38_10_25043685_25049585_25100349_25104868_RR	2030.307559	47	1.598
56	Hg38_1_229090863_229096006_229196083_229202342_FR	2179.775328	55	1.597
57	Hg38_13_105283036_105288043_105320265_105325556_RR	1894.786347	43	1.597
58	Hg38_12_103957683_103963295_104120354_104125638_RR	2134.567802	51	1.592
59	Hg38_6_114008656_114013787_114232226_114238214_RF	1834.397344	42	1.588
60	Hg38_8_140877455_140883144_140932435_140938098_RF	2969.154809	97	1.585
61	Hg38_4_136781505_136792883_136902701_136917925_FR	1926.209278	44	1.584
62	Hg38_17_44726208_44728331_44900687_44908527_FR	3766.109078	142	1.583
63	Hg38_8_116664671_116672423_116798829_116802256_RR	2372.310095	62	1.582
64	Hg38_3_105989527_105998279_106059965_106070080_FR	150657.5165	69345	1.581
65	Hg38_2_112740760_112742979_112765786_112772711_RF	2216.789753	56	1.58
66	Hg38_18_9337930_9343491_9573987_9583586_RR	2016.059075	46	1.58
67	Hg38_11_19074376_19084676_19339671_19348554_FR	2412.878673	65	1.579
68	Hg38_11_57219000_57228121_57426633_57429019_FF	52224.03779	6959	1.576
69	Hg38_11_12078291_12088535_12276885_12282796_FF	2992.859117	99	1.575
70	Hg38_4_152885427_152900293_153068111_153076707_FR	2107.102525	49	1.574
71	Hg38_1_47112037_47119435_47237146_47242526_FF	3119.590551	104	1.572
72	Hg38_13_27255589_27257567_27412662_27420769_FR	2412.337745	64	1.572
73	Hg38_8_31019968_31023828_31152507_31157947_FR	3265.30875	113	1.571
74	Hg38_7_30496219_30498858_30628404_30631817_FF	2885.244353	89	1.571
75	Hg38_X_41694532_41696489_41776262_41781759_FF	2614.17827	75	1.57
76	Hg38_6_51827509_51843341_51906482_51917695_FF	24590.08703	1846	1.568
77	Hg38_4_52550935_52553766_52741887_52744874_RF	2398.639908	63	1.568
78	Hg38_4_143208146_143211670_143254394_143265663_FR	117290.0204	40943	1.567
79	Hg38_2_79143668_79146500_79293195_79300892_FR	2822.115975	86	1.567
80	Hg38_3_386460_393029_417553_428199_RF	2371.626586	61	1.567

81	Hg38_8_105746180_105747310_105814873_105824107_FR	2281.090504	58	1.567
82	Hg38_20_47934845_47942853_47960362_47966156_RF	2812.677411	84	1.566
83	Hg38_1_193673926_193687017_193767073_193774723_FR	2511.193509	70	1.566
84	Hg38_X_55562087_55565924_55755522_55768422_RF	2890.107857	90	1.565
85	Hg38_12_22051055_22053335_22293062_22296971_FR	3103.749832	103	1.564
86	Hg38_5_168367648_168371678_168496703_168499633_RF	2705.325572	80	1.564
87	Hg38_9_13378184_13386623_13453370_13455410_RR	2293.493641	59	1.564
88	Hg38_4_13607623_13610565_13677034_13689726_RR	3789.680583	144	1.563
89	Hg38_1_158836157_158842400_158905246_158912243_FF	2663.851596	76	1.563
90	Hg38_2_59529259_59533399_59556418_59563869_RF	3642.187614	135	1.56
91	Hg38_1_172365073_172375924_172561646_172570053_RR	3195.829634	108	1.558
92	Hg38_1_167272741_167278581_167541602_167544034_FF	2582.676531	72	1.558
93	Hg38_1_27783032_27786599_27834284_27836433_FF	2679.371207	78	1.557
94	Hg38_2_144038117_144048675_144274589_144280493_FF	2464.995797	67	1.557
95	Hg38_17_41002849_41006661_41059440_41062968_RF	2959.335905	96	1.556
96	Hg38_11_90904893_90913850_91035518_91039190_FF	2939.352384	94	1.554
97	Hg38_1_247706861_247710350_247812273_247815652_FR	2718.801607	81	1.554
98	Hg38_12_23014365_23020377_23180775_23184338_RR	2861.202321	88	1.552
99	Hg38_4_28348510_28364344_28414655_28418162_FF	2688.720003	79	1.551
100	Hg38_17_35578150_35580887_35656691_35659920_FF	3346.702466	121	1.55

Table 1A (part 2a)

No.	pfp	P.value	Type	Probe sequence
				60 mer
51	0	0	SBMA	ATACAGGTATCAAATCATCTAGTTGTAAGTATGATGATATAAAAAATCACAAGCATTCTATAC
52	0	0	SBMA	TTTAGGGTCTTTCTTTATCCTTGATCTTCGAGAAGATGTTGAGTTTTATCAGATGCTTT
53	0	0	SBMA	TATTTGTTATCTATTACTTCTAACAATCGAGGACCTGAATTACTTATCACCCTTCTCA
54	0	0	SBMA	TCTGTTTAGCAAATAAACACAAAAAGTATCGACAGATTGACCAAGTTTTAGTTGTAGCAC
55	0	0	SBMA	ACTGAAGTCCAGTAGAACAGAGAATCGAAAGATTCTGAATGGGGAAAACTTACTC
56	0	0	SBMA	CACTTAAGAGCCAGCTATTTGACTGAATTCGAAAAGCTTCTACCAAAAAATCCTTAAAA
57	0	0	SBMA	TTTCCACTGTTTTCTTACAATTTCCCTTCGATTTGTCTTAGCAGACATTTAAGTTACA
58	0	0	SBMA	AATGGAAAAATTCCTGGATTAAGTTATGTCGATACAATCAAATTTTTAAGCATTAAAA
59	0	0	SBMA	CCCATGAGTAAATGTAGACCTATGTCTATCGACGTATACCCTATGGAGAGGATATCCCT
60	0	0	SBMA	CACATCTAACACAATTCACAGTACAAAATCGAATCAAAGCTGTGTACAAAATATGTAA
61	0	0	SBMA	TAAAAATGTAAACGGCTGTTTTTAACTCGATGTTTGATCATTTAAATGCATTATGTCT
62	0	0	SBMA	ATAATTTCCACATGTTCTATTGGTCCAATCGACTGAAGCACCAAAATTAATAATTTTT
63	0	0	SBMA	CTTGATCTACTGAACATATCTTGAGTTTTTCGACTGGTTTTCTCCTCATTATTTTCT
64	0.087 8738	0.0065 61035	SBMA	AGCCTGTGATGGCAAGACTTGCCAAAACCTCGAGTTGCCAGGTATGCATCTTTAGAAAGG
65	0	0	SBMA	AAAATCTTTCCAGAAGTTGTTTCCAGATCGAGACTTGGACTAGAATTAAGTCTGTGAAC
66	0	0	SBMA	TGCCTTGATGATTGGAAGAGATATAACTTCGAAAGTATAAAATCTCTAAATCTAATTTT
67	0	0	SBMA	CTGCCTTTTAATCCTATGTGGAAATGGTCGAGTTATTTTGACAATTGAACTTTTGGT
68	0.000 1820	0.0000 013638 285394	SBMA	ACCCAGAAGAAAGACTGCCAAATCTTCTCGAACCAAGAACATGGGAATGGTTCAGAGG
69	0	0	SBMA	TAGTCTATTTCTGTTCTAGTATTTATTGTGCAACACATTTCTCAATATCATCTATTTGGT
70	0	0	SBMA	CACTCAGAATGTTAATGTATGTAATTATTCGATCATGTCTCTTCCACATGTCTTCTCT
71	0	0	SBMA	AACAACTAGACATTGAAGAAATGTACCTCGATACTATTCTAATCTCCCATTTAGTAGGC

72	0	0	SBMA	AGATCCCTTG TACTGTACTGTTTGTGCAAACCTACGAGTCTAAATATAGTTC
73	0	0	SBMA	GATATTGGACAGGATCAACAAAAAGGAATCGACTCGTGATATGTTTGATATATCCACA
74	0	0	SBMA	CACTTTCGTAATTTGTCATCAGATAACTTCGATGAACCTGGCACCAAGGTCAGTATGAGA
75	0	0	SBMA	CTATATGTTTGTCCCTATCATGCCTTTCGATTACTCTAAGATTTAAAGTCATGTGGAG
76	0	0	SBMA	GGAATCACATGGGCAAGAGAGCTGAGACTCGAATGTCCCCACCATCTTACACATCATTG
77	0	0	SBMA	CATTACCTGACCAGGTCAATCCAGAATTTGACAAAAACATTGTAGGATGAAAAGAGGAG
78	0.024 2079 64	0.0010 67174	SBMA	TCCAAAGTTTCAACTTACAATCACATCTTCGACTCCTTGCATGTTTTCTTGCATCCACT
79	0	0	SBMA	CCTTTTCAAAAAAACAACCTCTCATTCTCGATGACATCAATGGTTTTGCAGTATTGAGC
80	0	0	SBMA	GGAATCTTCAAAGAATAAGTGTTTTTCATCGAACATCATAATGTTCTACTTGCAAAACAG
81	0	0	SBMA	TTAACTCCAAATTTCCAAGTCAGTTAACTCGACCTTTTTCTGTTTCAGTAACCAACCCAG
82	0	0	SBMA	ACTGCAGATCTGTACCCAAGTGATATGATCGACATTCAGTAAGACTTGTCTTTATTGG
83	0	0	SBMA	GGAACACTTCTCTAAGAACCTGAATTATTCGAGCTTCAAATACAAAACATTGGGCTCAA
84	0	0	SBMA	TAATCCCTTTCAATTTCTGTTAAGTTTCTCGATTAAAGCCATGCATTGATACCTGACCCAA
85	0	0	SBMA	ATGCAGTTCATCTTCCCTCAGTAGATATCGAGACTAAGAAACAAACACTTGTCAAATA
86	0	0	SBMA	TTATAAACATCTTTGGAGTTCTGTACTTCGAGTTTTGGAATCTGGCAGTGGAACCTCAG
87	0	0	SBMA	TTTCTTCCTAATTTGGTTAGCCAGTATCGAGTCTTAGAAGTATTCAATTTGCAATTTG
88	0	0	SBMA	AAATTGAAATGTAACAGTCTGCATTTGTGCGAAACAAATATTGTCTACTGCATTGTAA
89	0	0	SBMA	CATCACTTAAAAACCTTGTTAAACATCTTCGAGGTTACCATAACCCATTATTTAAGCTG
90	0	0	SBMA	TTTTAAAGATGCAGAAAAAACAATCGACAAACAGTTCACACAATAACACTATGTG
91	0	0	SBMA	TTTTAAAGTTATGTGTTTGAGTTTGAATCGAAAAGAAGTATTACACTATTTTGTCCCC
92	0	0	SBMA	ACGATGAAGATAATGTTACATTATCATTGAAAGTTAAAGTTTACTTTCACAGGACATAA
93	0	0	SBMA	TTGTCTATCTCTTTCCTTAGAAGACTCTCGAAAACAAAAACAAACAAAAAATAAAAAAT
94	0	0	SBMA	CTATGATTAACTTTACTTCATTAGGTATCGAATTACAACAAAAAACCCCAAAATCCT
95	0	0	SBMA	CTTGGAAAGTTCAATGTGAAAGAAAGAGTCGATTTTGAAATATTATATAGATTACAGGAGA
96	0	0	SBMA	AATTTATCTCATTTACAGATTGTATCAGTCGAATAATCCACAGGAAAACCAAGTTGGCC
97	0	0	SBMA	CATCATAGGTACCTTAAGAGGTAGACTTTCGAAATACATAGTCAGTTCACAGTTTGTATA
98	0	0	SBMA	TTGTATATGGGCTCAGTAAATGTGAATCGAACTTCTGCTTTTAAATACTCTACTCTC
99	0	0	SBMA	CAAAGAAATGTTGTTTCATGAACTTATATCGACATAAAGAGCGTTAGGGCAAATTATAAG
100	0	0	SBMA	AAAAAAAAGAAAACAGAAATTTGCAACTCGAAAAAGGAACCTTGATTCTCTGAGTGAAT

Table 1A (part 2b)

No.	Probe Location				
	Chr	Start1	End1	Start2	End2
51	4	37206229	37206258	37312442	37312471
52	3	98365697	98365726	98383507	98383536
53	21	16644392	16644421	16680073	16680102
54	2	42656273	42656302	42702637	42702666
55	10	25043687	25043716	25100351	25100380
56	1	229095975	229096004	229196085	229196114
57	13	105283038	105283067	105320267	105320296
58	12	103957685	103957714	104120356	104120385
59	6	114008658	114008687	114238183	114238212
60	8	140877457	140877486	140938067	140938096
61	4	136792852	136792881	136902703	136902732
62	17	44728300	44728329	44900689	44900718
63	8	116664673	116664702	116798831	116798860
64	3	105998248	105998277	106059967	106059996
65	2	112740762	112740791	112772680	112772709
66	18	9337932	9337961	9573989	9574018
67	11	19084645	19084674	19339673	19339702

68	11	57228090	57228119	57428988	57429017
69	11	12088504	12088533	12282765	12282794
70	4	152900262	152900291	153068113	153068142
71	1	47119404	47119433	47242495	47242524
72	13	27257536	27257565	27412664	27412693
73	8	31023797	31023826	31152509	31152538
74	7	30498827	30498856	30631786	30631815
75	X	41696458	41696487	41781728	41781757
76	6	51843310	51843339	51917664	51917693
77	4	52550937	52550966	52744843	52744872
78	4	143211639	143211668	143254396	143254425
79	2	79146469	79146498	79293197	79293226
80	3	386462	386491	428168	428197
81	8	105747279	105747308	105814875	105814904
82	20	47934847	47934876	47966125	47966154
83	1	193686986	193687015	193767075	193767104
84	X	55562089	55562118	55768391	55768420
85	12	22053304	22053333	22293064	22293093
86	5	168367650	168367679	168499602	168499631
87	9	13378186	13378215	13453372	13453401
88	4	13607625	13607654	13677036	13677065
89	1	158842369	158842398	158912212	158912241
90	2	59529261	59529290	59563838	59563867
91	1	172365075	172365104	172561648	172561677
92	1	167278550	167278579	167544003	167544032
93	1	27786568	27786597	27836402	27836431
94	2	144048644	144048673	144280462	144280491
95	17	41002851	41002880	41062937	41062966
96	11	90913819	90913848	91039159	91039188
97	1	247710319	247710348	247812275	247812304
98	12	23014367	23014396	23180777	23180806
99	4	28364313	28364342	28418131	28418160
100	17	35580856	35580885	35659889	35659918

Table 1A (part 2c)

No.	4 kb Sequence Location				
	Chr	Start1	End1	Start2	End2
51	4	37202259	37206258	37308472	37312471
52	3	98361727	98365726	98383507	98387506
53	21	16640422	16644421	16676103	16680102
54	2	42656273	42660272	42698667	42702666
55	10	25043687	25047686	25100351	25104350
56	1	229092005	229096004	229196085	229200084
57	13	105283038	105287037	105320267	105324266
58	12	103957685	103961684	104120356	104124355
59	6	114008658	114012657	114234213	114238212
60	8	140877457	140881456	140934097	140938096
61	4	136788882	136792881	136902703	136906702
62	17	44724330	44728329	44900689	44904688

63	8	116664673	116668672	116798831	116802830
64	3	105994278	105998277	106059967	106063966
65	2	112740762	112744761	112768710	112772709
66	18	9337932	9341931	9573989	9577988
67	11	19080675	19084674	19339673	19343672
68	11	57224120	57228119	57425018	57429017
69	11	12084534	12088533	12278795	12282794
70	4	152896292	152900291	153068113	153072112
71	1	47115434	47119433	47238525	47242524
72	13	27253566	27257565	27412664	27416663
73	8	31019827	31023826	31152509	31156508
74	7	30494857	30498856	30627816	30631815
75	X	41692488	41696487	41777758	41781757
76	6	51839340	51843339	51913694	51917693
77	4	52550937	52554936	52740873	52744872
78	4	143207669	143211668	143254396	143258395
79	2	79142499	79146498	79293197	79297196
80	3	386462	390461	424198	428197
81	8	105743309	105747308	105814875	105818874
82	20	47934847	47938846	47962155	47966154
83	1	193683016	193687015	193767075	193771074
84	X	55562089	55566088	55764421	55768420
85	12	22049334	22053333	22293064	22297063
86	5	168367650	168371649	168495632	168499631
87	9	13378186	13382185	13453372	13457371
88	4	13607625	13611624	13677036	13681035
89	1	158838399	158842398	158908242	158912241
90	2	59529261	59533260	59559868	59563867
91	1	172365075	172369074	172561648	172565647
92	1	167274580	167278579	167540033	167544032
93	1	27782598	27786597	27832432	27836431
94	2	144044674	144048673	144276492	144280491
95	17	41002851	41006850	41058967	41062966
96	11	90909849	90913848	91035189	91039188
97	1	247706349	247710348	247812275	247816274
98	12	23014367	23018366	23180777	23184776
99	4	28360343	28364342	28414161	28418160
100	17	35576886	35580885	35655919	35659918

Table 1A (part 2d)

No.	probe	Primer ID
51	Hg38_4_37200238_37206260_37300406_37312473_FF	OBD160.201
52	Hg38_3_98352533_98365728_98383505_98386616_FR	OBD160.205
53	Hg38_21_16639172_16644423_16670368_16680104_FF	OBD160.209
54	Hg38_2_42656271_42661181_42695432_42702668_RF	OBD160.213
55	Hg38_10_25043685_25049585_25100349_25104868_RR	OBD160.217
56	Hg38_1_229090863_229096006_229196083_229202342_FR	OBD160.221
57	Hg38_13_105283036_105288043_105320265_105325556_RR	OBD160.225
58	Hg38_12_103957683_103963295_104120354_104125638_RR	OBD160.229

59	Hg38_6_114008656_114013787_114232226_114238214_RF	OBD160.233
60	Hg38_8_140877455_140883144_140932435_140938098_RF	OBD160.237
61	Hg38_4_136781505_136792883_136902701_136917925_FR	OBD160.241
62	Hg38_17_44726208_44728331_44900687_44908527_FR	OBD160.245
63	Hg38_8_116664671_116672423_116798829_116802256_RR	OBD160.249
64	Hg38_3_105989527_105998279_106059965_106070080_FR	OBD160.253
65	Hg38_2_112740760_112742979_112765786_112772711_RF	OBD160.257
66	Hg38_18_9337930_9343491_9573987_9583586_RR	OBD160.261
67	Hg38_11_19074376_19084676_19339671_19348554_FR	OBD160.265
68	Hg38_11_57219000_57228121_57426633_57429019_FF	OBD160.269
69	Hg38_11_12078291_12088535_12276885_12282796_FF	OBD160.273
70	Hg38_4_152885427_152900293_153068111_153076707_FR	OBD160.277
71	Hg38_1_47112037_47119435_47237146_47242526_FF	OBD160.281
72	Hg38_13_27255589_27257567_27412662_27420769_FR	OBD160.285
73	Hg38_8_31019968_31023828_31152507_31157947_FR	OBD160.289
74	Hg38_7_30496219_30498858_30628404_30631817_FF	OBD160.293
75	Hg38_X_41694532_41696489_41776262_41781759_FF	OBD160.297
76	Hg38_6_51827509_51843341_51906482_51917695_FF	OBD160.301
77	Hg38_4_52550935_52553766_52741887_52744874_RF	OBD160.305
78	Hg38_4_143208146_143211670_143254394_143265663_FR	OBD160.309
79	Hg38_2_79143668_79146500_79293195_79300892_FR	OBD160.313
80	Hg38_3_386460_393029_417553_428199_RF	OBD160.317
81	Hg38_8_105746180_105747310_105814873_105824107_FR	OBD160.321
82	Hg38_20_47934845_47942853_47960362_47966156_RF	OBD160.325
83	Hg38_1_193673926_193687017_193767073_193774723_FR	OBD160.329
84	Hg38_X_55562087_55565924_55755522_55768422_RF	OBD160.333
85	Hg38_12_22051055_22053335_22293062_22296971_FR	OBD160.337
86	Hg38_5_168367648_168371678_168496703_168499633_RF	OBD160.341
87	Hg38_9_13378184_13386623_13453370_13455410_RR	OBD160.345
88	Hg38_4_13607623_13610565_13677034_13689726_RR	OBD160.349
89	Hg38_1_158836157_158842400_158905246_158912243_FF	OBD160.353
90	Hg38_2_59529259_59533399_59556418_59563869_RF	OBD160.357
91	Hg38_1_172365073_172375924_172561646_172570053_RR	OBD160.361
92	Hg38_1_167272741_167278581_167541602_167544034_FF	OBD160.365
93	Hg38_1_27783032_27786599_27834284_27836433_FF	OBD160.369
94	Hg38_2_144038117_144048675_144274589_144280493_FF	OBD160.373
95	Hg38_17_41002849_41006661_41059440_41062968_RF	OBD160.377
96	Hg38_11_90904893_90913850_91035518_91039190_FF	OBD160.381
97	Hg38_1_247706861_247710350_247812273_247815652_FR	OBD160.385
98	Hg38_12_23014365_23020377_23180775_23184338_RR	OBD160.389
99	Hg38_4_28348510_28364344_28414655_28418162_FF	OBD160.393
100	Hg38_17_35578150_35580887_35656691_35659920_FF	OBD160.397

Table 1A (part 2e)

No.	Sequence	Primer ID	Sequence
51	GGAATAGAGGGAAGAAAACCCATAAA	OBD160.203	CTCTCTGTTGTCTGTTATTGGTGTAT
52	AGTCTGTAAGGTTTCTATGAGAAGC	OBD160.207	GAAACGAATACCCCTGATGAAGATAG
53	CTCAGATTCTCACCTGTAGAGCAGT	OBD160.211	GGAAAAGTGAAGAATAAGCACCCATC
54	TTCTGGTAGCAGTGGTGGGAGTGTC	OBD160.215	AATGCCATACTCATACTCACCGTGCT

55	GCCTTGAGAACCTTAGAACAAATGCCA	OBD160.219	GGAGAAATCCCAGTTACACAGTTGGC
56	TAAGTCCAGGAGATTGAGGCTGC	OBD160.223	AGTAACTAAGTCTCTACCTTCTTTC
57	CAATGTGTCTAAGTAACGCCTGTGTG	OBD160.227	GAAGAACATAACTGCCCTGCTCCAG
58	TGCTGGCTGGGATTACAGGCGTA	OBD160.231	CCACAGACGGTCAACAACAAAATGT
59	GATTGGTAGAGGAAAGAGAAGCAGAGAA	OBD160.235	GTGCCAGAAAGGGTTATGCTGTTAGTGA
60	CTAAGAAGACAACACAACCTCCTC	OBD160.239	GTATGCTGCTTACACCAGATAACTTA
61	GAGGAACTCAGAAGACTGGCTTTAGG	OBD160.243	CACTGGAAAAGAGGCAGGTTTGAGAC
62	GCCACCTTCCCAGAAAGTGAGGC	OBD160.247	GACCCCAAAGCACTCTGGACATC
63	GCTCTACTCTTCCCTACAGGCTG	OBD160.251	AGGAATAGAAAAGTGTAGCCACCCTA
64	TTGTGCTGTCTGGAGTTGTAGGAGGG	OBD160.255	CCCTACTTCTCTCTCTACACACAA
65	TCATTGTGTGGCTCTGACTTCCAGT	OBD160.259	CCGAATAGCCAAGGCAGAACAGCATA
66	TACTTCTCTTACTTTTCTCCCAGA	OBD160.263	GTCCTCTGGTGTCTTGATACCTACG
67	CCATCTTTCATCCACTCATCCCTCCA	OBD160.267	GAATCCATCATAATGCTGACTCTGAA
68	CCCTGGGTCCCTCTCTTATCATC	OBD160.271	GCCTCCACTCCACATCTCCCATC
69	AGAGCCGAGTTGTCCCAGCAGAG	OBD160.275	GCAGGTCTCTGAGTAGGCACAAC
70	GAAAATGAGAGAGGGAGAAAGGGAGGG	OBD160.279	CCAATACGACTGGTGTCTTGTAAAG
71	CTCAGTAGACGCAGAAAACGCTT	OBD160.283	ATCTCTTATTCTCTATTTCCAGCCTA
72	GCTGGCAGGTTGCGGTGTCTGTG	OBD160.287	GGAAAAGTCTGGCTGGGAGATGC
73	CAGTTCACAGGTCAGTATCCTTCTG	OBD160.291	CTTTGCCAACTTTTGTCTTATTGCC
74	GTAATCACCACCACTGTGAAATAGC	OBD160.295	GGTAGGACCCAAGAGTCAGATTTA
75	CTATTGAGGATTCTAAAAGGAGGTC	OBD160.299	TGAGCAATGAGCCCTAAATACCAGG
76	GTGTCAGCAGATGTAGCCAGTAGCCA	OBD160.303	TGCCAGATGACAAAATGGGAAGCGTA
77	GATTGGAACCTGTGAGCCACCAG	OBD160.307	CTCACAGGCAAGATACTTCCACGGG
78	GGCTAAACTTCTTCTTCTCAGAATGC	OBD160.311	CTCAAGTTGGGAGGGCTGATGGAAAC
79	TGGGTCTTCTATTTTCTTAGTCTGGC	OBD160.315	ACACCCACAGAACTAAGCAGCCAGT
80	CTTGTTTCTCTGCTCACTGGCTACTC	OBD160.319	GGCTTTTGGTTTGTCTTTGGTGTCC
81	GCACTTCACTGCTCCCTTGCCAGC	OBD160.323	CTGTTCTCCCAAGTCTTAAGTGTAGGC
82	CCCCAGCCTCGTGAGAGAGTCTA	OBD160.327	CGAAGAGCCCCAACCCAACACAT
83	CCTGTGCTTCTGAAATGTGCTCTGCT	OBD160.331	GCTATTTACCCTCAGAGTAGTATCAT
84	TAGCCGACTCTTGGCATTATGAGGG	OBD160.335	GCACCCTGTATTACTTATCTATGGC
85	GCCTGGGTGACAGAGCAAGACTC	OBD160.339	CAGCAAATACCCCAATCCTGGA
86	TTCCAACCTCAGTGACAGAGTGA	OBD160.343	ACACAGTTAGTAAACACCACAGGTAT
87	GGAAGTTCAGGAATGTGGTGTGCTCT	OBD160.347	CAACTCTGGAAAATGCTTCTTGTGC
88	GGGATTGTGCTCTCCTTTGTTGACCA	OBD160.351	CAGAACTTTCACCTGAGGTCCCATCA
89	CCTGGGACACTCACTCAGAAAAGCATA	OBD160.355	GTAGAAAAGACTAAAAGACAAACCTCTCA
90	GCTGGAACAATGTATCACTTTAGGGA	OBD160.359	TATTGAAGTTTCCCTGTCCGCCAGC
91	CCTTAGAAAAACATAACACAATAC	OBD160.363	GACAAGAGTAGAGGTGAGTGGGTA
92	GGGACCTTGTCTGCTTACTCACTGC	OBD160.367	CAGTGTGGAGACTTATGGGAAAACAG
93	TATCCTCTGCCACCACTGTCACTT	OBD160.371	GAGAGTTATTCCTCAAGTGTCCAC
94	GCAGAGGTAAAACAGGTAGAAAGGTC	OBD160.375	GTCTCCTAAAGCCAAAACACCACCAT
95	CTAAAGTCAGGGAAGGCAAAGTAATC	OBD160.379	CAGTATGAACGAGGTACAGAGGGTA
96	TTTCTTAGAGATACAATCATTCTGGCAG	OBD160.383	CCTCATAGGCTGCTTCTTTGTTCTCC
97	GCCTCGGTGAGATGTTCAATGGCAGGAA	OBD160.387	TACTGGCTGAGGGATTCTTCCACCAT
98	TCAGTTTCAGAGACCTACCAACATTA	OBD160.391	GTCCTCAGAGAAAATCGCAGGGAGTC
99	GGGACTTACACAGCCCTATGCTTCTTG	OBD160.395	GCCGAGTGGGCTCTTCTGCTACACAAC
100	GGCAGGAGAATCACTTGAACCCG	OBD160.399	CTTGGTGTTACAGCCCCAGAAAT

Table 1A (part 2f)

No.	probe	Marker
51	Hg38_4_37200238_37206260_37300406_37312473_FF	OBD160.201.203
52	Hg38_3_98352533_98365728_98383505_98386616_FR	OBD160.205.207
53	Hg38_21_16639172_16644423_16670368_16680104_FF	OBD160.209.211
54	Hg38_2_42656271_42661181_42695432_42702668_RF	OBD160.213.215
55	Hg38_10_25043685_25049585_25100349_25104868_RR	OBD160.217.219
56	Hg38_1_229090863_229096006_229196083_229202342_FR	OBD160.221.223
57	Hg38_13_105283036_105288043_105320265_105325556_RR	OBD160.225.227
58	Hg38_12_103957683_103963295_104120354_104125638_RR	OBD160.229.231
59	Hg38_6_114008656_114013787_114232226_114238214_RF	OBD160.233.235
60	Hg38_8_140877455_140883144_140932435_140938098_RF	OBD160.237.239
61	Hg38_4_136781505_136792883_136902701_136917925_FR	OBD160.241.243
62	Hg38_17_44726208_44728331_44900687_44908527_FR	OBD160.245.247
63	Hg38_8_116664671_116672423_116798829_116802256_RR	OBD160.249.251
64	Hg38_3_105989527_105998279_106059965_106070080_FR	OBD160.253.255
65	Hg38_2_112740760_112742979_112765786_112772711_RF	OBD160.257.259
66	Hg38_18_9337930_9343491_9573987_9583586_RR	OBD160.261.263
67	Hg38_11_19074376_19084676_19339671_19348554_FR	OBD160.265.267
68	Hg38_11_57219000_57228121_57426633_57429019_FF	OBD160.269.271
69	Hg38_11_12078291_12088535_12276885_12282796_FF	OBD160.273.275
70	Hg38_4_152885427_152900293_153068111_153076707_FR	OBD160.277.279
71	Hg38_1_47112037_47119435_47237146_47242526_FF	OBD160.281.283
72	Hg38_13_27255589_27257567_27412662_27420769_FR	OBD160.285.287
73	Hg38_8_31019968_31023828_31152507_31157947_FR	OBD160.289.291
74	Hg38_7_30496219_30498858_30628404_30631817_FF	OBD160.293.295
75	Hg38_X_41694532_41696489_41776262_41781759_FF	OBD160.297.299
76	Hg38_6_51827509_51843341_51906482_51917695_FF	OBD160.301.303
77	Hg38_4_52550935_52553766_52741887_52744874_RF	OBD160.305.307
78	Hg38_4_143208146_143211670_143254394_143265663_FR	OBD160.309.311
79	Hg38_2_79143668_79146500_79293195_79300892_FR	OBD160.313.315
80	Hg38_3_386460_393029_417553_428199_RF	OBD160.317.319
81	Hg38_8_105746180_105747310_105814873_105824107_FR	OBD160.321.323
82	Hg38_20_47934845_47942853_47960362_47966156_RF	OBD160.325.327
83	Hg38_1_193673926_193687017_193767073_193774723_FR	OBD160.329.331
84	Hg38_X_55562087_55565924_55755522_55768422_RF	OBD160.333.335
85	Hg38_12_22051055_22053335_22293062_22296971_FR	OBD160.337.339
86	Hg38_5_168367648_168371678_168496703_168499633_RF	OBD160.341.343
87	Hg38_9_13378184_13386623_13453370_13455410_RR	OBD160.345.347
88	Hg38_4_13607623_13610565_13677034_13689726_RR	OBD160.349.351
89	Hg38_1_158836157_158842400_158905246_158912243_FF	OBD160.353.355
90	Hg38_2_59529259_59533399_59556418_59563869_RF	OBD160.357.359
91	Hg38_1_172365073_172375924_172561646_172570053_RR	OBD160.361.363
92	Hg38_1_167272741_167278581_167541602_167544034_FF	OBD160.365.367
93	Hg38_1_27783032_27786599_27834284_27836433_FF	OBD160.369.371
94	Hg38_2_144038117_144048675_144274589_144280493_FF	OBD160.373.375
95	Hg38_17_41002849_41006661_41059440_41062968_RF	OBD160.377.379
96	Hg38_11_90904893_90913850_91035518_91039190_FF	OBD160.381.383
97	Hg38_1_247706861_247710350_247812273_247815652_FR	OBD160.385.387
98	Hg38_12_23014365_23020377_23180775_23184338_RR	OBD160.389.391

99	Hg38_4_28348510_28364344_28414655_28418162_FF	OBD160.393.395
100	Hg38_17_35578150_35580887_35656691_35659920_FF	OBD160.397.399

Table 1A (part 2g)

No.	probe	RP/Rsum	Rprank	FC:(class1/class2)
101	Hg38_13_28438004_28449201_28551336_28558541_RR	5473.459527	216	1.548
102	Hg38_8_132637112_132642401_132681711_132690255_FR	3591.973084	130	1.545
103	Hg38_20_33827938_33830467_34035296_34047038_FR	3359.632084	122	1.545
104	Hg38_4_55932433_55939189_55969220_55974802_FF	2903.160734	91	1.545
105	Hg38_7_142995810_142998826_143057496_143064818_RR	3759.403871	140	1.544
106	Hg38_18_75676630_75682929_75700545_75706785_RR	2791.763006	83	1.544
107	Hg38_5_12486934_12496757_12590668_12597008_FF	2558.874957	71	1.544
108	Hg38_7_113374693_113380998_113411335_113420030_FR	2582.839821	73	1.542
109	Hg38_3_98493912_98497028_98612320_98617232_RF	2676.998144	77	1.54
110	Hg38_6_71312879_71323494_71524385_71527337_FR	2845.485946	87	1.539
111	Hg38_4_71700748_71714803_71741385_71749255_FF	3490.546135	128	1.537
112	Hg38_13_62231930_62237495_62330216_62339040_FR	2587.198527	74	1.537
113	Hg38_12_90700058_90702509_90796185_90802319_RF	3605.32438	131	1.536
114	Hg38_4_67686135_67693477_67782747_67789927_RR	2955.347004	95	1.536
115	Hg38_6_39611834_39623490_39813403_39823235_FF	3385.094489	123	1.535
116	Hg38_6_125238508_125249295_125290548_125297233_FF	3558.225301	129	1.534
117	Hg38_4_126064916_126070028_126094394_126106891_RR	3138.820724	105	1.534
118	Hg38_10_12235815_12238464_12383561_12388246_FR	2359.06621	60	1.534
119	Hg38_7_88599386_88615125_88740721_88745628_FF	2728.216	82	1.533
120	Hg38_2_52892382_52905124_52921980_52933672_RR	3219.804543	110	1.532
121	Hg38_1_74603597_74607998_74778978_74800362_FR	3742.651266	139	1.531
122	Hg38_Y_22721647_22725457_22859118_22870072_RF	3212.534981	109	1.53
123	Hg38_4_97463862_97470977_97576564_97590463_RR	3052.561735	101	1.53
124	Hg38_1_96357496_96364474_96392998_96404426_RF	2982.624056	98	1.53
125	Hg38_1_158905246_158912243_159126541_159136350_FF	2817.776717	85	1.53
126	Hg38_11_106098496_106106725_106275961_106290738_RR	3268.3717	114	1.529
127	Hg38_11_72859306_72866489_72925691_72936492_RF	3458.227037	127	1.525
128	Hg38_14_49020009_49028815_49076509_49078072_FR	4442.91003	165	1.524
129	Hg38_4_173125717_173130524_173207477_173215489_FR	3607.202568	132	1.524
130	Hg38_14_19825779_19829413_19968132_19975589_FF	3185.904497	107	1.524
131	Hg38_15_56425187_56434244_56691312_56696438_FR	2916.936995	92	1.524
132	Hg38_7_30612223_30619592_30804622_30809524_FR	4045.43792	152	1.523
133	Hg38_20_46372997_46377307_46622048_46631132_FF	3314.955421	118	1.523
134	Hg38_14_24423148_24425179_24517993_24525921_RR	5033.707838	189	1.522
135	Hg38_7_93821969_93826969_93960806_93964392_FR	3286.118138	115	1.522
136	Hg38_2_36912180_36914993_37085573_37089692_RR	3310.62397	117	1.521
137	Hg38_4_77717993_77727364_77982270_77985832_RR	3083.119716	102	1.521
138	Hg38_3_87991842_87995289_88126188_88133417_FF	3239.086494	111	1.518
139	Hg38_4_121310394_121315169_121339971_121354127_RF	3150.912042	106	1.518
140	Hg38_2_15677778_15684445_15733618_15739157_RR	4181.003667	156	1.517
141	Hg38_12_29701302_29708431_29828391_29843699_FF	3425.857677	124	1.517
142	Hg38_3_64067438_64075904_64228797_64236262_FR	3767.332371	143	1.516
143	Hg38_17_40700822_40703790_40868811_40875117_FR	3434.139591	125	1.516
144	Hg38_9_120795804_120798748_120831347_120833895_RR	3002.794717	100	1.515
145	Hg38_7_144246203_144258031_144391768_144394587_FR	5823.554282	235	1.513
146	Hg38_12_71685734_71687005_71771992_71780701_FR	4285.485291	160	1.513
147	Hg38_11_82067024_82073102_82131728_82146376_RF	3887.012897	147	1.513

148	Hg38_7_144153639_144162181_144246203_144258031_RF	6897.235002	308	1.512
149	Hg38_2_21769905_21774394_21960934_21972734_FR	5044.788457	190	1.512
150	Hg38_4_38385027_38395353_38450896_38455314_RF	3309.983405	116	1.512

Table 1A (part 3a)

No.	pfp	P.value	Type	Probe sequence
				60 mer
101	0	0	SBMA	AATAAAATGATGGTGTCTTAAGCATAAATCGATTGATGTAGGAGTATTAGTAGTAATTGA
102	0	0	SBMA	TCATGCTATTTCTCATGGAGAGATGGCATCGAAGATGAAATTAATTTTAAATGATTGTCT
103	0	0	SBMA	ATTTATTTTCTCAGTTCTGGAGACTCAGTCGAAGGCTAGAGTTATCAGAAAAATGTTAATT
104	0	0	SBMA	AGTTAATATAGAAACAACATTCTTTTCGACGTTTTATTCCATGTTCTAGTCTCATCC
105	0	0	SBMA	TTGTTTGTCTACTTTGCTATTGAGTCTTCGATTTCAGACATTCCATACGTCCTCTGA
106	0	0	SBMA	ACATCTGATTTAACCAAATCTTTGCCAATCGATTGTATCTTCTATAATTAGCAATAGCTA
107	0	0	SBMA	ATATATTTAATGAAATAAAATCTATATCGATTACACTCTGGGCTAGAGGTTCTCTAAAT
108	0	0	SBMA	CCATAATTTTTCAGCACATAAACTTTCTCGACAGAAGTGAAGAAACAATCCTGAAAAAA
109	0	0	SBMA	TGACATGATCTAAGATAATCTCCTTATCTCGAGGTGAGAATTAACACATTATTAATTA
110	0	0	SBMA	ATGTCAATAAAATGTACAGGATTACATTCGAAAAAACAAAAACAAACAAAAA
111	0	0	SBMA	ATAAACAGATGAATAGACTGTAAATAATCGACAGTAAATTTATAGCAGCTGAGTAGCCT
112	0	0	SBMA	ACTGAGTTTATACAACCTTTTAAATTTTCGAGAATAACTCAGGATAAAATAGATACAAG
113	0	0	SBMA	TATTGTGGGGTTTTTTTATTGTTGTTTTCGAGTAAAAACAGTTTTTGAATATCAAGT
114	0	0	SBMA	GTTCTTTCATAAAAGGGTGAATTTTAAATCGATGTTTACCATTTTGACTGAAGATATAAT
115	0	0	SBMA	AAAATGTACTATCTTGTTTCATAAAGTTCTCGATGTAGCCTTTCTTAATCTTTGGGCCCTTT
116	0	0	SBMA	ATTTTCCCTCTATTCTTTAAAACTTTTCGAGATTCTTAGTTGCAGAAAGGAATTAGCA
117	0	0	SBMA	TCTGCATTTAATGTTGCAACATGAGGAATCGATGTATAATGTTGTTTCAGTTAAACTATGT
118	0	0	SBMA	TGACTTTTTTCTCCTTTACAGTTGTGTTTCGAGCTTGTTATTTTCTTTCTTACCTAGT
119	0	0	SBMA	ACACAATATGATGCATAAGAAAAAATCGAATTTAAAAACAAAAAAGCCCTAATAT
120	0	0	SBMA	AATAACTGCAGAATATACATTTTCCCATCGAGTCTGATTGATTGAGCTCTGAAATCAA
121	0	0	SBMA	TATCATCACCCTTTACAAATGAGAAAAATCGAAAAATAGAACTTACGTTATCAGGTTCAA
122	0	0	SBMA	ACTATATTATGACCTGTATCAAGATGTATCGAAATACAAGAATCTAGTCTGATTAGATTA
123	0	0	SBMA	ATGGGATCTCAGAATAGAAAAAGAACATTCGACCTCTACATATCATCTAAAGAAATTAAC
124	0	0	SBMA	ATTTTAAAAATGAAAAAATGACATAATTCGACCTCTCTTTCTTGCTGGAAAAATATGCT
125	0	0	SBMA	CAGCTTAAATAATGGGTTATGGTAACCTCGAGGTAGATACATAGGAGGTGCAACACAA
126	0	0	SBMA	AAACATTCAAATTTTTTCTTTTACTAATCGAGGGATATGATGTTCTCAGTTGGATTTTT
127	0	0	SBMA	CAGTGTGATTTTATCAAATCAAGAATCTCGAGTATATGCAAGCTATGTAAGCTACTTGT
128	0	0	SBMA	ATTTTATAAAGCCAGAATAACCCTGATATCGAACCTATAAATACTGTTTTTCTATAA
129	0	0	SBMA	AATGTTATGAAATGAAGACATATGTGACTCGAAACCCTTTTCATACCATTAATATTTT
130	0	0	SBMA	GCTATTTTAAACAAAACATCATTTAATATCGATTTTGGAGGGACTTAATTTTCAGCTACC
131	0	0	SBMA	TTTGTTTCTGAGCATTCATTAATCTATTGATTGATAGATATACTGTAGGTACATT
132	0	0	SBMA	GGTTAAGAACATAAGTATACCTAACAGTCGATATCTGTTGAGTCTCACTATCTGACTG
133	0	0	SBMA	TTTATTACTTGTGAAATGGTAACGTTTCGAGAACCCTGGATTAAATGATCTCAGCTT
134	0	0	SBMA	AAATATTGTAGTACAAATGTCTACACTCTCGATTGTGGTTGTTGCCAGGAATGGAGGCA
135	0	0	SBMA	ACAGAAATGAGAAAAACAATAGAGAATATCGACTCTAAAGTCTATGTAGAGAAGCAAAGG
136	0	0	SBMA	ACCAATAAAAGGGAAAGAGTAGAGATACTCGAGAAAAATGAAGGAAATGATTGCCATAAAA
137	0	0	SBMA	AAACAGCTTAAGTTTATTTTGTGTATGATCGATAAGCTACCCCTCCTTAGGATAACAAAT
138	0	0	SBMA	CCGGATAATTTTTTATTTCTTACTTTTCGATCCTACCTATTTCCCAACCATTAATAT
139	0	0	SBMA	TTTGATTCCTATAGTTTTGCAGTATAATTCGAAGATCAAAACATGCAAACTAGCAGTC
140	0	0	SBMA	CAGGACTGTAAAAGAGCCTTTTCTTCTTCGATTGGAACCTTTATGTCTGGACTCTGAAA
141	0	0	SBMA	ACCAAAAGTCAGAGGAACAAATAATTTGTCGATCTTCAGAACTTCTGTATTTTAA
142	0	0	SBMA	ATTCTCTATCTCCATGAATTTAATTGTTTCGACCTTCAGAACTTCTGTAGGTAGAAT
143	0	0	SBMA	CTGCCTTTTTGGCCTTTATATACACACTTCGAAATCCTTTGTTGGATTTCAGATTTCTAAA

144	0	0	SBMA	AAACATCATTCTACCAGCAAGTTTATTTGGAACAATGTCATTGTTTTATTACACTTT
145	0	0	SBMA	AAACAGAACCCGGATTTTTACAGACTGATCGAAGTTAACTGCACATCCTTTTTTATCT
146	0	0	SBMA	GCCTTTAATAAATGCTTGTTGTGATAATTGAGTCATTAGGTTGAAAGGGACCAGTTGT
147	0	0	SBMA	GAATGCACAATGTAAACTATTAACCTTTGGAAGTTATCTCTATTTTACTGTACTGTGG
148	0	0	SBMA	AAACAGAACCCGGATTTTTACAGACTGATCGACTCAAAAATTACTGTATGTGATATGGGA
149	0	0	SBMA	TGTCCCAGTAAATCGCTGGGGAATAGAATCGATAAGAAGTATGAAAAATTTAATTTAAA
150	0	0	SBMA	ATCACTTTCAGAAAAGAATAGAGGTTTTTCGATATTCAAGCTCAGAAAATAAGCTCAAC

Table 1A (part 3b)

No.	Probe Location				
	Chr	Start1	End1	Start2	End2
101	13	28438006	28438035	28551338	28551367
102	8	132642370	132642399	132681713	132681742
103	20	33830436	33830465	34035298	34035327
104	4	55939158	55939187	55974771	55974800
105	7	142995812	142995841	143057498	143057527
106	18	75676632	75676661	75700547	75700576
107	5	12496726	12496755	12596977	12597006
108	7	113380967	113380996	113411337	113411366
109	3	98493914	98493943	98617201	98617230
110	6	71323463	71323492	71524387	71524416
111	4	71714772	71714801	71749224	71749253
112	13	62237464	62237493	62330218	62330247
113	12	90700060	90700089	90802288	90802317
114	4	67686137	67686166	67782749	67782778
115	6	39623459	39623488	39823204	39823233
116	6	125249264	125249293	125297202	125297231
117	4	126064918	126064947	126094396	126094425
118	10	12238433	12238462	12383563	12383592
119	7	88615094	88615123	88745597	88745626
120	2	52892384	52892413	52921982	52922011
121	1	74607967	74607996	74778980	74779009
122	Y	22721649	22721678	22870041	22870070
123	4	97463864	97463893	97576566	97576595
124	1	96357498	96357527	96404395	96404424
125	1	158912212	158912241	159136319	159136348
126	11	106098498	106098527	106275963	106275992
127	11	72859308	72859337	72936461	72936490
128	14	49028784	49028813	49076511	49076540
129	4	173130493	173130522	173207479	173207508
130	14	19829382	19829411	19975558	19975587
131	15	56434213	56434242	56691314	56691343
132	7	30619561	30619590	30804624	30804653
133	20	46377276	46377305	46631101	46631130
134	14	24423150	24423179	24517995	24518024
135	7	93826938	93826967	93960808	93960837
136	2	36912182	36912211	37085575	37085604
137	4	77717995	77718024	77982272	77982301

138	3	87995258	87995287	88133386	88133415
139	4	121310396	121310425	121354096	121354125
140	2	15677780	15677809	15733620	15733649
141	12	29708400	29708429	29843668	29843697
142	3	64075873	64075902	64228799	64228828
143	17	40703759	40703788	40868813	40868842
144	9	120795806	120795835	120831349	120831378
145	7	144258000	144258029	144391770	144391799
146	12	71686974	71687003	71771994	71772023
147	11	82067026	82067055	82146345	82146374
148	7	144153641	144153670	144258000	144258029
149	2	21774363	21774392	21960936	21960965
150	4	38385029	38385058	38455283	38455312

Table 1A (part 3c)

No.	4 kb Sequence Location				
	Chr	Start1	End1	Start2	End2
101	13	28438006	28442005	28551338	28555337
102	8	132638400	132642399	132681713	132685712
103	20	33826466	33830465	34035298	34039297
104	4	55935188	55939187	55970801	55974800
105	7	142995812	142999811	143057498	143061497
106	18	75676632	75680631	75700547	75704546
107	5	12492756	12496755	12593007	12597006
108	7	113376997	113380996	113411337	113415336
109	3	98493914	98497913	98613231	98617230
110	6	71319493	71323492	71524387	71528386
111	4	71710802	71714801	71745254	71749253
112	13	62233494	62237493	62330218	62334217
113	12	90700060	90704059	90798318	90802317
114	4	67686137	67690136	67782749	67786748
115	6	39619489	39623488	39819234	39823233
116	6	125245294	125249293	125293232	125297231
117	4	126064918	126068917	126094396	126098395
118	10	12234463	12238462	12383563	12387562
119	7	88611124	88615123	88741627	88745626
120	2	52892384	52896383	52921982	52925981
121	1	74603997	74607996	74778980	74782979
122	Y	22721649	22725648	22866071	22870070
123	4	97463864	97467863	97576566	97580565
124	1	96357498	96361497	96400425	96404424
125	1	158908242	158912241	159132349	159136348
126	11	106098498	106102497	106275963	106279962
127	11	72859308	72863307	72932491	72936490
128	14	49024814	49028813	49076511	49080510
129	4	173126523	173130522	173207479	173211478
130	14	19825412	19829411	19971588	19975587
131	15	56430243	56434242	56691314	56695313

132	7	30615591	30619590	30804624	30808623
133	20	46373306	46377305	46627131	46631130
134	14	24423150	24427149	24517995	24521994
135	7	93822968	93826967	93960808	93964807
136	2	36912182	36916181	37085575	37089574
137	4	77717995	77721994	77982272	77986271
138	3	87991288	87995287	88129416	88133415
139	4	121310396	121314395	121350126	121354125
140	2	15677780	15681779	15733620	15737619
141	12	29704430	29708429	29839698	29843697
142	3	64071903	64075902	64228799	64232798
143	17	40699789	40703788	40868813	40872812
144	9	120795806	120799805	120831349	120835348
145	7	144254030	144258029	144391770	144395769
146	12	71683004	71687003	71771994	71775993
147	11	82067026	82071025	82142375	82146374
148	7	144153641	144157640	144254030	144258029
149	2	21770393	21774392	21960936	21964935
150	4	38385029	38389028	38451313	38455312

Table 1A (part 3d)

No.	probe	Primer ID
101	Hg38_13_28438004_28449201_28551336_28558541_RR	OBD160.401
102	Hg38_8_132637112_132642401_132681711_132690255_FR	OBD160.405
103	Hg38_20_33827938_33830467_34035296_34047038_FR	OBD160.409
104	Hg38_4_55932433_55939189_55969220_55974802_FF	OBD160.413
105	Hg38_7_142995810_142998826_143057496_143064818_RR	OBD160.417
106	Hg38_18_75676630_75682929_75700545_75706785_RR	OBD160.421
107	Hg38_5_12486934_12496757_12590668_12597008_FF	OBD160.425
108	Hg38_7_113374693_113380998_113411335_113420030_FR	OBD160.429
109	Hg38_3_98493912_98497028_98612320_98617232_RF	OBD160.433
110	Hg38_6_71312879_71323494_71524385_71527337_FR	OBD160.437
111	Hg38_4_71700748_71714803_71741385_71749255_FF	OBD160.441
112	Hg38_13_62231930_62237495_62330216_62339040_FR	OBD160.445
113	Hg38_12_90700058_90702509_90796185_90802319_RF	OBD160.449
114	Hg38_4_67686135_67693477_67782747_67789927_RR	OBD160.453
115	Hg38_6_39611834_39623490_39813403_39823235_FF	OBD160.457
116	Hg38_6_125238508_125249295_125290548_125297233_FF	OBD160.461
117	Hg38_4_126064916_126070028_126094394_126106891_RR	OBD160.465
118	Hg38_10_12235815_12238464_12383561_12388246_FR	OBD160.469
119	Hg38_7_88599386_88615125_88740721_88745628_FF	OBD160.473
120	Hg38_2_52892382_52905124_52921980_52933672_RR	OBD160.477
121	Hg38_1_74603597_74607998_74778978_74800362_FR	OBD160.481
122	Hg38_Y_22721647_22725457_22859118_22870072_RF	OBD160.485
123	Hg38_4_97463862_97470977_97576564_97590463_RR	OBD160.489
124	Hg38_1_96357496_96364474_96392998_96404426_RF	OBD160.493
125	Hg38_1_158905246_158912243_159126541_159136350_FF	OBD160.497
126	Hg38_11_106098496_106106725_106275961_106290738_RR	OBD160.501

127	Hg38_11_72859306_72866489_72925691_72936492_RF	OBD160.505
128	Hg38_14_49020009_49028815_49076509_49078072_FR	OBD160.509
129	Hg38_4_173125717_173130524_173207477_173215489_FR	OBD160.513
130	Hg38_14_19825779_19829413_19968132_19975589_FF	OBD160.517
131	Hg38_15_56425187_56434244_56691312_56696438_FR	OBD160.521
132	Hg38_7_30612223_30619592_30804622_30809524_FR	OBD160.525
133	Hg38_20_46372997_46377307_46622048_46631132_FF	OBD160.529
134	Hg38_14_24423148_24425179_24517993_24525921_RR	OBD160.533
135	Hg38_7_93821969_93826969_93960806_93964392_FR	OBD160.537
136	Hg38_2_36912180_36914993_37085573_37089692_RR	OBD160.541
137	Hg38_4_77717993_77727364_77982270_77985832_RR	OBD160.545
138	Hg38_3_87991842_87995289_88126188_88133417_FF	OBD160.549
139	Hg38_4_121310394_121315169_121339971_121354127_RF	OBD160.553
140	Hg38_2_15677778_15684445_15733618_15739157_RR	OBD160.557
141	Hg38_12_29701302_29708431_29828391_29843699_FF	OBD160.561
142	Hg38_3_64067438_64075904_64228797_64236262_FR	OBD160.565
143	Hg38_17_40700822_40703790_40868811_40875117_FR	OBD160.569
144	Hg38_9_120795804_120798748_120831347_120833895_RR	OBD160.573
145	Hg38_7_144246203_144258031_144391768_144394587_FR	OBD160.577
146	Hg38_12_71685734_71687005_71771992_71780701_FR	OBD160.581
147	Hg38_11_82067024_82073102_82131728_82146376_RF	OBD160.585
148	Hg38_7_144153639_144162181_144246203_144258031_RF	OBD160.589
149	Hg38_2_21769905_21774394_21960934_21972734_FR	OBD160.593
150	Hg38_4_38385027_38395353_38450896_38455314_RF	OBD160.597

Table 1A (part 3e)

No.	Sequence	Primer ID	Sequence
101	GTGGACTTTCCTGTAACATCCTTTTA	OBD160.403	GGCTGGGTTCTAAAGATGAAGACTT
102	GTGGGCACTTGGCTCTGAGATGC	OBD160.407	GCCCTCAACGGTGGAGTAGGATA
103	GGTGGGAGAGACACTGAGGCTGT	OBD160.411	CACCACCTACCTGCCAAGTTGCT
104	GATGTCCCACTACCTTGCTGAGG	OBD160.415	GCAGGGAGACTTGGACCTATTGG
105	CCAGCAGTGATGAGGGCTCGCCTGTCT	OBD160.419	CACAGCAGCCTCTTTCATCACAGCCCAG
106	GGAATGATAGAGATAGGGAGAAATGGAA	OBD160.423	GAGAAGCAGACGGAAACTGTGACTGACA
107	CTCAAGCAACTCAGCAGCATAAAACACA	OBD160.427	CTTCCCCACTCATTTCTGTGATTCTAT
108	TTTATTTGTCAAGTGCCAAGGAATGC	OBD160.431	TAGGAAACACCAGTGAGTCCAAGGCT
109	CACAGTCCCCTCTTACTACAGCGTGAAA	OBD160.435	ACACTATTTCAATTGTAGAGGTTACCACG
110	CTTGGAATGTCAGACCCTTGCCCAT	OBD160.439	ATTGAGCCGTGTGTTTGGTGCTTGC
111	GGCTGGATGGCAGTAGAATGCTGTTC	OBD160.443	CTCCATTCATCGCACTCTACTTTAGC
112	CCTGCCTCAACCTCCCAAGTAGC	OBD160.447	CTGAGGTAACGGAGTAAAGGGTA
113	CTGTTGGTAGTTCCTAACCTCATA	OBD160.451	CAATAAGAAGTAAACAAAGCATAAC
114	GCCCCAAGGGAATAAACTAAGACTA	OBD160.455	CTTCTTCTCTTTCATCACACAGTC
115	CTTCTTGGTTGTCTATCCTTTCAGAT	OBD160.459	CAAGTTGGCACCGAGTGGTTTCCTAA
116	ACCAAAAGTTCTCACTGGAGGCACCA	OBD160.463	CTCGTCCACAATGTCCAGATTACCC
117	CCATCCCCAGGACCCCACTGTGC	OBD160.467	CAGACAAAGGTGACTTCAGAGCAAGAAC
118	GTGACTCCCATCTTTCCATAGAACCAG	OBD160.471	CACCTTTGTGTCGCTCCTGAGGCTA
119	CGGGATTCATAAAGGAGAAAGCAAGA	OBD160.475	GTGCCAACCCACAGAGCAACTTATG
120	GGAAAAGGAAGGACGCAAATGGTGTCAC	OBD160.479	GTCTTGTGCCAGTTTCAAAGGGAGAGC
121	TAAGATTATTGAGCACTCTCTGTG	OBD160.483	GGGTGTAGGGCACAGATTCTTAC
122	TCCAGCAAAAGTATCCTTCAACAGG	OBD160.487	CTGCTGTATGCTCAGGCTTTGCTCC

123	TACAGCAATAGAAAGGAGTGCGGTAT	OBD160.491	GTCAAAGCCAGTGTCAGAAAGGGTAT
124	GCCTCATTAGGAAAGTGTAGAAGAGA	OBD160.495	GACTATCCTGGAGACTCTGGAAAACCT
125	GTAGAAAGACTAAAAGACAAACCTCTC	OBD160.499	CACGCACAGCCTCCAAGAACTA
126	CTTGACCTTTATTTACTATGCTTGGC	OBD160.503	CAAGGGACCTCTCAAAGCAGAAGCAA
127	ATTTTGGTGACAGACTGGGCTTCT	OBD160.507	CATCTCTCTCTTCTTACAGTCCCC
128	AAGGATTGGTGAACCTCAAAGACAGGTTA	OBD160.511	GGTATTTTGAGAGAGAGTCCACATTGAC
129	CGGAACCTTAGCATCTGGAAGAAGAA	OBD160.515	CAACATCAGAGAGGTGAGAAACAACC
130	CAGTCTTTTGGTAGAGCAATCAGGAT	OBD160.519	GAACATCTCCTTGACAACCTCCCT
131	GTTGGCGACGCTCTTCAATAAGTTTT	OBD160.523	GGAGCAACACAAGCCAAACACAGCAG
132	CCATCCAGAGAAGTAACCACTATCCC	OBD160.527	GACTGCTTGGTCATTTTGTGCCTCAG
133	CCTGTGAGGTCCAGTTTGGTAGCCCC	OBD160.531	CCTTCAGTTTCTTGTGTGCTGTAGACA
134	ACTCACTCTTCCCTCAGCAGC	OBD160.535	ACTGCCTCAGGAGTTGGCTGCCT
135	ATGAAACAGAAATGAGAAAAACA	OBD160.539	TCTATGTAGAGAAGCAAAGGGCCAA
136	GTGATGTGTGTCTTAGAGGAGTAACC	OBD160.543	AGCCCTCTTGTCCCCTATCCAGTTG
137	TTGGGTGGGTTTTCTGCTCTGGAGGTAT	OBD160.547	ATCAGGAGAAGAGCAAGAGTTGAAATCA
138	CTCACCTCAGTCTCCCAAGTAGC	OBD160.551	GTGTGCCACTCCAATCACTGTAT
139	TTATTGAAGAGACTGTCTTTCCCTA	OBD160.555	GTGAATAGTGCCGCAATAAACATACG
140	ATTATGCCTCTACATTCCCTCCCCG	OBD160.559	CCTCCCTGTCTTCCCTGTTGATAAAA
141	GAATGAGTGAATACAGCCAGGGAATG	OBD160.563	TGGCTATGGAGATGTCACCTGAAGGG
142	ACCCATCCCCAAGCATTATCCTTTGTG	OBD160.567	GTTGCTGTGTTTTGCTGTCTTGTGTCC
143	GGCGAATAGGAGAGGTGATGACG	OBD160.571	GCCCTGTTCCCACGAGGTAGGA
144	GTCATCTAACTACCTCCCCAGGCAAGT	OBD160.575	GGTTTAGAATGGATGATTTGCGTAATGG
145	CAGCGGCAACACAGGCAGATGT	OBD160.579	CCCCAGAGCCCCATCCTGTCAAT
146	CCTCTGAATGGTTATGAATGGTTGTG	OBD160.583	CCTGCCTGGTCAACCCACAGAATCAT
147	ATTCAGTGTAATCCCTATCAAAAT	OBD160.587	TCTGCCATAAAGTCATTCTCAAAA
148	CCATTGAACAGTAGAGACAGGGTCCC	OBD160.591	GGCACTCTTCTGCTCTATTTTGTGG
149	GTTATTACTGGTTGATGACTCCACAT	OBD160.595	GCAATCTCAGAAATCAACACTAAAGAAC
150	GATGTCTGAGAATGTGGAGTGTGCTA	OBD160.599	TTTACCGCCTTTTCTCCACCTCTC

Table 1A (part 3f)

No.	probe	Marker
101	Hg38_13_28438004_28449201_28551336_28558541_RR	OBD160.401.403
102	Hg38_8_132637112_132642401_132681711_132690255_FR	OBD160.405.407
103	Hg38_20_33827938_33830467_34035296_34047038_FR	OBD160.409.411
104	Hg38_4_55932433_55939189_55969220_55974802_FF	OBD160.413.415
105	Hg38_7_142995810_142998826_143057496_143064818_RR	OBD160.417.419
106	Hg38_18_75676630_75682929_75700545_75706785_RR	OBD160.421.423
107	Hg38_5_12486934_12496757_12590668_12597008_FF	OBD160.425.427
108	Hg38_7_113374693_113380998_113411335_113420030_FR	OBD160.429.431
109	Hg38_3_98493912_98497028_98612320_98617232_RF	OBD160.433.435
110	Hg38_6_71312879_71323494_71524385_71527337_FR	OBD160.437.439
111	Hg38_4_71700748_71714803_71741385_71749255_FF	OBD160.441.443
112	Hg38_13_62231930_62237495_62330216_62339040_FR	OBD160.445.447
113	Hg38_12_90700058_90702509_90796185_90802319_RF	OBD160.449.451
114	Hg38_4_67686135_67693477_67782747_67789927_RR	OBD160.453.455
115	Hg38_6_39611834_39623490_39813403_39823235_FF	OBD160.457.459
116	Hg38_6_125238508_125249295_125290548_125297233_FF	OBD160.461.463
117	Hg38_4_126064916_126070028_126094394_126106891_RR	OBD160.465.467
118	Hg38_10_12235815_12238464_12383561_12388246_FR	OBD160.469.471

119	Hg38_7_88599386_88615125_88740721_88745628_FF	OBD160.473.475
120	Hg38_2_52892382_52905124_52921980_52933672_RR	OBD160.477.479
121	Hg38_1_74603597_74607998_74778978_74800362_FR	OBD160.481.483
122	Hg38_Y_22721647_22725457_22859118_22870072_RF	OBD160.485.487
123	Hg38_4_97463862_97470977_97576564_97590463_RR	OBD160.489.491
124	Hg38_1_96357496_96364474_96392998_96404426_RF	OBD160.493.495
125	Hg38_1_158905246_158912243_159126541_159136350_FF	OBD160.497.499
126	Hg38_11_106098496_106106725_106275961_106290738_RR	OBD160.501.503
127	Hg38_11_72859306_72866489_72925691_72936492_RF	OBD160.505.507
128	Hg38_14_49020009_49028815_49076509_49078072_FR	OBD160.509.511
129	Hg38_4_173125717_173130524_173207477_173215489_FR	OBD160.513.515
130	Hg38_14_19825779_19829413_19968132_19975589_FF	OBD160.517.519
131	Hg38_15_56425187_56434244_56691312_56696438_FR	OBD160.521.523
132	Hg38_7_30612223_30619592_30804622_30809524_FR	OBD160.525.527
133	Hg38_20_46372997_46377307_46622048_46631132_FF	OBD160.529.531
134	Hg38_14_24423148_24425179_24517993_24525921_RR	OBD160.533.535
135	Hg38_7_93821969_93826969_93960806_93964392_FR	OBD160.537.539
136	Hg38_2_36912180_36914993_37085573_37089692_RR	OBD160.541.543
137	Hg38_4_77717993_77727364_77982270_77985832_RR	OBD160.545.547
138	Hg38_3_87991842_87995289_88126188_88133417_FF	OBD160.549.551
139	Hg38_4_121310394_121315169_121339971_121354127_RF	OBD160.553.555
140	Hg38_2_15677778_15684445_15733618_15739157_RR	OBD160.557.559
141	Hg38_12_29701302_29708431_29828391_29843699_FF	OBD160.561.563
142	Hg38_3_64067438_64075904_64228797_64236262_FR	OBD160.565.567
143	Hg38_17_40700822_40703790_40868811_40875117_FR	OBD160.569.571
144	Hg38_9_120795804_120798748_120831347_120833895_RR	OBD160.573.575
145	Hg38_7_144246203_144258031_144391768_144394587_FR	OBD160.577.579
146	Hg38_12_71685734_71687005_71771992_71780701_FR	OBD160.581.583
147	Hg38_11_82067024_82073102_82131728_82146376_RF	OBD160.585.587
148	Hg38_7_144153639_144162181_144246203_144258031_RF	OBD160.589.591
149	Hg38_2_21769905_21774394_21960934_21972734_FR	OBD160.593.595
150	Hg38_4_38385027_38395353_38450896_38455314_RF	OBD160.597.599

Table 1A (part 3g)

No.	probe	RP/Rsum	Rprank	FC:(class1/class2)
151	Hg38_17_36023309_36028028_36272442_36275457_FF	181419.9448	102901	1.51
152	Hg38_12_78435225_78440781_78459801_78476525_RF	5179.767063	196	1.51
153	Hg38_X_40477200_40482652_40589768_40592788_RF	3846.655135	146	1.51
154	Hg38_Y_3584113_3585230_3719457_3726617_FF	5222.745707	200	1.508
155	Hg38_7_103380032_103385339_103627677_103636524_RR	3342.65815	120	1.508
156	Hg38_1_152724530_152728363_152991207_152992512_FR	3244.654375	112	1.508
157	Hg38_10_103825506_103831138_103895197_103900793_FR	4497.05848	167	1.504
158	Hg38_Y_2866835_2871971_2958559_2972902_RF	3649.087311	136	1.502
159	Hg38_4_142475549_142484776_142514277_142521702_RR	4031.321645	150	1.501
160	Hg38_4_124396134_124401011_124507033_124522866_FR	3626.70075	134	1.501
161	Hg38_12_31992399_31994148_32218403_32222271_RF	4824.003128	175	1.499
162	Hg38_X_2551528_2553681_2721164_2724566_FR	4920.501174	180	1.498
163	Hg38_4_12250997_12254184_12322283_12330696_FF	4300.114047	161	1.498
164	Hg38_2_203737190_203742853_203950615_203958558_RR	4856.527848	177	1.497
165	Hg38_4_171028618_171040398_171297049_171298480_FR	4401.334551	164	1.497

166	Hg38_18_74451499_74454993_74653959_74660559_RR	4203.559159	157	1.497
167	Hg38_7_10927538_10936617_11059573_11063361_FF	4045.05349	151	1.497
168	Hg38_2_199918581_199920573_200063524_200066499_FF	3765.522187	141	1.497
169	Hg38_20_40684507_40687277_40697330_40701314_RF	3823.485364	145	1.495
170	Hg38_1_69381686_69386805_69431002_69439637_FF	5021.561295	188	1.494
171	Hg38_X_80882210_80890038_81125945_81129443_RF	3947.387733	148	1.494
172	Hg38_X_81004388_81008183_81249768_81260862_RR	3665.225818	137	1.494
173	Hg38_2_43218506_43222954_43338993_43342008_RR	4532.348136	168	1.493
174	Hg38_12_78001793_78008398_78104543_78106544_FF	4479.616333	166	1.493
175	Hg38_8_138470025_138485193_138738624_138748013_FR	3670.508224	138	1.493
176	Hg38_12_85366513_85378853_85614124_85622896_FF	4696.514771	172	1.492
177	Hg38_7_112896017_112908366_113061946_113067988_RR	3616.071678	133	1.492
178	Hg38_2_200576039_200582576_200625910_200631991_FF	4070.103419	153	1.491
179	Hg38_15_30512275_30516087_30637530_30644724_RF	5643.964375	225	1.49
180	Hg38_7_25392695_25398339_25542599_25548176_FR	4947.457038	183	1.49
181	Hg38_6_56692561_56704365_56788190_56791583_FR	4933.771069	182	1.49
182	Hg38_9_63901466_63907814_64080352_64086066_RF	4265.343025	158	1.49
183	Hg38_13_21325011_21327390_21575413_21582625_RF	46100.56928	5384	1.488
184	Hg38_4_164713694_164729294_164967949_164972230_RF	5809.93205	233	1.488
185	Hg38_1_63238122_63243108_63375818_63382270_FR	4098.295424	154	1.488
186	Hg38_11_106045994_106053482_106098496_106106725_FR	5214.04095	199	1.486
187	Hg38_2_191681747_191683098_191825543_191836084_RF	5765.279979	232	1.485
188	Hg38_14_70326561_70339130_70362648_70369731_RR	5337.378645	208	1.485
189	Hg38_5_3428156_3436940_3502869_3506924_RF	97200.98548	27570	1.484
190	Hg38_9_93834125_93843642_94033256_94043963_RR	5264.953933	204	1.484
191	Hg38_4_166975421_166983791_167173650_167191011_FF	4931.651686	181	1.484
192	Hg38_12_114559051_114568056_114591211_114602162_FF	5641.122845	223	1.483
193	Hg38_13_91314238_91325788_91448901_91460521_RR	5289.858609	205	1.483
194	Hg38_X_107971578_107974327_108029689_108034634_RR	4958.888197	185	1.483
195	Hg38_8_24835942_24839566_24905842_24907666_FR	4823.525297	174	1.483
196	Hg38_8_115234769_115239118_115394021_115408137_FR	4268.313107	159	1.483
197	Hg38_12_126756498_126769103_126960572_126965968_RF	4607.573373	170	1.482
198	Hg38_11_93302415_93309584_93391985_93400931_RF	5161.045697	194	1.481
199	Hg38_3_81259865_81272497_81351596_81353868_RR	4609.489918	171	1.481
200	Hg38_3_38500849_38506870_38670653_38683212_FR	4308.252287	162	1.479

Table 1A (part 4a)

				Probe sequence
No.	pfp	P.value	Type	60 mer
151	0.201 2369 82	0.022 2958 9	SBMA	TGAGCTAATAAACTATTTCTGGTTTTGCTCGAGTTCACATTCTATACCATGTTTCTTTT
152	0	0	SBMA	TGTCTTCTGGATTTTATTATTTTCTGTCGAAATGATCATATAATTTTACTCCTTCAGT
153	0	0	SBMA	TTTTTTTTTTTTCAGATTTTCTGTGGTCGACAAGGAGGTAAGATTAGATACATACATC
154	0	0	SBMA	TACATTCGGTCACTGAAAACATTAGTTTTCGATGAGGGTGTCTTTTCTCCAGTTTATGTT
155	0	0	SBMA	TTTGAGTGTCTTTTCTTCTGTGGAATATCGATTGCTCAGTGTGGTTGTTAATAAACT
156	0	0	SBMA	GCATGTCAGGTAATGAAAACAGACATTATCGAAAGACATTTATACACGACTTTAACCGTT
157	0	0	SBMA	TGAATAATTTTAAATTTACATAAATGGATCGATTCTTTTAAACATATAGCACCAGGCAG
158	0	0	SBMA	AACTTCAGTTTGTCTTACTGTAAATGTCGACTTACTGTTGCTGAAGAGAGAGATAAGA
159	0	0	SBMA	GAATTGGGTTTCTTCTTTCTTTGAATGTCGACTTTAATTTATCCTTTCTTTGAAAGCCA
160	0	0	SBMA	TTCACTCATTGATTTTCAGATATTAAATCGAATTCTGTACATGTAAGTGGCAGATAAG

161	0	0	SBMA	CAGAAGATTGGAGTTATCAAATGAATTATCGAAGAGAAGCTTCAGTGCAGATGGATTGTA
162	0	0	SBMA	GCCAAGGCCAAACTCCAATTATTAGTTTTCGAAAGTTATATGTTTAGGTTTTTTGTTT
163	0	0	SBMA	AAGGGACTAGAAGAAGAAATCATTAAAGTTCGACAATTTTTAAATAACTGCCTGAAGATAA
164	0	0	SBMA	CTTAAAAATCAACCAAAGTACAGTATTTTCGAACTGCAGACTTAGAGCTGTCAAGCGGTT
165	0	0	SBMA	TAGCTTTGCATGAACATAAATGTCAAATTTGAAAAATTATACTGCGAGAAAATTCATACC
166	0	0	SBMA	GGCAAATCTCGTATAGATTTGTATTTTCATCGATATAATTTAATGAGTGTCAATTACAG
167	0	0	SBMA	TTAGAGGCCAAATATAACACAGATGAGATCGACATATTGCAAAATTTATACTGTGGTCAG
168	0	0	SBMA	AACTATAAAAAGGATTTAGATGAGCCCTTCGAGATTTAAAACACACACACACATATTT
169	0	0	SBMA	TCTAAACTTGGAGTCAGAAGAACTGAGTTCGAGCTAGAATTCGAAGCTTCTCTCTATTG
170	0	0	SBMA	TTGCTATTCTTTCTTCATTCACCTCTTCGATTTGTAACTTACAAAACCTAAACATTC
171	0	0	SBMA	CCATTTGTATTTCTGTCTGTGAATTTTCGAAATGTATGAATCAGAATAATTCAGAGGA
172	0	0	SBMA	TTCACTCAAAGCCTGAATGATTTTAGGGTCGAAAGAAACCAGAAAAGTAACATGCAAGTA
173	0	0	SBMA	CTGAAATAGAAAGGAAAGATATTAAAGGACTCGAGTGAAAAAAGGAAGGAAGCTATAACTTA
174	0	0	SBMA	TTGCTTGTGTCTGTGATTTGTTTTAATCGACAGAACATCTTCTGGTGTCTGTTCACC
175	0	0	SBMA	ATTCAGCAGAGTTTACAGACTGTAATTTGAGGCTCAGACCTCATGTCTCTCTTGTTC
176	0	0	SBMA	AGTAAGGCAGAAAGTATATTGTATGACTTCGAACTTTTTTTTTCTACTGCATACATATA
177	0	0	SBMA	TATGTAAGCTTTGCTGGAGAAGTTTTAGTCGAGTTTGAGGCACTAAGGTAATAAAACAT
178	0	0	SBMA	GCAGATTATAGCTGGAATTCACAATTTTCGAAAATCTGAGTTAAAAAAGAGCACAGA
179	0	0	SBMA	ATTTTCAGGTAGGATCATAAAGGACTTATCGAAAAGAAAAAAGAAATTATTAACCTAA
180	0	0	SBMA	CTTCAAGTAGTCACAGAGAATGACAGAATCGAAGTACTGTTTTGTTTATTGCTGTATCCC
181	0	0	SBMA	AGTCTTCATAGAGATCATTACATGTTTTCGAAAGTATTAAGTCTTCTTTTTTTTTTT
182	0	0	SBMA	CCATCTGATTACAGTTACATGTATCATATCGAATGACCTCCCTTCTATTCTCTGTTAATAA
183	0.000 0854 3833 5809 8068	0.000 0004 9528 5101 1781 33	SBMA	ACTTAACCTCCTCTAAAACAACCTTTTTCGACTTTAGTTGGTGACATCATCATCCCCCT
184	0	0	SBMA	CAGCTATTGACTGTGTATCTTTAGAAAATCGATCTCTAAATAAACTGCAGAGGAGGAGGT
185	0	0	SBMA	CCTTAAAAGATGTGAAACAGAGAACAGCTCGAATTATTTTGTAAATTTATATTTTCTAG
186	0	0	SBMA	AGTTTTTCCACCTATGACAAATAATCTATCGATTAGTAAAGAAAAAATTTGAATGTTT
187	0	0	SBMA	CTCCTCTTCATCTTCCACAATAGTCAAGTCGACAGAATTTTGTATTCTTTGTAATAG
188	0	0	SBMA	GTAGTTGATTTATTTGCTACAGTTGTAATCGAAAGATTAGTTACTTCATGAATCTTTGTT
189	0.008 3194 29	0.000 2469 61	SBMA	AATATTAGAATGGGCTACTCGCCTTTCCTCGAGACGTGGGCAATGTATTTAAAAGTCAT
190	0	0	SBMA	AAGTTCAACACAGTTGCAGAATATAGGATCGAAATGTTTCTCAGAATCATGTTTATAT
191	0	0	SBMA	CCCCTATGTGGAATTATGTAGTTATCTCTCGAAACAGTATGTTCTGGCATAAAAACAGAC
192	0	0	SBMA	CTGTACTTAGGGTATCATAAGGCTGAAATCGATTTCTGTCTTACCCACACATTCAGGCT
193	0	0	SBMA	GAATATTTTATTTGCCATTTCAACAAAATCGAAATGCGGCTGCTTTTCAAGGTAAGTGGA
194	0	0	SBMA	CCACCACCACAGTGGTCTCCAGTATTCGATGGAATAGTGAACCTTCACCAATTGC
195	0	0	SBMA	CTTCAACTCAATATAAATAAGATCTCTATCGAGGTAAGTGGTCTTTACTTGCCTGAATC
196	0	0	SBMA	GTGTCCTTTACATCCTAAGTACAGAGATTCGATGGAGAAAGTGGTGTGCACACCAGTACA
197	0	0	SBMA	AGAAACAAGTAAGAGATTCTAAAAGTCTCGATTTTGAAGGTAATTTGCACTTTTCTACT
198	0	0	SBMA	ATTTCAACACTTTTATTCAACATAATACTCGACAGAATGAAGAACAAAACGATTTGATC
199	0	0	SBMA	TTAAAATGATTTAGCAGGGCACAAAATGTGATAAATAATACGACATTTGCATCACTACC
200	0	0	SBMA	ATTTGTTTTTCAGAATAGAAATGTACTGTCGACCTATCTTCAGACTCACTGTTTCTTCC

Table 1A (part 4b)

No.	Probe Location				
	Chr	Start1	End1	Start2	End2
151	17	36027997	36028026	36275426	36275455

152	12	78435227	78435256	78476494	78476523
153	X	40477202	40477231	40592757	40592786
154	Y	3585199	3585228	3726586	3726615
155	7	103380034	103380063	103627679	103627708
156	1	152728332	152728361	152991209	152991238
157	10	103831107	103831136	103895199	103895228
158	Y	2866837	2866866	2972871	2972900
159	4	142475551	142475580	142514279	142514308
160	4	124400980	124401009	124507035	124507064
161	12	31992401	31992430	32222240	32222269
162	X	2553650	2553679	2721166	2721195
163	4	12254153	12254182	12330665	12330694
164	2	203737192	203737221	203950617	203950646
165	4	171040367	171040396	171297051	171297080
166	18	74451501	74451530	74653961	74653990
167	7	10936586	10936615	11063330	11063359
168	2	199920542	199920571	200066468	200066497
169	20	40684509	40684538	40701283	40701312
170	1	69386774	69386803	69439606	69439635
171	X	80882212	80882241	81129412	81129441
172	X	81004390	81004419	81249770	81249799
173	2	43218508	43218537	43338995	43339024
174	12	78008367	78008396	78106513	78106542
175	8	138485162	138485191	138738626	138738655
176	12	85378822	85378851	85622865	85622894
177	7	112896019	112896048	113061948	113061977
178	2	200582545	200582574	200631960	200631989
179	15	30512277	30512306	30644693	30644722
180	7	25398308	25398337	25542601	25542630
181	6	56704334	56704363	56788192	56788221
182	9	63901468	63901497	64086035	64086064
183	13	21325013	21325042	21582594	21582623
184	4	164713696	164713725	164972199	164972228
185	1	63243077	63243106	63375820	63375849
186	11	106053451	106053480	106098498	106098527
187	2	191681749	191681778	191836053	191836082
188	14	70326563	70326592	70362650	70362679
189	5	3428158	3428187	3506893	3506922
190	9	93834127	93834156	94033258	94033287
191	4	166983760	166983789	167190980	167191009
192	12	114568025	114568054	114602131	114602160
193	13	91314240	91314269	91448903	91448932
194	X	107971580	107971609	108029691	108029720
195	8	24839535	24839564	24905844	24905873
196	8	115239087	115239116	115394023	115394052
197	12	126756500	126756529	126965937	126965966
198	11	93302417	93302446	93400900	93400929
199	3	81259867	81259896	81351598	81351627
200	3	38506839	38506868	38670655	38670684

Table 1A (part 4c)

	4 kb Sequence Location
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No.	Chr	Start1	End1	Start2	End2
151	17	36024027	36028026	36271456	36275455
152	12	78435227	78439226	78472524	78476523
153	X	40477202	40481201	40588787	40592786
154	Y	3581229	3585228	3722616	3726615
155	7	103380034	103384033	103627679	103631678
156	1	152724362	152728361	152991209	152995208
157	10	103827137	103831136	103895199	103899198
158	Y	2866837	2870836	2968901	2972900
159	4	142475551	142479550	142514279	142518278
160	4	124397010	124401009	124507035	124511034
161	12	31992401	31996400	32218270	32222269
162	X	2549680	2553679	2721166	2725165
163	4	12250183	12254182	12326695	12330694
164	2	203737192	203741191	203950617	203954616
165	4	171036397	171040396	171297051	171301050
166	18	74451501	74455500	74653961	74657960
167	7	10932616	10936615	11059360	11063359
168	2	199916572	199920571	200062498	200066497
169	20	40684509	40688508	40697313	40701312
170	1	69382804	69386803	69435636	69439635
171	X	80882212	80886211	81125442	81129441
172	X	81004390	81008389	81249770	81253769
173	2	43218508	43222507	43338995	43342994
174	12	78004397	78008396	78102543	78106542
175	8	138481192	138485191	138738626	138742625
176	12	85374852	85378851	85618895	85622894
177	7	112896019	112900018	113061948	113065947
178	2	200578575	200582574	200627990	200631989
179	15	30512277	30516276	30640723	30644722
180	7	25394338	25398337	25542601	25546600
181	6	56700364	56704363	56788192	56792191
182	9	63901468	63905467	64082065	64086064
183	13	21325013	21329012	21578624	21582623
184	4	164713696	164717695	164968229	164972228
185	1	63239107	63243106	63375820	63379819
186	11	106049481	106053480	106098498	106102497
187	2	191681749	191685748	191832083	191836082
188	14	70326563	70330562	70362650	70366649
189	5	3428158	3432157	3502923	3506922
190	9	93834127	93838126	94033258	94037257
191	4	166979790	166983789	167187010	167191009
192	12	114564055	114568054	114598161	114602160
193	13	91314240	91318239	91448903	91452902
194	X	107971580	107975579	108029691	108033690
195	8	24835565	24839564	24905844	24909843
196	8	115235117	115239116	115394023	115398022
197	12	126756500	126760499	126961967	126965966
198	11	93302417	93306416	93396930	93400929
199	3	81259867	81263866	81351598	81355597
200	3	38502869	38506868	38670655	38674654

Table 1A (part 4d)

No.	probe	Primer ID
151	Hg38_17_36023309_36028028_36272442_36275457_FF	OBD160.601
152	Hg38_12_78435225_78440781_78459801_78476525_RF	OBD160.605
153	Hg38_X_40477200_40482652_40589768_40592788_RF	OBD160.609
154	Hg38_Y_3584113_3585230_3719457_3726617_FF	OBD160.613
155	Hg38_7_103380032_103385339_103627677_103636524_RR	OBD160.617
156	Hg38_1_152724530_152728363_152991207_152992512_FR	OBD160.621
157	Hg38_10_103825506_103831138_103895197_103900793_FR	OBD160.625
158	Hg38_Y_2866835_2871971_2958559_2972902_RF	OBD160.629
159	Hg38_4_142475549_142484776_142514277_142521702_RR	OBD160.633
160	Hg38_4_124396134_124401011_124507033_124522866_FR	OBD160.637
161	Hg38_12_31992399_31994148_32218403_32222271_RF	OBD160.641
162	Hg38_X_2551528_2553681_2721164_2724566_FR	OBD160.645
163	Hg38_4_12250997_12254184_12322283_12330696_FF	OBD160.649
164	Hg38_2_203737190_203742853_203950615_203958558_RR	OBD160.653
165	Hg38_4_171028618_171040398_171297049_171298480_FR	OBD160.657
166	Hg38_18_74451499_74454993_74653959_74660559_RR	OBD160.661
167	Hg38_7_10927538_10936617_11059573_11063361_FF	OBD160.665
168	Hg38_2_199918581_199920573_200063524_200066499_FF	OBD160.669
169	Hg38_20_40684507_40687277_40697330_40701314_RF	OBD160.673
170	Hg38_1_69381686_69386805_69431002_69439637_FF	OBD160.677
171	Hg38_X_80882210_80890038_81125945_81129443_RF	OBD160.681
172	Hg38_X_81004388_81008183_81249768_81260862_RR	OBD160.685
173	Hg38_2_43218506_43222954_43338993_43342008_RR	OBD160.689
174	Hg38_12_78001793_78008398_78104543_78106544_FF	OBD160.693
175	Hg38_8_138470025_138485193_138738624_138748013_FR	OBD160.697
176	Hg38_12_85366513_85378853_85614124_85622896_FF	OBD160.701
177	Hg38_7_112896017_112908366_113061946_113067988_RR	OBD160.705
178	Hg38_2_200576039_200582576_200625910_200631991_FF	OBD160.709
179	Hg38_15_30512275_30516087_30637530_30644724_RF	OBD160.713
180	Hg38_7_25392695_25398339_25542599_25548176_FR	OBD160.717
181	Hg38_6_56692561_56704365_56788190_56791583_FR	OBD160.721
182	Hg38_9_63901466_63907814_64080352_64086066_RF	OBD160.725
183	Hg38_13_21325011_21327390_21575413_21582625_RF	OBD160.729
184	Hg38_4_164713694_164729294_164967949_164972230_RF	OBD160.733
185	Hg38_1_63238122_63243108_63375818_63382270_FR	OBD160.737
186	Hg38_11_106045994_106053482_106098496_106106725_FR	OBD160.741
187	Hg38_2_191681747_191683098_191825543_191836084_RF	OBD160.745
188	Hg38_14_70326561_70339130_70362648_70369731_RR	OBD160.749
189	Hg38_5_3428156_3436940_3502869_3506924_RF	OBD160.753
190	Hg38_9_93834125_93843642_94033256_94043963_RR	OBD160.757
191	Hg38_4_166975421_166983791_167173650_167191011_FF	OBD160.761
192	Hg38_12_114559051_114568056_114591211_114602162_FF	OBD160.765
193	Hg38_13_91314238_91325788_91448901_91460521_RR	OBD160.769
194	Hg38_X_107971578_107974327_108029689_108034634_RR	OBD160.773
195	Hg38_8_24835942_24839566_24905842_24907666_FR	OBD160.777
196	Hg38_8_115234769_115239118_115394021_115408137_FR	OBD160.781
197	Hg38_12_126756498_126769103_126960572_126965968_RF	OBD160.785
198	Hg38_11_93302415_93309584_93391985_93400931_RF	OBD160.789
199	Hg38_3_81259865_81272497_81351596_81353868_RR	OBD160.793
200	Hg38_3_38500849_38506870_38670653_38683212_FR	OBD160.797

Table 1A (part 4e)

No.	Sequence	Primer ID	Sequence
151	TACGCCTGCCATCCACTCTGAAT	OBD160.603	GGATTACAGATGTGAGCCACCAC
152	ATGTGTTGCTCTACTGGTTTGTAAAGTTA	OBD160.607	AGACACATCCAATAAAGAAACTGCGGGC
153	GGTCTATGTGATGCTGAAGTTTTGGG	OBD160.611	GCCCTGGTTTTCTGTAGGCAATCAGC
154	ATGAAGGGAAAACATTGGAGTGGAAT	OBD160.615	CACACACCTACAGTGAACCTATTTTC
155	ATAGTGGTCAAAGTGAAAAGTCTGAGC	OBD160.619	GCACCTTGAGCAGCACCATAGGAGTTT
156	GCTCACAGTCTCCTGGCTGAACC	OBD160.623	GAGGGTCTGCGGTATCTGCCTA
157	AAGCATCCTTCCAGTCTGTGTTTGC	OBD160.627	TAATCATTTAGAGGCGGCTCAAAGC
158	CCAGAGGTTGATGGTGGTTTCTTGTC	OBD160.631	GGTTTATTTACTGGAGGGTCAGAGGA
159	CCTCCTCTGGTTGATTTTGCTGTTA	OBD160.635	CACCTTTGGTTGGAAGTTTAGGGAGG
160	CTACAACCAAGTGAAGATGGCTCCAA	OBD160.639	CTGCCATCCCCACTAATGTCACCTCT
161	GAATGCAGAAGATTGGAGTT	OBD160.643	TGCAGATGGATTTGAGATGC
162	GCACACTCTGAGGATTTAGACTTC	OBD160.647	CACAAATAGCCATCAAATGTCAACAAG
163	GAACAACCTACCTGTGCCTCAAAGAC	OBD160.651	CAACTCTGAAGCCTACTGTGTTTATC
164	CAACAGTTCTTCAGCACCCAAGT	OBD160.655	GAAGGCTGACTTAGGTTTCCACATA
165	GGGTGCTACTGTTCTTCCAGATAGC	OBD160.659	TCTTCTATTCTGGAACAACCGATTG
166	TCACAACCTCTGTTTGAATCGCCCT	OBD160.663	CTTCCTCAAATGGTCTTCAATAACA
167	ACCCATAGATTCCAATACGCTCTTTG	OBD160.667	GTAGTTCCAAGTTCAGGAGATACACC
168	ACTGTAGTTTCCAGGACCTCAGG	OBD160.671	AGCATTGACTTTTGTCCCTCTGGGC
169	CCTACCCCTCTCTTAGCCTCACT	OBD160.675	CCTGGAGGTAGTGATGGCTGAGG
170	CGTTTTCTCAATGCCCTTTATTCTA	OBD160.679	GTGAGAAGGGTAAAATCTTAGGCAGC
171	CTGGCACTGGAGAGCAGCACCAA	OBD160.683	GCGAACACTGCCTTGAATCTGCC
172	TTGTAAGGCATTGACCTGTTCTACCATA	OBD160.687	AAAAGCAAGTCCATAACTCCAGAACA
173	CCTTGGTGCCGCTGGCTGTCTGC	OBD160.691	CCGTTTTCCCTTCATTGTTGTGTGC
174	TTCCCACAGCAAGGCATAGGTTTCTA	OBD160.695	GTGAAGAGATACTCATTTGTGGATTG
175	TCAACGAGGTTTACCAAAGCCACCAAT	OBD160.699	CAGAGTTGCTGAATGAGAGGAGAGGACG
176	GCTGGCAGGAAAAGTGTAGACTGTTT	OBD160.703	GAGGCAAAGTAATAAGAGAGGAAAAC
177	CGCACACTCACCTGACTTTGTATC	OBD160.707	CCATTTGTAACTGCTGACTTCATTG
178	TTGCTCAGCCCCAGGAAATAACTTGG	OBD160.711	GTGGATAGGCAGAATCAATAATACTG
179	CAGATAATGAAACAACCACCATCGGT	OBD160.715	GACTTCCTATTCTGCTGCCTATGGT
180	TCATAACACCTCCCTCTGTGGAACA	OBD160.719	CCTTCGGGAGATGTATTTAGGAGTTGCG
181	ACCAAGGTATCTCCTGAAAGAACC	OBD160.723	TAATACTTAGGCTGGGAGCGATGGCT
182	GGAATGAAGCCAGTTGAGTTGC	OBD160.727	GCCCAAACCCGTGTGGTCCAACA
183	TTTCCTTTGACTTTTCCCCTAAT	OBD160.731	ATTGGCAGGAGGAATAAGGAAGAG
184	ATTGAGAGGACACCAGGTTTGAATCC	OBD160.735	GGTGATTAGGTTATGAGGGCTCCGTC
185	ATTTGAGTTACTTGTAGGGCTCCT	OBD160.739	CAATGGTTGAACAATGACTAACTGCCA
186	TATGCCTCTGGGTAATGGGCTAACAG	OBD160.743	CTTGACCTTTATTTACTATGCTTGGC
187	AGGATGGCACGGTGGCTCTAAGC	OBD160.747	ATCAAGCCCTCTCTATCCACCATA
188	CAGCCTTTTCCTTGTCTCTCAA	OBD160.751	GCCCAGGAGTTCAAGACCAGCCT
189	CAGAGACGGTTCCACGGTTGTC	OBD160.755	ACACCTGGGACTGGCTCCAACCTC
190	CACTTCGGTTCAACTTTTACTGGAGG	OBD160.759	ATGTTGCCTCCACAGAAACCAGAAAA
191	TAATGTCTCTGGGCTCATCCAT	OBD160.763	CTGCTCTATTGGTCTAAGTGCTG
192	GTTAGAAATCTGGTATGAAATGACTGG	OBD160.767	TTTATTAGGAATGCTGGAGAACTCAG
193	GCCTAACTCCTCAAATAATGCTAATGA	OBD160.771	AATGTTGGCAGACCTGGAAGAACCCTAT
194	GCTCAACTCTGCCATCTTACTGTGAA	OBD160.775	CTCACCTTCTCTACCTTTTGACCC
195	GGCTCAAAGAGAATGTGTAAGAGAGAAA	OBD160.779	GTCCCTGAACTTGATTGCCTGTGGTCTA
196	CTGTTTACTCCCTTGGCATCTGCTGC	OBD160.783	GGCTATTTGCTCTTGCTACTTCTTTC
197	GCTGCCTTCTGTTTGTATACCTGC	OBD160.787	AATACTACCAAATGACAGCCCAGCAT
198	GACTTCCAGTTTCAAATGGTGGC	OBD160.791	ATTGTGTTGAGGTATGTTCTTCCAT

199	GACATCTCTATCTTTACAGACTGCCCCCT	OBD160.795	GCCTCCCAAAGCACTGAGATTATGACAT
200	TTTCTTGGTATCTTTATAGGAAT	OBD160.799	AATAACAGCAGTGAAGAATACCTT

Table 1A (part 4f)

No.	probe	Marker
151	Hg38_17_36023309_36028028_36272442_36275457_FF	OBD160.601.603
152	Hg38_12_78435225_78440781_78459801_78476525_RF	OBD160.605.607
153	Hg38_X_40477200_40482652_40589768_40592788_RF	OBD160.609.611
154	Hg38_Y_3584113_3585230_3719457_3726617_FF	OBD160.613.615
155	Hg38_7_103380032_103385339_103627677_103636524_RR	OBD160.617.619
156	Hg38_1_152724530_152728363_152991207_152992512_FR	OBD160.621.623
157	Hg38_10_103825506_103831138_103895197_103900793_FR	OBD160.625.627
158	Hg38_Y_2866835_2871971_2958559_2972902_RF	OBD160.629.631
159	Hg38_4_142475549_142484776_142514277_142521702_RR	OBD160.633.635
160	Hg38_4_124396134_124401011_124507033_124522866_FR	OBD160.637.639
161	Hg38_12_31992399_31994148_32218403_32222271_RF	OBD160.641.643
162	Hg38_X_2551528_2553681_2721164_2724566_FR	OBD160.645.647
163	Hg38_4_12250997_12254184_12322283_12330696_FF	OBD160.649.651
164	Hg38_2_203737190_203742853_203950615_203958558_RR	OBD160.653.655
165	Hg38_4_171028618_171040398_171297049_171298480_FR	OBD160.657.659
166	Hg38_18_74451499_74454993_74653959_74660559_RR	OBD160.661.663
167	Hg38_7_10927538_10936617_11059573_11063361_FF	OBD160.665.667
168	Hg38_2_199918581_199920573_200063524_200066499_FF	OBD160.669.671
169	Hg38_20_40684507_40687277_40697330_40701314_RF	OBD160.673.675
170	Hg38_1_69381686_69386805_69431002_69439637_FF	OBD160.677.679
171	Hg38_X_80882210_80890038_81125945_81129443_RF	OBD160.681.683
172	Hg38_X_81004388_81008183_81249768_81260862_RR	OBD160.685.687
173	Hg38_2_43218506_43222954_43338993_43342008_RR	OBD160.689.691
174	Hg38_12_78001793_78008398_78104543_78106544_FF	OBD160.693.695
175	Hg38_8_138470025_138485193_138738624_138748013_FR	OBD160.697.699
176	Hg38_12_85366513_85378853_85614124_85622896_FF	OBD160.701.703
177	Hg38_7_112896017_112908366_113061946_113067988_RR	OBD160.705.707
178	Hg38_2_200576039_200582576_200625910_200631991_FF	OBD160.709.711
179	Hg38_15_30512275_30516087_30637530_30644724_RF	OBD160.713.715
180	Hg38_7_25392695_25398339_25542599_25548176_FR	OBD160.717.719
181	Hg38_6_56692561_56704365_56788190_56791583_FR	OBD160.721.723
182	Hg38_9_63901466_63907814_64080352_64086066_RF	OBD160.725.727
183	Hg38_13_21325011_21327390_21575413_21582625_RF	OBD160.729.731
184	Hg38_4_164713694_164729294_164967949_164972230_RF	OBD160.733.735
185	Hg38_1_63238122_63243108_63375818_63382270_FR	OBD160.737.739
186	Hg38_11_106045994_106053482_106098496_106106725_FR	OBD160.741.743
187	Hg38_2_191681747_191683098_191825543_191836084_RF	OBD160.745.747
188	Hg38_14_70326561_70339130_70362648_70369731_RR	OBD160.749.751
189	Hg38_5_3428156_3436940_3502869_3506924_RF	OBD160.753.755
190	Hg38_9_93834125_93843642_94033256_94043963_RR	OBD160.757.759
191	Hg38_4_166975421_166983791_167173650_167191011_FF	OBD160.761.763
192	Hg38_12_114559051_114568056_114591211_114602162_FF	OBD160.765.767
193	Hg38_13_91314238_91325788_91448901_91460521_RR	OBD160.769.771
194	Hg38_X_107971578_107974327_108029689_108034634_RR	OBD160.773.775

195	Hg38_8_24835942_24839566_24905842_24907666_FR	OBD160.777.779
196	Hg38_8_115234769_115239118_115394021_115408137_FR	OBD160.781.783
197	Hg38_12_126756498_126769103_126960572_126965968_RF	OBD160.785.787
198	Hg38_11_93302415_93309584_93391985_93400931_RF	OBD160.789.791
199	Hg38_3_81259865_81272497_81351596_81353868_RR	OBD160.793.795
200	Hg38_3_38500849_38506870_38670653_38683212_FR	OBD160.797.799

Table 1A (part 4g)

No	probe	RP/Rsum	Rprank	FC:(class 1/class2)	pfp
1	Hg38_3_100733021_100742761_100862282_100875494_RF	1276.982875	9	-1.862	0
2	Hg38_3_100750954_100758578_100862282_100875494_RF	1853.765048	19	-1.807	0
3	Hg38_5_150272362_150278699_150330165_150332483_FR	1170.349245	3	-1.745	0
4	Hg38_3_100862282_100875494_101052914_101071675_FF	3484.363128	62	-1.739	0
5	Hg38_5_150008962_150014465_150272362_150278699_RF	1191.048051	5	-1.715	0
6	Hg38_5_150272362_150278699_150382773_150387928_FF	1176.134465	4	-1.708	0
7	Hg38_12_69346683_69349534_69539751_69542024_FF	1240.559047	8	-1.633	0
8	Hg38_8_143073684_143079751_143219138_143224471_RF	891.0362935	1	-1.62	0
9	Hg38_1_32214585_32217213_32237144_32241139_RF	1916.433227	20	-1.612	0
10	Hg38_X_46498682_46508989_46616810_46620218_FR	1191.059693	6	-1.611	0
11	Hg38_10_8256256_8258992_8314718_8322822_FF	1997.333433	23	-1.604	0
12	Hg38_6_3027907_3030237_3146778_3149848_FR	1332.376903	10	-1.598	0
13	Hg38_7_27204432_27205465_27302548_27312509_FF	2411.122208	36	-1.597	0
14	Hg38_7_25370684_25382177_25542599_25548176_FF	2022.117984	24	-1.596	0
15	Hg38_6_2898813_2902737_3146778_3149848_RR	1435.327398	11	-1.59	0
16	Hg38_5_150036868_150040595_150272362_150278699_RF	2126.214981	28	-1.579	0
17	Hg38_8_142863175_142868397_143073684_143079751_RR	1054.173681	2	-1.578	0
18	Hg38_5_150194890_150198993_150272362_150278699_RF	2149.76038	31	-1.576	0
19	Hg38_3_100862282_100875494_101027240_101038115_FF	3687.763264	73	-1.572	0
20	Hg38_8_26561792_26565691_26638318_26644530_RR	2165.336533	32	-1.571	0
21	Hg38_7_27151628_27154280_27302548_27312509_FF	2361.083379	34	-1.57	0
22	Hg38_3_100677572_100682399_100862282_100875494_RF	3589.606187	67	-1.568	0
23	Hg38_9_84621528_84639678_84804816_84814325_RF	1828.923149	17	-1.564	0
24	Hg38_X_46498682_46508989_46571235_46574591_FR	1785.89045	15	-1.563	0
25	Hg38_7_25274699_25276258_25370684_25382177_RF	2139.963434	30	-1.563	0
26	Hg38_6_3146778_3149848_3232412_3234356_RF	1805.502041	16	-1.557	0
27	Hg38_Y_7774814_7781345_7901883_7918222_RR	2848.762302	43	-1.557	0
28	Hg38_6_47291785_47297630_47538465_47543792_RF	1946.170671	22	-1.556	0
29	Hg38_5_150272362_150278699_150390262_150397231_FR	2615.809608	40	-1.555	0
30	Hg38_6_2891780_2893777_3146778_3149848_FR	1661.21676	12	-1.555	0
31	Hg38_13_33481982_33488531_33704999_33717490_RF	1752.746474	13	-1.549	0
32	Hg38_6_3045545_3051391_3146778_3149848_FR	1924.507183	21	-1.549	0
33	Hg38_8_26561792_26565691_26776216_26787349_RR	3150.83329	51	-1.548	0
34	Hg38_6_2860707_2865436_3146778_3149848_FR	1839.184279	18	-1.544	0
35	Hg38_7_27250080_27251352_27302548_27312509_FF	2509.589873	38	-1.544	0
36	Hg38_12_114767229_114770912_114977828_114985191_RF	2775.735277	42	-1.54	0
37	Hg38_7_22390272_22396878_22624843_22634759_FF	7861.738142	308	-1.539	0
38	Hg38_12_91718135_91726240_91895416_91906634_FR	3218.63397	53	-1.538	0
39	Hg38_10_8256256_8258992_8533854_8544622_FF	3243.075285	57	-1.537	0
40	Hg38_8_142835475_142844052_143073684_143079751_FR	1213.884569	7	-1.535	0

41	Hg38_6_3146778_3149848_3207080_3212780_RF	2066.688372	25	-1.533	0
42	Hg38_10_102798644_102804186_102874567_102879563_RR	1775.993146	14	-1.527	0
43	Hg38_6_3146778_3149848_3196920_3199851_RF	2136.395315	29	-1.525	0
44	Hg38_12_114977828_114985191_115073537_115080207_FR	3454.341156	60	-1.521	0
45	Hg38_X_46498682_46508989_46621627_46624211_FF	2395.87684	35	-1.521	0
46	Hg38_5_150272362_150278699_150335788_150341587_FF	3220.31145	54	-1.518	0
47	Hg38_12_91718135_91726240_91888283_91891782_FR	3918.107486	81	-1.515	0
48	Hg38_X_46498682_46508989_46624211_46629863_FF	2684.932505	41	-1.514	0
49	Hg38_7_27201418_27203903_27302548_27312509_FF	3018.091514	48	-1.513	0
50	Hg38_5_132650160_132653783_132755645_132763810_RR	3592.88293	68	-1.51	0

Table 1B (part 1a)

			Probe sequence
No.	P.va lue	Type	60 mer
1	0	Healthy Control	CCCGATTGCTTAATCTCGGCATAGATTTCTGAATTATATTGATTGTCTTATCTCCTCA
2	0	Healthy Control	CCCGATTGCTTAATCTCGGCATAGATTTCTGAATCAAATAGTTTATTTAGAGAACCTCCA
3	0	Healthy Control	AGTGCCTGTGAAAGTGTCTGAATTCCTCGATCAGCTTCTCAGAAAAATGAAATTGACT
4	0	Healthy Control	CCCGATTGCTTAATCTCGGCATAGATTTCTGAATTACAGATTTTATCCAAAATATCTGTC
5	0	Healthy Control	AGTGCCTGTGAAAGTGTCTGAATTCCTCGACTCTTGCTTTTGATTATTGAAGAATC
6	0	Healthy Control	AGTGCCTGTGAAAGTGTCTGAATTCCTCGACAAAAATCAGAGGGGGTTTAATCACCTT
7	0	Healthy Control	AGTTATTTTATAGTTTGTACATAGTTGTCGAGTGTGTGAGGAAAAATTATCTGAAAAT
8	0	Healthy Control	CATGTTTTGGAGTCTTTATCTAGTTTATCGAGGAGACAGCCGTTGTCCTCCAGGGCTCCT
9	0	Healthy Control	AAGGGCTCGGGAGCTCCCTCGGCACACCTCGAGGAGTGCCAGGCATCTACTGCTCTGTCC
10	0	Healthy Control	ACAGAGCCCTCAGAAATAATGCCGCATATCGATGAGAAGTCTGATTCTTGCTTTTGGAG
11	0	Healthy Control	TGGGGTGATTGGGTTCATTTATGTATTATCGAGAGACATAACAATATTTATAAAGTTTGG
12	0	Healthy Control	AAACTTGGTATGTGTCTAATAAACAGCTTCGAGTGCTGGTTTGGGTCTGGAGTGCTGGTTC
13	0	Healthy Control	CTTTAAGTCAACAAATACACTGAAGACTTCGAAGTAATGAAGAGGGAGGTGGTTTCTTT
14	0	Healthy Control	AGCCAGCCATTGTTAACATAGTTCAACTTCGAAGGAATGATTCTTTTTCTTAACCATGC
15	0	Healthy Control	CCTCCAGTCTATTTCTTTTTTTTTTTCGAGTGCTGGTTTGGGTCTGGAGTGCTGGTTC
16	0	Healthy Control	AGTGCCTGTGAAAGTGTCTGAATTCCTCGAATTATTATGAGTCTCCGTCCACGCAGTG
17	0	Healthy Control	TCGTCTATGCATGGAATATTCTCCAAAATCGAGGAGACAGCCGTTGTCTCCAGGGCTCCT
18	0	Healthy Control	AGTGCCTGTGAAAGTGTCTGAATTCCTCGAGCGTACACCAATGGAGGAGGTATGGGCC
19	0	Healthy Control	CCCGATTGCTTAATCTCGGCATAGATTTCTGAAAGGCTGAGAAAAAAGGGAGCTGGTGG
20	0	Healthy Control	CAGCCAGCCAGTAGATCTTCATAGGAGCTCGAAATTTTGCTATAAATGTGAGCTTTGAAA
21	0	Healthy Control	ATGCTTTTGGAAATAAATATATTATTTTCGAAGTAATGAAGAGGGAGGTGGTTTCTTT
22	0	Healthy Control	CCCGATTGCTTAATCTCGGCATAGATTTCTGAAGAACTCCTTTTAGCATTCTTGTAGGT
23	0	Healthy Control	CTCTCAGGGGTGTGTGGAGTAAATAGCTCGAGGAAACCTAAAAGTGTATGTTATCCAT
24	0	Healthy Control	ACAGAGCCCTCAGAAATAATGCCGCATATCGAGGATCTATCTCTTCTCACCTGCTGG
25	0	Healthy Control	AGCCAGCCATTGTTAACATAGTTCAACTTCGATATTTTACATCATAATTTTGTGTTTATT
26	0	Healthy Control	GCCCCATTCTGAGAACTCTGATTGGATTGAGTGCTGGTTTGGGTCTGGAGTGCTGGTTC
27	0	Healthy Control	TGCCAGCCATTATTGATTTCTTTATGTGCAACTTGCCAACGGAAATTGAGGAAATTG
28	0	Healthy Control	TGGGTGTTAGGGTTTCAATATATGAATTCGAAGGCCTCTTCAATTCTGAAGTAAACAG
29	0	Healthy Control	AGTGCCTGTGAAAGTGTCTGAATTCCTCGAGTCCCTCATGAGATTTCCAGCGTAGTG
30	0	Healthy Control	TGAGGATGGTGAAAGATACCTAAGTCACTCGAGTGCTGGTTTGGGTCTGGAGTGCTGGTTC
31	0	Healthy Control	AAGGCGGGCAGATCACGAGTCTAGGCAATCGAAAAAAGAAAGAAAAAAGAAAGAAAAAAG G
32	0	Healthy Control	TGATCACTCCAACACCCAAAGGTGACTTCGAGTGCTGGTTTGGGTCTGGAGTGCTGGTTC
33	0	Healthy Control	CAGCCAGCCAGTAGATCTTCATAGGAGCTCGAATTCCTATCCAGCACTGGTCATTAGGGG
34	0	Healthy Control	AGTGGTGTAACCTCAGTTGACTGCAGCCTCGAGTGCTGGTTTGGGTCTGGAGTGCTGGTTC
35	0	Healthy Control	TTGTGAAAGTCATATCCTTGCGTCTTCATCGAAGTAATGAAGAGGGAGGTGGTTTCTTT

36	0	Healthy Control	GGCAGGGGCAGTATTCTCAGGTGGTTCCTCGAAGAACGGGCCTGGCCCAAGGCACTTTGG
37	0	Healthy Control	TGTCTTGAGGCTTACTAGTGCCTCCGTCGATGTATTCTACTAATAAAAAAGGAAGATTC
38	0	Healthy Control	GTCAGGGTCAGATATTGATTTAACGAAGTCGAAGAACTAAAACTTTTTCTAGTTTCAC
39	0	Healthy Control	TGGGGTGATTGGGTTCATTTATGTATTATCGACTCATAGATCCAGGTACAACGTATAATT
40	0	Healthy Control	AAGCAGTCTTGGGGAAAAAGAAAAAGCTCGAGGAGACAGCCGTTGTCCCAGGGCTCCT
41	0	Healthy Control	TCAAAGTCCAAGTTAGAATTCTGAGAACTCGAGTGCTGGTTTGGGTCGGAGTGCTGGTTC
42	0	Healthy Control	AAGGCGGGCAGATCACGAGGTCAACAGATCGACATTCATCTGTTCTCTTTAGATCAAA
43	0	Healthy Control	ACTATGGTGGATTTAAAAATAAATGCCCTCGAGTGCTGGTTTGGGTCGGAGTGCTGGTTC
44	0	Healthy Control	GGCAGGGGCAGTATTCTCAGGTGGTTCCTCGATACACTTCTCATAAAAAATGGCACTGAA
45	0	Healthy Control	ACAGAGCCCTCAGAAATAATGCCGCATATCGATAATTTGCTAGAATGACTCACAGAACAC
46	0	Healthy Control	AGTGCCTGTGAAAGTGTCTGAATTCCTCGATGTGTTTGGGGACTGAAAAGTCCTGCA
47	0	Healthy Control	GTCAGGGTCAGATATTGATTTAACGAAGTCGACATGCGATTTGAACAGGGACACAAATCC
48	0	Healthy Control	ACAGAGCCCTCAGAAATAATGCCGCATATCGAGGCTAATTTAGAGTATAACAGTTTGGGA
49	0	Healthy Control	AAAAGGAAAAAGGGAAACCAGGTTTAAATCGAAGTAATGAAGAGGGAGGTGGTTTTCTTT
50	0	Healthy Control	TCTTTTATTGAAGAGCGTGTTTTAAATCGAATATTAGTAGTCCCGTGGCAAGCCTTTG

Table 1B (part 1b)

No.	Probe Location				
	Chr	Start1	End1	Start2	End2
1	3	100733023	100733052	100875463	100875492
2	3	100750956	100750985	100875463	100875492
3	5	150278668	150278697	150330167	150330196
4	3	100875463	100875492	101071644	101071673
5	5	150008964	150008993	150278668	150278697
6	5	150278668	150278697	150387897	150387926
7	12	69349503	69349532	69541993	69542022
8	8	143073686	143073715	143224440	143224469
9	1	32214587	32214616	32241108	32241137
10	X	46508958	46508987	46616812	46616841
11	10	8258961	8258990	8322791	8322820
12	6	3030206	3030235	3146780	3146809
13	7	27205434	27205463	27312478	27312507
14	7	25382146	25382175	25548145	25548174
15	6	2898815	2898844	3146780	3146809
16	5	150036870	150036899	150278668	150278697
17	8	142863177	142863206	143073686	143073715
18	5	150194892	150194921	150278668	150278697
19	3	100875463	100875492	101038084	101038113
20	8	26561794	26561823	26638320	26638349
21	7	27154249	27154278	27312478	27312507
22	3	100677574	100677603	100875463	100875492
23	9	84621530	84621559	84814294	84814323
24	X	46508958	46508987	46571237	46571266
25	7	25274701	25274730	25382146	25382175
26	6	3146780	3146809	3234325	3234354
27	Y	7774816	7774845	7901885	7901914
28	6	47291787	47291816	47543761	47543790
29	5	150278668	150278697	150390264	150390293
30	6	2893746	2893775	3146780	3146809
31	13	33481984	33482013	33717459	33717488

32	6	3051360	3051389	3146780	3146809
33	8	26561794	26561823	26776218	26776247
34	6	2865405	2865434	3146780	3146809
35	7	27251321	27251350	27312478	27312507
36	12	114767231	114767260	114985160	114985189
37	7	22396847	22396876	22634728	22634757
38	12	91726209	91726238	91895418	91895447
39	10	8258961	8258990	8544591	8544620
40	8	142844021	142844050	143073686	143073715
41	6	3146780	3146809	3212749	3212778
42	10	102798646	102798675	102874569	102874598
43	6	3146780	3146809	3199820	3199849
44	12	114985160	114985189	115073539	115073568
45	X	46508958	46508987	46624180	46624209
46	5	150278668	150278697	150341556	150341585
47	12	91726209	91726238	91888285	91888314
48	X	46508958	46508987	46629832	46629861
49	7	27203872	27203901	27312478	27312507
50	5	132650162	132650191	132755647	132755676

Table 1B (part 1c)

No.	4 kb Sequence Location				
	Chr	Start1	End1	Start2	End2
1	3	100733023	100737022	100871493	100875492
2	3	100750956	100754955	100871493	100875492
3	5	150274698	150278697	150330167	150334166
4	3	100871493	100875492	101067674	101071673
5	5	150008964	150012963	150274698	150278697
6	5	150274698	150278697	150383927	150387926
7	12	69345533	69349532	69538023	69542022
8	8	143073686	143077685	143220470	143224469
9	1	32214587	32218586	32237138	32241137
10	X	46504988	46508987	46616812	46620811
11	10	8254991	8258990	8318821	8322820
12	6	3026236	3030235	3146780	3150779
13	7	27201464	27205463	27308508	27312507
14	7	25378176	25382175	25544175	25548174
15	6	2898815	2902814	3146780	3150779
16	5	150036870	150040869	150274698	150278697
17	8	142863177	142867176	143073686	143077685
18	5	150194892	150198891	150274698	150278697
19	3	100871493	100875492	101034114	101038113
20	8	26561794	26565793	26638320	26642319
21	7	27150279	27154278	27308508	27312507
22	3	100677574	100681573	100871493	100875492
23	9	84621530	84625529	84810324	84814323
24	X	46504988	46508987	46571237	46575236
25	7	25274701	25278700	25378176	25382175
26	6	3146780	3150779	3230355	3234354
27	Y	7774816	7778815	7901885	7905884

28	6	47291787	47295786	47539791	47543790
29	5	150274698	150278697	150390264	150394263
30	6	2889776	2893775	3146780	3150779
31	13	33481984	33485983	33713489	33717488
32	6	3047390	3051389	3146780	3150779
33	8	26561794	26565793	26776218	26780217
34	6	2861435	2865434	3146780	3150779
35	7	27247351	27251350	27308508	27312507
36	12	114767231	114771230	114981190	114985189
37	7	22392877	22396876	22630758	22634757
38	12	91722239	91726238	91895418	91899417
39	10	8254991	8258990	8540621	8544620
40	8	142840051	142844050	143073686	143077685
41	6	3146780	3150779	3208779	3212778
42	10	102798646	102802645	102874569	102878568
43	6	3146780	3150779	3195850	3199849
44	12	114981190	114985189	115073539	115077538
45	X	46504988	46508987	46620210	46624209
46	5	150274698	150278697	150337586	150341585
47	12	91722239	91726238	91888285	91892284
48	X	46504988	46508987	46625862	46629861
49	7	27199902	27203901	27308508	27312507
50	5	132650162	132654161	132755647	132759646

Table 1B (part 1d)

No.	probe	Primer ID
1	Hg38_3_100733021_100742761_100862282_100875494_RF	OBD160.801
2	Hg38_3_100750954_100758578_100862282_100875494_RF	OBD160.805
3	Hg38_5_150272362_150278699_150330165_150332483_FR	OBD160.809
4	Hg38_3_100862282_100875494_101052914_101071675_FF	OBD160.813
5	Hg38_5_150008962_150014465_150272362_150278699_RF	OBD160.817
6	Hg38_5_150272362_150278699_150382773_150387928_FF	OBD160.821
7	Hg38_12_69346683_69349534_69539751_69542024_FF	OBD160.825
8	Hg38_8_143073684_143079751_143219138_143224471_RF	OBD160.829
9	Hg38_1_32214585_32217213_32237144_32241139_RF	OBD160.833
10	Hg38_X_46498682_46508989_46616810_46620218_FR	OBD160.837
11	Hg38_10_8256256_8258992_8314718_8322822_FF	OBD160.841
12	Hg38_6_3027907_3030237_3146778_3149848_FR	OBD160.845
13	Hg38_7_27204432_27205465_27302548_27312509_FF	OBD160.849
14	Hg38_7_25370684_25382177_25542599_25548176_FF	OBD160.853
15	Hg38_6_2898813_2902737_3146778_3149848_RR	OBD160.857
16	Hg38_5_150036868_150040595_150272362_150278699_RF	OBD160.861
17	Hg38_8_142863175_142868397_143073684_143079751_RR	OBD160.865
18	Hg38_5_150194890_150198993_150272362_150278699_RF	OBD160.869
19	Hg38_3_100862282_100875494_101027240_101038115_FF	OBD160.873
20	Hg38_8_26561792_26565691_26638318_26644530_RR	OBD160.877
21	Hg38_7_27151628_27154280_27302548_27312509_FF	OBD160.881
22	Hg38_3_100677572_100682399_100862282_100875494_RF	OBD160.885
23	Hg38_9_84621528_84639678_84804816_84814325_RF	OBD160.889
24	Hg38_X_46498682_46508989_46571235_46574591_FR	OBD160.893

25	Hg38_7_25274699_25276258_25370684_25382177_RF	OBD160.897
26	Hg38_6_3146778_3149848_3232412_3234356_RF	OBD160.901
27	Hg38_Y_7774814_7781345_7901883_7918222_RR	OBD160.905
28	Hg38_6_47291785_47297630_47538465_47543792_RF	OBD160.909
29	Hg38_5_150272362_150278699_150390262_150397231_FR	OBD160.913
30	Hg38_6_2891780_2893777_3146778_3149848_FR	OBD160.917
31	Hg38_13_33481982_33488531_33704999_33717490_RF	OBD160.921
32	Hg38_6_3045545_3051391_3146778_3149848_FR	OBD160.925
33	Hg38_8_26561792_26565691_26776216_26787349_RR	OBD160.929
34	Hg38_6_2860707_2865436_3146778_3149848_FR	OBD160.933
35	Hg38_7_27250080_27251352_27302548_27312509_FF	OBD160.937
36	Hg38_12_114767229_114770912_114977828_114985191_RF	OBD160.941
37	Hg38_7_22390272_22396878_22624843_22634759_FF	OBD160.945
38	Hg38_12_91718135_91726240_91895416_91906634_FR	OBD160.949
39	Hg38_10_8256256_8258992_8533854_8544622_FF	OBD160.953
40	Hg38_8_142835475_142844052_143073684_143079751_FR	OBD160.957
41	Hg38_6_3146778_3149848_3207080_3212780_RF	OBD160.961
42	Hg38_10_102798644_102804186_102874567_102879563_RR	OBD160.965
43	Hg38_6_3146778_3149848_3196920_3199851_RF	OBD160.969
44	Hg38_12_114977828_114985191_115073537_115080207_FR	OBD160.973
45	Hg38_X_46498682_46508989_46621627_46624211_FF	OBD160.977
46	Hg38_5_150272362_150278699_150335788_150341587_FF	OBD160.981
47	Hg38_12_91718135_91726240_91888283_91891782_FR	OBD160.985
48	Hg38_X_46498682_46508989_46624211_46629863_FF	OBD160.989
49	Hg38_7_27201418_27203903_27302548_27312509_FF	OBD160.993
50	Hg38_5_132650160_132653783_132755645_132763810_RR	OBD160.997

Table 1B (part 1e)

No.	Primer Sequence	Primer ID	Primer Sequence
1	GCAGGTAGGACAGGTGCCATCATTCCC	OBD160.803	CCCAACCTGAAGAACAGAGAGAAGACTG
2	GGACACGAGCCAGGATGCTAAACAGTGA	OBD160.807	GCTGTGTAATGAGGACTGAATAAGACTG
3	GGGCAAGGGTGGAAGCGATGGC	OBD160.811	TTCCCTGCCACCATTTCCAGACGGGCG
4	GCAGGTAGGACAGGTGCCATCATTCCC	OBD160.815	CCTCCCACATCTGATACTCTCACCCC
5	AGCCCAGAAACCTTGCCAAACAGAAGAG	OBD160.819	GCACCCAATAAGGAAAACAGAAAAGTTC
6	GGGCAAGGGTGGAAGCGATGGC	OBD160.823	GAGGGTCAGGTGGGCTCTGGGAGTTGTG
7	TAGTTCCCTTCAGTCACTCTTTGTAT	OBD160.827	TGAGCCCTGGAGGTGGAGGTTGC
8	CCAACCAACTGATTTATGCCAGG	OBD160.831	GACGACGGCTGTCTCCTCAAACA
9	CGCCCTTTCCAGCCCCTCAGTCC	OBD160.835	CTCCCTCCTTGCTGCCTCTTCCCACCAG
10	AGATTTTGGGCTGAGACAATGGG	OBD160.839	GGGCATTCCATAACTACAAGAGAAAA
11	AGAGCAGAGGGAAGAAGGAAGTCT	OBD160.843	TATTATTATCCATTCTGCCAAAGC
12	GAAGGTCTCTGTGTAATGATGAACCC	OBD160.847	AACCAGCACTCGCCAAACCAGCA
13	CAACAAAACAGGAAACCAGGACTG	OBD160.851	CAACAGAGATGGGAGACTTGAAG
14	GCCCTATCCTTACTCCCTGAACCTTGGG	OBD160.855	GAAGTGGCATCTCACGAATCCTCCCTGC
15	ATCCATCAAACAGAGACAACCACCTTG	OBD160.859	CGCCCAAACCAGCACTCCGACCC
16	CAGCCAGCAGATGGGTGGGTGGGC	OBD160.863	ATAATGGGCTGCTACAGAGAAGGCACTG
17	CAACACCTCATTGACACCACTGGACAG	OBD160.867	CTCAAACAGGGACCACGAGGATGATGGC
18	GGGCAAGGGTGGAAGCGATGGC	OBD160.871	ACCCAGACACCCTCCGACAGGACCTCA
19	GCAGGTAGGACAGGTGCCATCATTCCC	OBD160.875	CACTCACTAAGGTGGGTGGAGGTAATCC
20	GAGCAGCAAGTGAGCCAGCATTACCGCC	OBD160.879	GCGTGTCTCTCAGGGAAGGCAGGATGC
21	GCCAGAGAAGGAGGGATTGATTC	OBD160.883	CAACAGAGATGGGAGACTTGAAG

22	GCAGGTAGGACAGGTGCCATCATTTCCC	OBD160.887	GGGATTTTCATCAACACCAGCCCTGACCT
23	CATTAGTTAGATTCTCATAAGGATGGC	OBD160.891	TCACGGCGAACCCTAATGTCTATT
24	AGATTTTGGGCTGAGACAATGGG	OBD160.895	AAACAAGCCTGCTGACCGCCAGA
25	GCCCTATCTTACTCCCTGAACCTTGGG	OBD160.899	GTCTGGAGAACACGGCAGTTTGGCAGG
26	GCATCCTGTGAGGGCACCTGTGTCATT	OBD160.903	CTCCGACCCAAACCAGCACTCCAGCCG
27	AGGTTACAGCCACTGAGCCTGGATGTG	OBD160.907	GGGAAATGAGTAAGTCTGAGGGAAACAA
28	GGGAGGGCAATGGTGGGCTGATGTCTCT	OBD160.911	AATCAGAGGGCTGCCACCAGGCGAGTG
29	ACAGGACAGGGCAGGAGAGGCAACGAGG	OBD160.915	GCCTTGCTGAATGCTGGTCACATCGCAG
30	GTAGATGGCATTGACAAGAACCAGCCTG	OBD160.919	CCGACCCAAACCAGCACTCCAGCCG
31	ATGCCCACTTTCACCACTGCTATTGGAC	OBD160.923	CGTCCACCTACATCTCCCTTACCTAT
32	GGTGGGTGCTGAGGAGTGGGCTC	OBD160.927	ACTCCGACCCAAACCAGCACTCCAGCCG
33	GAGCAGCAAGTGAGCCAGCATTACCGCC	OBD160.931	TGGGTGAGGTGGAGCCGAGTTTGGGTC
34	CCTTCCTCCCTCCCTCCCGCTT	OBD160.935	ACTCCGACCCAAACCAGCACTCCAGCCG
35	TAGTTAGATTCTCATAAGGATGGC	OBD160.939	TTTCGTCCTTCGTACATTCACGG
36	CTGGCTCAGAGGAGGTGGTGATTATGGA	OBD160.943	GCCGAGGTCTCCAGTAACACCCTTGC
37	CAGTCTTGATAGAGGTTGGTGAGTGT	OBD160.947	GATTTCAGAAGCACTCCCTCCCGAGC
38	CTTTGTCACTGCCTGTTGCCACCTTGGT	OBD160.951	CTGTGGAGGAAAATAGTTGAGCAGGAAC
39	GCTCTTGGGTAGGCAGCCAGCAGCC	OBD160.955	CCCCTTACTCTCTGACCTATCACCCAG
40	GTGTTTTGACAAGTTGGTGCCGAATGCT	OBD160.959	CTCAAAACAGGGACCACGAGGATGATGGC
41	CAGGGAGGGAGAAACCCAGACAG	OBD160.963	CAAACCAGCACTCCGACCCAAAC
42	AACAGCAAGCCAGCCAGGTGTGGTGG	OBD160.967	CACTCTCCTCTCACCTTCAGCACCCG
43	GTGAGCAGGAGGCTTGGGCAGGC	OBD160.971	ACTCCGACCCAAACCAGCACTCCAGCCG
44	CTGGCTCAGAGGAGGTGGTGATTATGGA	OBD160.975	CCAACCCAGCCACACACAGCAGACCC
45	AGATTTTGGGCTGAGACAATGGG	OBD160.979	GGCTATTTCCGAGTTGTATCCTTTAT
46	GGGCAAGGGTGGGAAGCGATGGC	OBD160.983	AGGTTGGCTGGCTGCTCCTGCTCCCTTG
47	TTTGTCAGTGCCTGTTGCCACCTTGGT	OBD160.987	GTTTTCTGAGGCTGATTTCTTGTGAGA
48	AGATTTTGGGCTGAGACAATGGG	OBD160.991	AGAGCCATTATCTTTCTTTGGTGAA
49	CAGGCATTAGTTAGATTCTCATAAGG	OBD160.995	TCACGGCGAACCCTAATGTCTATT
50	CAACCACTTCACCAAGGAGCCAGAGTTC	OBD160.999	GGGATGGAGGGAAGAGTCACAGGAAAGT

Table 1B (part 1f)

No.	probe	Markers
1	Hg38_3_100733021_100742761_100862282_100875494_RF	OBD160.801.803
2	Hg38_3_100750954_100758578_100862282_100875494_RF	OBD160.805.807
3	Hg38_5_150272362_150278699_150330165_150332483_FR	OBD160.809.811
4	Hg38_3_100862282_100875494_101052914_101071675_FF	OBD160.813.815
5	Hg38_5_150008962_150014465_150272362_150278699_RF	OBD160.817.819
6	Hg38_5_150272362_150278699_150382773_150387928_FF	OBD160.821.823
7	Hg38_12_69346683_69349534_69539751_69542024_FF	OBD160.825.827
8	Hg38_8_143073684_143079751_143219138_143224471_RF	OBD160.829.831
9	Hg38_1_32214585_32217213_32237144_32241139_RF	OBD160.833.835
10	Hg38_X_46498682_46508989_46616810_46620218_FR	OBD160.837.839
11	Hg38_10_8256256_8258992_8314718_8322822_FF	OBD160.841.843
12	Hg38_6_3027907_3030237_3146778_3149848_FR	OBD160.845.847
13	Hg38_7_27204432_27205465_27302548_27312509_FF	OBD160.849.851
14	Hg38_7_25370684_25382177_25542599_25548176_FF	OBD160.853.855
15	Hg38_6_2898813_2902737_3146778_3149848_RR	OBD160.857.859
16	Hg38_5_150036868_150040595_150272362_150278699_RF	OBD160.861.863
17	Hg38_8_142863175_142868397_143073684_143079751_RR	OBD160.865.867
18	Hg38_5_150194890_150198993_150272362_150278699_RF	OBD160.869.871

19	Hg38_3_100862282_100875494_101027240_101038115_FF	OBD160.873.875
20	Hg38_8_26561792_26565691_26638318_26644530_RR	OBD160.877.879
21	Hg38_7_27151628_27154280_27302548_27312509_FF	OBD160.881.883
22	Hg38_3_100677572_100682399_100862282_100875494_RF	OBD160.885.887
23	Hg38_9_84621528_84639678_84804816_84814325_RF	OBD160.889.891
24	Hg38_X_46498682_46508989_46571235_46574591_FR	OBD160.893.895
25	Hg38_7_25274699_25276258_25370684_25382177_RF	OBD160.897.899
26	Hg38_6_3146778_3149848_3232412_3234356_RF	OBD160.901.903
27	Hg38_Y_7774814_7781345_7901883_7918222_RR	OBD160.905.907
28	Hg38_6_47291785_47297630_47538465_47543792_RF	OBD160.909.911
29	Hg38_5_150272362_150278699_150390262_150397231_FR	OBD160.913.915
30	Hg38_6_2891780_2893777_3146778_3149848_FR	OBD160.917.919
31	Hg38_13_33481982_33488531_33704999_33717490_RF	OBD160.921.923
32	Hg38_6_3045545_3051391_3146778_3149848_FR	OBD160.925.927
33	Hg38_8_26561792_26565691_26776216_26787349_RR	OBD160.929.931
34	Hg38_6_2860707_2865436_3146778_3149848_FR	OBD160.933.935
35	Hg38_7_27250080_27251352_27302548_27312509_FF	OBD160.937.939
36	Hg38_12_114767229_114770912_114977828_114985191_RF	OBD160.941.943
37	Hg38_7_22390272_22396878_22624843_22634759_FF	OBD160.945.947
38	Hg38_12_91718135_91726240_91895416_91906634_FR	OBD160.949.951
39	Hg38_10_8256256_8258992_8533854_8544622_FF	OBD160.953.955
40	Hg38_8_142835475_142844052_143073684_143079751_FR	OBD160.957.959
41	Hg38_6_3146778_3149848_3207080_3212780_RF	OBD160.961.963
42	Hg38_10_102798644_102804186_102874567_102879563_RR	OBD160.965.967
43	Hg38_6_3146778_3149848_3196920_3199851_RF	OBD160.969.971
44	Hg38_12_114977828_114985191_115073537_115080207_FR	OBD160.973.975
45	Hg38_X_46498682_46508989_46621627_46624211_FF	OBD160.977.979
46	Hg38_5_150272362_150278699_150335788_150341587_FF	OBD160.981.983
47	Hg38_12_91718135_91726240_91888283_91891782_FR	OBD160.985.987
48	Hg38_X_46498682_46508989_46624211_46629863_FF	OBD160.989.991
49	Hg38_7_27201418_27203903_27302548_27312509_FF	OBD160.993.995
50	Hg38_5_132650160_132653783_132755645_132763810_RR	OBD160.997.999

Table 1B (part 1g)

No.	probe	RP/Rsum	Rprank	FC:(class1/class2)	pfp
51	Hg38_21_44826248_44830834_44873351_44875256_RF	2956.424781	46	-1.509	0
52	Hg38_6_3114019_3116008_3146778_3149848_RR	2593.745836	39	-1.508	0
53	Hg38_5_132755645_132763810_132924803_132929300_RF	3865.979955	80	-1.507	0
54	Hg38_6_2882362_2886326_3146778_3149848_FR	2479.56492	37	-1.504	0
55	Hg38_12_68747488_68752550_68814505_68818951_RR	2290.703965	33	-1.503	0
56	Hg38_18_46958975_46962799_47078769_47089265_FR	3240.639266	56	-1.5	0
57	Hg38_18_46958975_46962799_47114979_47119139_FR	3161.351495	52	-1.498	0
58	Hg38_19_34277524_34285717_34302513_34306297_RF	4267.515378	97	-1.497	0
59	Hg38_5_132755645_132763810_132929300_132935025_RF	3744.91901	77	-1.495	0
60	Hg38_5_132755645_132763810_132845490_132849804_RF	3637.844194	69	-1.491	0
61	Hg38_12_89512516_89520005_89567382_89573321_FF	3120.819609	49	-1.491	0
62	Hg38_18_46958975_46962799_47181285_47187993_FF	4071.28168	87	-1.489	0
63	Hg38_4_145441661_145450618_145639668_145646739_FR	4351.192236	102	-1.489	0
64	Hg38_8_65429758_65438145_65603423_65608237_FR	3669.316935	70	-1.488	0
65	Hg38_21_44873351_44875256_45009774_45011942_FR	3284.39733	59	-1.484	0

66	Hg38_7_27176915_27178105_27302548_27312509_FF	3462.395102	61	-1.481	0
67	Hg38_8_143073684_143079751_143187205_143191965_RF	2069.623189	26	-1.48	0
68	Hg38_21_44873351_44875256_44975178_44979847_FF	3715.369973	75	-1.477	0
69	Hg38_X_104167549_104169666_104260928_104265364_RF	2992.791924	47	-1.47	0
70	Hg38_X_46474993_46482135_46498682_46508989_RF	4532.171008	111	-1.469	0
71	Hg38_18_46958975_46962799_47152390_47157459_FR	4325.866296	101	-1.469	0
72	Hg38_18_46958975_46962799_47218671_47222248_FF	4552.140095	116	-1.467	0
73	Hg38_12_8943814_8945391_9061693_9073885_RR	3991.953624	85	-1.467	0
74	Hg38_18_46958975_46962799_47102132_47108776_FF	4425.666246	106	-1.465	0
75	Hg38_3_126843341_126854251_126975387_126980610_FR	4230.256246	96	-1.463	0
76	Hg38_X_46451412_46455647_46498682_46508989_RF	5850.564876	178	-1.463	0
77	Hg38_6_47538465_47543792_47623265_47631675_FR	3781.879009	78	-1.462	0
78	Hg38_1_69357288_69362673_69431002_69439637_RF	4224.385254	95	-1.461	0
79	Hg38_2_3461060_3464337_3620203_3628632_RR	4223.660735	94	-1.461	0
80	Hg38_3_126715028_126724613_126843341_126854251_RF	4187.552449	92	-1.459	0
81	Hg38_X_104123664_104126241_104260928_104265364_RF	3137.27664	50	-1.455	0
82	Hg38_X_147757585_147771392_148009858_148011061_RF	4078.660813	88	-1.454	0
83	Hg38_X_46402474_46404815_46498682_46508989_RF	5728.942859	169	-1.454	0
84	Hg38_2_191868245_191877609_192052829_192065719_RR	3706.781886	74	-1.453	0
85	Hg38_20_19501430_19515696_19750261_19752596_RF	4044.106873	86	-1.453	0
86	Hg38_3_13325884_13327571_13490970_13499186_FF	4953.040936	132	-1.452	0
87	Hg38_18_46958975_46962799_47093730_47099291_FF	4534.435881	112	-1.452	0
88	Hg38_4_145441661_145450618_145487239_145494181_FR	6098.1236	198	-1.451	0
89	Hg38_X_104171401_104174188_104260928_104265364_RF	3522.63992	64	-1.45	0
90	Hg38_5_150272362_150278699_150355072_150357974_FR	4630.538732	120	-1.449	0
91	Hg38_7_148757046_148761950_148843816_148853209_RF	3272.699272	58	-1.447	0
92	Hg38_X_46462567_46466475_46498682_46508989_RF	5873.726154	181	-1.447	0
93	Hg38_1_211900971_211908280_212023996_212027825_FF	3673.530159	71	-1.447	0
94	Hg38_7_27236651_27239035_27302548_27312509_FF	3973.626367	83	-1.447	0
95	Hg38_18_46917333_46922591_46958975_46962799_RF	6372.471571	218	-1.445	0
96	Hg38_17_17926103_17934669_18063962_18066155_RF	4609.709066	117	-1.443	0
97	Hg38_17_44261859_44271957_44545451_44548502_RF	6733.043227	242	-1.443	0
98	Hg38_4_145441661_145450618_145529286_145534613_FF	5808.960219	173	-1.443	0
99	Hg38_3_52542416_52548124_52787566_52791869_FR	3941.729282	82	-1.441	0
100	Hg38_2_27492451_27495056_27719544_27726504_FF	5608.079466	162	-1.439	0

Table 1B (part 2a)

No.	P.va lue	Type	Probe sequence
			60 mer
51	0	Healthy Control	TTTGAGGTGTGTGGTTAACACTATCCTTCGATGAGTTCCTTGAGAGTTCTGTATTGTTT
52	0	Healthy Control	AATATAAATTCAATTCATTAATAAATAATCGAGTGCTGGTTGGGTCGGAGTGCTGGTTC
53	0	Healthy Control	AAAATTTGATTTAATTCTCCAATTATCATCGAATATTAGTAGTCCCGTGGCAAGCCTTTG
54	0	Healthy Control	CAAATAAGCCAGAACTCACTACCTCGAGTGCTGGTTGGGTCGGAGTGCTGGTTC
55	0	Healthy Control	AGGCGGGCAGATCAGTTCAGAGTTCGAAGGAAAAGCTAAATTTAGTTAGAAGTT
56	0	Healthy Control	ATCGTCGGGAGAATCTTCCCTTGTAGTCTCGATTTTCTAAGCCCAAATAAATGGTTCA
57	0	Healthy Control	ATCGTCGGGAGAATCTTCCCTTGTAGTCTCGACAGGAAACCTCATTTTATAGGTAGCCAT
58	0	Healthy Control	AGGACTGTGGGTGAGAAAAGCTCTGGATTGATTAGATTTTATTGATTAGTATTTAGGCAA
59	0	Healthy Control	ATATAATTCTGAACATAATTTCCAACTTCGAATATTAGTAGTCCCGTGGCAAGCCTTTG

60	0	Healthy Control	AGTTTTTAATGTCAAATATGATATACAGTCGAATATTAGTAGTCCCGTGGCAAGCCTTTG
61	0	Healthy Control	GCCAAAGAGAGCTTTGGTACCAATAAATTCGAGTTTGGTGGGAGGAAATTTATCTTT
62	0	Healthy Control	ATCGTCGGGAGAATCTTCCCTGTAGTCTCGATAGTTAATTTCTAAGAGGAAAGTACT
63	0	Healthy Control	TCCAGCCCAGTGACAGAGTAAAAACATCGAATGGCGACTTTTTTACAAATATTTGGAT
64	0	Healthy Control	ACAGAGCCCTCAGAAATAATGCCACATATCGAGCAATTCATGTTTTAAAGTTGGACTCTA
65	0	Healthy Control	TTTGCAGGTGTGTGGTTAACACTATCCTTCGAAAAAAAGCCTTTTGAGACTTCAGTTGG
66	0	Healthy Control	CCTAATGAAAGATACCAGGTCTGAGATCGAAGTAATGAAGAGGGAGGTGGTTTTCTTT
67	0	Healthy Control	GATCGGTACAGACATTGCCATCTGTTGATCGAGGAGACAGCCGTTGTCCCGAGGGCTCCT
68	0	Healthy Control	TTTGCAGGTGTGTGGTTAACACTATCCTTCGATTACCGAGGGATTTCATGTTCTGCTCCT
69	0	Healthy Control	GGCAGGCAGATCACTTGAGGTCAAGTTCGATTCTCTTTTTTCTCCTCCTTTATT
70	0	Healthy Control	ACAGAGCCCTCAGAAATAATGCCGCATATCGAAACCATGAAGCTAGCAAACACTGGAATG
71	0	Healthy Control	ATCGTCGGGAGAATCTTCCCTGTAGTCTCGAATGTTTTACAATATTTGACTTCTAATG
72	0	Healthy Control	ATCGTCGGGAGAATCTTCCCTGTAGTCTCGACTTCCAGGTGATTCTCCTACCTCAGCC
73	0	Healthy Control	GTCGTGAGTGGTGATGATCTCTGCAATCGATCATGATGGCAGGCAATCAAAGAATCTT
74	0	Healthy Control	ATCGTCGGGAGAATCTTCCCTGTAGTCTCGAGCATCAGATGAAGAAAAAATTAATCCAC
75	0	Healthy Control	GCATATGCAGGTGTGGGCTTTTTAAAAATCGATTAAAGTTTTATTCTGATTATTGTATGT
76	0	Healthy Control	ACAGAGCCCTCAGAAATAATGCCGCATATCGATATATAAGATTGTTTTAATTTCTATCT
77	0	Healthy Control	TGGGTGTTAGGTTTCAATATATGAATTCGAAGCTAGCCAAAGCATGTATTGTTATGT
78	0	Healthy Control	GAATGTTTAGGTTTTGTAAGTTTACAAATCGAGTGGCCAGTTACAGAAATTTCTGGAGTT
79	0	Healthy Control	ATGGGTGTGGGAGTTAAGGTCTGCTTCGATTGGAGATTTTTGACTACAGAATCAGTC
80	0	Healthy Control	GCATATGCAGGTGTGGGCTTTTTAAAAATCGACTAGTTTTTAAAGTAGGTTGTCTGTTTT
81	0	Healthy Control	GGCAGGCAGATCACTTGAGGTCAAGTTCGACCTGTCATCTACATTAGGTATTTCTGCT
82	0	Healthy Control	AAGGCGGGCAGATCACGAGGTCAAGGATTCGATCTCATATAGATATAAACCAAGTCTGTG
83	0	Healthy Control	ACAGAGCCCTCAGAAATAATGCCGCATATCGACAAGCACTTTTCTGCTAGAATGTGATAT
84	0	Healthy Control	GGCGGGCAGATCACTTGAGGTCAAGGATTCGAAGTCCATCCTTAATGAAAGATACCTCTA
85	0	Healthy Control	AGAATGGGCGATGTTTCTCAGGGCTGCTTCGAAAAGCATTATTAACACCTACCTTGCT
86	0	Healthy Control	TGACTGAGGTCCAGGTGTGGCCCCAACTCGAAAAAGAAAAAAGAGCCTGGTGAAAAAG
87	0	Healthy Control	ATCGTCGGGAGAATCTTCCCTGTAGTCTCGACCAGAATCCTCTCTCCAGGCGGCGTAA
88	0	Healthy Control	TCCAGCCCAGTGACAGAGTAAAAACATCGAAAACAAATCACATTCTTAACCAAAAGCT
89	0	Healthy Control	GGCAGGCAGATCACTTGAGGTCAAGTTCGAAGTGTAGGTAACCTTCTCTAGTGGA
90	0	Healthy Control	AGTGCTGTGAAAGTGTCTGAATTCCTCGACAACCTCTCATCTTCTAGTGGAA
91	0	Healthy Control	GGCAGGCAGATCACTTGAGGTCAAGGATTCGATTTTCAAGCAAAGTGTGAATGGAATTT
92	0	Healthy Control	ACAGAGCCCTCAGAAATAATGCCGCATATCGACTCCCCTATTCTCTGGCTGTGTGACCTG
93	0	Healthy Control	GGCAGGCAGATCACTTGAGGTCAAGGATTCGATGCCAACCTTTTCAAAGTAGTTAAACAG
94	0	Healthy Control	CTCATCTACCTGCAAGTGTGAGATCCACTCGAAGTAATGAAGAGGGAGGTGGTTTTCTTT
95	0	Healthy Control	ATCGTCGGGAGAATCTTCCCTGTAGTCTCGAAATCCGCCATTTTATACCACCGCGGGC
96	0	Healthy Control	AGCAATGTTGACTTAGTAATTTTTATATCGAGGCCGAGTGAGTTGTGATCATACCACT
97	0	Healthy Control	GTTCTAGAAGGTTCTGGAAGACAAAATATCGAGGACACCCGGGATTACGCCAGGGAGGCC
98	0	Healthy Control	TCCAGCCCAGTGACAGAGTAAAAACATCGAGTCTTTAGACATTTAATTCACCTACAT
99	0	Healthy Control	TGTTGAGGGTGTCCCGGAGCATCAAATCTCGATAATATGTCCTTGTCTTCTACAGAGATG
100	0	Healthy Control	GGGCGGGGTCTGCGGAGCCCCAGGGCTCGAGAAGACTTATTGTTTTGTCTGCCAGAA

Table 1B (part 2b)

No.	Probe Location				
	Chr	Start1	End1	Start2	End2
51	21	44826250	44826279	44875225	44875254
52	6	3114021	3114050	3146780	3146809
53	5	132755647	132755676	132929269	132929298
54	6	2886295	2886324	3146780	3146809
55	12	68747490	68747519	68814507	68814536

56	18	46962768	46962797	47078771	47078800
57	18	46962768	46962797	47114981	47115010
58	19	34277526	34277555	34306266	34306295
59	5	132755647	132755676	132934994	132935023
60	5	132755647	132755676	132849773	132849802
61	12	89519974	89520003	89573290	89573319
62	18	46962768	46962797	47187962	47187991
63	4	145450587	145450616	145639670	145639699
64	8	65438114	65438143	65603425	65603454
65	21	44875225	44875254	45009776	45009805
66	7	27178074	27178103	27312478	27312507
67	8	143073686	143073715	143191934	143191963
68	21	44875225	44875254	44979816	44979845
69	X	104167551	104167580	104265333	104265362
70	X	46474995	46475024	46508958	46508987
71	18	46962768	46962797	47152392	47152421
72	18	46962768	46962797	47222217	47222246
73	12	8943816	8943845	9061695	9061724
74	18	46962768	46962797	47108745	47108774
75	3	126854220	126854249	126975389	126975418
76	X	46451414	46451443	46508958	46508987
77	6	47543761	47543790	47623267	47623296
78	1	69357290	69357319	69439606	69439635
79	2	3461062	3461091	3620205	3620234
80	3	126715030	126715059	126854220	126854249
81	X	104123666	104123695	104265333	104265362
82	X	147757587	147757616	148011030	148011059
83	X	46402476	46402505	46508958	46508987
84	2	191868247	191868276	192052831	192052860
85	20	19501432	19501461	19752565	19752594
86	3	13327540	13327569	13499155	13499184
87	18	46962768	46962797	47099260	47099289
88	4	145450587	145450616	145487241	145487270
89	X	104171403	104171432	104265333	104265362
90	5	150278668	150278697	150355074	150355103
91	7	148757048	148757077	148853178	148853207
92	X	46462569	46462598	46508958	46508987
93	1	211908249	211908278	212027794	212027823
94	7	27239004	27239033	27312478	27312507
95	18	46917335	46917364	46962768	46962797
96	17	17926105	17926134	18066124	18066153
97	17	44261861	44261890	44548471	44548500
98	4	145450587	145450616	145534582	145534611
99	3	52548093	52548122	52787568	52787597
100	2	27495025	27495054	27726473	27726502

Table 1B (part 2c)

No.	4 kb Sequence Location				
	Chr	Start1	End1	Start2	End2
51	21	44826250	44830249	44871255	44875254

52	6	3114021	3118020	3146780	3150779
53	5	132755647	132759646	132925299	132929298
54	6	2882325	2886324	3146780	3150779
55	12	68747490	68751489	68814507	68818506
56	18	46958798	46962797	47078771	47082770
57	18	46958798	46962797	47114981	47118980
58	19	34277526	34281525	34302296	34306295
59	5	132755647	132759646	132931024	132935023
60	5	132755647	132759646	132845803	132849802
61	12	89516004	89520003	89569320	89573319
62	18	46958798	46962797	47183992	47187991
63	4	145446617	145450616	145639670	145643669
64	8	65434144	65438143	65603425	65607424
65	21	44871255	44875254	45009776	45013775
66	7	27174104	27178103	27308508	27312507
67	8	143073686	143077685	143187964	143191963
68	21	44871255	44875254	44975846	44979845
69	X	104167551	104171550	104261363	104265362
70	X	46474995	46478994	46504988	46508987
71	18	46958798	46962797	47152392	47156391
72	18	46958798	46962797	47218247	47222246
73	12	8943816	8947815	9061695	9065694
74	18	46958798	46962797	47104775	47108774
75	3	126850250	126854249	126975389	126979388
76	X	46451414	46455413	46504988	46508987
77	6	47539791	47543790	47623267	47627266
78	1	69357290	69361289	69435636	69439635
79	2	3461062	3465061	3620205	3624204
80	3	126715030	126719029	126850250	126854249
81	X	104123666	104127665	104261363	104265362
82	X	147757587	147761586	148007060	148011059
83	X	46402476	46406475	46504988	46508987
84	2	191868247	191872246	192052831	192056830
85	20	19501432	19505431	19748595	19752594
86	3	13323570	13327569	13495185	13499184
87	18	46958798	46962797	47095290	47099289
88	4	145446617	145450616	145487241	145491240
89	X	104171403	104175402	104261363	104265362
90	5	150274698	150278697	150355074	150359073
91	7	148757048	148761047	148849208	148853207
92	X	46462569	46466568	46504988	46508987
93	1	211904279	211908278	212023824	212027823
94	7	27235034	27239033	27308508	27312507
95	18	46917335	46921334	46958798	46962797
96	17	17926105	17930104	18062154	18066153
97	17	44261861	44265860	44544501	44548500
98	4	145446617	145450616	145530612	145534611
99	3	52544123	52548122	52787568	52791567
100	2	27491055	27495054	27722503	27726502

Table 1B (part 2d)

No.	probe	Primer ID
51	Hg38_21_44826248_44830834_44873351_44875256_RF	OBD160.1001
52	Hg38_6_3114019_3116008_3146778_3149848_RR	OBD160.1005
53	Hg38_5_132755645_132763810_132924803_132929300_RF	OBD160.1009
54	Hg38_6_2882362_2886326_3146778_3149848_FR	OBD160.1013
55	Hg38_12_68747488_68752550_68814505_68818951_RR	OBD160.1017
56	Hg38_18_46958975_46962799_47078769_47089265_FR	OBD160.1021
57	Hg38_18_46958975_46962799_47114979_47119139_FR	OBD160.1025
58	Hg38_19_34277524_34285717_34302513_34306297_RF	OBD160.1029
59	Hg38_5_132755645_132763810_132929300_132935025_RF	OBD160.1033
60	Hg38_5_132755645_132763810_132845490_132849804_RF	OBD160.1037
61	Hg38_12_89512516_89520005_89567382_89573321_FF	OBD160.1041
62	Hg38_18_46958975_46962799_47181285_47187993_FF	OBD160.1045
63	Hg38_4_145441661_145450618_145639668_145646739_FR	OBD160.1049
64	Hg38_8_65429758_65438145_65603423_65608237_FR	OBD160.1053
65	Hg38_21_44873351_44875256_45009774_45011942_FR	OBD160.1057
66	Hg38_7_27176915_27178105_27302548_27312509_FF	OBD160.1061
67	Hg38_8_143073684_143079751_143187205_143191965_RF	OBD160.1065
68	Hg38_21_44873351_44875256_44975178_44979847_FF	OBD160.1069
69	Hg38_X_104167549_104169666_104260928_104265364_RF	OBD160.1073
70	Hg38_X_46474993_46482135_46498682_46508989_RF	OBD160.1077
71	Hg38_18_46958975_46962799_47152390_47157459_FR	OBD160.1081
72	Hg38_18_46958975_46962799_47218671_47222248_FF	OBD160.1085
73	Hg38_12_8943814_8945391_9061693_9073885_RR	OBD160.1089
74	Hg38_18_46958975_46962799_47102132_47108776_FF	OBD160.1093
75	Hg38_3_126843341_126854251_126975387_126980610_FR	OBD160.1097
76	Hg38_X_46451412_46455647_46498682_46508989_RF	OBD160.1101
77	Hg38_6_47538465_47543792_47623265_47631675_FR	OBD160.1105
78	Hg38_1_69357288_69362673_69431002_69439637_RF	OBD160.1109
79	Hg38_2_3461060_3464337_3620203_3628632_RR	OBD160.1113
80	Hg38_3_126715028_126724613_126843341_126854251_RF	OBD160.1117
81	Hg38_X_104123664_104126241_104260928_104265364_RF	OBD160.1121
82	Hg38_X_147757585_147771392_148009858_148011061_RF	OBD160.1125
83	Hg38_X_46402474_46404815_46498682_46508989_RF	OBD160.1129
84	Hg38_2_191868245_191877609_192052829_192065719_RR	OBD160.1133
85	Hg38_20_19501430_19515696_19750261_19752596_RF	OBD160.1137
86	Hg38_3_13325884_13327571_13490970_13499186_FF	OBD160.1141
87	Hg38_18_46958975_46962799_47093730_47099291_FF	OBD160.1145
88	Hg38_4_145441661_145450618_145487239_145494181_FR	OBD160.1149
89	Hg38_X_104171401_104174188_104260928_104265364_RF	OBD160.1153
90	Hg38_5_150272362_150278699_150355072_150357974_FR	OBD160.1157
91	Hg38_7_148757046_148761950_148843816_148853209_RF	OBD160.1161
92	Hg38_X_46462567_46466475_46498682_46508989_RF	OBD160.1165
93	Hg38_1_211900971_211908280_212023996_212027825_FF	OBD160.1169
94	Hg38_7_27236651_27239035_27302548_27312509_FF	OBD160.1173
95	Hg38_18_46917333_46922591_46958975_46962799_RF	OBD160.1177
96	Hg38_17_17926103_17934669_18063962_18066155_RF	OBD160.1181
97	Hg38_17_44261859_44271957_44545451_44548502_RF	OBD160.1185
98	Hg38_4_145441661_145450618_145529286_145534613_FF	OBD160.1189

99	Hg38_3_52542416_52548124_52787566_52791869_FR	OBD160.1193
100	Hg38_2_27492451_27495056_27719544_27726504_FF	OBD160.1197

Table 1B (part 2e)

No.	Primer Sequence	Primer ID	Primer Sequence
51	CTCTGTTCCGCCTACCCAGGTCCACACC	OBD160.1003	CCTTCTTCTGTCTCCTTCTCCTCCATC
52	CAGGGCACTCAGGCTGGGTGAAGG	OBD160.1007	AGCACTCGCCCAAACCAGCACTCCGACC
53	TTCCCACTGGTTGACACAAAGTAGGTGC	OBD160.1011	GGGATGGAGGGAAGAGTCACAGGAAAGT
54	TCACTTTGACATTCATCCCTGGG	OBD160.1015	TGATGGAGAAGTTTATGATGAAGGAATC
55	GGCTCACCCTGTAAACCCAGCG	OBD160.1019	CCAGGGATGCCCAAGAAGTCCTT
56	GCAGTGGCTGGGTGTGGGAGGCA	OBD160.1023	GGGAGATGGTGGGTTTATTCTGCTTTT
57	GCAGTGGCTGGGTGTGGGAGGCA	OBD160.1027	GGCACTGGCTGTGAACCTGAGGAGGCTG
58	TTTCTAAATGTGATTGCAAGCATAGGC	OBD160.1031	GATGAAGGAATCAGGCATAACACCT
59	GCTGGGTGCGGGTCTCTCTCAGAA	OBD160.1035	GGGATGGAGGGAAGAGTCACAGGAAAGT
60	GGCAATGGTCAAGGGCACGAACACAATG	OBD160.1039	GGGATGGAGGGAAGAGTCACAGGAAAGT
61	CCGTAAAGTTGGACACTAAATGACATAG	OBD160.1043	TTCAGCGTTTGACTTTTGAGAAGAGTGC
62	CCGTCGCAAGTTTCGTTCCCAACCCGC	OBD160.1047	CTCGGCACTGACTCCCAACCCGC
63	CTGCCCTCAGAGAGTAAAGAGACAGGAC	OBD160.1051	AGGCTGGGTTTACAGTCACTCCGAGAAA
64	CAAGTCTACAGTAACCAAAACAGCAT	OBD160.1055	TTTTGGAGACTGTTTGAATGTGACCA
65	CTCTGTTCCGCCTACCCAGGTCCACACC	OBD160.1059	CCATACCCAGCAACGGACAGCCAG
66	GCCAATAAGGGTCTCTCTCAGAA	OBD160.1063	GATGAAGGAATCAGGCATAACACC
67	GGAAGACCTCACAGGACTCTGC	OBD160.1067	GACGACGGCTGTCTCCTCAAACA
68	CTCTGTTCCGCCTACCCAGGTCCACACC	OBD160.1071	GTGGCAGCAGGTGTCCCATCGGC
69	AGTGCTGAGGTTGAGAAGCCCAAGTTA	OBD160.1075	TTGTGTAAGTCAGTCCATCCTAAGCCTT
70	AGATTTTGGGCTGAGACAATGGG	OBD160.1079	GATGACACCTCACTTCTTCCGAA
71	TATCCGTAAGGCAAGTCCTGAGT	OBD160.1083	TGGCTACACAGTGAGACTCCGTC
72	TATCCGTAAGGCAAGTCCTGAGT	OBD160.1087	GCCCAGGAGTTTGAGACCAGCCT
73	GCTCCATTTTCTGTGCCCTCCTCAGGT	OBD160.1091	ACCGATGTGGACAATGAAGACCTGTGGG
74	CCGTGCGAAGTTTCGTTCCCAACCCGC	OBD160.1095	CCCCACAGCCCCACCTAACCTGATG
75	GGCAGAAAGGAAAGAGCCTCGCAGCATT	OBD160.1099	GTCATAGCAAGAACCAGAGAAATGTCAG
76	AGATTTTGGGCTGAGACAATGGG	OBD160.1103	GAAAGTTGTTTATGAGGCACTGTTTACA
77	GGGAGGGCAATGGTGGGCTGATGTC	OBD160.1107	ATGGCATCACCTTCTCAAGAGTGC
78	TTGTGAGAAGGGTAAAATCTTAGGCAGC	OBD160.1111	CTATGCCCAAGCCAGAATGAAGCGGTT
79	CCGTGAGCACAGTTCTCGCTGGTAAAT	OBD160.1115	GCTGTAGCAAAGCGACAAAATAAGAGT
80	GGCAGAAAGGAAAGAGCCTCGCAGCATT	OBD160.1119	CCCCAGGGAGATGGACGGGCAGAGC
81	TAATCCCAGCAAGTTGAGAGGCT	OBD160.1123	TAGAGGAGGGATAGCATTAGCAG
82	CACCTAAGGAGCCAGCAACTGACAAGAG	OBD160.1127	GGGTCTGCTGTGCTCCACGGCTGAAGG
83	AGATTTTGGGCTGAGACAATGGG	OBD160.1131	TAGGAGTTTGTCTTGGGACTTGTTA
84	CACCTGTAATCCAGCACTTTGG	OBD160.1135	GGACAAGTTATTACACGCCAGTA
85	GCCTGACATTCTCTGCTTCTTAT	OBD160.1139	GCAAGTGTGAGATTTTGTGTCCTCAT
86	GGTGCTCTGCGTCCACACACGG	OBD160.1143	GTTGGGTTGGGTGGGCACATCCTGGGTC
87	CCGTGCGAAGTTTCGTTCCCAACCCGC	OBD160.1147	CTTCCCTTCTCTCCCTCCCTCAGTTCTC
88	CTGCCCTCAGAGAGTAAAGAGACAGGAC	OBD160.1151	GGTGGCTACAGCAGAGTGATGAAAATAC
89	TGGCTCATACCTGTAATCCAGCAAGTT	OBD160.1155	CAGATTATTCAAAGGAAAACACCCAAC
90	GGGCAAGGGTGGGAAGCGATGGC	OBD160.1159	GGGAGGGTGTGGTGGCAGTGGAGTTGA
91	CCCAACAGATACCAAAATCCACGAAGAC	OBD160.1163	CCAGGCCAACTGTGATGGTAGGGTCAGG
92	AGATTTTGGGCTGAGACAATGGG	OBD160.1167	GAGCCTAAGTAATAACCCAGGT
93	ATCTACTTTCAGGCAGTGGCTCACGCC	OBD160.1171	CTCTCTTCTTTTCTGTGCTGGACTTA
94	GCAAGGAGGTGACAGGAGTGGTC	OBD160.1175	CAACAGAGATGGGAGACTTGAAG
95	CGTCGCAAGTTTCGTTCCCAACCCGCA	OBD160.1179	TCGTTGGCGGCAGCGGGAGTGGGT

96	GTCCTGCTGGGCTGCCTCAGTC	OBD160.1183	CCGCATCTCCCCTGTGCCAGTCCAGAC
97	CCCATCACCCCAAGGACCCCTCC	OBD160.1187	CACTCAGGGCTCTGCCGTACCTTGGAG
98	CTGCCCTCAGAGAGTAAAGAGACAGGAC	OBD160.1191	AACTGAAAAGGAAGAACTGTGAGAGGG
99	ATTATCCTCCTTTGTTCTTCCCC	OBD160.1195	GCCACTTACTCCTTCTGGGTCCC
100	TCCGCCCTGCCACACCCACCTC	OBD160.1199	GGTGTGAGATTGAAGGAGACTGTCAGG

Table 1B (part 2f)

No.	probe	Markers
51	Hg38_21_44826248_44830834_44873351_44875256_RF	OBD160.1001.1003
52	Hg38_6_3114019_3116008_3146778_3149848_RR	OBD160.1005.1007
53	Hg38_5_132755645_132763810_132924803_132929300_RF	OBD160.1009.1011
54	Hg38_6_2882362_2886326_3146778_3149848_FR	OBD160.1013.1015
55	Hg38_12_68747488_68752550_68814505_68818951_RR	OBD160.1017.1019
56	Hg38_18_46958975_46962799_47078769_47089265_FR	OBD160.1021.1023
57	Hg38_18_46958975_46962799_47114979_47119139_FR	OBD160.1025.1027
58	Hg38_19_34277524_34285717_34302513_34306297_RF	OBD160.1029.1031
59	Hg38_5_132755645_132763810_132929300_132935025_RF	OBD160.1033.1035
60	Hg38_5_132755645_132763810_132845490_132849804_RF	OBD160.1037.1039
61	Hg38_12_89512516_89520005_89567382_89573321_FF	OBD160.1041.1043
62	Hg38_18_46958975_46962799_47181285_47187993_FF	OBD160.1045.1047
63	Hg38_4_145441661_145450618_145639668_145646739_FR	OBD160.1049.1051
64	Hg38_8_65429758_65438145_65603423_65608237_FR	OBD160.1053.1055
65	Hg38_21_44873351_44875256_45009774_45011942_FR	OBD160.1057.1059
66	Hg38_7_27176915_27178105_27302548_27312509_FF	OBD160.1061.1063
67	Hg38_8_143073684_143079751_143187205_143191965_RF	OBD160.1065.1067
68	Hg38_21_44873351_44875256_44975178_44979847_FF	OBD160.1069.1071
69	Hg38_X_104167549_104169666_104260928_104265364_RF	OBD160.1073.1075
70	Hg38_X_46474993_46482135_46498682_46508989_RF	OBD160.1077.1079
71	Hg38_18_46958975_46962799_47152390_47157459_FR	OBD160.1081.1083
72	Hg38_18_46958975_46962799_47218671_47222248_FF	OBD160.1085.1087
73	Hg38_12_8943814_8945391_9061693_9073885_RR	OBD160.1089.1091
74	Hg38_18_46958975_46962799_47102132_47108776_FF	OBD160.1093.1095
75	Hg38_3_126843341_126854251_126975387_126980610_FR	OBD160.1097.1099
76	Hg38_X_46451412_46455647_46498682_46508989_RF	OBD160.1101.1103
77	Hg38_6_47538465_47543792_47623265_47631675_FR	OBD160.1105.1107
78	Hg38_1_69357288_69362673_69431002_69439637_RF	OBD160.1109.1111
79	Hg38_2_3461060_3464337_3620203_3628632_RR	OBD160.1113.1115
80	Hg38_3_126715028_126724613_126843341_126854251_RF	OBD160.1117.1119
81	Hg38_X_104123664_104126241_104260928_104265364_RF	OBD160.1121.1123
82	Hg38_X_147757585_147771392_148009858_148011061_RF	OBD160.1125.1127
83	Hg38_X_46402474_46404815_46498682_46508989_RF	OBD160.1129.1131
84	Hg38_2_191868245_191877609_192052829_192065719_RR	OBD160.1133.1135
85	Hg38_20_19501430_19515696_19750261_19752596_RF	OBD160.1137.1139
86	Hg38_3_13325884_13327571_13490970_13499186_FF	OBD160.1141.1143
87	Hg38_18_46958975_46962799_47093730_47099291_FF	OBD160.1145.1147
88	Hg38_4_145441661_145450618_145487239_145494181_FR	OBD160.1149.1151
89	Hg38_X_104171401_104174188_104260928_104265364_RF	OBD160.1153.1155
90	Hg38_5_150272362_150278699_150355072_150357974_FR	OBD160.1157.1159
91	Hg38_7_148757046_148761950_148843816_148853209_RF	OBD160.1161.1163
92	Hg38_X_46462567_46466475_46498682_46508989_RF	OBD160.1165.1167

93	Hg38_1_211900971_211908280_212023996_212027825_FF	OBD160.1169.1171
94	Hg38_7_27236651_27239035_27302548_27312509_FF	OBD160.1173.1175
95	Hg38_18_46917333_46922591_46958975_46962799_RF	OBD160.1177.1179
96	Hg38_17_17926103_17934669_18063962_18066155_RF	OBD160.1181.1183
97	Hg38_17_44261859_44271957_44545451_44548502_RF	OBD160.1185.1187
98	Hg38_4_145441661_145450618_145529286_145534613_FF	OBD160.1189.1191
99	Hg38_3_52542416_52548124_52787566_52791869_FR	OBD160.1193.1195
100	Hg38_2_27492451_27495056_27719544_27726504_FF	OBD160.1197.1199

Table 1B (part 2g)

No.	probe	RP/Rsum	Rprank	FC:(class1 /class2)	pfp
101	Hg38_7_148843816_148853209_149049131_149053931_FF	3724.759194	76	-1.439	0
102	Hg38_5_150134627_150137703_150272362_150278699_RF	5047.498487	139	-1.438	0
103	Hg38_X_46398622_46399662_46498682_46508989_RF	6153.043315	200	-1.438	0
104	Hg38_3_52542416_52548124_52688436_52689750_FR	4290.852063	98	-1.438	0
105	Hg38_13_77929805_77933751_77995325_78000878_FR	4895.079027	128	-1.437	0
106	Hg38_X_77891626_77893835_78036858_78043877_RR	4737.136557	123	-1.437	0
107	Hg38_5_132755645_132763810_132995308_132998933_RF	5427.156748	152	-1.436	0
108	Hg38_8_65429758_65438145_65628655_65630980_FF	5313.744389	148	-1.436	0
109	Hg38_5_94505842_94514405_94641711_94646370_FR	5118.072112	141	-1.436	0
110	Hg38_2_13845156_13854426_13990532_13998047_FF	4209.708849	93	-1.435	0
111	Hg38_18_46958975_46962799_47121690_47124504_FR	5139.553936	144	-1.435	0
112	Hg38_X_46498682_46508989_46603634_46604788_FF	7085.42019	267	-1.435	0
113	Hg38_11_83253501_83261801_83434843_83442656_RF	4953.072097	133	-1.435	0
114	Hg38_5_34366017_34372954_34527904_34530421_RR	4740.961086	124	-1.434	0
115	Hg38_18_46958975_46962799_47058015_47062163_FR	6552.392969	229	-1.434	0
116	Hg38_19_45210518_45212404_45410404_45414235_FF	4098.241985	89	-1.433	0
117	Hg38_3_126755033_126764525_126843341_126854251_RF	5104.936168	140	-1.433	0
118	Hg38_12_6595585_6598606_6681014_6683610_FF	4353.353812	103	-1.432	0
119	Hg38_9_87096089_87101882_87143570_87148986_RR	5684.666484	166	-1.431	0
120	Hg38_3_52542416_52548124_52699561_52701305_FF	4512.767485	108	-1.43	0
121	Hg38_17_17926103_17934669_18141138_18142995_RF	4946.982257	131	-1.429	0
122	Hg38_3_126604176_126607234_126843341_126854251_RF	5936.323554	185	-1.429	0
123	Hg38_2_27492451_27495056_27657039_27659544_FR	6695.897118	239	-1.428	0
124	Hg38_20_45581538_45584773_45643172_45649623_FR	6225.863337	205	-1.426	0
125	Hg38_3_126627400_126630792_126843341_126854251_RF	5809.854722	174	-1.425	0
126	Hg38_4_112653708_112659532_112867641_112872043_RR	4539.896621	114	-1.425	0
127	Hg38_17_17840582_17849843_17926103_17934669_FR	5118.63214	142	-1.424	0
128	Hg38_15_88873420_88883875_88904252_88906658_FF	3854.072433	79	-1.424	0
129	Hg38_5_132755645_132763810_132790667_132795213_RF	5630.548983	163	-1.423	0
130	Hg38_8_65429758_65438145_65633322_65635344_FR	5572.230006	159	-1.422	0
131	Hg38_4_145339443_145344834_145441661_145450618_RF	7036.536906	262	-1.422	0
132	Hg38_X_155860883_155870741_155953718_155958970_FR	5391.94258	150	-1.422	0
133	Hg38_3_39518499_39534447_39571894_39578360_RF	5227.376758	147	-1.422	0
134	Hg38_18_34889295_34890326_35083399_35092622_RR	7546.609989	292	-1.421	0
135	Hg38_3_52500907_52509286_52542416_52548124_RF	5037.934163	138	-1.421	0
136	Hg38_3_52542416_52548124_52570196_52574410_FF	4864.647822	126	-1.421	0
137	Hg38_X_109485286_109494606_109613112_109617390_RR	6064.912335	194	-1.42	0
138	Hg38_7_148843816_148853209_148905600_148909514_FF	4627.431815	119	-1.42	0
139	Hg38_11_7448008_7457037_7491523_7495793_RR	7829.755413	306	-1.419	0
140	Hg38_21_44873351_44875256_45059036_45065042_FF	5784.979186	171	-1.418	0

Table 1B (part 3a)79

136	0	Healthy Control	TGTTGAGGGTGTCCGGAGCATCAAATCTCGAAATTCATGACTTAAAGTGTAAATCCCTAG
137	0	Healthy Control	AGGGTTAGGTGAAAAATCTAAAGGAAGGTCGATGATGAAAATGTTTGGAGTTGATAGTG
138	0	Healthy Control	GGCAGGCAGATCACTTGAGGTCAGGAATTCGAAGACTAAATTGTACTACTTAAAAAGAAA
139	0	Healthy Control	TGGTGAGGGTGTTCATTAGCTTTTCGATTTATTATTTTAGAGGTTCTCTATCTA
140	0	Healthy Control	TTTGCAGGTGTGTGGTTAACACTATCCTTCGAGGAGAAAAGTCTCTGCCGTCCTGTGCGG
141	0	Healthy Control	TATAATTGAGGGTGTAATTGCAATGGGCTCGAGTGTGTTTGGGTCGGAGTGTGCTGTTT
142	0	Healthy Control	CCATGCTAATGCTTACCAAAGTGTGACCTCGAGGAGACAGCCGTTGTCCCGAGGGCTCCT
143	0	Healthy Control	TAGATGATCATATATCATACAAACCACTTCGAGGACACCCGGGATTAGCCAGGGAGGCC
144	0	Healthy Control	GACAGGCAGATCACTTGAGGTCAGGCATTGCAACATGCTCCTTAAGGACCACCGCTACA
145	0	Healthy Control	CCAAATAGAACTTACTTTTTTTTTTTCGAGGCCGAGTGAGTTGTGATCATACCACT
146	0	Healthy Control	GGCAGGTGGATCACTTGAGGTCAGCAATTCGAACACCTACCAATGTTATTTTTTTCACC
147	0	Healthy Control	TGTAGCCAGAGTGGATGTTATCTAATATCGAATATTAGTAGTCCCGTGGCAAGCCTTTG
148	0	Healthy Control	GGCAGGCAGATCACTTGAGGCCAGGAATTCGACAATAGCAAGACCACCTTTGCTAGCCAG
149	0	Healthy Control	CAGGCAGGCAGAATGCACCATCAATGAATCGATTCTGATGACATGGTTGTTCTCTCTGTT
150	0	Healthy Control	GGCAGGTGGATCATTTGTGGTCAGCAGTTCGATCTCCTGGATTCAATTGATCCTCGCATC

Table 1B (part 3b)

No.	Probe Location				
	Chr	Start1	End1	Start2	End2
101	7	148853178	148853207	149053900	149053929
102	5	150134629	150134658	150278668	150278697
103	X	46398624	46398653	46508958	46508987
104	3	52548093	52548122	52688438	52688467
105	13	77933720	77933749	77995327	77995356
106	X	77891628	77891657	78036860	78036889
107	5	132755647	132755676	132998902	132998931
108	8	65438114	65438143	65630949	65630978
109	5	94514374	94514403	94641713	94641742
110	2	13854395	13854424	13998016	13998045
111	18	46962768	46962797	47121692	47121721
112	X	46508958	46508987	46604757	46604786
113	11	83253503	83253532	83442625	83442654
114	5	34366019	34366048	34527906	34527935
115	18	46962768	46962797	47058017	47058046
116	19	45212373	45212402	45414204	45414233
117	3	126755035	126755064	126854220	126854249
118	12	6598575	6598604	6683579	6683608
119	9	87096091	87096120	87143572	87143601
120	3	52548093	52548122	52701274	52701303
121	17	17926105	17926134	18142964	18142993
122	3	126604178	126604207	126854220	126854249
123	2	27495025	27495054	27657041	27657070
124	20	45584742	45584771	45643174	45643203
125	3	126627402	126627431	126854220	126854249
126	4	112653710	112653739	112867643	112867672
127	17	17849812	17849841	17926105	17926134
128	15	88883844	88883873	88906627	88906656
129	5	132755647	132755676	132795182	132795211
130	8	65438114	65438143	65633324	65633353

131	4	145339445	145339474	145450587	145450616
132	X	155870710	155870739	155953720	155953749
133	3	39518501	39518530	39578329	39578358
134	18	34889297	34889326	35083401	35083430
135	3	52500909	52500938	52548093	52548122
136	3	52548093	52548122	52574379	52574408
137	X	109485288	109485317	109613114	109613143
138	7	148853178	148853207	148909483	148909512
139	11	7448010	7448039	7491525	7491554
140	21	44875225	44875254	45065011	45065040
141	6	3041216	3041245	3146780	3146809
142	8	142903861	142903890	143073686	143073715
143	17	44261861	44261890	44489969	44489998
144	1	224692839	224692868	224812314	224812343
145	17	17735039	17735068	17926105	17926134
146	4	36105086	36105115	36290918	36290947
147	5	132681704	132681733	132755647	132755676
148	7	143128015	143128044	143341325	143341354
149	22	29469297	29469326	29549135	29549164
150	2	223382063	223382092	223446118	223446147

Table 1B (part 3c)

No.	4 kb Sequence Location				
	Chr	Start1	End1	Start2	End2
101	7	148849208	148853207	149049930	149053929
102	5	150134629	150138628	150274698	150278697
103	X	46398624	46402623	46504988	46508987
104	3	52544123	52548122	52688438	52692437
105	13	77929750	77933749	77995327	77999326
106	X	77891628	77895627	78036860	78040859
107	5	132755647	132759646	132994932	132998931
108	8	65434144	65438143	65626979	65630978
109	5	94510404	94514403	94641713	94645712
110	2	13850425	13854424	13994046	13998045
111	18	46958798	46962797	47121692	47125691
112	X	46504988	46508987	46600787	46604786
113	11	83253503	83257502	83438655	83442654
114	5	34366019	34370018	34527906	34531905
115	18	46958798	46962797	47058017	47062016
116	19	45208403	45212402	45410234	45414233
117	3	126755035	126759034	126850250	126854249
118	12	6594605	6598604	6679609	6683608
119	9	87096091	87100090	87143572	87147571
120	3	52544123	52548122	52697304	52701303
121	17	17926105	17930104	18138994	18142993
122	3	126604178	126608177	126850250	126854249
123	2	27491055	27495054	27657041	27661040
124	20	45580772	45584771	45643174	45647173
125	3	126627402	126631401	126850250	126854249
126	4	112653710	112657709	112867643	112871642

127	17	17845842	17849841	17926105	17930104
128	15	88879874	88883873	88902657	88906656
129	5	132755647	132759646	132791212	132795211
130	8	65434144	65438143	65633324	65637323
131	4	145339445	145343444	145446617	145450616
132	X	155866740	155870739	155953720	155957719
133	3	39518501	39522500	39574359	39578358
134	18	34889297	34893296	35083401	35087400
135	3	52500909	52504908	52544123	52548122
136	3	52544123	52548122	52570409	52574408
137	X	109485288	109489287	109613114	109617113
138	7	148849208	148853207	148905513	148909512
139	11	7448010	7452009	7491525	7495524
140	21	44871255	44875254	45061041	45065040
141	6	3041216	3045215	3146780	3150779
142	8	142899891	142903890	143073686	143077685
143	17	44261861	44265860	44485999	44489998
144	1	224692839	224696838	224808344	224812343
145	17	17731069	17735068	17926105	17930104
146	4	36101116	36105115	36290918	36294917
147	5	132677734	132681733	132755647	132759646
148	7	143128015	143132014	143337355	143341354
149	22	29465327	29469326	29549135	29553134
150	2	223382063	223386062	223446118	223450117

Table 1B (part 3d)

No.	probe	Primer ID
101	Hg38_7_148843816_148853209_149049131_149053931_FF	OBD160.1201
102	Hg38_5_150134627_150137703_150272362_150278699_RF	OBD160.1205
103	Hg38_X_46398622_46399662_46498682_46508989_RF	OBD160.1209
104	Hg38_3_52542416_52548124_52688436_52689750_FR	OBD160.1213
105	Hg38_13_77929805_77933751_77995325_78000878_FR	OBD160.1217
106	Hg38_X_77891626_77893835_78036858_78043877_RR	OBD160.1221
107	Hg38_5_132755645_132763810_132995308_132998933_RF	OBD160.1225
108	Hg38_8_65429758_65438145_65628655_65630980_FF	OBD160.1229
109	Hg38_5_94505842_94514405_94641711_94646370_FR	OBD160.1233
110	Hg38_2_13845156_13854426_13990532_13998047_FF	OBD160.1237
111	Hg38_18_46958975_46962799_47121690_47124504_FR	OBD160.1241
112	Hg38_X_46498682_46508989_46603634_46604788_FF	OBD160.1245
113	Hg38_11_83253501_83261801_83434843_83442656_RF	OBD160.1249
114	Hg38_5_34366017_34372954_34527904_34530421_RR	OBD160.1253
115	Hg38_18_46958975_46962799_47058015_47062163_FR	OBD160.1257
116	Hg38_19_45210518_45212404_45410404_45414235_FF	OBD160.1261
117	Hg38_3_126755033_126764525_126843341_126854251_RF	OBD160.1265
118	Hg38_12_6595585_6598606_6681014_6683610_FF	OBD160.1269
119	Hg38_9_87096089_87101882_87143570_87148986_RR	OBD160.1273
120	Hg38_3_52542416_52548124_52699561_52701305_FF	OBD160.1277
121	Hg38_17_17926103_17934669_18141138_18142995_RF	OBD160.1281
122	Hg38_3_126604176_126607234_126843341_126854251_RF	OBD160.1285
123	Hg38_2_27492451_27495056_27657039_27659544_FR	OBD160.1289

124	Hg38_20_45581538_45584773_45643172_45649623_FR	OBD160.1293
125	Hg38_3_126627400_126630792_126843341_126854251_RF	OBD160.1297
126	Hg38_4_112653708_112659532_112867641_112872043_RR	OBD160.1301
127	Hg38_17_17840582_17849843_17926103_17934669_FR	OBD160.1305
128	Hg38_15_88873420_88883875_88904252_88906658_FF	OBD160.1309
129	Hg38_5_132755645_132763810_132790667_132795213_RF	OBD160.1313
130	Hg38_8_65429758_65438145_65633322_65635344_FR	OBD160.1317
131	Hg38_4_145339443_145344834_145441661_145450618_RF	OBD160.1321
132	Hg38_X_155860883_155870741_155953718_155958970_FR	OBD160.1325
133	Hg38_3_39518499_39534447_39571894_39578360_RF	OBD160.1329
134	Hg38_18_34889295_34890326_35083399_35092622_RR	OBD160.1333
135	Hg38_3_52500907_52509286_52542416_52548124_RF	OBD160.1337
136	Hg38_3_52542416_52548124_52570196_52574410_FF	OBD160.1341
137	Hg38_X_109485286_109494606_109613112_109617390_RR	OBD160.1345
138	Hg38_7_148843816_148853209_148905600_148909514_FF	OBD160.1349
139	Hg38_11_7448008_7457037_7491523_7495793_RR	OBD160.1353
140	Hg38_21_44873351_44875256_45059036_45065042_FF	OBD160.1357
141	Hg38_6_3041214_3044157_3146778_3149848_RR	OBD160.1361
142	Hg38_8_142901645_142903892_143073684_143079751_FR	OBD160.1365
143	Hg38_17_44261859_44271957_44488590_44490000_RF	OBD160.1369
144	Hg38_1_224692837_224704390_224807715_224812345_RF	OBD160.1373
145	Hg38_17_17728293_17735070_17926103_17934669_FR	OBD160.1377
146	Hg38_4_36078971_36105117_36290916_36293184_FR	OBD160.1381
147	Hg38_5_132679860_132681735_132755645_132763810_FR	OBD160.1385
148	Hg38_7_143128013_143133284_143335881_143341356_RF	OBD160.1389
149	Hg38_22_29467180_29469328_29549133_29556322_FR	OBD160.1393
150	Hg38_2_223382061_223395131_223446116_223450606_RR	OBD160.1397

Table 1B (part 3e)

No.	Primer Sequence	Primer ID	Primer Sequence
101	CATTAGTTAGATTCTCATAAGGATGGC	OBD160.1203	GGAATCTCAGTCACTCAACTACAAAAT
102	ACAGGACAGGGCAGGAGAGGCAACGAG	OBD160.1207	CGTGGGCTTCTCCCTAATGATGCCGAG
103	AGATTTTGGGCTGAGACAATGGG	OBD160.1211	GCTGCTACATTGTGGTAACCTCTTA
104	ATTATCCTCCTTTGTTCTTCCCC	OBD160.1215	ATGCTTACAGGCAGAACCAAGTTTGTGC
105	GTGGTAAAGTGTGAGGATGGCA	OBD160.1219	CTTGGGAGAAAGAGACAGATAGC
106	CTATTGCTAAATGGAATGCTACCTGCT	OBD160.1223	TTTCCCAATACCGTCCCTCCTGTGG
107	GAGGTTGTGGAGGAGGCTGAGGATGAGG	OBD160.1227	GGGATGGAGGGAAGAGTCACAGGAAAGT
108	CAAGTCTACAGTAACCAAAACAGCAT	OBD160.1231	GCAGTTGGTGCTCTGTATCCACA
109	ATCTCAAACCTGGTAATAATCAGC	OBD160.1235	AATGCTGAGAAAGCCCCAAACCCA
110	GCCTACCACTCTGCCTCACTTGCTCC	OBD160.1239	GCACAAGGGAAAATGGAGGGAGAAAGGA
111	GGCAGTGGCTGGGTGTGGGAGGC	OBD160.1243	AAAGGTAACCTGAGAGTGGAGATGCGGG
112	AGATTTTGGGCTGAGACAATGGG	OBD160.1247	GGGATTACAGGCATAAGCCACTG
113	CCAGGATGAGCCAGAAGGAGTTTCACAA	OBD160.1251	TCACTGAAGGTTCCAAATCTCCCAAT
114	GCACCTTACTTACTGTATCTCTTCAG	OBD160.1255	CCTGCCTCAGCCTCCAAAGTAGC
115	CCGTCGCAAGTTTCGTTCCCAACCCGC	OBD160.1259	GTCCCTGTCTTCCCCGCTGTGG
116	CTCCCTCTACCTCCACTACCTGCCAG	OBD160.1263	AGGAGGGCAGGGCTGGGTACAG
117	GGCAGAAAGGAAAGAGCCTCGCAGCATT	OBD160.1267	CCAGCCAGGGATGTTACCCAGAGCCCC
118	TGCCTGAAATCCAGCACCTTGG	OBD160.1271	TGGCACACACCTGTAGTCCCAGC
119	GAGCCCTGAGCCCTCCTGACCA	OBD160.1275	GAAGCCAGGAGAAATGAAATGATGGGTG
120	ATTATCCTCCTTTGTTCTTCCCC	OBD160.1279	CACTTGACAAACCCACAGCACAGAAA

121	CTCCCCACTACCCCAACCCAGGC	OBD160.1283	CCGCATCTCCCCTTGCCAGTCCAGAC
122	GGCAGAAAGGAAAGAGCCTCGCAGCATT	OBD160.1287	GCAAACAAGGAAACCCCAAGCAGAGAAG
123	CCTATTTTCTCTACGCCCTCCCGCCCC	OBD160.1291	GGTGAGGCGACCCTGTTGAAAAGTGGGC
124	GGTAAAGTGTGGGAAGGCGAAA	OBD160.1295	CAGAGATGAGGTTTTCTATGTTGGC
125	GTCATTCTCCCCTCTCATCTTACCTA	OBD160.1299	CACACTCCTTAGGTAACAGAACATTTT
126	TGTCTGTAATCCAGCACTTTGG	OBD160.1303	CCAAGAGAAATGAAAATGTTATGTCCAC
127	TCCCCTCCCTGTCTGGACCCTGG	OBD160.1307	CCGCATCTCCCCTTGCCAGTCCAGAC
128	AGTGGCTCACGCCTGTAATCCTA	OBD160.1311	TGGACCACAGCCCTTCTTTCGGG
129	CAAGGACAATCAATGGCTGCTCACATCA	OBD160.1315	GGGATGGAGGGAAGAGTCACAGGAAAGT
130	CAAGTCTACAGTAACCAAAACAGCAT	OBD160.1319	TGAGATAACTGAGGCTCTAAGAACTT
131	CTGCCCTCAGAGAGTAAAGAGACAGGAC	OBD160.1323	CTGTTAGGCTCAAAGGTTGGGTATGGGC
132	TCTCTACCTCTCTACACACTTTATTGA	OBD160.1327	CAAGAGTCTAATCCCAAAACCCCAACCAG
133	TGGTAAAGTGTTAGGACGGTGAAAAT	OBD160.1331	GGAAGTATTTTCAGTGTATTTTCAGAGAC
134	GTCAGGACTTGGCTGGGCACCTACC	OBD160.1335	GCACTGGGAGCACAGGGCAGGAATGGTG
135	ATTATCCTCCTTGTTCTTCCCC	OBD160.1339	TGCCACTTCCCCTGCTCAGGG
136	ATTATCCTCCTTGTTCTTCCCC	OBD160.1343	CCCATTGAGACAGAGCAGACCCATTT
137	GCTAACAGTGCCAGTTGAAAGGAGATGC	OBD160.1347	CCCAGACAGGAGTGCCTTTGGAGTGGC
138	CATTAGTAGATTCTCATAAGGATGGC	OBD160.1351	GAATAGGACTGCCTGATAACTTGTAT
139	GCCTCCCCATTTCTCCTCAGTTTCACAA	OBD160.1355	CTATGGCAAGGAGAGGCTGTAGGAGC
140	CTCTGTTCGCTACCCAGGTCCACACC	OBD160.1359	GGCGGGAGACCCCTTGCCCTGAA
141	ACTTGTCTCCATTCTGGTGTGTTGG	OBD160.1363	CCGACCCAAACCAGCACTCCAGCCG
142	CAGAGAACAGAGAGGACTGAAGC	OBD160.1367	GACGACGGCTGTCTCCTCAAACA
143	GCCTCCTAACCCACCTCCCCACC	OBD160.1371	CACCTAGGGCTCTGCCGTACCTTGGAG
144	CGTCTTCCACCCTGGGCTGTTCGTCCC	OBD160.1375	CGGACCCATCAACAGTGAGCCAAGCATC
145	CCTGCCTGTGTCTGCGTGTGAGC	OBD160.1379	CCGCATCTCCCCTTGCCAGTCCAGAC
146	GGCTCCCACCCTGTTAGAGATGTGACG	OBD160.1383	CCTAACCACTCTTCTTCCACAGCCCACA
147	GCTGGAGTGGGCTCACCGAGGATAGGG	OBD160.1387	GGGATGGAGGGAAGAGTCACAGGAAAGT
148	TGTCCACAGTATGATTCTCGGGTTTCA	OBD160.1391	TACAGTGGTGTACAGGTTATGGGAGGG
149	CCTCTTCCCAATGTCTCTTTTAGC	OBD160.1395	GGAGGAAAATAGTTGAGCAGGAACAAT
150	CGATGGCTCATAGTCTGTAATCCAAGC	OBD160.1399	CACCTTGAGAGCCTGAAGCAGCAGCATC

Table 1B (part 3f)

No.	probe	Markers
101	Hg38_7_148843816_148853209_149049131_149053931_FF	OBD160.1201.1203
102	Hg38_5_150134627_150137703_150272362_150278699_RF	OBD160.1205.1207
103	Hg38_X_46398622_46399662_46498682_46508989_RF	OBD160.1209.1211
104	Hg38_3_52542416_52548124_52688436_52689750_FR	OBD160.1213.1215
105	Hg38_13_77929805_77933751_77995325_78000878_FR	OBD160.1217.1219
106	Hg38_X_77891626_77893835_78036858_78043877_RR	OBD160.1221.1223
107	Hg38_5_132755645_132763810_132995308_132998933_RF	OBD160.1225.1227
108	Hg38_8_65429758_65438145_65628655_65630980_FF	OBD160.1229.1231
109	Hg38_5_94505842_94514405_94641711_94646370_FR	OBD160.1233.1235
110	Hg38_2_13845156_13854426_13990532_13998047_FF	OBD160.1237.1239
111	Hg38_18_46958975_46962799_47121690_47124504_FR	OBD160.1241.1243
112	Hg38_X_46498682_46508989_46603634_46604788_FF	OBD160.1245.1247
113	Hg38_11_83253501_83261801_83434843_83442656_RF	OBD160.1249.1251
114	Hg38_5_34366017_34372954_34527904_34530421_RR	OBD160.1253.1255
115	Hg38_18_46958975_46962799_47058015_47062163_FR	OBD160.1257.1259
116	Hg38_19_45210518_45212404_45410404_45414235_FF	OBD160.1261.1263
117	Hg38_3_126755033_126764525_126843341_126854251_RF	OBD160.1265.1267

118	Hg38_12_6595585_6598606_6681014_6683610_FF	OBD160.1269.1271
119	Hg38_9_87096089_87101882_87143570_87148986_RR	OBD160.1273.1275
120	Hg38_3_52542416_52548124_52699561_52701305_FF	OBD160.1277.1279
121	Hg38_17_17926103_17934669_18141138_18142995_RF	OBD160.1281.1283
122	Hg38_3_126604176_126607234_126843341_126854251_RF	OBD160.1285.1287
123	Hg38_2_27492451_27495056_27657039_27659544_FR	OBD160.1289.1291
124	Hg38_20_45581538_45584773_45643172_45649623_FR	OBD160.1293.1295
125	Hg38_3_126627400_126630792_126843341_126854251_RF	OBD160.1297.1299
126	Hg38_4_112653708_112659532_112867641_112872043_RR	OBD160.1301.1303
127	Hg38_17_17840582_17849843_17926103_17934669_FR	OBD160.1305.1307
128	Hg38_15_88873420_88883875_88904252_88906658_FF	OBD160.1309.1311
129	Hg38_5_132755645_132763810_132790667_132795213_RF	OBD160.1313.1315
130	Hg38_8_65429758_65438145_65633322_65635344_FR	OBD160.1317.1319
131	Hg38_4_145339443_145344834_145441661_145450618_RF	OBD160.1321.1323
132	Hg38_X_155860883_155870741_155953718_155958970_FR	OBD160.1325.1327
133	Hg38_3_39518499_39534447_39571894_39578360_RF	OBD160.1329.1331
134	Hg38_18_34889295_34890326_35083399_35092622_RR	OBD160.1333.1335
135	Hg38_3_52500907_52509286_52542416_52548124_RF	OBD160.1337.1339
136	Hg38_3_52542416_52548124_52570196_52574410_FF	OBD160.1341.1343
137	Hg38_X_109485286_109494606_109613112_109617390_RR	OBD160.1345.1347
138	Hg38_7_148843816_148853209_148905600_148909514_FF	OBD160.1349.1351
139	Hg38_11_7448008_7457037_7491523_7495793_RR	OBD160.1353.1355
140	Hg38_21_44873351_44875256_45059036_45065042_FF	OBD160.1357.1359
141	Hg38_6_3041214_3044157_3146778_3149848_RR	OBD160.1361.1363
142	Hg38_8_142901645_142903892_143073684_143079751_FR	OBD160.1365.1367
143	Hg38_17_44261859_44271957_44488590_44490000_RF	OBD160.1369.1371
144	Hg38_1_224692837_224704390_224807715_224812345_RF	OBD160.1373.1375
145	Hg38_17_17728293_17735070_17926103_17934669_FR	OBD160.1377.1379
146	Hg38_4_36078971_36105117_36290916_36293184_FR	OBD160.1381.1383
147	Hg38_5_132679860_132681735_132755645_132763810_FR	OBD160.1385.1387
148	Hg38_7_143128013_143133284_143335881_143341356_RF	OBD160.1389.1391
149	Hg38_22_29467180_29469328_29549133_29556322_FR	OBD160.1393.1395
150	Hg38_2_223382061_223395131_223446116_223450606_RR	OBD160.1397.1399

Table 1B (part 3g)

No.	probe	RP/Rsum	Rprank	FC:(class1 /class2)	pfp
151	Hg38_3_52542416_52548124_52606123_52609751_FF	5189.071535	145	-1.414	0
152	Hg38_8_143012831_143021167_143073684_143079751_FR	3503.491132	63	-1.414	0
153	Hg38_1_212366521_212376213_212547138_212548374_RR	4620.284986	118	-1.413	0
154	Hg38_X_46498682_46508989_46602210_46603634_FR	6204.522114	202	-1.412	0
155	Hg38_21_44873351_44875256_44906478_44910319_FR	6433.604863	223	-1.412	0
156	Hg38_9_78097129_78101713_78276332_78285196_FF	6925.240863	254	-1.412	0
157	Hg38_3_126673758_126686020_126843341_126854251_RF	6344.512786	216	-1.411	0
158	Hg38_17_68575027_68578789_68785810_68796098_RF	5846.061342	177	-1.411	0
159	Hg38_5_24349034_24361029_24564285_24566267_FR	5934.820934	184	-1.411	0
160	Hg38_11_7448008_7457037_7633311_7640164_RR	8160.203972	325	-1.411	0
161	Hg38_7_27161846_27163700_27302548_27312509_FF	4965.220225	134	-1.411	0
162	Hg38_13_80339373_80340696_80530340_80535867_RF	6070.077564	196	-1.409	0
163	Hg38_9_4966910_4970390_5177459_5185304_FR	5825.482506	175	-1.409	0

164	Hg38_3_126843341_126854251_127025761_127027674_FR	6302.840977	212	-1.409	0
165	Hg38_2_13845156_13854426_13894360_13900303_FR	4127.259421	90	-1.409	0
166	Hg38_3_126619219_126620249_126843341_126854251_RF	6736.278815	243	-1.409	0
167	Hg38_11_19587032_19595878_19772073_19777708_RF	5137.562086	143	-1.408	0
168	Hg38_3_107106310_107120834_107363175_107364266_RF	4138.382317	91	-1.408	0
169	Hg38_2_172327203_172330194_172401667_172407636_FF	7018.881201	259	-1.408	0
170	Hg38_2_27492451_27495056_27626184_27635183_FF	7280.572764	284	-1.407	0
171	Hg38_6_108138075_108144989_108280425_108286846_RR	5889.114204	182	-1.407	0
172	Hg38_12_95793441_95797455_95929302_95940423_FR	4522.319776	109	-1.407	0
173	Hg38_17_34470224_34473967_34596926_34605729_RF	181704.137	102782	-1.406	0.2035 24936
174	Hg38_3_52542416_52548124_52770196_52773754_FR	5666.285584	164	-1.405	0
175	Hg38_1_186902459_186905074_187113187_187139713_RR	6803.129009	247	-1.405	0
176	Hg38_X_46498682_46508989_46576307_46579924_FR	5869.244424	180	-1.405	0
177	Hg38_6_3017794_3021910_3146778_3149848_RR	6256.127058	207	-1.403	0
178	Hg38_1_32149028_32153363_32237144_32241139_RF	6853.104399	250	-1.402	0
179	Hg38_11_316800_318015_481419_487611_FR	7179.47109	277	-1.402	0
180	Hg38_15_53424923_53427397_53442412_53454683_FF	7090.153633	268	-1.401	0
181	Hg38_17_68666853_68670189_68785810_68796098_RF	6909.88586	253	-1.401	0
182	Hg38_11_7448008_7457037_7610329_7615891_RR	9210.499261	399	-1.401	0
183	Hg38_17_77934896_77938750_78117632_78120001_RF	6333.571605	214	-1.4	0
184	Hg38_5_43590188_43596508_43695191_43701837_RR	5995.126969	190	-1.4	0
185	Hg38_1_60428956_60435934_60549270_60560051_FR	6237.112636	206	-1.399	0
186	Hg38_5_150272362_150278699_150370575_150373999_FF	6930.555298	255	-1.398	0
187	Hg38_9_130859900_130867193_130899377_130901466_RR	6344.951249	217	-1.398	0
188	Hg38_1_91404825_91416231_91606200_91614477_FR	3987.770204	84	-1.397	0
189	Hg38_14_91576230_91580637_91629033_91639298_RR	5505.97469	156	-1.397	0
190	Hg38_2_27349601_27353190_27492451_27495056_RF	7684.120774	302	-1.396	0
191	Hg38_5_150051979_150055894_150272362_150278699_RF	6705.504005	240	-1.396	0
192	Hg38_1_185167238_185172841_185287397_185290374_FR	6618.356808	234	-1.395	0
193	Hg38_3_112416500_112418982_112549606_112554897_FF	6393.210055	220	-1.395	0
194	Hg38_6_132376734_132385044_132542354_132547678_FR	6379.766204	219	-1.395	0
195	Hg38_1_189027657_189033909_189210801_189218947_FR	5745.204415	170	-1.395	0
196	Hg38_2_233409972_233419808_233475741_233480083_FR	8183.893064	330	-1.395	0
197	Hg38_17_35250006_35254814_35287155_35289074_RF	7536.563459	291	-1.395	0
198	Hg38_5_140984243_140987011_141123576_141128793_FF	5530.550379	157	-1.394	0
199	Hg38_13_40670004_40674221_40797038_40804771_RR	6292.929057	210	-1.394	0
200	Hg38_15_34800440_34807454_35007401_35010342_RR	5850.979126	179	-1.393	0

Table 1B (part 4a)

No.	P.v.a lue	Type	Probe sequence
			60 mer
151	0	Healthy Control	TGTTGAGGGTGTCCCGGAGCATCAAATCTCGAAGTCACATGATGGCCAACAAGTACCAAG
152	0	Healthy Control	CTGTGTGTTTGAGTGTCTGCTTGACCTGCTCGAGGAGACAGCCGTTGTCCCGAGGGTCTCT
153	0	Healthy Control	GAGGCAGGCGGATCACGAGGTCATAAGATCGAATTTCCAGTTTCTAAAAAGTTAAGAAT
154	0	Healthy Control	ACAGAGCCCTCAGAAATAATGCCGCATATCGAAGGCTCCAAGGTTTTCGTGATCTTTCA
155	0	Healthy Control	TTTGAGGTGTGTGGTTAACACTATCCTTCGAAACAGGTGCTCTGGTCAAGTCAGTTTGG
156	0	Healthy Control	AGTGTGTGTGAGGAAATGCAGGGGTGAATCGAGCCCCTGCTTTCAATTCTTTGGATATA
157	0	Healthy Control	GCATATGCAGGTGTGGGCTTTTAAAAATCGAAATCCAGCTCCACTACTCACTAGTTGGT

158	0	Healthy Control	ATAATGGGCGATGTTTCTCAGGGCTGCTTCGATAGGTACAACATTATGTATCAATATTT
159	0	Healthy Control	GGAGGGGAACATTACACACTGGGGCTGTCGAATGCTTTATCTGGACCTACTTTTGTGAA
160	0	Healthy Control	TGGTGAGGGTGTGTTTTCATTAGCTTTTTCGAAGCTTTCTAGGGAAGGCCATGCTTCTC
161	0	Healthy Control	TGACCTGCCTCTCGGTGAGGTTGAGCAGTCGAAGTAATGAAGAGGGAGGTGGTTTTCTTT
162	0	Healthy Control	CAGGTGTGCCATGATTAACTTTTAATTCGAGAGAAAAAAGATATCATATTTCTT
163	0	Healthy Control	GGCAGGCGGATCACTTGAGGCCAGGATTGACACACAGAGCTGTGTGGAGTCTCAGCAG
164	0	Healthy Control	GCATATGCAGGTGTGGGCTTTTAAAAATCGACAGATGAATGAATAAGCAAAATGTGGTC
165	0	Healthy Control	GGCAGGCAGATCACTTGAGGTACAGAGTTCGATCATTTCAAGAACCTACCTTCAAGTTCA
166	0	Healthy Control	GCATATGCAGGTGTGGGCTTTTAAAAATCGAAAGGAAAGAATCAGTGTATCAAAAAGAT
167	0	Healthy Control	GGAGGTGTGTGTGTTTAAACCAGGAAAGTCGAGCTTCACGGCCGCTTTGTTTACCTACTC
168	0	Healthy Control	GGCGGGCAGATCACTTGAGGTGAGAACTTCGAACCTGCTTTCTATTTTACGAGCATTG
169	0	Healthy Control	AGGGCAGGGGCTAGGATGAAAGGCCGTCGATCAATGGATAAAAAACAAATATAAGAGCT
170	0	Healthy Control	GGGCGCGGGTCTGCGGAGCCCCCAGGGCTCGATGTGTCCATTACATAGATGACAACTGTT
171	0	Healthy Control	AAGGCAGGCGGATCACGAGGTGAGTAGATCGAAGATTACTCTGTGATTTTCTCCAATTAT
172	0	Healthy Control	GGCAGGCAGATCACTTGAGGTGAGGAATTCGAGGTGCCATCTGTCACCCCTTTCTTTGAC
	0.0 225 233		
173	05	Healthy Control	GAAACAGTGAGTGTTTATTTCTCGTGAGTCGAAGCCTTTATCAAAGTCTCAAAGGGGTCT
174	0	Healthy Control	TGTTGAGGGTGTCGGGAGCATCAAATCTCGAGTTTAAAGTAATCCAGCAGTCTACAGT
175	0	Healthy Control	ATAATGGGCGATGTTTCTCAGGGCTGCTTCGATACAAAGAGATGGCCAGATTTTATCTGA
176	0	Healthy Control	ACAGAGCCCTCAGAAATAATGCCGATATCGACAAGACCTCAGGGTTGGGTGTCCTCCAC
177	0	Healthy Control	CCCCTCAAGAACGAGCTCTCCCTGTCTCGAGTGCTGGTTGGGTGCGAGTGCTGGTTC
178	0	Healthy Control	AAGGGCTCGGGAGCTCCCTCGGCACACCTCGATTCTGTTTCTTTCTTCTTCTTTATT
179	0	Healthy Control	GAGCTGGGTTAGGGTTGGGAAGACAGCTTCGAATCTGCAAGCTGTTTGGGAGTAGTGT
180	0	Healthy Control	AGAATGGGCGATGTTTCTCAGGGCTGCTTCGAGCATATGCTACACAGTGGAGCAACCTTC
181	0	Healthy Control	ATAATGGGCGATGTTTCTCAGGGCTGCTTCGAATGGTAGTTCTGCGTTTACTCTTTGAG
182	0	Healthy Control	TGGTGAGGGTGTGTTTTCATTAGCTTTTTCGATCTGATGACTGAAGTGTCTGAGCTGAAG
183	0	Healthy Control	TTTTATTATTATTAATTCATATATTCTCGAAGGTGTGTGGATTCTTCTGTTTCTGCT
184	0	Healthy Control	AGCAGGCAGATCACTTGAGGTGAGGAGTTCGAAAACAATTTCTACTTGTCTGGGCAAAA
185	0	Healthy Control	AGGGACAGCCAGCCAGCCACAGATGATGTCGATCAGACTAGATATCTGTTTGTGAGCTA
186	0	Healthy Control	AGTGCCTGTGAAAGTGTCTGAATTCCTCGATCAGCTTCACACTCTCACTCCTGGAG
187	0	Healthy Control	AAGGAGGGCAGATCACGAGGTGAGGCGTTCGATAAACTGGATTTTATTAATAAACTC
188	0	Healthy Control	ATGTGTTTGCTTATTTATCATTAAATTCGAACATCTTAGAGACCAAGACCAAAAGGGG
189	0	Healthy Control	GGCAGGAGGATCACTTGAGGCCAGGCATTGAAAACCTATATCTATACAAAACCTGCAAA
190	0	Healthy Control	GGGCGCGGGTCTGCGGAGCCCCAGGGCTCGAATTTAGGGGGGAAACATTAATAGGAAT
191	0	Healthy Control	AGTGCCTGTGAAAGTGTCTGAATTCCTCGACAATGCCACTCACTATTACCTCTACAAC
192	0	Healthy Control	GCCGAGGTGGGCAGATCACGAGGTCAAATCGAAAGGATCAGGAATTGGAATAATTCCTCT
193	0	Healthy Control	AGAATGGGCGATGTTTCTCAGGGCTGCTTCGAAGTAAAAGAACAGAAACATAAAGTTTCT
194	0	Healthy Control	GAGAGGTGGGCAGGTGTTAGATTTAGTTTCGATTAAATCTTTTATATTTAAAAAAGTTGCC
195	0	Healthy Control	GGCAGGCAGATCACTTGAGGTGAGCAGTTCGACACAGACACCCTCCCAAGACTAAACCAG
196	0	Healthy Control	GGGTGTGGGTGGATTTCACCTTGTCTGTCGAAGGCAAAGCTTTTACGCGATTTCATTAA
197	0	Healthy Control	ATTGTTTAAGCCAGCCAGCCTATGGTATTGAACTACAGTTGAAGGCCTTATATGCAAA
198	0	Healthy Control	GGCAGGCAGATCACTTGAGGTGAGTTCGAAAAAAGAGTATTTCTTTTAGT
199	0	Healthy Control	TCGCTAGGCTGGAGCAGTGGTGTGATCTCGATCTTTGAGAACCTACTAGGTGTCAGTCT
200	0	Healthy Control	GGCGGCAGATCACTTGAGGCCAGGAGCTCGATCAGTGATGTTAAATTAATGAGCAGGA

Table 1B (part 4b)

No.	Probe Location				
	Chr	Start1	End1	Start2	End2
151	3	52548093	52548122	52609720	52609749
152	8	143021136	143021165	143073686	143073715

153	1	212366523	212366552	212547140	212547169
154	X	46508958	46508987	46602212	46602241
155	21	44875225	44875254	44906480	44906509
156	9	78101682	78101711	78285165	78285194
157	3	126673760	126673789	126854220	126854249
158	17	68575029	68575058	68796067	68796096
159	5	24360998	24361027	24564287	24564316
160	11	7448010	7448039	7633313	7633342
161	7	27163669	27163698	27312478	27312507
162	13	80339375	80339404	80535836	80535865
163	9	4970359	4970388	5177461	5177490
164	3	126854220	126854249	127025763	127025792
165	2	13854395	13854424	13894362	13894391
166	3	126619221	126619250	126854220	126854249
167	11	19587034	19587063	19777677	19777706
168	3	107106312	107106341	107364235	107364264
169	2	172330163	172330192	172407605	172407634
170	2	27495025	27495054	27635152	27635181
171	6	108138077	108138106	108280427	108280456
172	12	95797424	95797453	95929304	95929333
173	17	34470226	34470255	34605698	34605727
174	3	52548093	52548122	52770198	52770227
175	1	186902461	186902490	187113189	187113218
176	X	46508958	46508987	46576309	46576338
177	6	3017796	3017825	3146780	3146809
178	1	32149030	32149059	32241108	32241137
179	11	317984	318013	481421	481450
180	15	53427366	53427395	53454652	53454681
181	17	68666855	68666884	68796067	68796096
182	11	7448010	7448039	7610331	7610360
183	17	77934898	77934927	78119970	78119999
184	5	43590190	43590219	43695193	43695222
185	1	60435903	60435932	60549272	60549301
186	5	150278668	150278697	150373968	150373997
187	9	130859902	130859931	130899379	130899408
188	1	91416200	91416229	91606202	91606231
189	14	91576232	91576261	91629035	91629064
190	2	27349603	27349632	27495025	27495054
191	5	150051981	150052010	150278668	150278697
192	1	185172810	185172839	185287399	185287428
193	3	112418951	112418980	112554866	112554895
194	6	132385013	132385042	132542356	132542385
195	1	189033878	189033907	189210803	189210832
196	2	233419777	233419806	233475743	233475772
197	17	35250008	35250037	35289043	35289072
198	5	140986980	140987009	141128762	141128791
199	13	40670006	40670035	40797040	40797069
200	15	34800442	34800471	35007403	35007432

Table 1B (part 4c)

No.	4 kb Sequence Location				
	Chr	Start1	End1	Start2	End2
151	3	52544123	52548122	52605750	52609749
152	8	143017166	143021165	143073686	143077685
153	1	212366523	212370522	212547140	212551139
154	X	46504988	46508987	46602212	46606211
155	21	44871255	44875254	44906480	44910479
156	9	78097712	78101711	78281195	78285194
157	3	126673760	126677759	126850250	126854249
158	17	68575029	68579028	68792097	68796096
159	5	24357028	24361027	24564287	24568286
160	11	7448010	7452009	7633313	7637312
161	7	27159699	27163698	27308508	27312507
162	13	80339375	80343374	80531866	80535865
163	9	4966389	4970388	5177461	5181460
164	3	126850250	126854249	127025763	127029762
165	2	13850425	13854424	13894362	13898361
166	3	126619221	126623220	126850250	126854249
167	11	19587034	19591033	19773707	19777706
168	3	107106312	107110311	107360265	107364264
169	2	172326193	172330192	172403635	172407634
170	2	27491055	27495054	27631182	27635181
171	6	108138077	108142076	108280427	108284426
172	12	95793454	95797453	95929304	95933303
173	17	34470226	34474225	34601728	34605727
174	3	52544123	52548122	52770198	52774197
175	1	186902461	186906460	187113189	187117188
176	X	46504988	46508987	46576309	46580308
177	6	3017796	3021795	3146780	3150779
178	1	32149030	32153029	32237138	32241137
179	11	314014	318013	481421	485420
180	15	53423396	53427395	53450682	53454681
181	17	68666855	68670854	68792097	68796096
182	11	7448010	7452009	7610331	7614330
183	17	77934898	77938897	78116000	78119999
184	5	43590190	43594189	43695193	43699192
185	1	60431933	60435932	60549272	60553271
186	5	150274698	150278697	150369998	150373997
187	9	130859902	130863901	130899379	130903378
188	1	91412230	91416229	91606202	91610201
189	14	91576232	91580231	91629035	91633034
190	2	27349603	27353602	27491055	27495054
191	5	150051981	150055980	150274698	150278697
192	1	185168840	185172839	185287399	185291398
193	3	112414981	112418980	112550896	112554895
194	6	132381043	132385042	132542356	132546355
195	1	189029908	189033907	189210803	189214802
196	2	233415807	233419806	233475743	233479742
197	17	35250008	35254007	35285073	35289072
198	5	140983010	140987009	141124792	141128791
199	13	40670006	40674005	40797040	40801039

200	15	34800442	34804441	35007403	35011402
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Table 1B (part 4d)

No.	probe	Primer ID
151	Hg38_3_52542416_52548124_52606123_52609751_FF	OBD160.1401
152	Hg38_8_143012831_143021167_143073684_143079751_FR	OBD160.1405
153	Hg38_1_212366521_212376213_212547138_212548374_RR	OBD160.1409
154	Hg38_X_46498682_46508989_46602210_46603634_FR	OBD160.1413
155	Hg38_21_44873351_44875256_44906478_44910319_FR	OBD160.1417
156	Hg38_9_78097129_78101713_78276332_78285196_FF	OBD160.1421
157	Hg38_3_126673758_126686020_126843341_126854251_RF	OBD160.1425
158	Hg38_17_68575027_68578789_68785810_68796098_RF	OBD160.1429
159	Hg38_5_24349034_24361029_24564285_24566267_FR	OBD160.1433
160	Hg38_11_7448008_7457037_7633311_7640164_RR	OBD160.1437
161	Hg38_7_27161846_27163700_27302548_27312509_FF	OBD160.1441
162	Hg38_13_80339373_80340696_80530340_80535867_RF	OBD160.1445
163	Hg38_9_4966910_4970390_5177459_5185304_FR	OBD160.1449
164	Hg38_3_126843341_126854251_127025761_127027674_FR	OBD160.1453
165	Hg38_2_13845156_13854426_13894360_13900303_FR	OBD160.1457
166	Hg38_3_126619219_126620249_126843341_126854251_RF	OBD160.1461
167	Hg38_11_19587032_19595878_19772073_19777708_RF	OBD160.1465
168	Hg38_3_107106310_107120834_107363175_107364266_RF	OBD160.1469
169	Hg38_2_172327203_172330194_172401667_172407636_FF	OBD160.1473
170	Hg38_2_27492451_27495056_27626184_27635183_FF	OBD160.1477
171	Hg38_6_108138075_108144989_108280425_108286846_RR	OBD160.1481
172	Hg38_12_95793441_95797455_95929302_95940423_FR	OBD160.1485
173	Hg38_17_34470224_34473967_34596926_34605729_RF	OBD160.1489
174	Hg38_3_52542416_52548124_52770196_52773754_FR	OBD160.1493
175	Hg38_1_186902459_186905074_187113187_187139713_RR	OBD160.1497
176	Hg38_X_46498682_46508989_46576307_46579924_FR	OBD160.1501
177	Hg38_6_3017794_3021910_3146778_3149848_RR	OBD160.1505
178	Hg38_1_32149028_32153363_32237144_32241139_RF	OBD160.1509
179	Hg38_11_316800_318015_481419_487611_FR	OBD160.1513
180	Hg38_15_53424923_53427397_53442412_53454683_FF	OBD160.1517
181	Hg38_17_68666853_68670189_68785810_68796098_RF	OBD160.1521
182	Hg38_11_7448008_7457037_7610329_7615891_RR	OBD160.1525
183	Hg38_17_77934896_77938750_78117632_78120001_RF	OBD160.1529
184	Hg38_5_43590188_43596508_43695191_43701837_RR	OBD160.1533
185	Hg38_1_60428956_60435934_60549270_60560051_FR	OBD160.1537
186	Hg38_5_150272362_150278699_150370575_150373999_FF	OBD160.1541
187	Hg38_9_130859900_130867193_130899377_130901466_RR	OBD160.1545
188	Hg38_1_91404825_91416231_91606200_91614477_FR	OBD160.1549
189	Hg38_14_91576230_91580637_91629033_91639298_RR	OBD160.1553
190	Hg38_2_27349601_27353190_27492451_27495056_RF	OBD160.1557
191	Hg38_5_150051979_150055894_150272362_150278699_RF	OBD160.1561
192	Hg38_1_185167238_185172841_185287397_185290374_FR	OBD160.1565
193	Hg38_3_112416500_112418982_112549606_112554897_FF	OBD160.1569
194	Hg38_6_132376734_132385044_132542354_132547678_FR	OBD160.1573
195	Hg38_1_189027657_189033909_189210801_189218947_FR	OBD160.1577
196	Hg38_2_233409972_233419808_233475741_233480083_FR	OBD160.1581

197	Hg38_17_35250006_35254814_35287155_35289074_RF	OBD160.1585
198	Hg38_5_140984243_140987011_141123576_141128793_FF	OBD160.1589
199	Hg38_13_40670004_40674221_40797038_40804771_RR	OBD160.1593
200	Hg38_15_34800440_34807454_35007401_35010342_RR	OBD160.1597

Table 1B (part 4e)

No.	Primer Sequence	Primer ID	Primer Sequence
151	ATTATCCTCCTTTGTTCTTCCCC	OBD160.1403	CCCTCCAGGTCTCTGCGTGTTTC
152	GCTCCCAGCAGAGGGCTCACCCG	OBD160.1407	ATCCCAGGACGACGGCTGTCTC
153	CTTCACAGCAGTCAAGTGGTGGTATCAC	OBD160.1411	CTCCTTGTTTGACTGACTTAGTTTCTCA
154	AGATTTTGGGCTGAGACAATGGG	OBD160.1415	CAGAACTCAAGAACATACTCCATAAAGT
155	CTCTGTTCCGCTACCCAGTCCACACC	OBD160.1419	CCCAGCCCTTACCATCGGTGCC
156	GCTCTAACTGATGCTTTCTCCAAG	OBD160.1423	TGAGTAACAAAGTGAGACCTTATGTC
157	GGCAGAAAGGAAAGAGCCTCGCAGCATT	OBD160.1427	TCCTCATCCTTGCTTTCTCATCTGTGA
158	CTGGCTATTTTCACTTCTTTGTGGA	OBD160.1431	GCAAGGCTGTGTCCCTCTGAG
159	GTGGGAGTTGAACAATGAGAACAC	OBD160.1435	AATGCCACCACCAGTAATGTTTCTAT
160	GCCTCCCCATTTCTCTCAGTTTCACAA	OBD160.1439	GGCTCTGGAGACTCAGCACCATTCTGGG
161	CATTTTCATCCTGCGGTTCTGGA	OBD160.1443	CAACAGAGATGGGAGACTTGAAG
162	CGTGGCTCTACAGAACTCCATA	OBD160.1447	AAAGCAGTTTCTGTGTCCGTTTGCCCCA
163	GCCTCTCTCCCATCAACATCCTTCAGAC	OBD160.1451	ATGGCGGCTGCCCTCTCCAGG
164	GGCAGAAAGGAAAGAGCCTCGCAGCATT	OBD160.1455	CTCAGACTCTCCAGCCCCACTCAGG
165	AATAGGGAACAGGTGTGTGACCCATAGC	OBD160.1459	GAAATGCCAGAGAAGAAAGACAACAAC
166	GGCAGAAAGGAAAGAGCCTCGCAGCATT	OBD160.1463	CTCCCCATCCTCCCTTTACCCTACCC
167	CTTGGTATTTCCCTTATTGTTTTGAAGC	OBD160.1467	CCACCATTGCTGAGGCTTGAGTA
168	CCACATCTTCCACCCCTGACACC	OBD160.1471	GGTGGAGGAGAACCGTTTGATGC
169	CTCCCCAAGCCTCCCAAGCAGG	OBD160.1475	GCTGGTGTGGATTGAATAGGAGGAAGA
170	TCCGCCCTGCCACACCCACCTCC	OBD160.1479	GCACACCCTGCCTAAAGTGGTTTTCCCT
171	CAGTGTCTCTGCTACAGGCTACAACATC	OBD160.1483	CAAAGAATAAACAAGGAGACAAGGGCTT
172	GTGCGGTGGCTCACACTTGTAAT	OBD160.1487	AGCCGAAGCAGGGCAAGGCATTG
173	CCACCCTGCTGTCTGCTTGGGC	OBD160.1491	GAGTTGGGAGGAATCTAAGGGTTACCT
174	ATTATCCTCCTTTGTTCTTCCCC	OBD160.1495	CTCGGATGGCGTTTCTCAGGGA
175	AGGAGAAGGAATGTACAAGGTAAGGTC	OBD160.1499	GTAGAGAAGGACAATGGTATGGGTTTCTAG
176	AGATTTTGGGCTGAGACAATGGG	OBD160.1503	AAGGCTCCATCTGTCAAACGGAT
177	TAGGAGGAGAAAACAGCAAATGGTCGGG	OBD160.1507	CCGACCCAAACCAGCACTCCAGCCG
178	GCCCTTTCCAGCCCTCAGTCTGTAGC	OBD160.1511	CCATCCCTCAGGAAGCCAGAGACTG
179	CCAGGAATGTCAGGCGACCCCTCAGGTG	OBD160.1515	GCCATCCCATCTTCAAGGACTGACGGAG
180	TGAAGCTTGAGGCGGCGAAAAT	OBD160.1519	GGTAACCAACATCTTGTATTGTATTAGC
181	CTGGCTATTTTCACTTCTTTGTGGA	OBD160.1523	GTTGTGGAAAGCAGTATCTGTGATTTC
182	GCCTCCCATTCTCTCAGTTTCACAA	OBD160.1527	CTGCTTCTCCTCTGCTCTCTCTGCTCC
183	GGGCTGGAGCACAGTGACGCAATCGTGG	OBD160.1531	GACTCCCTTTGTTCTGCCTGGCTTCTGA
184	CTCTGCCTCCTCTGCCCTGTTCTACTG	OBD160.1535	GCCACCACAACACACTGCTGCCTCACAC
185	CACACAGATAAAGATGAGCAGGAGGGAC	OBD160.1539	GCTCTCCTGGACTTGAGTGTGGAAGGG
186	GGGCAAGGGTGGGAAGCGATGGC	OBD160.1543	AGGGAGCCAGAGACAGAGGAGGCAGTGG
187	AGGTGCTCAGTCAGGGCTGCTGCCTCTC	OBD160.1547	TCCTGTGGGTCCCTGTGGCTGGG
188	GTAACATACATCGCTCCCACTTTCAATG	OBD160.1551	CTGCTCCTTTGCCCTTCCAGAGAGACAA
189	ACATTTCTTGCCCACTGTTTCAAGCGAT	OBD160.1555	CCCTCACCCCTGGCAACCACCGAT
190	CCTGCCACACCCACCTCCGCCG	OBD160.1559	GGCAACAGAGAGAGGCTCCGTCT
191	ACAGGACAGGGCAGGAGAGGCAACGAGG	OBD160.1563	CCCAAGGCGGTAGAGGGTGTACCG
192	ACCACTATGACCTCTTCCCAAATG	OBD160.1567	CTGTGGCTATTACTGTGTACAAT
193	GCCTGACATTCTGCCGTCTTAT	OBD160.1571	GTGACACCCACATACTTGCCAAAT

194	CAGTGCCCAAAGAGGTCCCTGAGGTC	OBD160.1575	GTGGCTTTACAACCTCACTCTGAACCTT
195	CTGGGCTATTCTAAATGCCAACTAAT	OBD160.1579	ATTCAGAGATTCAACTTCTTCTGGT
196	GGCAGCAGGTAAGAGCCCCAGGG	OBD160.1583	CCGCTCAGGAGACTCGCACTGGGTGTAG
197	TCTACTAACCAGAAAGACAGCCCTCACC	OBD160.1587	GATGGTGTGTGGGTAGGCACTACTGGG
198	ATTCTCAGGATGGAGGCTGGGTGTGGT	OBD160.1591	GGAAAGCATCTCAAGACCAAAGTCAAAG
199	GTCACCCTTCAGAGATGGCAACATTTAC	OBD160.1595	TAGCAACAACCTGTCTCCCGTCTCTGC
200	CCTCTTTCCAAATGTCATCTTTAG	OBD160.1599	GGAGGAAAATAGTTGAGCAGGAACA

Table 1B (part 4f)

No.	Probe	Markers
151	Hg38_3_52542416_52548124_52606123_52609751_FF	OBD160.1401.1403
152	Hg38_8_143012831_143021167_143073684_143079751_FR	OBD160.1405.1407
153	Hg38_1_212366521_212376213_212547138_212548374_RR	OBD160.1409.1411
154	Hg38_X_46498682_46508989_46602210_46603634_FR	OBD160.1413.1415
155	Hg38_21_44873351_44875256_44906478_44910319_FR	OBD160.1417.1419
156	Hg38_9_78097129_78101713_78276332_78285196_FF	OBD160.1421.1423
157	Hg38_3_126673758_126686020_126843341_126854251_RF	OBD160.1425.1427
158	Hg38_17_68575027_68578789_68785810_68796098_RF	OBD160.1429.1431
159	Hg38_5_24349034_24361029_24564285_24566267_FR	OBD160.1433.1435
160	Hg38_11_7448008_7457037_7633311_7640164_RR	OBD160.1437.1439
161	Hg38_7_27161846_27163700_27302548_27312509_FF	OBD160.1441.1443
162	Hg38_13_80339373_80340696_80530340_80535867_RF	OBD160.1445.1447
163	Hg38_9_4966910_4970390_5177459_5185304_FR	OBD160.1449.1451
164	Hg38_3_126843341_126854251_127025761_127027674_FR	OBD160.1453.1455
165	Hg38_2_13845156_13854426_13894360_13900303_FR	OBD160.1457.1459
166	Hg38_3_126619219_126620249_126843341_126854251_RF	OBD160.1461.1463
167	Hg38_11_19587032_19595878_19772073_19777708_RF	OBD160.1465.1467
168	Hg38_3_107106310_107120834_107363175_107364266_RF	OBD160.1469.1471
169	Hg38_2_172327203_172330194_172401667_172407636_FF	OBD160.1473.1475
170	Hg38_2_27492451_27495056_27626184_27635183_FF	OBD160.1477.1479
171	Hg38_6_108138075_108144989_108280425_108286846_RR	OBD160.1481.1483
172	Hg38_12_95793441_95797455_95929302_95940423_FR	OBD160.1485.1487
173	Hg38_17_34470224_34473967_34596926_34605729_RF	OBD160.1489.1491
174	Hg38_3_52542416_52548124_52770196_52773754_FR	OBD160.1493.1495
175	Hg38_1_186902459_186905074_187113187_187139713_RR	OBD160.1497.1499
176	Hg38_X_46498682_46508989_46576307_46579924_FR	OBD160.1501.1503
177	Hg38_6_3017794_3021910_3146778_3149848_RR	OBD160.1505.1507
178	Hg38_1_32149028_32153363_32237144_32241139_RF	OBD160.1509.1511
179	Hg38_11_316800_318015_481419_487611_FR	OBD160.1513.1515
180	Hg38_15_53424923_53427397_53442412_53454683_FF	OBD160.1517.1519
181	Hg38_17_68666853_68670189_68785810_68796098_RF	OBD160.1521.1523
182	Hg38_11_7448008_7457037_7610329_7615891_RR	OBD160.1525.1527
183	Hg38_17_77934896_77938750_78117632_78120001_RF	OBD160.1529.1531
184	Hg38_5_43590188_43596508_43695191_43701837_RR	OBD160.1533.1535
185	Hg38_1_60428956_60435934_60549270_60560051_FR	OBD160.1537.1539
186	Hg38_5_150272362_150278699_150370575_150373999_FF	OBD160.1541.1543
187	Hg38_9_130859900_130867193_130899377_130901466_RR	OBD160.1545.1547
188	Hg38_1_91404825_91416231_91606200_91614477_FR	OBD160.1549.1551
189	Hg38_14_91576230_91580637_91629033_91639298_RR	OBD160.1553.1555
190	Hg38_2_27349601_27353190_27492451_27495056_RF	OBD160.1557.1559

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191	Hg38_5_150051979_150055894_150272362_150278699_RF	OBD160.1561.1563
192	Hg38_1_185167238_185172841_185287397_185290374_FR	OBD160.1565.1567
193	Hg38_3_112416500_112418982_112549606_112554897_FF	OBD160.1569.1571
194	Hg38_6_132376734_132385044_132542354_132547678_FR	OBD160.1573.1575
195	Hg38_1_189027657_189033909_189210801_189218947_FR	OBD160.1577.1579
196	Hg38_2_233409972_233419808_233475741_233480083_FR	OBD160.1581.1583
197	Hg38_17_35250006_35254814_35287155_35289074_RF	OBD160.1585.1587
198	Hg38_5_140984243_140987011_141123576_141128793_FF	OBD160.1589.1591
199	Hg38_13_40670004_40674221_40797038_40804771_RR	OBD160.1593.1595
200	Hg38_15_34800440_34807454_35007401_35010342_RR	OBD160.1597.1599

Table 1B (part 4g)

CLAIMS

1. A method of detecting the muscular atrophy status in an individual, comprising determining the presence or absence of one or more chromosome interactions represented by the probes shown in Table
 5 1, to thereby detect muscular atrophy in the individual.

2. A method according to claim 1 wherein:
 (i) at least 5 chromosome interactions are typed from Table 1A, and/or
 (ii) at least 5 chromosome interactions are typed from Table 1B.

10

3. A method according to claim 1 or 2 wherein the chromosome interactions are typed:
 - in a sample from an individual, and/or
 - by detecting the presence or absence of a DNA loop at the site of the chromosome interactions, and/or
 - detecting the presence or absence of distal regions of a chromosome being brought together in a
 15 chromosome conformation, and/or
 - by detecting the presence of a ligated nucleic acid which is generated during said typing and whose sequence comprises two regions each corresponding to the regions of the chromosome which come together in the chromosome interaction, and/or
 - by a process which detects the proximity of the chromosome regions which have come together in the
 20 chromosome interaction.

4. A method according to any one of the preceding claims wherein said detecting of the presence or absence of the chromosome interactions is by a process comprising:
 (i) in vitro crosslinking of epigenetic chromosomal interactions which are present;
 25 (ii) optionally isolating the cross-linked DNA;
 (iii) subjecting said cross-linked DNA to cleaving;
 (iv) ligating said cross-linked cleaved DNA ends to form ligated DNA; and
 (v) identifying the presence or absence of said ligated DNA;
 to thereby determine the presence or absence of the chromosome interaction.

30

5. A method according to claim 3 or 4 wherein said ligated DNA is detected by PCR or by use of a probe.

6. A method according to claim 5 wherein:

(i) detection is by use of a probe, wherein said probe has at least 70% identity to any of the probes shown in Table 1, or

(ii) detection is by use of PCR, wherein the PCR uses a primer pair that has at least 70% identity to any of the primer pairs shown in Table 1.

5

7. A method according to any one of the preceding claims wherein:

(i) the method is carried out to select an individual for receiving therapy or a treatment for muscular atrophy, and/or

10 (ii) the method is carried out on individual that has been preselected based on a physical characteristic, risk factor or the presence of a symptom, and/or

(iii) the method is carried out to diagnose muscular atrophy or to determine prognosis for muscular atrophy, and preferably to determine severity of muscular atrophy.

15 8. A method according to claim 7(ii) wherein the individual is preselected for one or more of the following characteristics:

(a) being male, and/or

(b) being aged 30 to 60, and/or

(c) having gynecomastia, and/or

(d) having testicular atrophy, and/or

20 (e) having androgen insensitivity, and/or

(e) having reduced fertility, preferably as a result of androgen insensitivity.

9. A method according to any one of the preceding claims wherein at least 5 chromosome interactions are typed which are selected from:

25 (i) interaction numbers 1 to 40 from Table 1A, or

(ii) interaction numbers 1 to 40 from Table 1B.

30 10. A method according to any one of the preceding claims, wherein the typing or detecting comprises specific detection of the ligated product by quantitative PCR (qPCR) which uses primers capable of amplifying the ligated product and a probe which binds the ligation site during the PCR reaction, wherein said probe comprises sequence which is complementary to sequence from each of the chromosome regions that have come together in the chromosome interaction, wherein preferably said probe comprises:

- an oligonucleotide which specifically binds to said ligated product, and/or
 - a fluorophore covalently attached to the 5' end of the oligonucleotide, and/or
 - a quencher covalently attached to the 3' end of the oligonucleotide, and optionally
- 5 - said fluorophore is selected from HEX, Texas Red and FAM; and/or
- said probe comprises a nucleic acid sequence of length 10 to 40 nucleotide bases, preferably a length of
 - 20 to 30 nucleotide bases.
11. An anti-muscular atrophy therapeutic agent for use in treating muscular atrophy in an individual that
- 10 has been identified as having muscular atrophy according to any one of the preceding claims.