(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
30 April 2020 (30.04.2020)

WIPO | PCT

(10) International Publication Number
WO 2020/084289 A1

(51) International Patent Classification:
C12Q 1/6876 (2018.01)

(21) International Application Number:
PCT/GB2019/052996

(22) International Filing Date:
21 October 2019 (21.10.2019)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

1817181.9	22 October 2018 (22.10.2018)	GB
1904066.6	25 March 2019 (25.03.2019)	GB

(71) Applicant: **OXFORD BIODYNAMICS LIMITED** [GB/GB]; 26 Beaumont Street, Oxford Oxfordshire OX1 2NP (GB).

(72) Inventors: **HUNTER, Ewan**; Oxford BioDynamics Limited, 26 Beaumont Street, Oxford Oxfordshire OX1 2NP (GB). **RAMADASS, Aroul**; Oxford BioDynamics Limited, 26 Beaumont Street, Oxford Oxfordshire OX1 2NP (GB). **AKOULITCHEV, Alexandre**; Oxford BioDynamics Limited, 26 Beaumont Street, Oxford Oxfordshire OX1 2NP (GB).

(74) Agent: **AVIDITY IP**; Broers Building, Hauser Forum, 21 J J Thomson Ave, Cambridge Cambridgeshire CB3 0FA (GB).

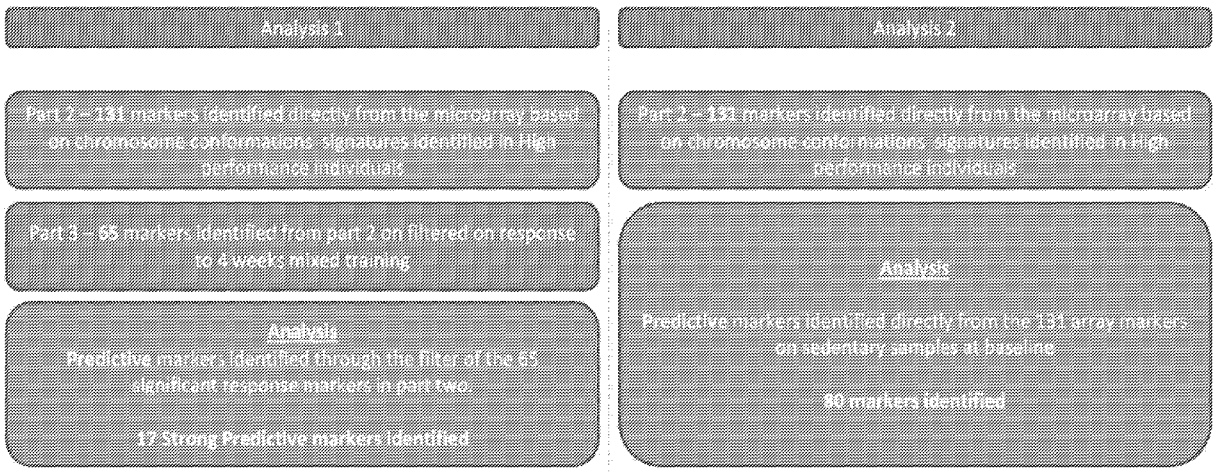
(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report (Art. 21(3))*

(54) Title: CHROMOSOME BIOMARKER

Figure 1



(57) Abstract: A process for analysing chromosome regions and interactions relating to physical performance.

WO 2020/084289 A1

Chromosome Biomarker

Field of the Invention

The invention relates to detecting chromosome interactions.

Background of the Invention

Physical performance is complex and cannot be predicted using available methods. It is clear coordination, flexibility, precision, power, speed, endurance, balance, awareness efficiency, and timing are relevant to performance.

Summary of the Invention

The inventors have identified chromosomal interactions relevant to physical performance using an approach which analyses subgroups in a population. The inventors' work allows physical performance to be typed and modulated in an entirely new way which is more sensitive and personalised than genomic or protein typing, and which reflects the individual history of the individual. This has applications in fitness and physical training regimes, as well as in sports medicine.

Accordingly, the invention provides a process for detecting a chromosome state which represents a subgroup in a population comprising determining whether a chromosome interaction relating to that chromosome state is present or absent within a defined region of the genome, wherein said subgroup relates to physical performance in an individual; and

- wherein said chromosome interaction has optionally been identified by a method of determining which chromosomal interactions are relevant to a chromosome state corresponding to a physical performance 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 pattern of hybridisation between the first and second set of nucleic acids allows a determination of which chromosomal interactions are specific to a physical performance subgroup; and

- wherein the chromosome interaction either:

(i) corresponds to any one of the chromosome interactions shown in any of Tables 3, 7, 8, 9, 25 and 30; and/or

(ii) corresponds to any one of the chromosome interactions shown in any of Tables 13, 14, 18, 22, 23 and 24; and/or

(iii) corresponds to any one of the chromosome interactions shown in Table 31 or 32; and/or

(iv) is present in a 4,000 base region which comprises or which flanks (i), (ii) or (iii); and/or

(v) is present in any one of the regions or genes listed in Table 21, 24, 25, 30, 31 or 32.

In a preferred embodiment, the invention provides a process for detecting a chromosome state which represents a subgroup in a population comprising determining whether a chromosome interaction relating to that chromosome state is present or absent within a defined region of the genome, wherein said subgroup relates to physical performance in an individual; and wherein the chromosome interaction either:

(a) corresponds to any one of the chromosome interactions shown in any of Tables 33, 34, 35, 36, 37, 38, 39, 40 or 41, or in any of Figures 16, 17 or 18; and/or

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

Detailed Description of the Invention

Aspects of the Invention

The inventions concerns a panel of epigenetic markers which relate to the regulation and stratification of physical performance, in particular strength and endurance. The markers are preferably stable and may allow detection of a predisposition in physiology to a specific stimulus, such as physical training.

The invention also includes monitoring of physical performance or responsiveness of physical performance to a specific stimulus, such as a specific training regimen. The invention therefore provides in one aspect a 'live' ongoing readout of physical performance status allowing a personalised stimulus to be given to the individual which reflects the individual's needs.

The inventions provided a method of selecting an individual for a given physical task, such as racing or specific training. The invention also provides a method of selecting or designing a training or fitness regime, for example for a specific individual.

The invention also provides methods of predicting physical performance, including whether an individual would have high strength or endurance or both, for example as measured in any specific way described herein.

The invention allows categorisation of individuals into 'fit', 'strong', or 'sedentary'. The invention allows stratification of 'baseline' individuals entering training programmes for better predisposition for either strength, or endurance - de facto predictive biomarkers for response. The invention also allows stratification of early biomarker evidence of response to training in individuals - de facto early response biomarkers for monitoring training progress.

Any marker disclosed herein may be used in the method of the invention, including any marker disclosed in any table or Figure. Preferred markers are shown in:

- Tables 3, 7, 8, 9, 25 and 30; and

- Tables 13, 14, 18, 22, 23 and 24; and

- Table 31 or 32; and

- Tables 33 to 41; and

- Figures 16 to 18.

Physical Performance

The invention relates to determining physical performance. The process of the invention may detect responsiveness to a stimulus relating to physical performance, for example to training, such as strength or endurance training. The training typically comprises subjecting the individual to physical exertion, for example in terms of the applying force, moving physically, running or carrying out a specific physical activity (for example as disclosed herein) over a certain time period. The process of the invention may be used to detect a high or low response to the stimulus, such as a high or low response to any specific training or physical activity disclosed herein. Preferably the invention detects the response to strength or endurance training.

The invention can be used to select an individual suitable for a physical activity, such as a sport. Preferred sports including strength or endurance sports. A preferred endurance sport is racing or running. Thus the invention may be used to select an individual that is suited to any particular activity mentioned herein, such as training.

The Process of the Invention

The process of the invention comprises a typing system for detecting chromosome interactions relevant to physical performance. This typing may be performed using the *EpiSwitch*™ system mentioned herein which is based on cross-linking regions of chromosome which have come together in the chromosome interaction, subjecting the chromosomal DNA to cleavage and then ligating the nucleic acids present in the cross-linked entity to derive a ligated nucleic acid with sequence from both the regions which formed the chromosomal interaction. Detection of this ligated nucleic acid allows determination of the presence or absence of a particular chromosome interaction.

The chromosomal interactions may be identified using the above described method in which populations of first and second nucleic acids are used. These nucleic acids can also be generated using *EpiSwitch*™ technology.

The Epigenetic Interactions Relevant to the Invention

As used herein, the term 'epigenetic' and 'chromosome' interactions typically refer to interactions between distal regions of a chromosome, said interactions being dynamic and altering, forming or breaking depending upon the status of the region of the chromosome.

In particular processes of the invention chromosome interactions are typically detected by first generating a ligated nucleic acid that comprises sequence from both regions of the chromosomes that are part of the interactions. In such processes the regions can be cross-linked by any suitable means. In a preferred embodiment, 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 and optionally 2 to 10 Angstroms apart.

The chromosome interaction may reflect the status of the region of the chromosome, for example, if it is being transcribed or repressed. Chromosome interactions which are specific to subgroups as defined herein have been found to be stable, thus providing a reliable means of measuring the differences between the two subgroups.

In addition, chromosome interactions specific to a characteristic (such as physical performance) will normally occur early in a biological process, for example compared to other epigenetic markers such as methylation or changes to binding of histone proteins, and are also capable of providing a 'live' readout of the status of the individual. Thus the process of the invention is able to detect early stages of a biological process as well as allowing continuous monitoring. Chromosome interactions also reflect the current state of the individual and therefore can be used to assess changes to physical performance. 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 interrogate 500,000 different interactions.

Preferred Marker Sets

Herein the term 'marker' or 'biomarker' refers to a specific chromosome interaction which can be detected (typed) in the invention. Specific markers are disclosed herein, any of which may be used in the invention or any of which may be used in any combination with other specific markers or combinations disclosed herein. Preferably sets of markers may be used, for example in the combinations or numbers disclosed herein. The specific markers disclosed in the tables herein are preferred as well as markers presents in genes and regions mentioned in the tables herein are preferred. These may be typed by any

suitable method, for example the PCR or probe based methods disclosed herein, including a qPCR method. The markers are defined herein by location or by probe and/or primer sequences.

Location and Causes of Epigenetic Interactions

Epigenetic chromosomal interactions may overlap and include the regions of chromosomes shown to encode relevant or undescribed genes, but equally may be in intergenic regions. The chromosome interactions which are detected in the invention could be caused by changes to the underlying DNA sequence, by environmental factors, DNA methylation, non-coding antisense RNA transcripts, non-mutagenic carcinogens, histone modifications, chromatin remodelling and specific local DNA interactions. The changes which lead to the chromosome interactions may be caused 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 embodiment 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 is preferably within any of the genes mentioned in Table 21. However it may also be upstream, for example up to 50,000, up to 30,000, up to 20,000, up to 10,000 or up to 5000 bases upstream from the gene. It may be downstream, for example up to 50,000, up to 30,000, up to 20,000, up to 10,000 or up to 5000 bases downstream from the gene. It may be upstream or downstream from coding sequences, for example by any of these specific numbers of bases.

Subgroups, Time Points and Personalisation

One aim of the present invention is to determine a characteristic relevant to physical performance. This may be at one or more defined time points for the same individual, for example at at least 1, 2, 5, 8 or 10 different time points. The durations between the time points may be at least 20, 50, 80 or 100 days. Typically testing of the individual (by the process of the invention) may occur before a physical stimulus is applied, or during or after. The testing may determine the predisposition to certain types of response, or the actual response to the stimulus.

As used herein, a “subgroup” preferably refers to a population subgroup (a subgroup in a population), more preferably a subgroup in the population of a human or horse population. The invention includes detecting and applying a physical stimulus to particular subgroups in a population. The inventors have discovered that chromosome interactions differ between subsets (for example at least two subsets) in a given population. Identifying these differences will allow categorisation of individuals and this allows

personalised stimuli to be given, such a personalised training, or allows selection of the individual for particular physical activities.

Generating Ligated Nucleic Acids

Certain embodiments of the invention utilise ligated nucleic acids, in particular ligated DNA. These comprise sequences from both of the regions that come together in a chromosome interaction and therefore provide information about the interaction. The EpiSwitch™ method described herein uses generation of such ligated nucleic acids to detect chromosome interactions.

Thus a process of the invention may comprise a step of generating ligated nucleic acids (e.g. DNA) by the following steps (including a method comprising these steps):

(i) cross-linking of epigenetic chromosomal interactions present at the chromosomal locus, preferably *in vitro*;

(ii) optionally isolating the cross-linked DNA from said chromosomal locus;

(iii) subjecting said cross-linked DNA to cutting, for example by restriction digestion with an enzyme that cuts it at least once (in particular an enzyme that cuts at least once within said chromosomal locus);

(iv) ligating said cross-linked cleaved DNA ends (in particular to form DNA loops); and

(v) optionally identifying the presence of said ligated DNA and/or said DNA loops, in particular using techniques such as PCR (polymerase chain reaction), to identify the presence of a specific chromosomal interaction.

These steps may be carried out to detect the chromosome interactions for any embodiment mentioned herein. The steps may also be carried out to generate the first and/or second set of nucleic acids mentioned herein.

PCR (polymerase chain reaction) may be used to detect or identify the ligated nucleic acid, for example the size of the PCR product produced may be indicative of the specific chromosome interaction which is present, and may therefore be used to identify the status of the locus. In preferred embodiments at least 1, 2 or 3 primers or primer pairs as shown in Table 24, 25 or 30 are used in the PCR reaction. In other preferred embodiments at least 1, 2 or 3 primers or primer pairs as shown in Table 31 or 32 are used in the PCR reaction. The skilled person will be aware of numerous restriction enzymes which can be used to cut the DNA within the chromosomal locus of interest. It will be apparent that the particular enzyme used will depend upon the locus studied and the sequence of the DNA located therein. A non-limiting example of a restriction enzyme which can be used to cut the DNA as described in the present invention is TaqI.

Embodiments such as 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. Embodiments 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 embodiment the processing time is 3 hours to 6 hours.

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 embodiment 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.

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, including Table 21. Typically preferred nucleic acids comprise the specific probe sequences mentioned in Table 24, 25 or 30; or fragments and/or homologues of such sequences. Preferred nucleic acids also comprise the specific probe sequences mentioned in Table 31 or 32; 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 embodiment.

The primers shown in Table 24, 25 or 30 may also be used in the invention as mentioned herein. In one embodiment primers are used which comprise any of: the sequences shown in Table 24, 25 or 30; or fragments and/or homologues of any sequence shown in Table 24, 25 or 30.

The primers shown in Table 31 or 32 may also be used in the invention as mentioned herein. In one embodiment primers are used which comprise any of: the sequences shown in Table 31 or 32; or fragments and/or homologues of any sequence shown in Table 31 or 32.

The Second Set of Nucleic Acids – the 'Index' Sequences

The second set of nucleic acid sequences has the function of being a set of index sequences, and is essentially a set of nucleic acid sequences which are suitable for identifying subgroup specific sequence. They can represents 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 represent a larger population group than the first set of nucleic acids. In one particular embodiment, the second set of nucleic acids represents all possible epigenetic chromosomal interactions in a specific set of genes. In another particular embodiment, 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 embodiment, the second set of nucleic acids represents at least 50% or at least 80% of epigenetic 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 physical characteristic. The second set of nucleic acids typically comprises sequences representing epigenetic interactions both relevant and not relevant to a physical performance subgroup.

In one particular embodiment 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 additions of one or more nucleotide base pairs. In one particular embodiment, 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 embodiment, 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.

Properties of the Second Set of Nucleic Acids

In one particular embodiment, 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% or these would correspond to different chromosomal interactions.

In one particular embodiment, 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 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 embodiment, 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 embodiment, the second set of nucleic acids comprises nucleic acid sequences of between 17 and 25 base pairs. In one embodiment 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 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

The first set of nucleic acids are typically from subgroups relevant to physical performance. 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.

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

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. A library may for example comprise all of the nucleic acids disclosed in any table disclosed herein, or all of the probe sequences disclosed in any table herein.

Hybridisation

The invention requires a means for allowing wholly or partially complementary nucleic acid sequences from the first set of nucleic acids and the second set of nucleic acids to hybridise. In one embodiment 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. 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 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 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.

Selecting a Subgroup with Particular Characteristics

The invention provides a process which comprises detecting the presence or absence of chromosome interactions, typically 5 to 20 or 5 to 500 such interactions, preferably 20 to 300 or 50 to 100 interactions, in order to determine the presence or absence of a characteristic relating to physical performance in an individual. Preferably the chromosome interactions are those in any of the genes mentioned herein or in any Table herein. In one embodiment the chromosome interactions which are typed are those represented in any of Tables 3, 7, 8, 9, 25 and 30. In another embodiment the chromosome interactions are those represented in any of Tables 13, 14, 18, 22, 23 and 24. In a preferred embodiment the chromosome interactions which are typed are those represented in Table 31 or 32. In one embodiment the chromosome interactions which are typed are those from any of Tables 33, 34, 35, 36, 37, 38, 39 or 40 or in any of Figures 16, 17 or 18. The relevant chromosome interaction may be present or absent for a given characteristic, and therefore either presence or absence of the interaction will indicate the presence of the characteristic.

The Individual that is Tested

The individual that is tested is preferably a human or horse. The human be an athlete or sportsman. The human is typically 30 years old or less. The horse may be any type of horse mentioned herein, such as a Thoroughbred. The horse may be racing horse. The horse may be one which is not a racing horse, but which optionally is being considered for selection as a race horse. The horse may be less than 500 days old, such as less than 200 or less than 100 days old.

Preferred Gene Regions, Loci, Genes and Chromosome Interactions

For all aspects of the invention preferred gene regions, loci, genes and chromosome interactions are mentioned in the tables, for example in any of Tables 3, 7, 8, 9, 25 and 30 (preferably for typing humans) or in any of Tables 13, 14, 18, 22, 23 and 24 (preferably for typing horses), or in Table 31 or 32 (preferably for typing humans). Typically in the processes of the invention chromosome interactions are detected from at least 1, 2, 10, 30 or 50 genes listed in Table 21. The chromosome interaction may be upstream or downstream of any of the genes mentioned herein, for example 50 kb upstream or 20 kb downstream, for example from the coding sequence.

In one embodiment at least 5, 10 or all of the chromosome interactions of Table 3 are typed. In one embodiment at least the interactions with the top 5 or 10 highest odds ratio of Table 3 are typed.

In one embodiment at least 5, 10, 15 or all of the chromosome interactions in Table 7 are typed. In one embodiment at least the interactions with the smallest 5, 10 or 15 mean p values of Table 7 are typed.

In one embodiment at least 5, 10, 15, 20 or all of the chromosome interactions in Table 8 are typed. In one embodiment at least the interactions with the smallest 5, 10, 15 or 20 mean p values of Table 8 are typed.

In one embodiment at least 5, 10, 15, 20 or all of the chromosome interactions in Table 9 are typed. In one embodiment at least the interactions with the smallest 5, 10, 15 or 20 mean p values of Table 9 are typed.

In one embodiment at least 5, 10, 15 or all of the chromosome interactions in Table 13 are typed. In one embodiment at least the interactions with the smallest 5 or 10 Exact Boschloo p value of Table 13 are typed.

In one embodiment at least 5, 10, 15 or all of the chromosome interactions in Table 14 are typed.

In one embodiment at least 5, 10, 20, 30 or all of the chromosome interactions in Table 18 are typed. In one embodiment at least the interactions with the smallest 5, 10, 20 or 30 Exact Boschloo p value of Table 18 are typed.

In one embodiment at least 5, 10 or all of the chromosome interactions of Table 22 are typed. In one embodiment at least the interactions with the top 5 or 10 highest odds ratio of Table 22 are typed.

In one embodiment at least 5, 10, 15 or all of the chromosome interactions of Table 23 are typed.

In one embodiment at least 5, 10, 20, 30 or all of the chromosome interactions of Table 24 are typed. In one embodiment at least the interactions with the top 5, 10, 20, 30 GLMNET values of Table 24 are typed.

In one embodiment at least 5, 10, 20, 30, 40, 50 or all of the chromosome interactions of Table 25 are typed. In one embodiment at least the interactions with the smallest 5, 10, 20, 30, 40, 50 adjusted p values of Table 25 are typed. In one embodiment at least the markers numbered 1 to 30 in Table 25 are typed. In another at least the markers numbers 31 to 77 in Table 25 are typed.

In one embodiment at least 5, 10, 20, 30, 40, 50, 150, 180 or all of the chromosome interactions of Table 30 are typed. In one embodiment at least the interactions with the smallest 5, 10, 20, 30, 40, 50, 150, or 180 adjusted p values of Table 30 are typed. In one embodiment at least the markers numbered 1 to 50 in Table 30 are typed. In another embodiment at least the markers numbered 51 to 100 in Table 30 are typed. In another embodiment at least the markers numbered 101 to 150 in Table 30 are typed. In one embodiment at least the markers numbered 151 to 202 in Table 30 are typed.

In one embodiment at least 5, 10 or all of the chromosome interactions of Table 31 are typed.

In one embodiment at least 5 or all of the chromosome interactions of Table 32 are typed.

In one embodiment at least 5, 10, 20, 30, 40, 50, 150, 180, 200, 250 or all of the chromosome interactions of Table 33 are typed. In one embodiment at least the interactions with the smallest 5, 10, 20, 30, 40, 50, 150, 180 or 250 adjusted p values of Table 33 are typed. In one embodiment at least the markers numbered 1 to 50 in Table 33 are typed. In another embodiment at least the markers numbered 51 to 100 in Table 33 are typed. In another embodiment at least the markers numbered 101 to 150 in Table 33 are typed. In one embodiment at least the markers numbered 151 to 202 in Table 33 are typed. In one embodiment at least the markers numbered 202 to 320 in Table 33 are typed.

In one embodiment at least 5, 10, 20, 30, 40, 50 or all of the chromosome interactions of Table 34 are typed.

In one embodiment at least 5, 10, 20, 30 or all of the chromosome interactions of Table 35 are typed.

In one embodiment at least 5, 10, 15 or all of the chromosome interactions of Table 36 are typed.

In one embodiment at least 5, 10, 20, 30, 40, 50, 150, 180 or all of the chromosome interactions of Table 37 are typed. In one embodiment at least the interactions with the smallest 5, 10, 20, 30, 40, 50, 150, or 180 adjusted p values of Table 37 are typed. In one embodiment at least the markers numbered 1 to 50 in Table 37 are typed. In another embodiment at least the markers numbered 51 to 100 in Table 37 are typed. In another embodiment at least the markers numbered 101 to 150 in Table 37 are typed. In one embodiment at least the markers numbered 151 to 202 in Table 37 are typed.

In one embodiment at least 5, 10 or all of the chromosome interactions of Table 38 are typed.

In one embodiment at least 5 or all of the chromosome interactions of Table 39 are typed.

In one embodiment at least 5, 10 or all of the chromosome interactions of Table 40 are typed. In one embodiment at least the 3 'shared' chromosome interactions of Table 40 are typed. In one embodiment at least the 7 'strength' chromosome interactions of Table 40 are typed.

In one embodiment at least 5, 10, 20, 30, 40, 50 or all of the chromosome interactions of Table 41 are typed. In one embodiment at least the interactions with the smallest 5, 10, 20, 30, 40, 50 adjusted p values of Table 41 are typed. In one embodiment at least the markers numbered 1 to 30 in Table 41 are typed. In another at least the markers numbers 31 to 77 in Table 41 are typed. [Table 41 is shown in abbreviated form to avoid duplicating information from Table 25 which relates to the same marker set. It is understood that smallest p values mentioned here can be obtained from Table 25]

In one embodiment at least 5, 8 or all of the chromosome interactions of Figure 16 are typed.

In one embodiment at least 5, 10 or all of the chromosome interactions of Figure 17 are typed.

In one embodiment at least 5, 8 or all of the chromosome interactions of Figure 18 are typed.

Typically at least 5, 10, 15, 20, 30, 40 or 70 chromosome interactions are typed from any of genes or regions disclosed the tables herein, or parts of tables disclosed herein. Typically the chromosome interactions which are typed are present in at least 20, 50 or all of the genes mentioned in Table 21.

For all aspects of the invention preferred gene regions, loci, genes and chromosome interactions are mentioned in Tables 24 and 30.

In one embodiment 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 24 or 30.

Thus typically sequence from both regions of the probe (i.e. from both sites of the chromosome interaction) could be detected. In preferred embodiments 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 embodiments probes are used which comprise sequence which is homologous to any of the probe sequences shown in the tables.

Tables Provided Herein

The tables show probe (Episwitch™ marker) data and gene data representing chromosome interactions relevant to physical performance. The probe sequences show sequence which can be used to detect a ligated product generated from both sites of gene regions that have come together in chromosome interactions, i.e. the probe will comprise sequence which is complementary to sequence in the ligated product. The 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:

- HyperG_Stats: p-value for the probability of finding that number of significant EpiSwitch™ markers in the locus based on the parameters of hypergeometric enrichment
- Probe Count Total: Total number of EpiSwitch™ Conformations tested at the locus
- Probe Count Sig: Number of EpiSwitch™ Conformations found to be statistically significant at the locus
- FDR HyperG: Multi-test (Fimmunoresposivenesse Discovery Rate) corrected hypergeometric p-value
- Percent Sig: Percentage of significant EpiSwitch™ markers relative the number of markers tested at the locus
- logFC: logarithm base 2 of Epigenetic Ratio (FC)

- AveExpr: average log2-expression for the probe over all arrays and channels
- T: moderated t-statistic
- p-value: raw p-value
- adj. p-value: adjusted p-value or q-value
- B - B-statistic (lods or B) is the log-odds that that gene is differentially expressed.
- FC - non-log Fold Change
- FC_1 - non-log Fold Change centred around zero
- LS – Binary value this relates to FC_1 values. FC_1 value below -1.1 it is set to -1 and if the FC_1 value is above 1.1 it is set to 1. Between those values the value is 0

The tables also shows genes where a relevant chromosome interaction has been found to occur. The p-value in the loci table is the same as the HyperG_Stats (p-value for the probability of finding that number of significant EpiSwitch™ markers in the locus based on the parameters of hypergeometric enrichment).

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

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

GLMNET values related to procedures for fitting the entire lasso or elastic-net regularization (Lambda set to 0.5 (elastic-net)).

Preferred Embodiments for Sample Preparation and Chromosome Interaction Detection

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

Typically the sample will contain at least 2 x10^5 cells. The sample may contain up to 5 x10^5 cells. In one embodiment, the sample will contain 2 x10^5 to 5.5 x10^5 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 embodiments, 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 embodiment, 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 embodiment of the EpiSwitch method 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 embodiment after digestion of the protein, for example Proteinase K digestion, there is no cross-link reversal or phenol DNA extraction step.

In one embodiment 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 14 shows a preferred method 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 method of 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:

- the locus may be any of the loci, regions or genes mentioned in any table, and/or

- wherein the chromosomal interaction may be any of the chromosome interactions mentioned herein or corresponding to any of the probes disclosed in any table, 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 any table herein; or (ii) sequence which is complementary to (ii).

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 absence of physical performance, and/or
- the chromosome state may be at any locus, region or gene mentioned in any table; and/or
- the chromosome interaction may be any of those mentioned in any table or corresponding to any of the probes disclosed in that table.

The process of the invention can be described as a method of 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:

- the locus may be any of the loci, regions or genes mentioned in any table, and/or

- wherein the chromosomal interaction may be any of the chromosome interactions mentioned herein or corresponding to any of the probes disclosed in any table, 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 any table; or (ii) sequence which is complementary to (ii).

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 absence of physical performance, and/or
- the chromosome state may be at any locus, region or gene mentioned in any table; and/or
- the chromosome interaction may be any of those mentioned in any table or corresponding to any of the probes disclosed in that table.

The invention includes detecting chromosome interactions at any locus, gene or regions mentioned in any table, such as Table 24 or 30. The invention includes use of the nucleic acids and probes mentioned herein to detect chromosome interactions, for example use of at least 1, 5, 10, 50, 100 such nucleic acids or probes to detect chromosome interactions, preferably in at least 1, 5, 10, 50, 100 different loci or genes. The invention includes detection of chromosome interactions using any of the primers or primer pairs listed in Table 24 or 30 or using variants of these primers as described herein (sequences comprising the primer sequences or comprising fragments and/or homologues of the primer sequences).

The invention includes detecting chromosome interactions at any locus, gene or regions mentioned Table 24 or 30. The invention includes use of the nucleic acids and probes mentioned herein to detect chromosome interactions, for example use of at least 1, 5, 10, 50, 100, 200, 250, 300 such nucleic acids or probes to detect chromosome interactions, preferably in at least 1, 5, 10, 50, 100, 200, 250, 300 different loci or genes. The invention includes detection of chromosome interactions using any of the primers or primer pairs listed in Table 24 or 30 or using variants of these primers as described herein (sequences comprising the primer sequences or comprising fragments and/or homologues of the primer sequences).

When analysing whether a chromosome interaction occurs 'within' a defined gene, region or location, either both the parts of the chromosome which have together in the interaction are within the defined gene, region or location or in some embodiments only one part of the chromosome is within the defined, gene, region or location.

Use of the Method of the Invention to Identify New Training or Fitness Regimens

Knowledge of chromosome interactions can be used to identify new fitness or training regimens. The invention provides methods and uses of chromosomes interactions defined herein to identify or design new agents.

Homologues

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 calculated on the basis of nucleotide identity (sometimes referred to as "hard homology").

Therefore, in a particular embodiment, 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, 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.

For example the UWGCG Package provides the BESTFIT program which can be used to calculate 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.

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 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 W5 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 % 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.

Arrays

The second set of nucleic acids may be bound to an array, and in one embodiment there are at least 15,000, 45,000, 100,000 or 250,000 different second nucleic acids bound to the array, which preferably represent at least 300, 900, 2000 or 5000 loci. In one embodiment one, or more, or all of the different populations of second 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.

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 physical performance. 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.

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.

Detection Methods

In one embodiment 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 method 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 method typically allows particular interactions to be 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.

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 embodiment the fluorophore is attached to the 5'end of the oligonucleotide, and the quencher is covalently attached to the 3' end of the oligonucleotide. Fluorophores that can be used in the methods 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.

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 methods 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 method 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 embodiment 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 embodiment 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.

Particular Embodiments

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

In particular embodiments 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 embodiments chromosome interactions are not typed in any of the genes mentioned here, for example in any gene mentioned in Table 21.

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.

Tables

Table 1 shows patient sample for the human study.

Table 2 shows the classification of responders in the human study.

Tables 3 and 4 show markers from the human study which are preferably used for typing humans.

Table 5 illustrates for the human study predispositions present in subjects.

Table 6 shows markers from the human study, which are preferably used for typing humans.

Table 7 shows predictive markers for strength training response, which are preferably used for typing humans.

Table 8 shows predictive markers for endurance training response, which are preferably used for typing humans.

Table 9 shows predictive markers for either strength or endurance training response, which are preferably used for typing humans.

Table 10 shows the samples for the equine study.

Table 11 defines the 'sex' description used in Table 10.

Table 12 shows the sex distribution in the equine study.

Table 13 shows the top markers for Stayer versus Sprinter phenotype (n=32, 16 Stayer, 16 Sprinter), which are preferably used to type horses.

Table 14 shows markers discovered in humans that applicable to horses, and the closest genomic loci, which can be used to type horses.

Table 15 shows classifier calls for Sprinters and Stayers

Table 16 shows probability scores for the equine study.

Table 17 shows classifier calls of naïve samples from young Thoroughbreds.

Table 18 shows the informative markers from the equine study, which are preferably used to type horses.

Tables 19 and 20 show the subjects for the human study.

Table 21 shows preferred genes for carrying out the invention.

Table 22 and 23 shows preferred markers from the equine study and the traits they relate to, which are preferably used to type horses.

Table 24 shows markers identified in the equine study, which are preferably used to type horses.

Table 25 shows markers identified in the human study, which are preferably used to type humans.

Table 26 shows another set of preferred genes for carrying out the invention.

Table 27 shows pathway analysis for genes locations for 171 chromosome interactions shared between the strength and endurance groups.

Table 28 shows pathway analysis for genes locations for the top 79 chromosome interactions which are unique to the endurance group.

Table 29 shows pathway analysis for genes locations for the top 79 chromosome interactions which are unique to the strength group.

Tables 30 to 32 show markers identified in the human study, which are preferably used to type humans. To clarify the nomenclature used in the tables, including Table 30:

E_Trn refers to presence in Endurance Training

Str_Trn refers to presence in Strength Training

E_Ctrl refers to presence in Endurance Control (i.e. absence in Endurance Training)

Str_Ctrl refers to presence in Strength Control (i.e. absence in Strength Training)

Table 33 shows markers from an equine study, which are preferably used to type horses. In LS column: 1 means present in Sprinters, while (-1) means present in Stayers. The 'Loop detection' column is de facto decoding what +1 and -1 means in terms of detection.

Table 34 shows markers from a human study, which are preferably used to type humans.

Table 35 shows preferred markers from a horse study, which are preferably used to type horses.

Table 36 shows preferred markers from a human study, which are preferably used to type humans.

Table 37 shows an updated version of Table 30. The same markers are typed in this study in humans, preferably used to type humans.

Table 38 shows an updated version of Table 31. The same markers are typed in a human study and preferably used to type humans.

Table 39 shows an updated version of Table 32. The same markers are typed in a human study and preferably used to type humans.

Table 40 shows markers corresponding to those shown in Figure 15, which are preferably used to type humans.

Table 41 shows updated results for Table 25, where the markers are from a human study and are preferably used to type human.

Figures 16 and 17 shows markers from a human study, which preferably can be used to type humans.

Figure 18 shows markers from a horse study, which preferably can be used to type horses.

Preferred Methods

The following numbered paragraphs define preferred methods:

1. A process for detecting a chromosome state which represents a subgroup in a population comprising determining whether a chromosome interaction relating to that chromosome state is present or absent within a defined region of the genome, wherein said subgroup relates to physical performance in an individual; and

- wherein said chromosome interaction has optionally been identified by a method of determining which chromosomal interactions are relevant to a chromosome state corresponding to a physical performance 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 pattern of hybridisation between the first and second set of nucleic acids allows a determination of which chromosomal interactions are specific to a physical performance subgroup; and

- wherein the chromosome interaction either:

(i) corresponds to any one of the chromosome interactions shown in any of Tables 3, 7, 8, 9, 25 and 30; and/or

(ii) corresponds to any one of the chromosome interactions shown in any of Tables 13, 14, 18, 22, 23 and 24; and/or

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

(iv) is present in any one of the regions or genes listed in Table 21, 24, 25 or 30.

2. A process according to paragraph 1 wherein:

- the individual is a human and the subgroup is a human subgroup

- the individual is a horse and the subgroup is a horse subgroup, and

wherein optionally:

(i) the process is carried out to determining physical performance ability, and/or

(ii) the process is carried out to detect responsiveness to a stimulus relating to physical performance, which is preferably physical training, and optionally strength or endurance training; and/or

(iii) the process is carried out to select an individual suitable for a physical activity, which is preferably a sport; and/or

(iv) the process is carried out to select a stimulus relating to physical performance to give to the individual, wherein said stimulus is a type of physical training.

3. A process according to paragraph 1 or 2 wherein a specific combination of chromosome interactions are typed:

(i) comprising all of the chromosome interactions represented in any of Tables 3, 7, 8, 9, 25 and 30 or any of Tables 13, 14, 18, 22, 23; and/or

(ii) comprising at least 10%, 20%, 50%, or 80% of the chromosome interactions in any of Tables 3, 7, 8, 9, 25 and 30 or any of Tables 13, 14, 18, 22, 23; and/or

(iii) which together are present in at least 10, 50 or 100 of the regions or genes listed in any of Tables 21, 24, 25 or 30; and/or

(iv) wherein at least 10, 50, 100, 150, 200 or 300 chromosome interactions are typed which are present in a 4,000 base region which comprises or which flanks the chromosome interactions represented in any of Tables 3, 7, 8, 9, 25 and 30 or any of Tables 13, 14, 18, 22, 23.

4. A process according to any one of the preceding paragraphs in which 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 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, wherein detection of the ligated nucleic acid is preferably by using either:

(i) a probe that has at least 70% identity to any of the specific probe sequences mentioned in Table 24, 25 or 30, and/or (ii) by a primer pair which has at least 70% identity to any primer pair in Table 24, 25 or 30.

5. A process according to any one of the preceding paragraphs, wherein:

- the second set of nucleic acids is from a larger group of individuals than the first set of nucleic acids; and/or

- the first set of nucleic acids is from at least 8 individuals; and/or

- the first set of nucleic acids is from at least 4 individuals from a first subgroup and at least 4 individuals from a second subgroup which is preferably non-overlapping with the first subgroup.

6. A process according to any one of the preceding paragraphs wherein:

- the second set of nucleic acids represents an unselected group; and/or

- wherein the second set of nucleic acids is bound to an array at defined locations; and/or

- wherein the second set of nucleic acids represents chromosome interactions in least 100 different genes; and/or

- wherein the second set of nucleic acids comprises at least 1,000 different nucleic acids representing at least 1,000 different chromosome interactions; and/or

- wherein the first set of nucleic acids and the second set of nucleic acids comprise at least 100 nucleic acids with length 10 to 100 nucleotide bases.

7. A process according to any one of the preceding paragraphs, wherein the first set of nucleic acids is obtainable in a process comprising the steps of: -

(i) cross-linking of chromosome regions which have come together in a chromosome interaction;

(ii) subjecting said cross-linked regions to cleavage, optionally by restriction digestion cleavage with an enzyme; and

(iii) ligating said cross-linked cleaved DNA ends to form the first set of nucleic acids (in particular comprising ligated DNA).

8. A process according to any one of the preceding paragraphs:

- wherein at least 10 to 50 different chromosome interactions are typed, preferably in 10 to 50 different regions or genes optionally as defined in Table 21, 24, 25 or 30;

and/or

- which is:

(i) carried out on a human or horse athlete; and/or

(ii) carried out as part of a training regime, preferably after the start of the training regime; and/or

(iii) carried out on a Thoroughbred horse, preferably a racing horse; or

(iv) carried out on a human individual of who is less than 20 years old or is carried out on a horse that is less than 18 months old, and/or

(v) which is carried out at multiple time points to assess physical performance characteristics at specific time points, wherein the process is optionally carried out at at least 3 time points, which are preferably at least 30 days apart from each other.

9. A process according to any one of the preceding paragraphs wherein said defined region of the genome:

(i) comprises a single nucleotide polymorphism (SNP); and/or

(ii) expresses a microRNA (miRNA); and/or

(iii) expresses a non-coding RNA (ncRNA); and/or

(iv) expresses a nucleic acid sequence encoding at least 10 contiguous amino acid residues; and/or

(v) expresses a regulating element; and/or

(vii) comprises a CTCF binding site.

10. A process according to any one of the preceding paragraphs:

- which is carried out to identify an individual that is suited to endurance training, and preferably the identified individual is then subject to endurance training, which optionally occurs on at least 100 days out of the next 365 days after the identification; or

- which is carried out to identify an individual that is suited to strength training, and preferably the identified individual is then subject to strength training, which optionally occurs on at least 100 days out of the next 365 days after the identification.

11. A process according to any one of the preceding paragraphs which is carried out to select the individual for racing.

12. A process according to any one of the preceding paragraphs which is carried out to identify or design a an agent that affects physical performance, wherein said process is used to detect whether a candidate agent is able to cause a change to a chromosome state which is associated with a different physical performance state; wherein

- the chromosomal interaction is any specific interaction or combination of interactions defined in any paragraph and/or is present in any one of the regions or genes listed in Table 21, 24, 25 or 30; and/or

- the change in chromosomal interaction is monitored using (i) a probe that has at least 70% identity to any of the specific probe sequences mentioned in Table 24, 25 or 30, and/or (ii) by a primer pair which has at least 70% identity to any primer pair in Table 24, 25 or 30.

13. A process according to paragraph 12 which comprises selecting a target based on detection of chromosome interactions, and preferably screening for a modulator of the target to identify an agent which affects physical performance, wherein said target is optionally a protein.

14. A process according to any one of the preceding paragraphs, 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

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.

15. A process according to any one of the proceeding paragraphs which further comprises:

- producing a report on the physical performance characteristics of the individual based on the results of the process, or

- inputting the results of the process into a database, or

- assigning a specific fitness or training regime to the individual based on the results of the process, or

- designing a specific fitness or training regime for the individual based on the results of the process.

Specific Embodiments

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 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) <=30% that are <=-1.1 or =>1.1 and pass the p<=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.

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 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 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.

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.

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 translation.

Array design and processing

Array Design

1. Genetic loci are processed using the SII software (currently v3.2) to:
    a. Pull out the sequence of the genome at these specific genetic loci (gene sequence with 50kb upstream and 20kb downstream)
    b. Define the probability that a sequence within this region is involved in CCs
    c. Cut the sequence using a specific RE
    d. Determine which restriction fragments are likely to interact in a certain orientation
    e. Rank the likelihood of different CCs interacting together.
2. Determine array size and therefore number of probe positions available (x)
3. Pull out x/4 interactions.
4. 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.
5. Create list of x/4 probes plus defined control probes and replicate 4 times to create list to be created on array
6. Upload list of probes onto Agilent Sure design website for custom CGH array.
7. Use probe group to design Agilent custom CGH array.

Array Processing

1. Process samples using EpiSwitch™ Standard Operating Procedure (SOP) for template production.
2. Clean up with ethanol precipitation by array processing laboratory.
3. 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
4. Scan using Agilent C Scanner using Agilent feature extraction software.

EpiSwitch™

EpiSwitch™ biomarker signatures demonstrate high robustness, sensitivity and specificity in the stratification of complex disease phenotypes. This technology takes advantage of the latest breakthroughs in the science of epigenetics, monitoring and evaluation of chromosome conformation signatures as a highly informative class of epigenetic biomarkers. Current research methodologies 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 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 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 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.

Example 1

This work concerns human epigenetic biomarkers which monitor physiological differences and predispositions associated with physical fitness training programs. Defined biomarkers have been discovered and evaluated to assist in the determination of epigenetic predisposition for either strength or endurance training, with monitoring after 4 weeks of mixed training and 8 weeks of specialized training.

Participant Recruitment:

Participants were recruited using posted fly paper, electronic newsletter, local print and radio media, targeted recruitment at local athletics clubs and word of mouth. To be eligible for enrolment to the study, participants were required to meet the following '*performance*' criteria.

Group 1: strength athlete: Participant should be a regular weight-lifter. Example provided: 100kg body mass and have a current accumulated total of 550kg across; bench-press + squat + deadlift exercise.

Group 2: fitness athlete: Participant should be a regular fitness athlete. Example provided: current 10km run time: <40 mins; or current 5km run time <19 mins.

Group 3: sedentary non-athlete: has not been participating in sport or any form of structured exercise that causes physical exertion for >3 years.

Study Enrolment

Requisite criteria for potential enrolment were subjective (participant) reporting of athletic ability in order to meet one of three distinct phenotypes; 1) strength athlete 2) fitness athlete 3) sedentary non-athlete. Subsequently, eighty five (n=85) male participants aged 18-54 years, provided written informed consent prior to enrolling to the study. To confirm the meeting of enrolment criteria, comprehensive medical and athletic history were obtained before familiarisation protocol, blood sampling and performance tests were performed.

Familiarisation Protocol

Prior to physiological assessment, participants were acquainted with study procedures, personnel and provided with triaxial accelerometers (ActiGraph GT3X+, ActiGraph Corp), which were worn for 7-days in order to objectively determine participant physical activity, prior to physiological assessment.

Blood sampling

Following overnight fast, morning blood samples were drawn from an antecubital vein by venepuncture, using 22 gauge needle into a 6ml EDTA (BD Vacutainer®) blood tube. The blood tubes underwent 12 gentle inversions and immediately frozen at -80°C.

Anthropometrics

Height was determined using a portable stadiometer (Seca, Birmingham, U.K.). Body mass was measured to the nearest 0.1 kg by commercially available scales (body composition analyser TBF-300, Tanita, Tokyo, Japan). Total body fat percentage was calculated using bioelectrical impedance analysis (BIA) using a commercially available analyser (body composition analyser TBF-300, Tanita, Tokyo, Japan).

Strength Tests

For the 1RM tests, each subject attempted a weight that he believed could be lifted only once using maximum effort. The subject then added weight in increments of 2.2–4.5 kg until the heaviest load that could be successfully lifted once was determined. The subjects rested for approximately 3–5 minutes between attempts. The criterion for participant *maximum strength* was the combined 1RM max lifts (kg) for Squat + Bench Press + Deadlift exercises. Participant *relative strength ratio* was calculated as [Maximum Strength: Body Mass (kg:kg)]

Squat Exercise, 1 Rep Maximum (SQ 1RM)

During the SQ 1RM test, each lifter assumed an upright position, with the top of the bar not more than 3.0 cm below the top of the anterior deltoids. With both hands grasping the bar, the bar was removed from the rack, and the lifter moved back to assume a ready position, with knees extended, looking forward

at the chief referee. On command, the lifter bent the knees and lowered the body in one smooth descent, until the top surface of the legs at the hip joint were lower than the top of the knees. The lifter then raised himself from the deepest point of the SQ to a standing position, with the knees extended. On command, the lifter replaced the weight back onto the rack with the aid of a spotter.

Bench Press, 1 Rep Maximum (BP 1RM)

The participant placed himself in a supine position, keeping his head, shoulders, and buttocks in constant contact with the weightlifting bench. The lifter's feet remained flat and motionless on the floor during the attempt. The participant received the bar at full arm's length from a spotter located behind the head of the bench. The bar was then lowered to the chest at a point 1–2 cm below the nipple line along the chest. When the bar became motionless on the chest, "press" command was issued and the participant extended his arms, returning the weight back to its starting position. Once the arms were completely extended, the chief referee gave a rack command, and the spotter aided the participant in returning the weight back to the racks on the bench.

Dead-lift, 1 Rep Maximum (DL 1RM)

For the DL 1RM, the participants feet and hands were spaced evenly from the centre of the bar and were allowed to be placed close to its centre (power style), or farther from the centre (sumo style). The participant lifted the bar vertically from the floor with one smooth motion until the knees and back extended the body to an erect position. When the knees became fully extended, upon command, and the participant lowered the bar to the floor.

Peak Aerobic Capacity

Peak aerobic capacity ($\dot{V}O_2peak$) was obtained indirect calorimetery on an electronically braked cycle ergometer (Velotron, RacerMate, Seattle, WA, USA). Gas exchange was collected throughout the test using a metabolic cart (Moxus, AEI Technologies, Pittsburgh, PA, USA). The test consisted unloaded pedalling for 1 min, followed by a step-wise increase to 50 W for 2 min. Subsequently, work rate was increased by 30 W min^{-1} until the participant reached volitional fatigue (determined by the inability to maintain a minimum cadence above 60 rpm, blood lactate >7mmol.l^{-1}, respiratory exchange ratio >1.15; reaching >90% of age predicted heart rate maximum). $\dot{V}O_2peak$ values were confirmed as the highest value during the final stage of the ramp protocol. Work rate (WR) was collected continuously throughout the test and peak aerobic power was calculated using the average WR from the last 30 s of the test.

Phenotype Confirmation

Group 1: Participants were required to meet at least the 90th percentile for strength

STRENGHT PHENOTYPE: Relative Strength Ratio* (RSR) > 4.5 kg:kg

*RSR = [(*SQ1RM* kg+ *BP1RM* kg + *DL1RM kg) ÷ Body Mass (kg)*]

Group 2: Participants were required to meet at least the 90th percentile for aerobic capacity **FITNESS PHENOTYPE:** $\dot{V}O_2peak > 51.4ml.kg^{-1}$

Group 3: Participants were required to be on or below the 50th percentile for strength and aerobic capacity

Strength: ***Relative Strength Ratio* (RSR) < 3 kg:kg***

Fitness: 50th Percentile: $\dot{V}O_2peak < 40.8ml.kg^{-1}$

Samples and Processing

The samples used in the study are shown in Table 1. The EpiSwitch™ template was prepared for each of the samples using the EpiSwitch TM extraction procedure. The 3C template library was quantified and the amount standardised to 1ng/µl. A serial dilution was created and Nested PCR performed according to the EpiSwitch TM protocols.

Nested PCR was performed using the created serial dilutions for each sample for all 65 markers identified in part 2. For each marker the appropriate controls were included, these consisted of a no template control (NTC, all other reagents minus any DNA template) to monitor for any potential contamination of PCR reagents and a genomic control (negative control) to ensure the PCR products being detected are specific 3C products. The Nested PCR was analysed using high throughput capillary gel electrophoresis (LabChip GX Touch HT, Perkin Elmer) to identify and size the PCR products.

Training Response Annotations

The Nested PCR data was analysed using the retrospective annotation of end-point outcome for high and low response to exercise. To generate the annotations for each training group the individuals increase in physiological measurements due to undertaking the specified training regime, was ranked. The top 5 individuals in the ranking system were classed as High Responders for that training regime, the bottom 5 individuals were classed as Low responders (see table 2).

Results Overview

The analysis for part three of the project has been performed in two separate ways. The first is a direct analysis for predictive capability of 65 markers identified through the response analysis in part two and now screened in the third part of the project. The second is a parallel analysis of all the top 131 markers originally translated from EpiSwitch™ array of the high achieving Endurance and Strength Athletes. In this analysis the markers were evaluated strictly for their predictive potential using their baseline readouts and retrospective annotations of end-point outcome as High and Low response to specialized training by the end of 8 weeks of training. Figure 1 provides a graphical representation and overview of the analysis.

When compared, the two analysis streams have an overlap of 40.8%. The second analysis identifies 38 additional markers from the 131 original markers at the start of part 2 that are prime candidates to be predictive markers for training response. The overlap is shown in Figure 2, with a circle marking the markers identified in the section 2 analysis stream that have not been processed. [Figure 2 shows a Venn diagram of 80 potential markers identified in Analysis 2 compared to the 65 markers identified in part 2 and screened in part 3 based on exercise response]

Analysis 1

Analysis 1 was based on 3 comparisons. These three questions were designed to identify the markers from the 65 that were originally filtered on their responsiveness to mixed exercise and were predictive of an individual's outcome to specific training regimes or training in general. To that end the nested PCR data was analysed in three stratification groups:

1. High versus Low response (H/L) for Strength Training – to identify markers that were predictive at baseline to the end-point outcome of high or low response to Strength training.
2. High versus Low response (H/L) for Cardiovascular Endurance Training – to identify markers that are predicative at baseline to the end-point outcome of high or low response to Strength training at baseline.
3. High versus Low (H/L) response independent of training, grouping Strength and Endurance together – to identify markers that are predictive at baseline to the end-point outcome of a response to any/a training program at baseline.

The annotations of the outcome response to the training regimes at 8 weeks (after 4 weeks of specific cardio or strength training) were used to identify markers that are statistically significant for exercise response for the individual training regimes the third group looked at markers that were significant in both training programs.

To ensure the markers were predictive of training response H/L outcome and not just response markers, the binary nature of the marker at baseline and 8 weeks was investigated. Only markers that showed concordance between the two time points were selected. Filtering chromosome conformations that are stably detected before and after training that also show statistical significance between low and high response to the training programs selects for high quality markers that represent an inherent stable regulation framework in individuals that pre-disposes them to physiologically advance well or poorly to the final outcome of physical training of particular type.

Out of the 65 markers filtered through exercise response to 4-week of mixed training, 17 were found to be statistically significant. These are detailed in Table 3 and 4. These 17 markers represent a pool of high quality markers for the predisposition of training response in individuals at baseline (naïve) before training

commences. The odds ratio shown in Table 3 is the measure of how strongly the absence and detection of the individual marker is associated with High/Low predicted outcome response to training in the sample population. An odds ratio of 1 indicates there is no difference between the two subpopulations (High and low response). The data strongly suggest that 17 discovered predictive markers are strongly associated with the successful outcome of training in the sample population with odds ratios of between 2 and 12.

Each marker was also individually assessed using Welch's t-test. This is a statistical test used to compare two sample populations and ascertain if the populations have equal means. An equal mean demonstrating that the two populations are not significant different. The p values shown in Table 5 are a measure of confidence that the inequality in the population means is due to actual differences and not be chance sampling.

A p value cut off of 0.3 is used to determine if the difference in detection of chromosome conformations are statistically significant. As will be seen in other literature this differs from the normally used 0.05 values. The 0.3 limit was experimentally derived to assure capturing markers that provide useful information gain, for example in the machine learning classifiers, strengthening the classifier performance.

The significant p values for each marker show the statistical significance of the odds ratios (OR) between training types in Table 3. The data in Tables 3 and 4 demonstrate quality and robustness of the 17 predictive markers identified.

Binary data from the marker OBD142_081.083_1.4x, as shown in Table 5 gives a useful example of both the higher detection rates between High and Low responders to exercise, in this case cardio endurance training and the predisposition already present at baseline before training commences. The data also represents a documented phenomenon of interference by mixed training causing disruption to the regulation before the chromatin regulation is reprogrammed back to its original predisposition state.

We identified the regulatory frame work for predictive advantage and predisposition of High response outcome in individuals being present at onset. The regulatory frame work in the low responders either preprogrammes to match that of the high responders, which they inherently possess already or fails to change at all. The markers represented in Figure 3 are all marker for high response in strength training. Figure 6. showing changes in detection for specific markers from baseline and after 8 weeks of training (4 weeks mixed, 4 weeks strength training), Y axis detection state 0 = no detection, 1 = detection, X axis 1 = baseline, 2 = 8 weeks. Figure 3A shows High responders is fixed with Low responders reprogramming causing the marker to become detectable due to the training programme. Figure 3B shows High responders is fixed with Low responders reprogramming causing the marker to become undetectable due to the training programme. Figure 3C shows High responders is fixed with Low responders also fixed, showing no modification of the chromatin landscape for this particular interaction.

Three of the 17 markers identified are anchored in the 3' UTR of the DKK3 genetic locus (Table 6). It is evident that the DKK3 3'UTR is a hub of epigenetic control for this specific genetic locus with differential genomic architecture changing the regulation and accessibility creating predisposition for training response.

Analysis 2

The rationale for the second analysis was to look at the 131 markers screened at baseline in part 2 against retrospective annotations of end-point outcome of High or Low response to specialised training after 8 weeks. Many potential predictive markers may have been excluded in Analysis 1 as they were largely insensitive to the 4 weeks of mixed training. In contrast to analysis 1, which identified predictive markers with additional feature of responsiveness to mixed exercise, Analysis 2 was designed only to identify markers that were predictive of an individual's response to specific training programs.

Analysis 2 was based on the same three comparisons.

1. High versus Low response for Strength Training – to identify markers that were predictive at baseline to the end-point outcome of high or low response to Strength training at baseline.
2. High versus Low response for Cardiovascular Endurance Training – to identify markers that are predicative at baseline to the end-point outcome of high or low response to Strength training at baseline.
3. High versus Low response independent of training, grouping Strength and Endurance together – to identify markers that are predictive at baseline to the end-point outcome of a response to any/a training program at baseline.

Welch's t - test was used to investigate the three comparisons. The test was cross validated by performing 1000 repeats with randomised sample selection. This gives 1000 different sample populations to test for the same 131 markers. Resampling and cross validation are used to ensure that the markers can generalise to an independent data set. The analysis output statistics for the predictive markers are shown in tables 7, 8 and 9. When duplications between the comparisons were removed the analysis identified 80 potential predictive markers. These 80 contained all 17 good predictive markers identified in Analysis 1.

Figure 4 shows the analysis overlap. The circle on the left represents 38 additional predictive markers from Analysis 2. The circle in the middle shows the 42 overlapping predictive markers that have been investigated in part 2 and 3. These include the 17 markers detailed in Analysis 1. The circle on the right shows 23 markers investigated in part 2 and 3 that are Responsive markers to training. The composition of the 80 markers identified in Analysis two is shown in the Venn diagram in Figure 5.

It is important to mention, that as an independent validation of the methodology in general and individual markers in particular, top significant markers with predictive powers for strength or endurance training

outcome have been successfully translated into markers in an equine study. Based on the evolutionary conservation of genetic and epigenetic regulatory mechanisms underlying those markers, equine study of stayers and sprinters achieved 93,75% accuracy in classification of the development cohort of 32 (Figure 6 which shows confusion matrix results).

Conclusions

1. Existing chromosome conformation signatures can be predictive of later response outcome to training phenotypes. This is consistent with a number of validated studies for development of the predictive biomarkers to response to various treatments.
2. Statistically significant disseminating EpiSwitch™ markers identified and evaluated in strength/endurance training for human participants have been successfully translated into statistically significant equine markers for stratification of verified Sprinters and Stayers.
3. The 10 discovered markers classify between Sprinter and Stayer phenotypes with an accuracy of 93.75% on the available set of 32 validated samples.

Analysis 2 has identified 80 strong predictive markers, these include all the 17 predictive/response markers earlier reported in analysis 1 and an additional 38 markers that are predictive for H/L outcome to training response phenotypes when measured at baseline.

Summary

We have successfully identified and evaluated significant predictive biomarkers for H/L outcome of the strength/endurance training. These results achieve the objective of the project.

- 17 high quality robust predictive stable markers, with sensitivity to mixed training, have been developed for use in baseline prediction of an individual's response outcome to specialized training regimes
- A further 38 strictly predictive markers, independent of response to mixed training, have been identified and evaluated at baseline, for use in baseline prediction of an individual's response outcome to specialized training regimes.

Example 2

Identification of validated signatures contain binary CCSs which are either present, or absent as conditional biomarkers of epigenetic regulation in equine individuals in strength or endurance training.

We identified CCSs biomarkers to successfully distinguish between Thoroughbreds, trained as either sprinters or a stayers. These markers can be used to determine predisposition and monitoring of young

unraced Thoroughbreds as they are selected and undergo the training programs for sprinters and stayers. The markers are relevant to training potential, physiological monitoring and epigenetic reprogramming through training.

Project Approach

The top 50 EpiSwitch™ markers, identified from the work in human was translated into EpiSwitchTM designed Equine nested PCR assays and tested by the EpiSwitch™ PCR platform using Thoroughbreds with a defined phenotype: 1) sprinting 2) long-distance (Stayers) for evaluation of best disseminating markers for Sprinters and Stayers.

Samples

A total of 48 Samples were used as shown in Table 10:

- 16 Untrained young Thoroughbreds.
- 16 Trained Thoroughbreds classed as Sprinters.
- 16 Trained Thoroughbreds classed as Stayers.

The sex distribution between the sprinter and stayer sample types is balanced. The untrained male samples are skewed towards Colts against their castrated peers (Gelding), table 4. This skew will be accounted for in the biostatistical analysis.

Genome Conversion

The 131 markers identified on the Human array and translated to Nested PCR were translated from the GRCh38 Human Genome assembly to the EquCab2.0 Equine genome assembly using LiftOver (USSC). In total 114 of these were successfully translated. OBD's internal primer design application was used to design Nested primer sets for PCR, 65 of the 114 markers met the strict criteria for the successful primer design according to EpiSwitchTM operational procedures and methodology. The top 50 markers were selected for EpiSwitchTM equine nested PCR interrogation.

Nested PCR screening

The EpiSwitch™ template was prepared for each of the samples using the EpiSwitch TM extraction standard operation procedure. The 3C template library was quantified and the amount standardised to 1ng/µl. A serial dilution was created and Nested PCR performed according to the EpiSwitch TM protocols

Nested PCR was performed using the created serial dilutions for each sample for all 50 markers selected. The Nested PCR was analysed using high throughput capillary gel electrophoresis (LabChip GX Touch HT, Perkin Elmer) to identify and size the PCR products. The data for the 16 Sprinters and 16 stayers was analysed using Boschloos' Test with resampling. The top 17 markers are shown in table 13.

In total, 17 of the 50 markers investigated were found to be statistically significant using a Boschloo p value cut off of 0.2. Importantly, this selection is produced using dilution individual titres, so each marker is produced by p-values based on the specific titres. Resampling of the data set was performed 100 times with a 66.7% partition, from the dataset of 32, 22 samples were selected at random and the statistical tests performed. This was repeated 100 times with the median result of this documented in table 13. These 17 markers represent interactions spaced around 16 genomic loci. The markers OBD154_045/047 and OBD154_049/051 are unique interactions that are across the same genomic location, see Table 4. The data show that a number of translated markers, discovered originally in a human cohort, are also applicable to horses.

MTFR1 (mitochondrial fission regulator 1) is notable from amongst identified loci as this was indicated in the most significant region from the Horse genetics for selection in thoroughbred Horses. Mitochondrial function and the management of reactive oxygen species are important for favorable exercise responses and therefore MTFR1 may impose strong selection pressure in Thoroughbreds by protection of mitochondria-rich tissue against oxidative stress. As such it is an excellent region for racing performance and endurance.

Classification

A classifier based on the Sprinter vs Stayer markers identified on the trained samples was developed to enable the classification of the untrained samples. Glmnet (Lasso and Elastic-Net Regularized Generalized Linear Models) was used to rank the markers in their ability to classify between sample types. The top 14 markers identified in Glmnet were then compared to the top 11 markers based on Boschloos' p value (Table 13). As shown in Figure 7, 10 of the markers showed concordance and were shared between the two statistical analyses. The 10 concordant markers were selected to develop the classifier. XGBoost was used to model the markers and build a classifier.

The XGBoost model is an ensemble-based classifier that uses a series of weak classifying models to produce one overall strong model. In this gradient boosting methodology an initial model is created from the training data, a second model is then created that attempts to correct any errors in classification from the first model. This process is repeated n number of times to produce a final model that will classify the training set. A process of early stopping, ending the classifier build chain earlier then the initially set n value, is used to prevent the model over fitting the training set. A classification of the training set based on Sprinters and Stayers is shown in Figure 6. Based on the 10 markers, the EpiSwitchTM test classifies well between Sprinters and Stayers, with an accuracy of 93.75%.

The probability calls of the 10 markers classifier are shown in Table 15. By default, a probability score >0.5 by the classifier is considered a call for a Sprinter, while < 0.5 is considered a call for Stayer. On the basis of the results of classification in Table 15, the original probability scores (>0.5 for Sprinter, <0.5 for Stayer)

were adjusted for quality classification calls on naïve samples from young Thoroughbreds. The established cut offs for the classifier calls are shown in Table 16.

The classifier was applied to the data for the naïve samples from young Thoroughbreds with the call results in Table 17. For 4 of the samples the classifier was unable to call the phenotype with high enough certainty and they fell into the unclassified limits. The remaining 12 samples were successfully called with a prediction of epigenetic profile conducive for the potential good Sprinter or Stayer. The 10 discovered markers classify between Sprinter and Stayer phenotypes with an accuracy of 93.75% on the available set of 32 validated samples.

Example 3

Further Work on the Human Study

A multinomial Glmnet regression analysis was performed based on three annotation groups, High responder, Medium responder and Low responder to each training type. Each CCS identified as predictive at baseline relative to training response outcomes was then compared across the time points for the sedentary controls to remove any CCS that showed variation due to effects other than the training under investigation. In total 18 CCS were identified as predictive for response to Strength training and 7 for response to Endurance training. Two of the CCS are shared between the training types (Mixed). Results are shown in tables 31 and 32.

Loop detected, or EpiSwitch marker present, are strict categories of predictive and stable markers for strength or endurance training. 'High-responder' markers are parts of epigenetic profile that conducive to very good physiological response to training program (using VO2 maximum and one-repetition maximum strength tests), i.e responders in our use of term. 'Low -responders' is the data analysis term that marks the stable predictive markers for individuals who will not change much their physiological performance after the training program ('non-responders').

Considering that 'high response' is the physiological data analysis term for 'responder' biomarker, and 'low-response' for 'non-responders', the majority of predictive response biomarkers are strength or endurance specific. However, several biomarkers reflect a dual function and provide information for good response in both endurance and strength.

The loop detected refers to array data, however Table 31 refers to strength and Table 32 refers to endurance based on PCR data. In regards to marker definitions and marker categories used by data analysis on array data:

Strength control: these are is just reference controls on the untrained side - readouts on the group of sedentary individuals before training at baseline. This is a physiological baseline control group.

Endurance control: same as above, but for endurance.

Strength training: these are reference controls, retrospective and ultimate positive controls, on high achievers in strength read out on the group of strength trained individuals after successful training. This is a physiological, positive control group.

Endurance training: same as before but for endurance.

This group of markers should be evaluated based on the following rules: the high responder markers as predictive and stable (from baseline onwards) responder markers, while low responder are the opposite side - predictive and stable markers of non-response to training. Generally predictive markers are specific for either strength or endurance as they were developed separately on either strength or endurance programmes and control groups. However there is some overlap, probably reflecting physiological overlap of the relevant regulatory networks - several markers are good predictive marker for good response in both strength or endurance training.

Overall Review of the Work

The original pool of genetic sites on the screening array was comprised of 1) inflammatory genes, 2) loci associated with micro-satellite differences in Thoroughbred horses and translated into humans. Thoroughbreds are highly inbred and the input of genetic component into phenotypical differences is highly limited in those subjects - this was considered the right model to search for any associations with epigenetic control sites, in terms of chromosome conformations. The fact that statistically significant sites are associated broadly with some of the well-known genes functionally linked to strength and endurance is the consequence of an independent selection. Importantly, screening of the potential candidates for chromosome conformation markers was driven by proprietary EpiSwitch annotations within non-coding parts of the genome within 100 kb windows of the referenced loci: upstream, downstream or encompassing the whole genes within the chromatin domain. At any part of the selection of CCS marker leads, no comparative assessment for any gene expression of any genes in the vicinity were made to assist the selection, thus excluding any link or correlation to gene expression changes of any of the genes and their known functional link to physical training outcomes.

Tables 34 to 36 show preferred powerful markers. The odds ratio shown in Table 36 is the measure of how strongly the absence and detection of the individual marker is associated with High/Low predicted outcome response to training in the sample population. An odds ratio of 1 indicates there is no difference between the two subpopulations (High and low response). The data strongly suggest that 17 discovered predictive markers are strongly associated with the successful outcome of training in the sample population with odds ratios of between 2 and 12.

Each marker was also individually assessed using Welch's t-test. This is a statistical test used to compare two sample populations and ascertain if the populations have equal means. An equal mean demonstrating that the two populations are not significant different. The p values shown are a measure of confidence that the inequality in the population means is due to actual differences and not be chance sampling.

We used a p value cut off of 0.3 to determine if the difference in detection of chromosome conformations are statistically significant. As will be seen in other literature this differs from the normally used 0.05 values. Through our previous projects, assay type and know-how the 0.3 limit was experimentally derived to assure capturing markers that provide useful information gain in the machine learning classifiers, strengthening the classifier performance. The significant p values for each marker show the statistical significance of the odds ratios (OR) between training types in this table. The data in this table demonstrates quality and robustness of the 17 predictive markers identified.

Figure 15 is a VENN Diagram of Significant Markers for CV and Strength Baseline and 8 weeks. These markers are show in Table 40.

Figure 16 shows baseline CV markers based on High and Low CV groups Exact P-values for association. These are the top 10 significant markers for the subjects at baseline based on the CV ranges. The range for Strength is a significant at baseline also. This indicates the close association between CV and strength ranges in these markers.

Figure 17 shows baseline Strength markers based on high and Low Strength group Exact P-values for association. These are the top 20 significant markers for the subjects at baseline based on the Strength ranges. The range for CV is a significant at baseline also. This indicates the close association between CV and strength ranges in these markers.

Figure 18 shows 10 Episwitch horse markers Identified from a UK cohort. The figure shows the genomic location in horses and the homologous region in the Human genome and the type of the marker: Sprinter or Stayer. The same 10 markers were used to classify the Singaporean Horses.

Patient Sample ID	Phenotype	Response
B16.3	Control	-
B17.3	Strength	-
B26.3	Cardio	High
B33.3	Cardio	-
B34.3	Cardio	High
B37.3	Strength	High
B38.3	Cardio	Low
B39.3	Strength	High
B40.3	Cardio	High
B43.3	Cardio	Low
B44.3	Cardio	High
B45.3	Strength	Low
B46.3	Strength	High
B51.3	Strength	-
B52.3	Control	-
B61.3	Cardio	High
B62.3	Strength	Low
B63.3	Excluded	-
B64.3	Strength	Low
B68.3	Cardio	-
B70.3	Strength	High
B71.3	Cardio	Low
B72.3	Strength	High
B73.3	Cardio	Low
B74.3	Strength	-
B76.3	Strength	Low
B77.3	Cardio	Low
B78.3	Strength	-
B79.3	Excluded	-
B80.3	Cardio	-
B83.3	Strength	Low
B85.3	Cardio	-

Table 1

Individual	Rank	Label
A	1	High response
B	2	High response
C	3	High response
D	4	High response
E	5	High response
F	6	-
G	7	-
H	8	-
I	9	-
J	10	Low response
K	11	Low response
L	12	Low response
M	13	Low response
N	14	Low response

Table 2

Marker	Training	Odds Ratio
OBD142_029.031_1x	Presence in Endurance and Strength	7.2
OBD142_061.063_1.8x	Presence in Endurance and Strength	8.2
OBD142_069.071_1.2x	Presence in Endurance and Strength	8
OBD142_089.091_1x	Presence in Endurance and Strength	2.9
OBD142_137.139_1.2x	Presence in Endurance and Strength	8
OBD142_081.083_1.4x	Presence in Endurance	6
OBD142_189.191_1x	Presence in Endurance	4.5
OBD142_213.215_1.4x	Presence in Endurance	2.25
OBD142_017.019_1.2x	Presence in Strength	4
OBD142_037.039_1x	Presence in Strength	12
OBD142_065.067_1x	Presence in Strength	5
OBD142_133.135_1x	Presence in Strength	4
OBD142_253.255_1.2x	Presence in Strength	12
OBD142_353.355_1x	Presence in Strength	9
OBD142_477.479_1x	Presence in Strength	9
OBD142_181.183_1.4x	Presence in Strength	2
OBD142_397.399_1x	Presence in Strength	2

Table 3

Marker	Training type		
	Combined	Cardio	Strength
OBD142_029.031_1x	0.01668097	0.066688	0.01613009
OBD142_061.063_1.8x	0.01851064	0.11741215	0.10680154
OBD142_069.071_1.2x	0.00255609	0.066688	0.05766889
OBD142_089.091_1x	0.12375267	0.40122897	0.18059725
OBD142_137.139_1.2x	0.06270144	0.11741215	0.18262433
OBD142_081.083_1.4x	0.13923948	0.070484	0.7999889
OBD142_189.191_1x	0.11969458	0.11741215	0.84528948
OBD142_213.215_1.4x	1	0.69409048	0.13523206
OBD142_017.019_1.2x	0.72495046	0.54542431	0.28124028
OBD142_037.039_1x	0.15251771	1	0.02525659
OBD142_065.067_1x	0.13191103	0.54542431	0.05766889
OBD142_133.135_1x	0.46156086	1	0.01613009
OBD142_253.255_1.2x	0.44960749	0.61010368	0.02421162
OBD142_353.355_1x	0.11969458	1	0.01615402

OBD142_477.479_1x	0.42751765	1	0.02525659
OBD142_181.183_1.4x	0.75595814	0.74070856	0.17780781
OBD142_397.399_1x	0.15163712	0.66842823	0.09667637

Table 4

Trainee	Base line	4 weeks	8 weeks	Response to training
B26	1	0	1	High
B34	1	0	1	High
B40	1	0	1	High
B44	0	0	0	High
B61	0	0	0	High
B38	0	0	0	Low
B43	0	0	0	Low
B71	0	0	0	Low
B73	0	1	0	Low
B77	0	1	0	Low

Table 5

Marker	High or low response	Training type
OBD142_061.063_1.8x	High	Both
OBD142_069.071_1.2x	High	Both
OBD142_065.067_1x	High	Strength

Table 6

Marker with Dilution	Marker	Freq	Rank Sum	Rank Mean	Rank Median	Mean p value	Median p value
OBD142_437.439_1.2x	OBD142_437.439	1000	198	1.98	2	0.01576	0.01562
OBD142_025.027_1x	OBD142_025.027	1000	1224.5	12.245	8.5	0.08678	0.09375
OBD142_417.419_1x	OBD142_417.419	1000	1369	13.69	13	0.09328	0.12500
OBD142_517.519_1.2x	OBD142_517.519	1000	1251.5	12.515	13	0.09312	0.12500
OBD142_065.067_1x	OBD142_065.067	971	3903	39.03	35.5	0.20758	0.13696
OBD142_513.515_1.2x	OBD142_513.515	971	3903	39.03	35.5	0.20758	0.13696
OBD142_017.019_1x	OBD142_017.019	977	4446	44.46	40	0.23382	0.28125
OBD142_029.031_1x	OBD142_029.031	972	4681.5	46.815	40.5	0.23992	0.28125
OBD142_069.071_1.2x	OBD142_069.071	972	5103.5	51.035	40	0.26566	0.28125
OBD142_085.087_1.2x	OBD142_085.087	972	4667	46.67	41	0.24252	0.28125
OBD142_093.095_1x	OBD142_093.095	1000	3945	39.45	40	0.22246	0.28125
OBD142_117.119_1.2x	OBD142_117.119	1000	4206.5	42.065	38.5	0.23621	0.28125
OBD142_125.127_1.2x	OBD142_125.127	977	4446	44.46	40	0.23382	0.28125
OBD142_157.159_1.4x	OBD142_157.159	1000	3707.5	37.075	38	0.22324	0.28125
OBD142_233.235_1.4x	OBD142_233.235	1000	3707.5	37.075	38	0.22324	0.28125
OBD142_285.287_1.4x	OBD142_285.287	975	4749	47.49	37.75	0.24953	0.28125
OBD142_325.327_1.4x	OBD142_325.327	1000	4206.5	42.065	38.5	0.23621	0.28125
OBD142_449.451_1x	OBD142_449.451	1000	3738	37.38	38.25	0.21652	0.28125
OBD142_461.463_1.4x	OBD142_461.463	972	4667	46.67	41	0.24252	0.28125
OBD142_469.471_1x	OBD142_469.471	975	4749	47.49	37.75	0.24953	0.28125
OBD142_133.135_1x	OBD142_133.135	504	14009	140.09	86.5	0.60112	0.34375
OBD142_181.183_1.4x	OBD142_181.183	504	14009	140.09	86.5	0.60112	0.34375
OBD142_397.399_1x	OBD142_397.399	504	14009	140.09	86.5	0.60112	0.34375

OBD142_253.255_1.2x	OBD142_253.255	867	7643	76.43	109.25	0.62216	0.34375
OBD142_181.183_1.4x	OBD142_181.183	504	14009	140.09	86.5	0.60112	0.34375
OBD142_037.039_1x	OBD142_037.039	779	8626.5	86.265	113	0.35984	0.45312
OBD142_353.355_1x	OBD142_353.355	699	8585.5	85.855	113	0.35078	0.45312

Table 7 shows predictive markers for strength training response, which are preferably used for typing humans. (Present in strength training in humans)

Marker with Dilution	Marker	Freq	Rank Sum	Rank Mean	Rank Median	Mean p value	Median p value
OBD142_005.007_1x	OBD142_005.007	527	12594.5	125.945	76.5	0.57000	0.28906
OBD142_009.011_1.4x	OBD142_009.011	737	9784	97.84	44.5	0.44750	0.18750
OBD142_025.027_1.2x	OBD142_025.027	1000	11604	116.04	42	0.53687	0.18750
OBD142_029.031_1.4x	OBD142_029.031	1000	2760.5	27.605	38	0.13594	0.18750
OBD142_041.043_1.2x	OBD142_041.043	737	9784	97.84	44.5	0.44750	0.18750
OBD142_045.047_1x	OBD142_045.047	525	13251.5	132.515	77.5	0.60297	0.28906
OBD142_057.059_1.8x	OBD142_057.059	715	11959.5	119.595	51.5	0.55312	0.18750
OBD142_061.063_1.4x	OBD142_061.063	814	10698.5	106.985	44.5	0.49625	0.18750
OBD142_065.067_1.2x	OBD142_065.067	1000	859.5	8.595	9.5	0.05469	0.07031
OBD142_069.071_1.2x	OBD142_069.071	967	10625.5	106.255	43	0.48812	0.18750
OBD142_081.083_1.4x	OBD142_081.083	1000	2686	26.86	34	0.13008	0.18750
OBD142_097.099_1.8x	OBD142_097.099	1000	11838	118.38	51.5	0.54500	0.18750
OBD142_101.103_1x	OBD142_101.103	1000	5050	50.5	70	0.21125	0.28906
OBD142_109.111_1.2x	OBD142_109.111	1000	11604	116.04	42	0.53687	0.18750
OBD142_121.123_1.8x	OBD142_121.123	814	10698.5	106.985	44.5	0.49625	0.18750
OBD142_133.135_1.8x	OBD142_133.135	737	9784	97.84	44.5	0.44750	0.18750
OBD142_137.139_1.2x	OBD142_137.139	1000	3052	30.52	39	0.14414	0.18750
OBD142_141.143_1.4x	OBD142_141.143	737	9784	97.84	44.5	0.44750	0.18750
OBD142_145.147_1.4x	OBD142_145.147	523	12431.5	124.315	81.5	0.56711	0.28906
OBD142_153.155_1.4x	OBD142_153.155	1000	914	9.14	10	0.05781	0.07031
OBD142_157.159_1.4x	OBD142_157.159	514	13293.5	132.935	83.5	0.60250	0.28906
OBD142_165.167_1x	OBD142_165.167	1000	4818.5	48.185	69.5	0.20031	0.28906
OBD142_185.187_1.4x	OBD142_185.187	1000	3161	31.61	39	0.15117	0.18750
OBD142_189.191_1x	OBD142_189.191	1000	2760.5	27.605	38	0.13594	0.18750
OBD142_197.199_1.4x	OBD142_197.199	1000	2795	27.95	38	0.13711	0.18750
OBD142_201.203_1.4x	OBD142_201.203	1000	2903.5	29.035	38.5	0.14180	0.18750
OBD142_213.215_1.4x	OBD142_213.215	151	19515.5	195.155	212	0.90047	1.00000
OBD142_233.235_1.2x	OBD142_233.235	505	12737	127.37	81.5	0.57758	0.28906
OBD142_241.243_1x	OBD142_241.243	1000	2820.5	28.205	38	0.13828	0.18750
OBD142_253.255_1.2x	OBD142_253.255	1000	5334.5	53.345	70	0.22125	0.28906
OBD142_257.259_1.2x	OBD142_257.259	1000	11995.5	119.955	51.5	0.55312	0.18750
OBD142_261.263_1x	OBD142_261.263	1000	5144	51.44	69.5	0.21031	0.28906
OBD142_265.267_1.4x	OBD142_265.267	967	9975.5	99.755	41.5	0.46375	0.18750
OBD142_273.275_1.4x	OBD142_273.275	962	12527	125.27	51.5	0.58562	0.18750
OBD142_277.279_1.2x	OBD142_277.279	1000	3060	30.6	38.5	0.14766	0.18750
OBD142_297.299_1.2x	OBD142_297.299	1000	847.5	8.475	9.5	0.05531	0.07031
OBD142_309.311_1.4x	OBD142_309.311	806	9550	95.5	42	0.43937	0.18750
OBD142_313.315_1x	OBD142_313.315	1000	2760.5	27.605	38	0.13594	0.18750
OBD142_321.323_1.2x	OBD142_321.323	1000	11995.5	119.955	51.5	0.55312	0.18750
OBD142_325.327_1.2x	OBD142_325.327	1000	4958.5	49.585	69.5	0.20344	0.28906
OBD142_329.331_1.4x	OBD142_329.331	1000	2795	27.95	38	0.13711	0.18750
OBD142_337.339_1x	OBD142_337.339	817	10759.5	107.595	43	0.49625	0.18750
OBD142_357.359_1.4x	OBD142_357.359	962	12527	125.27	51.5	0.58562	0.18750

OBD142_361.363_1.2x	OBD142_361.363	932	11406.5	114.065	43	0.52875	0.18750
OBD142_373.375_1x	OBD142_373.375	1000	2903.5	29.035	38.5	0.14180	0.18750
OBD142_393.395_1.2x	OBD142_393.395	1000	921.5	9.215	10.5	0.05781	0.07031
OBD142_401.403_1x	OBD142_401.403	1000	2820.5	28.205	38	0.13828	0.18750
OBD142_405.407_1x	OBD142_405.407	537	11739.5	117.395	73.5	0.52570	0.28906
OBD142_413.415_1.2x	OBD142_413.415	638	10473	104.73	45.5	0.48812	0.18750
OBD142_433.435_1x	OBD142_433.435	1000	2969.5	29.695	39	0.14297	0.18750
OBD142_437.439_1x	OBD142_437.439	1000	5144	51.44	69.5	0.21031	0.28906
OBD142_445.447_1.2x	OBD142_445.447	752	10351.5	103.515	45	0.48000	0.18750
OBD142_457.459_1x	OBD142_457.459	1000	3016	30.16	38.5	0.14414	0.18750
OBD142_469.471_1.2x	OBD142_469.471	1000	2829	28.29	38.5	0.13594	0.18750
OBD142_477.479_1.2x	OBD142_477.479	752	10351.5	103.515	45	0.48000	0.18750
OBD142_489.491_1x	OBD142_489.491	937	9975.5	99.755	41.5	0.46375	0.18750
OBD142_501.503_1x	OBD142_501.503	537	11739.5	117.395	73.5	0.52570	0.28906
OBD142_509.511_1.8x	OBD142_509.511	970	11725.5	117.255	43.25	0.54500	0.18750
OBD142_517.519_1x	OBD142_517.519	1000	914	9.14	10	0.05781	0.07031

Table 8 shows predictive markers for endurance training response, which are preferably used for typing humans. (Present in endurance training in humans).

Marker with Dilution	Marker	Freq	Rank Sum	Rank Mean	Rank Median	Mean p value	Median p value
OBD142_005.007_1x	OBD142_005.007	731	10275.5	102.755	71.5	0.33252	0.23486
OBD142_017.019_1x	OBD142_017.019	657	8644	86.44	57.5	0.28238	0.23486
OBD142_025.027_1.2x	OBD142_025.027	1000	1075	10.75	6.25	0.04110	0.03613
OBD142_029.031_1x	OBD142_029.031	971	4960.5	49.605	39.5	0.17457	0.13770
OBD142_041.043_1.4x	OBD142_041.043	837	9882.5	98.825	83.75	0.33162	0.28271
OBD142_045.047_1.2x	OBD142_045.047	817	7944	79.44	52	0.25580	0.19141
OBD142_057.059_1.4x	OBD142_057.059	707	8843	88.43	56.25	0.28852	0.19141
OBD142_061.063_1.8x	OBD142_061.063	906	5038	50.38	28.5	0.16971	0.09229
OBD142_065.067_1x	OBD142_065.067	992	2771.5	27.715	18.25	0.10043	0.05800
OBD142_069.071_1.2x	OBD142_069.071	998	2877.5	28.775	16.25	0.10248	0.05800
OBD142_085.087_1.4x	OBD142_085.087	783	13339.5	133.395	88.75	0.44247	0.28271
OBD142_089.091_1x	OBD142_089.091	214	21704.5	217.045	221.25	0.70459	0.58105
OBD142_097.099_1.8x	OBD142_097.099	986	4753	47.53	36.75	0.16534	0.13770
OBD142_101.103_1x	OBD142_101.103	692	10572.5	105.725	74.75	0.34013	0.26685
OBD142_113.115_1.2x	OBD142_113.115	633	11276	112.76	76.75	0.36933	0.26685
OBD142_117.119_1.2x	OBD142_117.119	586	11545	115.45	80.75	0.36613	0.26685
OBD142_121.123_1.8x	OBD142_121.123	785	12882.5	128.825	91.75	0.42484	0.28271
OBD142_137.139_1.2x	OBD142_137.139	811	8486.5	84.865	55	0.28375	0.19751
OBD142_145.147_1.2x	OBD142_145.147	779	9565.5	95.655	67	0.31244	0.23486
OBD142_153.155_1.2x	OBD142_153.155	996	2110.5	21.105	13.5	0.08214	0.07031
OBD142_157.159_1.4x	OBD142_157.159	901	4935	49.35	24	0.16512	0.09229
OBD142_181.183_1.2x	OBD142_181.183	726	13631.5	136.315	88.5	0.44859	0.28271
OBD142_185.187_1.4x	OBD142_185.187	800	7477.5	74.775	54.5	0.24398	0.19141
OBD142_189.191_1.2x	OBD142_189.191	990	2092.5	20.925	13.75	0.08116	0.07031
OBD142_197.199_1.4x	OBD142_197.199	806	10234	102.34	88	0.34598	0.28271
OBD142_201.203_1.4x	OBD142_201.203	752	10967	109.67	93	0.36080	0.28271
OBD142_225.227_1.2x	OBD142_225.227	910	9781	97.81	83.75	0.32891	0.28271
OBD142_233.235_1.2x	OBD142_233.235	886	6386	63.86	29.75	0.21925	0.09229
OBD142_241.243_1x	OBD142_241.243	883	4360.5	43.605	30.5	0.15074	0.11284
OBD142_253.255_1.2x	OBD142_253.255	986	2287.5	22.875	18	0.08839	0.09229
OBD142_257.259_1.2x	OBD142_257.259	961	6557.5	65.575	39.75	0.22005	0.13770
OBD142_261.263_1x	OBD142_261.263	894	5356.5	53.565	26.25	0.17615	0.09229
OBD142_273.275_1.4x	OBD142_273.275	864	10216.5	102.165	88	0.34298	0.28271
OBD142_309.311_1.2x	OBD142_309.311	762	10278	102.78	64	0.33810	0.23486

OBD142_321.323_1x	OBD142_321.323	958	5677.5	56.775	42.25	0.18968	0.13770
OBD142_325.327_1.4x	OBD142_325.327	958	4037	40.37	20.75	0.13814	0.09229
OBD142_329.331_1x	OBD142_329.331	943	6060.5	60.605	45	0.19830	0.13770
OBD142_349.351_1x	OBD142_349.351	689	10674	106.74	74.75	0.35113	0.24731
OBD142_353.355_1x	OBD142_353.355	743	9010.5	90.105	65.5	0.29709	0.23486
OBD142_361.363_1.2x	OBD142_361.363	741	9202	92.02	59.5	0.30628	0.23486
OBD142_373.375_1x	OBD142_373.375	952	5814	58.14	41.75	0.19707	0.13770
OBD142_389.391_1x	OBD142_389.391	855	10445	104.45	84.75	0.35071	0.28271
OBD142_393.395_1.2x	OBD142_393.395	961	5026	50.26	30.75	0.16382	0.10229
OBD142_405.407_1x	OBD142_405.407	661	9730.5	97.305	74.25	0.32788	0.26685
OBD142_433.435_1x	OBD142_433.435	663	10280.5	102.805	69	0.33826	0.23486
OBD142_437.439_1.2x	OBD142_437.439	679	11065	110.65	77	0.36270	0.25977
OBD142_445.447_1.2x	OBD142_445.447	959	5236.5	52.365	39	0.18092	0.13770
OBD142_461.463_1.4x	OBD142_461.463	946	6240	62.4	36.5	0.21435	0.13770
OBD142_469.471_1.2x	OBD142_469.471	832	8858.5	88.585	56.75	0.29436	0.19917
OBD142_477.479_1x	OBD142_477.479	629	12148	121.48	74.75	0.40365	0.25977
OBD142_489.491_1.2x	OBD142_489.491	748	7759.5	77.595	58.5	0.24931	0.20083
OBD142_497.499_1.2x	OBD142_497.499	675	10138.5	101.385	77.25	0.33286	0.26331
OBD142_509.511_1.8x	OBD142_509.511	988	4712	47.12	33	0.16110	0.10229
OBD142_521.523_1.4x	OBD142_521.523	747	13280	132.8	93.5	0.44187	0.28271

Table 9 shows predictive markers for either strength or endurance training response, which are preferably used for typing humans. (Present in strength and endurance training in humans).

Patient Sample ID	Basic Annotation	Sex
Brigand	Horse - Sprinter	Gelding
Brigand	Horse - Sprinter	Gelding
Headway	Horse - Sprinter	Colt
Headway	Horse - Sprinter	Colt
Barton Mills	Horse - Sprinter	Colt
Barton Mills	Horse - Sprinter	Colt
Muthmir	Horse - Sprinter	Gelding
Muthmir	Horse - Sprinter	Gelding
One Master	Horse - Sprinter	Filly
One Master	Horse - Sprinter	Filly
Move Swiftly	Horse - Sprinter	Filly
Move Swiftly	Horse - Sprinter	Filly
Island of life	Horse - Sprinter	Filly
Island of life	Horse - Sprinter	Filly
Juthoor	Horse - Sprinter	Colt
Juthoor	Horse - Sprinter	Colt
Pretty Baby	Horse - Sprinter	Filly
Pretty Baby	Horse - Sprinter	Filly
Robin Weathers	Horse - Sprinter	Colt
Robin Weathers	Horse - Sprinter	Colt
Beshaayir	Horse - Sprinter	Filly
Beshaayir	Horse - Sprinter	Filly
Mashaheer	Horse - Sprinter	Gelding
Mashaheer	Horse - Sprinter	Gelding
Mubtasim	Horse - Sprinter	Gelding
Mubtasim	Horse - Sprinter	Gelding

Tasleet	Horse - Sprinter	Colt
Tasleet	Horse - Sprinter	Colt
Important Mission	Horse - Sprinter	Gelding
Important Mission	Horse - Sprinter	Gelding
Algaffaal	Horse - Sprinter	Colt
Algaffaal	Horse - Sprinter	Colt
Carpio	Horse - Untrained	Colt
Carpio	Horse - Untrained	Colt
ex Donnellys Hollow	Horse - Untrained	Filly
ex Donnellys Hollow	Horse - Untrained	Filly
ex Marika	Horse - Untrained	Colt
ex Marika	Horse - Untrained	Colt
Narina	Horse - Untrained	Filly
Narina	Horse - Untrained	Filly
Setenta	Horse - Untrained	Colt
Setenta	Horse - Untrained	Colt
To Be Wild	Horse - Untrained	Colt
To Be Wild	Horse - Untrained	Colt
Starkers	Horse - Untrained	Filly
Starkers	Horse - Untrained	Filly
Soloist	Horse - Untrained	Filly
Soloist	Horse - Untrained	Filly
Field Gun	Horse - Untrained	Gelding
Field Gun	Horse - Untrained	Gelding
ex No Song	Horse - Untrained	Colt
ex No Song	Horse - Untrained	Colt
ex Celtic Lynn	Horse - Untrained	Colt
ex Celtic Lynn	Horse - Untrained	Colt
flare of firelight	Horse - Untrained	Colt
flare of firelight	Horse - Untrained	Colt
Second Thought	Horse - Untrained	Colt
Second Thought	Horse - Untrained	Colt
Dance Pearl	Horse - Untrained	Filly
Dance Pearl	Horse - Untrained	Filly
ex Yosoldina	Horse - Untrained	Filly
ex Yosoldina	Horse - Untrained	Filly
Queen of Mean	Horse - Untrained	Colt
Queen of Mean	Horse - Untrained	Colt
Al Muffrih	Horse - Stayer	Stayer
Al Muffrih	Horse - Stayer	Stayer
Dal Harraild	Horse - Stayer	Gelding
Dal Harraild	Horse - Stayer	Gelding
Humble Hero	Horse - Stayer	Colt
Humble Hero	Horse - Stayer	Colt
Istanbul Sultan	Horse - Stayer	Gelding
Istanbul Sultan	Horse - Stayer	Gelding
Young Rascal	Horse - Stayer	Colt
Young Rascal	Horse - Stayer	Colt
Give & Take	Horse - Stayer	Filly
Give & Take	Horse - Stayer	Filly

Alexana	Horse - Stayer	Filly
Alexana	Horse - Stayer	Filly
Call To Mind	Horse - Stayer	Colt
Call To Mind	Horse - Stayer	Colt
Cristal Spirit	Horse - Stayer	Gelding
Cristal Spirit	Horse - Stayer	Gelding
Heart of Grace	Horse - Stayer	Filly
Heart of Grace	Horse - Stayer	Filly
Mam'Selle	Horse - Stayer	Filly
Mam'Selle	Horse - Stayer	Filly
Smashed	Horse - Stayer	Colt
Smashed	Horse - Stayer	Colt
Dramatic Queen	Horse - Stayer	Filly
Dramatic Queen	Horse - Stayer	Filly
Nicklaus	Horse - Stayer	Colt
Nicklaus	Horse - Stayer	Colt
Reverend Jacobs	Horse - Stayer	Gelding
Reverend Jacobs	Horse - Stayer	Gelding
The Grand Visir	Horse - Stayer	Colt
The Grand Visir	Horse - Stayer	Colt

Table 10

Sex	Description
Colt	Male horse less than three years old
Gelding	Castrated Male horse less than three years old
Filly	Female horse less than three years old

Table 11

	Untrained	Sprinter	Stayer
Colt	9	6	7
Gelding	1	5	4
Filly	6	5	5

Table 12

N	Marker	Exact_Boschloo_p.value	Median_Boshloo	Dilution	Type
1	OBD154_125/OBD154_127	0.00631	0.037817955	OBD154_125/OBD154_127_1:2x	Present in Sprinter
2	OBD154_085/OBD154_087	0.03886	0.088156223	OBD154_085/OBD154_087_1:2x	Present in Sprinter
3	OBD154_157/OBD154_159	0.03886	0.088156223	OBD154_157/OBD154_159_1:2x	Present in Stayer
4	OBD154_013/OBD154_015	0.05011	0.13798237	OBD154_013/OBD154_015_1x	Present in Sprinter
5	OBD154_245/OBD154_247	0.05011	0.13798237	OBD154_245/OBD154_247_1x	Present in Sprinter
6	OBD154_229/OBD154_231	0.05419	0.239017755	OBD154_229/OBD154_231_1x	Present in Sprinter
7	OBD154_093/OBD154_095	0.07514	0.239017755	OBD154_093/OBD154_095_1:2x	Present in Sprinter
8	OBD154_049/OBD154_051	0.11993	0.243710751	OBD154_049/OBD154_051_1:4x	Present in Sprinter
9	OBD154_201/OBD154_203	0.11993	0.243710751	OBD154_201/OBD154_203_1:2x	Present in Stayer
10	OBD154_041/OBD154_043	0.12508	0.239017755	OBD154_041/OBD154_043_1:4x	Present in Stayer
11	OBD154_073/OBD154_075	0.12508	0.239017755	OBD154_073/OBD154_075_1x	Present in Stayer
12	OBD154_205/OBD154_207	0.12508	0.239017755	OBD154_205/OBD154_207_1:2x	Present in Sprinter
13	OBD154_009/OBD154_011	0.18007	0.239017755	OBD154_009/OBD154_011_1:2x	Present in Sprinter
14	OBD154_045/OBD154_047	0.18007	0.287077538	OBD154_045/OBD154_047_1x	Present in Stayer
15	OBD154_141/OBD154_143	0.18007	0.287077538	OBD154_141/OBD154_143_1x	Present in Sprinter
16	OBD154_165/OBD154_167	0.18007	0.287077538	OBD154_165/OBD154_167_1x	Present in Sprinter
17	OBD154_213/OBD154_215	0.18007	0.265394144	OBD154_213/OBD154_215_1:2x	Present in Stayer

Table 13 shows the top markers for Stayer versus Sprinter phenotype (n=32, 16 Stayer, 16 Sprinter), which are preferably used to type horses.

Marker	Nearest Gene/loci	Type
OBD154_045/OBD154_047	MC1R/NM_001081945	Present in Stayer
OBD154_073/OBD154_075	MIRLET7A-2/PPARA	Present in Stayer
OBD154_009/OBD154_011	MIR1898	Present in Sprinter
OBD154_041/OBD154_043	TAGLN/MIR125B	Present in Stayer
OBD154_093/OBD154_095	MIR1248/TFRC	Present in Sprinter
OBD154_085/OBD154_087	SYNJ2BP	Present in Sprinter
OBD154_013/OBD154_015	AMPP/ARNTL	Present in Sprinter
OBD154_049/OBD154_051	MC1R/NM_001081945	Present in Sprinter
OBD154_125/OBD154_127	CCDC146	Present in Sprinter
OBD154_165/OBD154_167	MIR17	Present in Sprinter
OBD154_201/OBD154_203	GSN	Present in Stayer
OBD154_229/OBD154_231	ALPHA4GNT	Present in Sprinter
OBD154_213/OBD154_215	BMP7	Present in Stayer
OBD154_205/OBD154_207	S100G/NROB1	Present in Sprinter
OBD154_157/OBD154_159	EEF1A1	Present in Stayer
OBD154_245/OBD154_247	MIR218	Present in Sprinter
OBD154_141/OBD154_143	NME1/SRSF1	Present in Sprinter

Table 14 shows markers discovered in humans that applicable to horses, and the closest genomic loci, which can be used to type horses.

5

Sample ID	Horse Name	Phenotype	Probability	Comments
Holo009	One Master	Sprinter	0.887	Correct
Holo013	Island of life	Sprinter	0.962	Correct
Holo019	Robin Weathers	Sprinter	0.321	Misclassified
Holo017	Pretty Baby	Sprinter	0.872	Correct
Holo015	Juthoor	Sprinter	0.974	Correct
Holo023	Mashaheer	Sprinter	0.960	Correct
Holo003	Headway	Sprinter	0.852	Correct
Holo011	Move Swiftly	Sprinter	0.993	Correct
Holo007	Muthmir	Sprinter	0.732	Correct
Holo031	Algaffaal	Sprinter	0.958	Correct
Holo005	Barton Mills	Sprinter	0.974	Correct
Holo021	Beshaayir	Sprinter	0.961	Correct
Holo001	Brigand	Sprinter	0.991	Correct
Holo025	Mubtasim	Sprinter	0.835	Correct
Holo027	Tasleet	Sprinter	0.958	Correct
Holo029	Important Mission	Sprinter	0.670	Correct
Holo065	Al Muffrih	Stayer	0.150	Correct
Holo077	Alexana	Stayer	0.014	Correct
Holo069	Humble Hero	Stayer	0.550	Misclassified

Holo091	Nicklaus	Stayer	0.086	Correct
Holo071	Istanbul Sultan	Stayer	0.265	Correct
Holo075	Give & Take	Stayer	0.271	Correct
Holo083	Heart of Grace	Stayer	0.032	Correct
Holo067	Dal Harraild	Stayer	0.298	Correct
Holo089	Dramatic Queen	Stayer	0.027	Correct
Holo079	Call To Mind	Stayer	0.032	Correct
Holo095	The Grand Visir	Stayer	0.283	Correct
Holo081	Cristal Spirit	Stayer	0.032	Correct
Holo093	Reverend Jacobs	Stayer	0.095	Correct
Holo087	Smashed	Stayer	0.167	Correct
Holo073	Young Rascal	Stayer	0.166	Correct
Holo085	Mam'Selle	Stayer	0.014	Correct

Table 15

Probability Score	Classifier Call
<0.3	Stayer
0.31 – 0.69	Unclassified
>0.7	Sprinter

Table 16

Sample	Horse Name	Probability	Call
Holo053	ex Celtic Lynn	0.383045197	Unclassified
Holo045	Starkers	0.165671632	Stayer
Holo035	ex Donnellys Hollow	0.549999774	Unclassified
Holo051	ex No Song	0.973659277	Sprinter
Holo057	Second Thought	0.271233022	Stayer
Holo059	Dance Pearl	0.549999774	Unclassified
Holo039	Narina	0.871761441	Sprinter
Holo043	To Be Wild	0.092756219	Stayer
Holo061	ex Yosoldina	0.031833708	Stayer
Holo055	Flare of Firelight	0.889145136	Sprinter
Holo063	Queen of Mean	0.004074222	Stayer
Holo047	Soloist	0.025709741	Stayer
Holo033	Carpio	0.0436165	Stayer
Holo041	Setenta	0.549999774	Unclassified
Holo049	Field Gun	0.094702385	Stayer
Holo037	ex Marika	0.882559121	Sprinter

Table 17

Marker	Exact_Boschloo_p.value	Type
OBD154_001/OBD154_003_1:2x	0.597203758	Present in Sprinter
OBD154_009/OBD154_011_1:2x	0.180069259	Present in Sprinter
OBD154_013/OBD154_015_1x	0.050106528	Present in Sprinter
OBD154_033/OBD154_035_1:4x	0.283703806	Present in Sprinter
OBD154_037/OBD154_039_1:8x	0.523402567	Present in Sprinter
OBD154_041/OBD154_043_1x	0.64299739	Present in Sprinter
OBD154_045/OBD154_047_1x	0.180069259	Present in stayer
OBD154_049/OBD154_051_1:4x	0.11992508	Present in Sprinter
OBD154_053/OBD154_055_1:2x	0.597203758	Present in Sprinter
OBD154_057/OBD154_059_1:2x	0.663949317	Present in Sprinter
OBD154_061/OBD154_063_1x	0.663949317	Present in stayer
OBD154_069/OBD154_071_1x	0.23718116	Present in Sprinter
OBD154_073/OBD154_075_1x	0.125083174	Present in stayer
OBD154_077/OBD154_079_1x	0.422463565	Present in Sprinter
OBD154_085/OBD154_087_1:2x	0.038860637	Present in Sprinter
OBD154_093/OBD154_095_1:2x	0.075142123	Present in Sprinter
OBD154_097/OBD154_099_1x	0.523402567	Present in Sprinter
OBD154_105/OBD154_107_1:2x	0.210490032	Present in Sprinter
OBD154_109/OBD154_111_1:2x	0.387940572	Present in stayer
OBD154_113/OBD154_115_1:4x	0.523402567	Present in stayer
OBD154_117/OBD154_119_1x	0.659282164	Present in Sprinter
OBD154_121/OBD154_123_1x	0.659282164	Present in stayer
OBD154_125/OBD154_127_1:2x	0.006313179	Present in Sprinter
OBD154_133/OBD154_135_1:2x	0.32961205	Present in Sprinter
OBD154_137/OBD154_139_1x	0.663949317	Present in stayer
OBD154_141/OBD154_143_1x	0.180069259	Present in Sprinter
OBD154_149/OBD154_151_1:2x	0.678620772	Present in stayer
OBD154_153/OBD154_155_1:8x	0.523402567	Present in Sprinter
OBD154_157/OBD154_159_1:2x	0.038860637	Present in stayer
OBD154_161/OBD154_163_1:2x	0.422463565	Present in stayer
OBD154_165/OBD154_167_1x	0.180069259	Present in Sprinter
OBD154_169/OBD154_171_1:4x	0.283703806	Present in Sprinter
OBD154_177/OBD154_179_1x	0.23718116	Present in Sprinter
OBD154_185/OBD154_187_1x	0.64299739	Present in stayer
OBD154_201/OBD154_203_1x	0.11992508	Present in stayer
OBD154_205/OBD154_207_1:2x	0.125083174	Present in Sprinter
OBD154_209/OBD154_211_1:2x	0.253032887	Present in Sprinter
OBD154_213/OBD154_215_1:2x	0.180069259	Present in stayer
OBD154_217/OBD154_219_1x	0.387940572	Present in Sprinter
OBD154_229/OBD154_231_1x	0.054191604	Present in stayer

OBD154_237/OBD154_239_1x	0.23718116	Present in Sprinter
OBD154_245/OBD154_247_1x	0.050106528	Present in stayer

Table 18 shows the informative markers from the equine study, which are preferably used to type horses.

RANKING (*Elite Athlete)	Code	Age	Height (cm)	T. Body Mass (kg)	VO2max/kg	COMBINED 3 Lifts (kg)	Relative Strength (kg/kg)
*1	C29	27	186.5	67	74.5	210	3.13
*2	C49	29	172.4	60	73.3	255	4.25
*3	C6	27	182	70.5	71.7	245	3.48
*4	C10	30	185.5	75	65.5	240	3.20
*5	C66	21	190.7	76	64.6	335	4.41
*6	C69	44	171	66	62.3	280	4.24
*7	C27	28	176	57	62.4	250	4.39
8	C8	21	183.3	75	61.3	325	4.33
9	C23	43	189.5	77	60.2	240	3.12
10	C28	33	193	72.5	60.2	225	3.10
11	C15	25	183	77	59.6	350	4.55
12	C67	43	179.3	74	58.4	240	3.24
13	B86	33	181	77.5	57.65	325	4.19
14	C32	47	166.6	67	57.5	170	2.54
15	C24	18	183	81	56.2	335	4.14
16	C25	51	184	75	56.1	210	2.80
17	C4	21	174	73	55.4	245	3.36
18	C9	24	185.5	70.5	55.1	260	3.69
19	C14	40	179.5	70	54.7	280	4.00
20	A50	24	173.1	65	54.6	355	5.46
21	C60	24	180	77.5	54.6	335	4.32
22	C19	29	188	88	52.7	260	2.95
23	C35	43	173.3	68	51	200	2.94
24	A57	28	171.6	60	49.7	355	5.92
25	C12	48	175	92	49.5	295	3.21
26	B48	21	170.5	55	49.4	195	3.55
27	A21	30	188.5	80	48.9	415	5.19
28	B52	45	181.9	68.5	48.7	155	2.26
29	A20	37	168	69	48.4	465	6.74
30	A54	18	163	69	47.8	425	6.16
31	A31	25	181.2	78	47.1	465	5.96
32	A56	25	176.6	82.5	46.4	380	4.61
33	A55	18	163	67.5	45.7	435	6.44
34	A3	28	174	70	44.6	390	5.57
35	B70	28	172.4	63.5	44.4	200	3.15
36	A13	28	172	75	44	300	4.00
37	B63	49	181.6	90	42.9	170	1.89
38	A2	26	181	92.5	42.3	475	5.14
38	A36	20	189.2	92	42.1	540	5.87
40	A5	42	176	88	42	487.5	5.54
41	A41	27	175.3	79.5	41.8	475	5.97
42	A22	28	176	85	41	530	6.24
43	A59	27	184.8	80	39.3	400	5.00
44	**A11**	**29**	**158**	**65.5**	**39.1**	**385**	**5.88**
45	B46	44	180.6	75	39	270	3.60

46	B43	42	187.4	73	38.85	125	1.71
47	A30	24	183.5	81	37	530	6.54
48	B74	34	178.4	77.5	37	320	4.13
48	B44	44	170.9	77	36.9	190	2.47
50	A53	23	173	68	36.8	350	5.15
51	B78	27	188.2	98	36.5	250	2.55
52	A7	22	178	85	36	490	5.76
53	B77	45	169.1	88.5	35.9	300	3.39
54	B45	41	175.4	88.5	35.7	230	2.60
55	B68	42	176.5	88	35.5	275	3.13
56	B85	39	184.9	106	35.3	330	3.11
57	A58	23	175	70	35.1	350	5.00
58	B37	31	192.5	123	34.7	310	2.52
59	B62	33	199.6	109.5	34.5	280	2.56
60	B33	44	177.4	88.5	33.3	255	2.88
61	B75	22	178.5	99	33.2	330	3.33
62	B42	45	168.1	79	32.8	250	3.16
63	B79	54	179	71	32.6	140	1.97
64	B73	46	175.1	106.5	32.1	270	2.54
65	B64	36	181.5	89.5	32.1	285	3.18
66	B18	25	172.5	82	32	165	2.01
67	B82	35	170.3	88	32	315	3.58
68	B71	42	184	95	31.8	260	2.74
69	B16	41	174.5	79	31.1	260	3.29
70	B61	29	180.9	97.5	31	190	1.95
71	B65	33	181	65.5	31	145	2.21
72	B38	21	194.2	73.5	30.5	130	1.77
73	B83	43	186.7	94	30	290	3.09
74	B81	43	174.8	86.5	29.9	280	3.24
75	B80	47	185.6	85	29.9	170	2.00
76	B17	31	171.5	89.5	29.1	345	3.85
77	A1	29	176.5	89.5	28.1	467	5.22
78	B39	26	185	97	28	200	2.06
79	B87	34	187.1	101	27.9	235	2.33
80	B72	33	183.5	134.5	27.8	280	2.08
81	B26	30	197.5	131.5	27.1	275	2.09
82	B51	33	175.4	99	27	270	2.73
83	B34	25	175.5	92.5	25.9	300	3.24
84	B76	24	196.7	74	24.5	144.5	1.95
85	B40	34	169.8	78.5	24.3	170	2.17

Table 19

KEY:

RELATIVE STRENGTH (STRONG GROUP) = BLUE

RELATIVE FITNESS (CARDIO GROUP) = ORANGE

SEDENTARY (UNTRAINED GROUP) = GREEN

*DIDN"T MEET CRITERIA (PERFORMANCE) = RED)

GENETIC DISORDER = BLACK

RANKING	Code	Age	Height (cm)	T. Body Mass (kg)	VO2max/kg	COMBINED 3 Lifts (kg)	Relative Strength (kg/kg)
1	A20	37	168	69	48.4	465	6.74
2	A30	24	183.5	81	37	530	6.54
3	A55	18	163	67.5	45.7	435	6.44

4	A22	28	176	85	41	530	6.24
5	A54	18	163	69	47.8	425	6.16
6	A41	27	175.3	79.5	41.8	475	5.97
7	A31	25	181.2	78	47.1	465	5.96
8	A57	28	171.6	60	49.7	355	5.92
***9**	**A11**	**29**	**158**	**65.5**	**39.1**	**385**	**5.88**
10	A36	20	189.2	92	42.1	540	5.87
11	A7	22	178	85	36	490	5.76
12	A3	28	174	70	44.6	390	5.57
13	A5	42	176	88	42	487.5	5.54
14	A50	24	173.1	65	54.6	355	5.46
15	A1	29	176.5	89.5	28.1	467	5.22
16	A21	30	188.5	80	48.9	415	5.19
17	A53	23	173	68	36.8	350	5.15
18	A2	26	181	92.5	42.3	475	5.14
19	A58	23	175	70	35.1	350	5.00
20	A59	27	184.8	80	39.3	400	5.00
21	A56	25	176.6	82.5	46.4	380	4.61
22	C15	25	183	77	59.6	350	4.55
23	C66	21	190.7	76	64.6	335	4.41
24	C27	28	176	57	62.4	250	4.39
25	C8	21	183.3	75	61.3	325	4.33
26	C60	24	180	77.5	54.6	335	4.32
27	C49	29	172.4	60	73.8	255	4.25
28	C69	44	171	66	63.3	280	4.24
29	B86	33	181	77.5	57.65	325	4.19
30	C24	18	183	81	56.2	335	4.14
31	B74	34	178.4	77.5	37	320	4.13
32	A13	28	172	75	44	300	4.00
33	C14	40	179.5	70	54.7	280	4.00
34	B17	31	171.5	89.5	29.1	345	3.85
35	C9	24	185.5	70.5	55.1	260	3.69
36	B46	44	180.6	75	39	270	3.60
37	B82	35	170.3	88	32	315	3.53
38	B48	21	170.5	55	49.4	195	3.55
38	C6	27	182	70.5	71.7	245	3.49
40	B77	45	169.1	88.5	35.9	300	3.39
41	C4	21	174	73	55.4	245	3.36
42	B75	22	178.5	99	33.2	330	3.33
43	B16	41	174.5	79	31.1	260	3.29
44	C67	43	179.3	74	58.4	240	3.24
45	B34	25	175.5	92.5	25.9	300	3.24
46	B81	43	174.8	86.5	29.9	280	3.24
47	C12	48	175	92	49.5	295	3.21
48	C10	30	185.5	75	65.5	240	3.20
48	B64	36	181.5	89.5	32.1	285	3.18
50	B42	45	168.1	79	32.9	250	3.16
51	B70	28	172.4	63.5	44.4	200	3.15
52	C29	27	186.5	67	74.5	210	3.13
53	B68	42	176.5	88	35.5	275	3.13
54	C23	43	189.5	77	60.2	240	3.12
55	B85	39	184.9	106	35.3	330	3.11
56	C28	33	193	72.5	60.2	225	3.10
57	B83	43	186.7	94	30	290	3.09
58	C19	29	188	88	53.7	260	2.95
59	C35	43	173.3	68	51	200	2.94

60	B33	44	177.4	88.5	33.3	255	2.88
61	C25	51	184	75	56.1	210	2.80
62	B71	42	184	95	31.8	260	2.74
63	B51	33	175.4	99	27	270	2.73
64	B45	41	175.4	88.5	35.7	230	2.60
65	B62	33	199.6	109.5	34.5	280	2.56
66	B78	27	188.2	98	36.5	250	2.55
67	C32	47	166.6	67	57.5	170	2.54
68	B73	46	175.1	106.5	32.1	270	2.54
69	B37	31	192.5	123	34.7	310	2.52
70	B44	44	170.9	77	36.9	190	2.47
71	B87	34	187.1	101	27.9	235	2.33
72	B52	45	181.9	68.5	48.7	155	2.26
73	B65	33	181	65.5	31	145	2.21
74	B40	34	169.8	78.5	24.3	170	2.17
75	B26	30	197.5	131.5	27.1	275	2.09
76	B72	33	183.5	134.5	27.8	280	2.08
77	B39	26	185	97	28	200	2.06
78	B18	25	172.5	82	32	165	2.01
79	B80	47	185.6	85	29.9	170	2.00
80	B79	54	179	71	32.6	140	1.97
81	B76	24	196.7	74	24.5	144.5	1.95
82	B61	29	180.9	97.5	31	190	1.95
83	B63	49	181.6	90	42.9	170	1.89
84	B38	21	194.2	73.5	30.5	130	1.77
85	B43	42	187.4	73	38.85	125	1.71

Table 20

***REMOVE – KALLMANS SYNDROME**

KEY:

RELATIVE STRENGTH (STRONG GROUP) = BLUE

RELATIVE FITNESS (CARDIO GROUP) = ORANGE

SEDENTARY (UNTRAINED GROUP) = GREEN

DIDN"T MEET CRITERIA (PERFORMANCE) = RED)

GENETIC DISORDER = BLACK

Gene	Gene Name	Function
ACACB	Acetyl-CoA Carboxylase Beta	Protein Coding gene. Biotin Deficiency. Diabetes Mellitus. Noninsulin-Dependent. Associated with Metformin pathways, Pharmacodynamics and Regulation of cholestrol biosynthesis by SREBP.
ACBD6	Acyl-CoA Binding Domain Containing 6	Protein Coding gene. Related to Fatty-Acyl-CoA Biosynthesis and Metabolism.
ADRB3	Adrenoceptor Beta 3	Protein Coding gene. Body Mass Index Quantitative Trait Locus 11. Low Compliance Bladder. Related to Monoamine GPCRs and Peptide ligand-binding receptors pathways.
ALDH1A2	Aldehyde Dehydrogenase 1 Family Member A2	Protein Coding Gene. Associated with Diaphragm Disease and Neural Tube Defects.
ANO2	Anoctamin 2	Protein Coding Gene. Associated with Von Willebrand disease and Scrotal Carcinoma. Related to Olfactory Signaling Pathway and Ion channel transport.
B3GAT1	Beta-1,3-Glucuronyltransferase 1	Protein Coding Gene. Associated with Renal Adenoma and Malignant Glandular Tumor Of Peripheral Nerve Sheath. Related to Glycosaminoglycan metabolism and Metabolism pathways.

B3GAT2	Beta-1,3-Glucuronyltransferase 2	Protein Coding gene. Diseases associated with B3GAT2 include Colonic Benign Neoplasm. Among its related pathways are Glycosaminoglycan metabolism and Metabolism. Involved in the biosynthesis of L2/HNK-1 carbohydrate epitope on both glycolipids and glycoproteins.
BMP7	Bone Morphogenetic Protein 7	Protein Coding gene. Diseases associated with BMP7 include Spondylolisthesis and Renal Fibrosis. Among its related pathways are Apoptotic Pathways in Synovial Fibroblasts and PEDF Induced Signaling. Induces cartilage and bone formation. May be the osteoinductive factor responsible for the phenomenon of epithelial osteogenesis. Plays a role in calcium regulation and bone homeostasis.
C1GALT1	Core 1 Synthase, Glycoprotein-N-Acetylgalactosamine	Protein Coding gene. Diseases associated with C1GALT1 include Iga Glomerulonephritis and Hypersensitivity Vasculitis. Among its related pathways are Ectoderm Differentiation and Metabolism of proteins.
CALCR	Calcitonin Receptor	Protein Coding gene. Diseases associated with CALCR include Osteoporosis and Bone Mineral Density Quantitative Trait Locus 15. Among its related pathways are RANK Signaling in Osteoclasts and Osteoclast differentiation.
CARD11	Caspase Recruitment Domain Family Member 11	Protein Coding gene. Diseases associated with CARD11 include B-Cell Expansion With Nfkb And T-Cell Anergy and Immunodeficiency 11. Involved in the costimulatory signal essential for T-cell receptor (TCR)-mediated T-cell activation.
CASP9	Caspase 9	Protein Coding gene. Diseases associated with CASP9 include Brain Meningioma and Inflammatory Bowel Disease 7. Among its related pathways are Constitutive Signaling by AKT1 E17K in Cancer and Apoptotic Pathways in Synovial Fibroblasts.
CBL	Cbl Proto-Oncogene	Protein Coding gene. Diseases associated with CBL include Noonan Syndrome-Like Disorder With Or Without Juvenile Myelomonocytic Leukemia and Juvenile Myelomonocytic Leukemia. Among its related pathways are Negative regulation of FGFR3 signaling and RANK Signaling in Osteoclasts.
CD36	CD36 Molecule	Protein Coding gene. Diseases associated with CD36 include Platelet Glycoprotein Iv Deficiency and Malaria. Among its related pathways are Cytokine Signaling in Immune system and Aryl Hydrocarbon Receptor.
COL13A1	Collagen Type XIII Alpha 1 Chain	Protein Coding gene. Diseases associated with COL13A1 include Myasthenic Syndrome, Congenital, 19and Postsynaptic Congenital Myasthenic Syndromes. Among its related pathways are Integrin Pathway and ERK Signaling.
COL25A1	Collagen Type XXV Alpha 1 Chain	Protein Coding gene. Diseases associated with COL25A1 include Fibrosis Of Extraocular Muscles, Congenital, 5 and Congenital Ptosis. Among its related pathways are Integrin Pathway and ERK Signaling.
COL4A2	Collagen Type IV Alpha 2 Chain	Protein Coding gene. Diseases associated with COL4A2 include Porencephaly 2 and Hemorrhage, Intracerebral. Among its related pathways are Integrin Pathway and ERK Signaling.
COL5A1	Collagen Type V Alpha 1 Chain	Protein Coding gene. Diseases associated with COL5A1 include Ehlers-Danlos Syndrome, Classic Type, 1and Ehlers-Danlos Syndrome Type 2. Among its related pathways are Integrin Pathway and ERK Signaling.
CYGB	Cytoglobin	Protein Coding gene. Diseases associated with CYGB include Ancylostomiasis. Among its related pathways are Metabolism and eNOS activation and regulation.
DGKH	Diacylglycerol Kinase Eta	Protein Coding gene. Diseases associated with DGKH include Adrenal Medulla Cancer and Extra-Adrenal Pheochromocytoma. Among its related pathways are Response to elevated platelet cytosolic Ca2+ and Signaling by GPCR.
DIAPH3	Diaphanous Related Formin 3	Protein Coding gene. Diseases associated with DIAPH3 include Auditory Neuropathy, Autosomal Dominant, 1and Autosomal Dominant Non-Syndromic Sensorineural Deafness Type Dfna. Among its related pathways are Actin Nucleation by ARP-WASP Complex and G-protein signaling_RhoB regulation pathway.

DKK3	Dickkopf WNT Signaling Pathway Inhibitor 3	Protein Coding gene. Diseases associated with DKK3 include Oral Submucous Fibrosis. Among its related pathways are CDK-mediated phosphorylation and removal of Cdc6 and Regulation of Wnt/B-catenin Signaling by Small Molecule Compounds.
DLK1	Delta Like Non-Canonical Notch Ligand 1	Protein Coding gene. Diseases associated with DLK1 include Temple Syndrome and Idiopathic Central Precocious Puberty. Among its related pathways are Signaling by NOTCH1 and NOTCH2 Activation and Transmission of Signal to the Nucleus.
DOK5	Docking Protein 5	Protein Coding gene. Among its related pathways are Developmental Biology and Brain-Derived Neurotrophic Factor (BDNF) signaling pathway.
EGR3	Early Growth Response 3	Protein Coding gene. Diseases associated with EGR3 include Patella, Chondromalacia Of and Ancylostomiasis. Among its related pathways are Circadian rythm related genes and Viral carcinogenesis.
EHD1	EH Domain Containing 1	Protein Coding gene. Diseases associated with EHD1 include Venous Hemangioma and Photoallergic Dermatitis. Among its related pathways are Response to elevated platelet cytosolic Ca2+ and Angiopoietin Like Protein 8 Regulatory Pathway.
EMCN	Endomucin	Protein Coding gene. mucin-like sialoglycoprotein that interferes with the assembly of focal adhesion complexes and inhibits interaction between cells and the extracellular matrix.
ETS1	ETS Proto-Oncogene 1, Transcription Factor	Protein Coding gene. Diseases associated with ETS1 include Jacobsen Syndrome and Bone Ewing's Sarcoma. Among its related pathways are Neural Crest Differentiation and ErbB signaling pathway.
EYA1	EYA Transcriptional Coactivator And Phosphatase 1	Protein Coding gene. Diseases associated with EYA1 include Otofaciocervical Syndrome 1and Branchiootorenal Syndrome 1. Among its related pathways are DNA Double-Strand Break Repair and DNA Double Strand Break Response.

Table 21.a

Gene	Gene Name	Function
FBLN2	Fibulin 2	Protein Coding gene. Diseases associated with FBLN2 include Familial Osteochondritis Dissecans and Osteochondritis Dissecans. Among its related pathways are Cell adhesion_Cell-matrix glycoconjugates and Elastic fibre formation.
FBXO32	F-Box Protein 32	Protein Coding gene. Diseases associated with FBXO32 include Muscle Hypertrophy and Muscle Tissue Disease. Among its related pathways are Innate Immune System and FoxO family signaling.
FOXO1	Forkhead Box O1	Protein Coding gene. Diseases associated with FOXO1 include Rhabdomyosarcoma 2 and Rhabdomyosarcoma. Among its related pathways are Constitutive Signaling by AKT1 E17K in Cancer and Cytokine Signaling in Immune system.
FOXO3	Forkhead Box O3	Protein Coding gene. Diseases associated with FOXO3 include Chromosome 6Q Deletion and Rhabdomyosarcoma. Among its related pathways are Constitutive Signaling by AKT1 E17K in Cancer and NFAT and Cardiac Hypertrophy.
FTO	FTO, Alpha-Ketoglutarate Dependent Dioxygenase	Protein Coding gene. Diseases associated with FTO include Growth Retardation, Developmental Delay, And Facial Dysmorphism and Body Mass Index Quantitative Trait Locus 14. Among its related pathways are DNA Damage Reversaland FTO Obesity Variant Mechanism.
GPC5	Glypican 5	Protein Coding gene. Diseases associated with GPC5 include Simpson-Golabi-Behmel Syndrome and Tetralogy Of Fallot. Among its related pathways are Glycosaminoglycan metabolism and CDK-mediated phosphorylation and removal of Cdc6.
GPC6	Glypican 6	Protein Coding gene. Diseases associated with GPC6 include Omodysplasia 1 and Omodysplasia. Among its related pathways are Apoptotic Pathways in Synovial Fibroblasts and PAK Pathway.

GRB10	Growth Factor Receptor Bound Protein 10	Protein Coding gene. Diseases associated with GRB10 include Silver-Russell Syndrome and Albright's Hereditary Osteodystrophy. Among its related pathways are Beta-Adrenergic Signaling and RET signaling.
GSN	Gelsolin	Protein Coding gene. Diseases associated with GSN include Amyloidosis, Finnish Type and Lattice Corneal Dystrophy Type Ii. Among its related pathways are N-cadherin signaling events and Apoptosis and survival Caspase cascade.
HDAC9	Histone Deacetylase 9	Protein Coding gene. Diseases associated with HDAC9 include Gastrointestinal Neuroendocrine Tumor and Cutaneous T Cell Lymphoma. Among its related pathways are PEDF Induced Signaling and Signaling by NOTCH1.
HOXC6	Homeobox C6	Protein Coding gene. Gene Ontology (GO) annotations related to this gene include *DNA binding transcription factor activity* and *transcription corepressor activity*.
IGF1R	Insulin Like Growth Factor 1 Receptor	Protein Coding gene. Diseases associated with IGF1R include Insulin-Like Growth Factor I and Ring Chromosome 15. Among its related pathways are Apoptotic Pathways in Synovial Fibroblasts and NFAT and Cardiac Hypertrophy.
IL1RAP	Interleukin 1 Receptor Accessory Protein	Protein Coding gene. Diseases associated with IL1RAP include Stromal Keratitis and Chromosome Xp21 Deletion Syndrome. Among its related pathways are Bacterial infections in CF airways and IL-1 signaling pathway.
KDM1A	Lysine Demethylase 1A	Protein Coding gene. Diseases associated with KDM1A include Cleft Palate, Psychomotor Retardation, And Distinctive Facial Features and Kbg Syndrome. Among its related pathways are Response to elevated platelet cytosolic Ca2+ and Activated PKN1 stimulates transcription of AR (androgen receptor) regulated genes KLK2 and KLK3.
LAMA2	Laminin Subunit Alpha 2	Protein Coding gene. Diseases associated with LAMA2 include Muscular Dystrophy, Congenital Merosin-Deficient, 1Aand Congenital Muscular Dystrophy Type 1A. Among its related pathways are MET promotes cell motility and Integrin Pathway.
LCK	LCK Proto-Oncogene, Src Family Tyrosine Kinase	Protein Coding gene. Diseases associated with LCK include Immunodeficiency 22 and Cd45 Deficiency. Among its related pathways are G-protein signaling N-RAS regulation pathway and Cytokine Signaling in Immune system.
LDB2	LIM Domain Binding 2	Protein Coding gene. Diseases associated with LDB2 include Retinal Detachment. Among its related pathways are Ectoderm Differentiation.
LMO4	LIM Domain Only 4	Protein Coding gene. Diseases associated with LMO4 include Precursor T-Cell Acute Lymphoblastic Leukemia. Among its related pathways are IL-6 signaling pathway and Embryonic and Induced Pluripotent Stem Cell Differentiation Pathways and Lineage-specific Markers.
MAPK10	Mitogen-Activated Protein Kinase 10	Protein Coding gene. Diseases associated with MAPK10 include Pertussis and Pneumococcal Meningitis. Among its related pathways are PEDF Induced Signaling and Toll-like receptor signaling pathway.
MBNL1	Muscleblind Like Splicing Regulator 1	Protein Coding gene. Diseases associated with MBNL1 include Myotonic Dystrophy and Myotonic Dystrophy 1. Among its related pathways are Adipogenesis.
MYBPC1	Myosin Binding Protein C, Slow Type	Protein Coding gene. Diseases associated with MYBPC1 include Arthrogryposis, Distal, Type 1B and Lethal Congenital Contracture Syndrome 4. Among its related pathways are Cardiac conduction and Striated Muscle Contraction.
MYH1	Myosin Heavy Chain 1	Protein Coding gene. Diseases associated with MYH1 include Retinitis Pigmentosa 67. Among its related pathways are PAK Pathway and ERK Signaling.
MYO18B	Myosin XVIIIB	Protein Coding gene. Diseases associated with MYO18B include Klippel-Feil Syndrome 4, Autosomal Recessive, With Nemaline Myopathy And Facial Dysmorphism and Lung Large Cell Carcinoma.
NCAM1	Neural Cell Adhesion Molecule 1	Protein Coding gene. Diseases associated with NCAM1 include Rabies and Blastic Plasmacytoid Dendritic Cell. Among its related pathways are RET signaling and Cytokine Signaling in Immune system.

NECTIN2	Nectin Cell Adhesion Molecule 2	Protein Coding gene. Diseases associated with NECTIN2 include Herpes Simplex and Ovarian Cystic Teratoma. Among its related pathways are PAK Pathway and Innate Immune System. An important paralog of this gene is PVR.
NFKB1	Nuclear Factor Kappa B Subunit 1	Protein Coding gene. Diseases associated with NFKB1 include Immunodeficiency, Common Variable, 12and Common Variable Immunodeficiency. Among its related pathways are RANK Signaling in Osteoclasts and PEDF Induced Signaling.
NR4A1	Nuclear Receptor Subfamily 4 Group A Member 1	Protein Coding gene. Diseases associated with NR4A1 include Fetal Adenoma and Tracheal Cancer. Among its related pathways are Constitutive Signaling by AKT1 E17K in Cancer and Aldosterone synthesis and secretion.
NRXN1	Neurexin 1	Protein Coding gene. Diseases associated with NRXN1 include Pitt-Hopkins-Like Syndrome 2 and Chromosome 2P16.3 Deletion Syndrome. Among its related pathways are Transmission across Chemical Synapses and Protein-protein interactions at synapses.
NTRK2	Neurotrophic Receptor Tyrosine Kinase 2	Protein Coding gene. Diseases associated with NTRK2 include Obesity, Hyperphagia, And Developmental Delay and Epileptic Encephalopathy, Early Infantile, 58. Among its related pathways are Apoptotic Pathways in Synovial Fibroblasts and ERK Signaling.
PAG1	Phosphoprotein Membrane Anchor With Glycosphingolipid Microdomains	Protein Coding gene. Among its related pathways are Innate Immune System and B cell receptor signaling pathway (KEGG).

Table 21.b

Gene	Gene Name	Function
PCK1	Phosphoenolpyruvate Carboxykinase 1	Protein Coding gene. Diseases associated with PCK1 include Phosphoenolpyruvate Carboxykinase Deficiency, Cytosolic and Pepck 1 Deficiency. Among its related pathways are Estrogen Receptor Pathway and Glycosaminoglycan metabolism.
PDK3	Pyruvate Dehydrogenase Kinase 3	Protein Coding gene. Diseases associated with PDK3 include Charcot-Marie-Tooth Disease, X-Linked Dominant, 6 and X-Linked Charcot-Marie-Tooth Disease. Among its related pathways are Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins. and Metabolism.
PHTF2	Putative Homeodomain Transcription Factor 2	Protein Coding gene. An important paralog of this gene is PHTF1. May play a role in transcription regulation.
PIK3C3	Phosphatidylinositol 3-Kinase Catalytic Subunit Type 3	Protein Coding gene. Diseases associated with PIK3C3 include Amyotrophic Lateral Sclerosis 1. Among its related pathways are wtCFTR and deltaF508 traffic / Late endosome and Lysosome (norm and CF) and Delta508-CFTR traffic / Sorting endosome formation in CF.
PIK3R1	Phosphoinositide-3-Kinase Regulatory Subunit 1	Protein Coding gene. Diseases associated with PIK3R1 include Short Syndrome and Agammaglobulinemia 7, Autosomal Recessive. Among its related pathways are Development EGFR signaling via small GTPases and N-cadherin signaling events.
PLCXD2	Phosphatidylinositol Specific Phospholipase C X Domain Containing 2	Protein Coding gene. Diseases associated with PLCXD2 include Narcolepsy.
PPARGC1A	PPARG Coactivator 1 Alpha	Protein Coding gene. Diseases associated with PPARGC1A include Amyotrophic Lateral Sclerosis 1 and Huntington Disease. Among its related pathways are Metformin Pathway, Pharmacodynamics and Organelle biogenesis and maintenance.

PPP3CA	Protein Phosphatase 3 Catalytic Subunit Alpha	Protein Coding gene. Diseases associated with PPP3CA include Epileptic Encephalopathy, Infantile Or Early Childhood, 1 and Undetermined Early-Onset Epileptic Encephalopathy. Among its related pathways are NFAT and Cardiac Hypertrophy and Circadian entrainment.
PRDX6	Peroxiredoxin 6	Protein Coding gene. Diseases associated with PRDX6 include Gnathomiasis and Fuchs' Endothelial Dystrophy. Among its related pathways are Innate Immune System and Detoxification of Reactive Oxygen Species.
PRKCQ	Protein Kinase C Theta	Protein Coding gene. Diseases associated with PRKCQ include Gastrointestinal Stromal Tumor and Smallpox. Among its related pathways are VEGF Signaling Pathway and NFAT and Cardiac Hypertrophy.
PTPRC	Protein Tyrosine Phosphatase, Receptor Type C	Protein Coding gene. Diseases associated with PTPRC include Severe Combined Immunodeficiency, Autosomal Recessive, T Cell-Negative, B Cell-Positive, Nk Cell-Positive and Hepatitis C Virus. Among its related pathways are PAK Pathway and Semaphorin interactions.
PYGM	Glycogen Phosphorylase, Muscle Associated	Protein Coding gene. Diseases associated with PYGM include Glycogen Storage Disease V and Glycogen Storage Disease. Among its related pathways are Glycosaminoglycan metabolism and Glycogen Metabolism.
RGS6	Regulator Of G Protein Signaling 6	Protein Coding gene. Diseases associated with RGS6 include Early-Onset Familial Alzheimer Disease and Alcoholic Cardiomyopathy. Among its related pathways are Signaling by GPCR and Chaperonin-mediated protein folding.
RORA	RAR Related Orphan Receptor A	Protein Coding gene. Diseases associated with RORA include Atrial Tachyarrhythmia With Short Pr Intervaland Hypoxia. Among its related pathways are Cytokine Signaling in Immune system and Innate Immune System.
RUNX3	Runt Related Transcription Factor 3	Protein Coding gene. Diseases associated with RUNX3 include Testicular Yolk Sac Tumor and Esophagus Squamous Cell Carcinoma. Among its related pathways are TGF-beta Receptor Signaling (WikiPathways) and Th17 cell differentiation.
RYR1	Ryanodine Receptor 1	Protein Coding gene. Diseases associated with RYR1 include Malignant Hyperthermia 1 and Central Core Disease Of Muscle. Among its related pathways are Cardiac conduction and Cell-type Dependent Selectivity of CCK2R Signaling.
SGCZ	Sarcoglycan Zeta	Protein Coding gene. Diseases associated with SGCZ include Generalized Epilepsy With Febrile Seizures Plus. An important paralog of this gene is SGCG.
SLC35B1	Solute Carrier Family 35 Member B1	Protein Coding gene. Encodes a nucleotide sugar transporter which is a member of solute carrier family 35. The transporters in this family are highly conserved hydrophobic proteins with multiple transmembrane domains.
SLC35D1	Solute Carrier Family 35 Member D1	Protein Coding gene. Diseases associated with SLC35D1 include Schneckenbecken Dysplasia and Fibrochondrogenesis. Among its related pathways are Metabolism and Cytochrome P450 - arranged by substrate type.
SMAD7	SMAD Family Member 7	Protein Coding gene. Diseases associated with SMAD7 include Colorectal Cancer 3 and Keloids. Among its related pathways are Immune response IFN gamma signaling pathway and TGF-beta Receptor Signaling
STIM1	Stromal Interaction Molecule 1	Protein Coding gene. Diseases associated with STIM1 include Myopathy, Tubular Aggregate, 1 and Immunodeficiency 10. Among its related pathways are Cardiac conduction and Platelet homeostasis.
STK39	Serine/Threonine Kinase 39	Protein Coding gene. Diseases associated with STK39 include Epilepsy, Familial Temporal Lobe, 4 and Renal Tubular Transport Disease. Among its related pathways are Diuretics Pathway, Pharmacodynamics and Sweet Taste Signaling.
STXBP4	Syntaxin Binding Protein 4	Protein Coding gene. Among its related pathways are Angiopoietin Like Protein 8 Regulatory Pathway and Glucose / Energy Metabolism.

SULF2	Sulfatase 2	Protein Coding gene. Diseases associated with SULF2 include Juvenile Astrocytoma. Gene Ontology (GO) annotations related to this gene include *calcium ion binding* and *arylsulfatase activity*. An important paralog of this gene is SULF1.
SYK	Spleen Associated Tyrosine Kinase	Protein Coding gene. Diseases associated with SYK include Hantavirus Pulmonary Syndrome and Mycobacterium Abscessus. Among its related pathways are RANK Signaling in Osteoclasts and Role of phospholipids in phagocytosis.
TBX21	T-Box 21	Protein Coding gene. Diseases associated with TBX21 include Asthma, Nasal Polyps, And Aspirin Intolerance and Genital Herpes. Among its related pathways are Th1 Differentiation Pathway and Th17 cell differentiation.
TGFB2	Transforming Growth Factor Beta 2	Protein Coding gene. Diseases associated with TGFB2 include Loeys-Dietz Syndrome 4 and Holt-Oram Syndrome. Among its related pathways are Apoptotic Pathways in Synovial Fibroblasts and PAK Pathway.
TGFBR2	Transforming Growth Factor Beta Receptor 2	Protein Coding gene. Diseases associated with TGFBR2 include Loeys-Dietz Syndrome 2 and Colorectal Cancer, Hereditary Nonpolyposis, Type 6. Among its related pathways are PAK Pathway and Chronic myeloid leukemia.
THADA	THADA, Armadillo Repeat Containing	Protein Coding gene. Diseases associated with THADA include Adenoma.
THNSL2	Threonine Synthase Like 2	Protein Coding gene. A similar enzyme in mouse can catalyze the degradation of O-phospho-homoserine to a-ketobutyrate, phosphate, and ammonia. This protein also has phospho-lyase activity on both gamma and beta phosphorylated substrates.
TLR2	Toll Like Receptor 2	Protein Coding gene. Diseases associated with TLR2 include Leprosy 3 and Colorectal Cancer. Among its related pathways are Bacterial infections in CF airways and Toll-like receptor signaling pathway.
TNFRSF25	TNF Receptor Superfamily Member 25	Protein Coding gene. Diseases associated with TNFRSF25 include Type 1 Diabetes Mellitus 18 and Type 1 Diabetes Mellitus 17. Among its related pathways are PEDF Induced Signaling and Apoptosis Modulation and Signaling.

Table 21.c

Gene	Gene Name	Function
TTN	Titin	Protein Coding gene. Diseases associated with TTN include Hereditary Myopathy With Early Respiratory Failure and Tibial Muscular Dystrophy, Tardive. Among its related pathways are Cardiac conduction and Response to elevated platelet cytosolic Ca2+.
UACA	Uveal Autoantigen With Coiled-Coil Domains And Ankyrin Repeats	Protein Coding gene. Diseases associated with UACA include Panuveitis and Graves' Disease. An important paralog of this gene is RAI14.
WASL	Wiskott-Aldrich Syndrome Like	Protein Coding gene. Diseases associated with WASL include Wiskott-Aldrich Syndrome and Vaccinia. Among its related pathways are Development EGFR signaling via small GTPases and PAK Pathway.
ZEB1	Zinc Finger E-Box Binding Homeobox 1	Protein Coding gene. Diseases associated with ZEB1 include Corneal Dystrophy, Fuchs Endothelial, 6and Corneal Dystrophy, Posterior Polymorphous, 3. Among its related pathways are PAK Pathway and Cytokine Signaling in Immune system.
ZFHX3	Zinc Finger Homeobox 3	Protein Coding gene. Diseases associated with ZFHX3 include Prostate Cancer and Atrial Fibrillation. Among its related pathways are Circadian rythm related genes and Signaling pathways regulating pluripotency of stem cells.

AGT	Angiotensinogen	Protein Coding gene. Diseases associated with AGT include Renal Tubular Dysgenesis and Hypertension, Essential. Among its related pathways are Signaling events mediated by PRL and Peptide hormone metabolism.
BMPR1B	Bone Morphogenetic Protein Receptor Type 1B	Protein Coding gene. Diseases associated with BMPR1B include Acromesomelic Dysplasia, Demirhan Type and Brachydactyly, Type A1, D. Among its related pathways are Akt Signaling and Ovarian Infertility Genes.
HTR2A	5-Hydroxytryptamine Receptor 2A	Protein Coding gene. Diseases associated with HTR2A include Major Depressive Disorder and Obsessive-Compulsive Disorder. Among its related pathways are Monoamine GPCRs and Peptide ligand-binding receptors.
PPARA	Peroxisome Proliferator Activated Receptor Alpha	Protein Coding gene. Diseases associated with PPARA include Fatty Liver Disease and Alcoholic Cardiomyopathy. Among its related pathways are Estrogen Receptor Pathway and Organelle biogenesis and maintenance.
SOS1	SOS Ras/Rac Guanine Nucleotide Exchange Factor 1	Protein Coding gene. Diseases associated with SOS1 include Noonan Syndrome 4 and Fibromatosis, Gingival, 1. Among its related pathways are G-protein signaling N-RAS regulation pathway and RET signaling.
SVEP1	Sushi, Von Willebrand Factor Type A, EGF And Pentraxin Domain Containing 1	Protein Coding gene. Related to calcium ion binding and chromatin binding.
UBE3A	Ubiquitin Protein Ligase E3A	Protein Coding gene. Diseases associated with UBE3A include Angelman Syndrome and Angelman Syndrome Due To A Point Mutation. Among its related pathways are PI3K-Akt signaling pathway and Innate Immune System.
HADHA	Hydroxyacyl-CoA Dehyrdogenase Trifunctional Multienzyme Complex Subunit Alpha	Protein Coding gene. Diseases associated with HADHA include Long-Chain 3-Hydroxyacyl-Coa Dehydrogenase Deficiency and Mitochondrial Trifunctional Protein Deficiency. Among its related pathways are Glycerophospholipid biosynthesis and Mitochondrial Fatty Acid Beta-Oxidation.
MTFR1	Mitochondrial Fission Regulator 1	Protein Coding gene. May play a role in mitochondrial aerobic respiration, organisation and fission. Chicken homolog promotes mitochondrial fission and mouse homolog protects cells from oxadative stress.
MYL1	Myosin Light Chain 1	Protein Coding gene. Among its related pathways are Cardiac conduction and PAK Pathway. Related to calcium ion binding and structural constituent of muscle.
MYOD1	Myogenic Differentiation 1	Protein Coding gene. Diseases associated with MYOD1 include Pleomorphic Rhabdomyosarcoma and Spindle Cell Rhabdomyosarcoma. Among its related pathways are Development NOTCH1-mediated pathway for NF-KB activity modulation and miRs in Muscle Cell Differentiation.
NECTIN3	Nectin Cell Adhesion Molecule 3	Protein Coding gene. Among its related pathways are PAK Pathway and T Cell Co-Signaling Pathway: Ligand-Receptor Interactions. Plays a role in ocular development involving the ciliary body. Mutations are believed to result in congenital ocular defects.
PON1	Paraoxonase 1	Protein Coding gene. Diseases associated with PON1 include Microvascular Complications Of Diabetes 5 and Amyotrophic Lateral Sclerosis 1. Among its related pathways are Metabolism and Arachidonic acid metabolism. Polymorphisms in the gene may be associated with coronary heart disease and diabetic retinopathy.
COL1A2	Collagen Type I Alpha 2 Chain	rotein Coding gene. Diseases associated with COL1A2 include Osteogenesis Imperfecta, Type Iii and Type Iv, atypical Marfan syndrome, Ehlers-Danos syndrome type VIIB and recessive Ehlers-Danos syndrome. Among its related pathways are Cytokine Signaling in Immune system and Integrin Pathway.
COX6A1	Cytochrome C Oxidase Subunit 6A1	Protein Coding gene. Diseases associated with COX6A1 include Charcot-Marie-Tooth Disease, Recessive Intermediate D and Charcot-Marie-Tooth Disease, Axonal, Type 2R. Among its related pathways are Respiratory

		electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins. and Gene Expression.
GGPS1	Geranylgeranyl Diphosphate Synthase 1	Protein Coding gene. Diseases associated with GGPS1 include Osteogenesis Imperfecta, Type V. Among its related pathways are Regulation of cholesterol biosynthesis by SREBP (SREBF) and Terpenoid backbone biosynthesis.
MUSK	Muscle Associated Receptor Tyrosine Kinase	Protein Coding gene. Diseases associated with MUSK include Myasthenic Syndrome, Congenital, 9, Associated With Acetylcholine Receptor Deficiency and Fetal Akinesia Deformation Sequence. Among its related pathways are ERK Signaling and ECM proteoglycans.
MYOT	Myotilin	Protein Coding gene. Diseases associated with MYOT include Myopathy, Myofibrillar, 3 and Muscular Dystrophy, Limb-Girdle, Type 1A.
PPP1R9A	Protein Phosphatase 1 Regulatory Subunit 9A	Protein Coding gene. Diseases associated with PPP1R9A include Hepatosplenic T-Cell Lymphoma. Among its related pathways are Beta-Adrenergic Signaling and Activation of cAMP-Dependent PKA. Also related to actin binding and cytoiskeleton reorganisation.
RB1	RB Transcriptional Corepressor 1	Protein Coding gene. Diseases associated with RB1 include Retinoblastoma and Bladder Cancer. Among its related pathways are Mitotic Prophase and Chronic myeloid leukemia.
SLC25A13	Solute Carrier Family 25 Member 13	Protein Coding gene. Diseases associated with SLC25A13 include Citrullinemia, Type Ii, Neonatal-Onset and Citrullinemia, Type Ii, Adult-Onset. Among its related pathways are Glycosaminoglycan metabolism and Metabolism.
ACE2	Angiotensin I Converting Enzyme 2	Protein Coding gene. Diseases associated with ACE2 include Severe Acute Respiratory Syndrome and Neurogenic Hypertension. Among its related pathways are Peptide hormone metabolism and Collagen chain trimerization. May play a role in the regulation of cardiovasuclar and renal function and fertility.
DNAH5	Dynein Axonemal Heavy Chain 5	Protein Coding gene. Diseases associated with DNAH5 include Ciliary Dyskinesia, Primary, 3, Primary Ciliary Dyskinesia and Kartagener syndrome. Among its related pathways are Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.
ITGAV	Integrin Subunit Alpha V	Protein Coding gene. Diseases associated with ITGAV include West Nile Virus and Cerebral Hypoxia. Among its related pathways are VEGF Signaling Pathway and Primary Focal Segmental Glomerulosclerosis FSGS. Protein may regulate angiogenesis and cancer progression.
MSTN	Myostatin	Protein Coding gene. Diseases associated with MSTN include Muscle Hypertrophy and Myostatin-Related Muscle Hypertrophy. Among its related pathways are Hypertrophy Model and Factors and pathways affecting insulin-like growth factor (IGF1)-Akt signaling.
SOCS7	Suppressor Of Cytokine Signaling 7	Protein Coding gene. Among its related pathways are Jak-STAT signaling pathway (KEGG) and Jak/STAT Signaling Pathway Intracellular Regulation. Functions in insulin signaling and glucose homeostasis.
SRI	Sorcin	Protein Coding gene. Regulates intracellular calcium homeostasis. Diseases associated with SRI include Interstitial Myocarditis and Apical Myocardial Infarction. Among its related pathways are Cardiac conduction and Response to elevated platelet cytosolic Ca2+.

Table 21.d

			Training type		
Marker	Training	Odds Ratio	Combined	Cardio	Strength
OBD142_029.031_1x	Present in Endurance and Strength	7.2	0.016681	0.06669	0.01613
OBD142_061.063_1.8x	Present in Endurance and Strength	8.2	0.0185106	0.11741	0.1068
OBD142_069.071_1.2x	Present in Endurance and Strength	8	0.0025561	0.06669	0.05767
OBD142_089.091_1x	Present in Endurance and Strength	2.9	0.1237527	0.40123	0.1806
OBD142_137.139_1.2x	Present in Endurance and Strength	8	0.0627014	0.11741	0.18262

OBD142_081.083_1.4x	Present in Endurance	6	0.1392395	0.07048	0.79999
OBD142_189.191_1x	Present in Endurance	4.5	0.1196946	0.11741	0.84529
OBD142_213.215_1.4x	Present in Endurance	2.25	1	0.69409	0.13523
OBD142_017.019_1.2x	Present in Strength	4	0.7249505	0.54542	0.28124
OBD142_037.039_1x	Present in Strength	12	0.1525177	1	0.02526
OBD142_065.067_1x	Present in Strength	5	0.131911	0.54542	0.05767
OBD142_133.135_1x	Present in Strength	4	0.4615609	1	0.01613
OBD142_253.255_1.2x	Present in Strength	12	0.4496075	0.6101	0.02421
OBD142_353.355_1x	Present in Strength	9	0.1196946	1	0.01615
OBD142_477.479_1x	Present in Strength	9	0.4275177	1	0.02526
OBD142_181.183_1.4x	Present in Strength	2	0.7559581	0.74071	0.17781
OBD142_397.399_1x	Present in Strength	2	0.1516371	0.66843	0.09668

Table 22 shows preferred markers from the equine study and the traits they relate to, which are preferably used to type horses.

5

PCR Marker	Phenotype
OBD154_125/OBD154_127	Sprinter
OBD154_085/OBD154_087	Sprinter
OBD154_157/OBD154_159	Stayer
OBD154_013/OBD154_015	Sprinter
OBD154_245/OBD154_247	Sprinter
OBD154_229/OBD154_231	Sprinter
OBD154_093/OBD154_095	Sprinter
OBD154_049/OBD154_051	Sprinter
OBD154_201/OBD154_203	Stayer
OBD154_041/OBD154_043	Stayer
OBD154_073/OBD154_075	Stayer
OBD154_205/OBD154_207	Sprinter
OBD154_009/OBD154_011	Sprinter
OBD154_045/OBD154_047	Stayer
OBD154_141/OBD154_143	Sprinter
OBD154_165/OBD154_167	Sprinter
OBD154_213/OBD154_215	Stayer

Table 23 shows preferred markers from the equine study and the traits they relate to, which are preferably used to type horses.

No.	Probe	GeneLocus
1	ORF2_1_133335365_133342248_133252663_133254033_RR	ORF2
2	ORF17_21_46168522_46170441_46128519_46131714_FR	ORF17
3	ORF37_7_80905043_80905799_80946828_80948039_FF	ORF37
4	ORF5_22_44079168_44079873_44099430_44101885_RR	ORF5
5	ORF33_23_51893485_51894717_51879777_51881452_RR	ORF33
6	ORF24_7_26919921_26921163_26962320_26963327_RF	ORF24
7	ORF1_3_38982976_38984987_38897821_38902754_RR	ORF1
8	ORF39_3_37427338_37427846_37369331_37372145_FF	ORF39
9	ORF21_27_18057476_18059723_18216584_18221307_FF	ORF21
10	ORF9_9_19477415_19483037_19371208_19377216_RF	ORF9

11	ORF11_25_15754740_15756330_15827853_15831235_FR	ORF11
12	ORF41_2_44125472_44130831_44114366_44115500_FR	ORF41
13	ORF12_28_42033251_42034839_42111316_42112829_FR	ORF12
14	ORF42_14_38556059_38561196_38515585_38519701_RR	ORF42
15	ORF31_24_18025107_18025879_18089550_18090204_FR	ORF31
16	ORF28_19_27971050_27974189_28029396_28030610_FR	ORF28
17	ORF3_3_39072647_39081470_38902754_38905559_RR	ORF3
18	ORF87_4_38678592_38682251_38712668_38720224_RF	ORF87
19	ORF95_2_30297289_30298973_30249858_30251319_RF	ORF95
20	ORF72_5_76755446_76755869_76713081_76716746_FR	ORF72
21	ORF44_8_11915509_11916086_11887773_11890590_RR	ORF44
22	ORF90_5_9229073_9235994_9247952_9249817_FR	ORF90
23	ORF51_4_788561_790967_729450_732106_FR	ORF51
24	ORF67_15_69928382_69930519_69848008_69851513_FF	ORF67
25	ORF109_1_110780529_110783525_110809348_110820887_FF	ORF109
26	ORF99_11_29755642_29761616_29820061_29826391_RR	ORF99
27	ORF46_27_7694409_7697820_7673458_7673882_FR	ORF46
28	ORF107_15_17634193_17641147_17623423_17624089_FR	ORF107
29	ORF86_19_45858761_45861211_45775880_45782396_RR	ORF86
30	ORF71_5_76755446_76755869_76727262_76728348_FF	ORF71
31	ORF62_17_64192230_64193405_64341970_64343229_FF	ORF62
32	ORF69_1_104390566_104392857_104321461_104322189_RF	ORF69
33	ORF76_7_85946864_85949922_85987651_85988101_FR	ORF76
34	ORF79_23_5314583_5315708_5202402_5204544_FR	ORF79
35	ORF64_25_24906776_24910177_25031046_25032151_FF	ORF64
36	ORF85_X_18614272_18616544_18648509_18649030_FR	ORF85
37	ORF58_22_41701255_41702998_41789282_41790782_RF	ORF58
38	ORF81_22_44079168_44079873_44118479_44121814_RR	ORF81
39	ORF84_X_18614272_18616544_18641258_18647069_FR	ORF84
40	ORF73_16_84538528_84540820_84582113_84585716_FR	ORF73
41	ORF106_15_55284305_55291596_55156691_55157175_FF	ORF106
42	ORF88_3_100800337_100801373_100744664_100751637_FF	ORF88

Table 24.a [Table 24 shows markers identified in the equine study, which are preferably used to type horses.]

	Probe sequence
No.	**60 mer**
1	TTTAAAACTAAGTCTAACCGCCTGAAAGTCGAGAGGGAAGTGCTACGCATCCCGCGCACA
2	AGAGGCTCAAAACTTCTGTCTGGTAAATTCGATTTTCTCCTATTGCTCTACATCACTCGG
3	CCCCATAGGAGGCTTCTGGGAAGCCCAGTCGAGATGCATCCATGTTGTCATGGGTATAAG
4	TTCCTACCACCCAAATTCTATTATTCTATCGAGAGGCACCAGGATGCTGAGAGGATGAGA
5	TCGTGTTAGTTAAATCGGCCGATTTGTCTCGAGAAAAGAGAAGGACTGGGTCATGGTGGG
6	CCGCCTCGCCACAGCTCTCCAGTGAGATTCGATCCTTTTAAACTTTGTTAGGCAAGACCA
7	TTGATCTTTTTTAAAATAGGGATGGGGTTCGAGAGAAGGAGAATGAAGCAGAAAGCTTGT
8	CTGTAACCAGAGGAGCAGAGTCTGCACATCGATTCCTCTTACTGCACTGCAGGTCCAGGG
9	ACCCAAAATTTACTTGCAATCACTTTAATCGAGCTCTTGGATGTCTGGGGATTGTTCTGC
10	GATAGAATTAAACATTGAAGGCAAACTTTCGATTAGGGTTTTAGTTTTCTTTAAGTTTTT
11	GAGCACAGGTGCTGGATTCAGGCTTCCTTCGATTCAAACTTCCCTCACACTGACATTTTT
12	GGAGAAAAAGGGGCTTTACGCAGTCCATTCGATGCAGTCAGGAGTCAGGACAGCATCTCC
13	CACAATGCCTTCCCCTCTTCCACCCCTTTCGATCACTGTCCTTCGTACACTCAAGATATA
14	GTAAAAACCAGCTTCCAGGGACCAGATGTCGAGATCAGTATTGAAATGCACCATTTCATT
15	CATAAGAGATGACTGGCCTTTTGCTGTTTCGATGGCCCGGCTTCCTCTTTGGGACTTCAG
16	TAATGAAATTGTCTTTTTGTGTCTTTCTTCGAGGATTTCTAGACTTTCTGTGCATCACTA
17	AAGCATAAATTCGTTTTCCCCTTGACTTTCGAGACTCCATAAAGCACACGCACAAAGGCC
18	GTAACATGCTGAATAACAACATTTCAGTTCGAGCGTTGTGGCAGAGCTTCCTTGTTACTG
19	ACAGTGCTGCCTCTTCTGTGCAGATGCTTCGAAACCCATGTAATTTCATAGCTATGATGG

20	TTGCCTCCATTTTAAAATTGAAGAAACTTCGAATAAAATTGAAACATCCTACCACCAACA
21	CAGCTGGAGCTCAGCCGGATGCGCAACTTCGAGAAGAGATATTTGCACATCCGTGTTCGT
22	AGTGGGCCACCACTGCCTAAGAACTACTTCGAGGCCAATACTACTGTCGGCCGCATCCGT
23	GCCGTCGGTGGAGAAATTTAAAACTATTTCGAGTCAGTAACTGGACTCAGTTAAGGAAGG
24	CACTGAGCTGCACGAAGATGCTGCCATCGATTCTCAATTGGGAAAAGCACATGGGATATG
25	TTAAAAGTAAAGTAAGTAGAGGTCAGTCTCGAAGCTTTGAAGATTAGTTTTTGAACAGTG
26	CAAGAATCAGTTCTGAGAAATCAATGCCTCGAGAACCAACGAAACACTGGGCCGCCTGCA
27	TGAACATTATCCAGGAGCTCATACTGCTTCGATGACCACAGAGGCGCCAGAAGGCCACAG
28	CAATGTACAATCTACCAGGAACTGAAGTTCGAGCAGCACTTGGCTTTCTTCCTTTTTAGA
29	GAAAGCTGGGTATGGGAGTGTGCACACTTCGAGATCTCAGAAAGGGCATAACTGTATTTT
30	ATTGCCTCCATTTTAAAATTGAAGAAACTCGATGGAGTTTGGGTTTAAGCACTGCTTTTT
31	AGGCCTCGCCTATGAATAGCATACCAGCTCGATTATTCTTCTCTCACACAATTTCTGAAG
32	CTCCGCCCGCCAGCTCTGCAGCTTCCCTTCGACGCTTCCTACTTTTCTCCAGGAAATTAT
33	TCACTCCAGGACCCCCCCAGCCCTGTGTTCGAGGTTGTTTTGCCAGTCGTCTGTTTGGCA
34	GGAAACACAAAGTTCTTGGCAAAGCTTCGAGTCTTGGAGGTGTTGTTATTTGCCCAAAGC
35	GTGGCCTTATTTTGCAAAGGGGCAAACTTCGAAGGTGATGAAACGGAGGCCCAGAGAGGG
36	TACCTCCAGTCTTGGTTATTCTGAGAGTTCGAGTCAGGATTCAGACCCAAGTCTAACTCT
37	GGGTCCAAACCTGCAAATCCCCAGCTGTTCGAAAATGTGTCTGCTTTTTCATGGACACCA
38	TTCCTACCACCCAAATTCTATTATTCTATCGAGAGGCTGAGATGAACAAGGCAGACGCAG
39	TACCTCCAGTCTTGGTTATTCTGAGAGTTCGACAAGTGCGCTAGTGCCGCTTGTCAAGAG
40	ATAAATTCCTTTGTGAATTTTGATCTCTTCGAAGACTTGTTCTGTTGGAGGCATGTCCCT
41	CTTCCCCAAGAATTTTGGATTATATCTCTCGAGAAAGGGTAAGGAAGAGTCAAAGCTGTA
42	CAATTTCTGGGGATACAGTAGTGAAGAGTCGATGGCATGGGATCTCTGCTATTTATCTCT

Table 24.b

	Probe Location					4 kb Sequence Location	
No.	Chr	Start1	End1	Start2	End2	Chr	Start1
1	1	133335365	133335396	133252663	133252694	1	133335365
2	21	46170410	46170441	46128519	46128550	21	46166440
3	7	80905768	80905799	80948008	80948039	7	80901798
4	22	44079168	44079199	44099430	44099461	22	44079168
5	23	51893485	51893516	51879777	51879808	23	51893485
6	7	26919921	26919952	26963296	26963327	7	26919921
7	3	38982976	38983007	38897821	38897852	3	38982976
8	3	37427815	37427846	37372114	37372145	3	37423845
9	27	18059692	18059723	18221276	18221307	27	18055722
10	9	19477415	19477446	19377185	19377216	9	19477415
11	25	15756299	15756330	15827853	15827884	25	15752329
12	2	44130800	44130831	44114366	44114397	2	44126830
13	28	42034808	42034839	42111316	42111347	28	42030838
14	14	38556059	38556090	38515585	38515616	14	38556059
15	24	18025848	18025879	18089550	18089581	24	18021878
16	19	27974158	27974189	28029396	28029427	19	27970188
17	3	39072647	39072678	38902754	38902785	3	39072647
18	4	38678592	38678623	38720193	38720224	4	38678592
19	2	30297289	30297320	30251288	30251319	2	30297289
20	5	76755838	76755869	76713081	76713112	5	76751868
21	8	11915509	11915540	11887773	11887804	8	11915509
22	5	9235963	9235994	9247952	9247983	5	9231993
23	4	790936	790967	729450	729481	4	786966
24	15	69930488	69930519	69851482	69851513	15	69926518
25	1	110783494	110783525	110820856	110820887	1	110779524
26	11	29755642	29755673	29820061	29820092	11	29755642
27	27	7697789	7697820	7673458	7673489	27	7693819
28	15	17641116	17641147	17623423	17623454	15	17637146
29	19	45858761	45858792	45775880	45775911	19	45858761

30	5	76755838	76755869	76728317	76728348	5	76751868
31	17	64193374	64193405	64343198	64343229	17	64189404
32	1	104390566	104390597	104322158	104322189	1	104390566
33	7	85949891	85949922	85987651	85987682	7	85945921
34	23	5315677	5315708	5202402	5202433	23	5311707
35	25	24910146	24910177	25032120	25032151	25	24906176
36	X	18616513	18616544	18648509	18648540	X	18612543
37	22	41701255	41701286	41790751	41790782	22	41701255
38	22	44079168	44079199	44118479	44118510	22	44079168
39	X	18616513	18616544	18641258	18641289	X	18612543
40	16	84540789	84540820	84582113	84582144	16	84536819
41	15	55291565	55291596	55157144	55157175	15	55287595
42	3	100801342	100801373	100751606	100751637	3	100797372

Table 24.c

	4 kb Sequence Location				
No.	End1	Start2	End2	PCR-Primer1_ID	PCR_Primer1
1	133339366	133252663	133256664	OBD154_001	GGTATTGGAACTTCAGAGAGGTAGGC
2	46170441	46128519	46132520	OBD154_009	GAGGAGGGAGAGTGCTACTTGCC
3	80905799	80944038	80948039	OBD154_013	GCCCCATTGAGCATCACAGAGGG
4	44083169	44099430	44103431	OBD154_033	TCCCCACTTCTCCTCCACAAGGC
5	51897486	51879777	51883778	OBD154_037	CCCCAGGAGTGATGGCTCAGAAT
6	26923922	26959326	26963327	OBD154_041	GCCTCCCAAACCATTCCCTCGGA
7	38986977	38897821	38901822	OBD154_045	GCCCCATACACTGCTCACTGGCT
8	37427846	37368144	37372145	OBD154_049	CACTCCTGCCGCTGAGATTCCTG
9	18059723	18217306	18221307	OBD154_053	CCGCCATTGGGTTGTTTTGCCCC
10	19481416	19373215	19377216	OBD154_057	GCCTTGAGCATACCCACTGTCAG
11	15756330	15827853	15831854	OBD154_061	ACCAAGCACAGTGGCTGACACATCTG
12	44130831	44114366	44118367	OBD154_069	AAGCCCTGGAGTGGGAGATTGCT
13	42034839	42111316	42115317	OBD154_073	CAACCTGGAGTCCTGAAGACCCC
14	38560060	38515585	38519586	OBD154_077	CCACCTTGGCAAATGGCTTCTCTGCT
15	18025879	18089550	18093551	OBD154_085	CTCCCTGCCCTCCATTTGCCTTT
16	27974189	28029396	28033397	OBD154_093	GCACTGAGTTGTGGGTTTTCAAAGGT
17	39076648	38902754	38906755	OBD154_097	GCTATTTGCGTGGTGGTGACAATGAT
18	38682593	38716223	38720224	OBD154_105	ATCATCACCTTAGTATCCCCACCTCT
19	30301290	30247318	30251319	OBD154_109	AAGTGTCAGCCTCTGCCCGTAGC
20	76755869	76713081	76717082	OBD154_113	GGGTGAGGTTCTTTCCCTGTAGG
21	11919510	11887773	11891774	OBD154_117	GTCTCTTCTTCTCTCTGGTCGGC
22	9235994	9247952	9251953	OBD154_121	CCCACACCTCCAGTTGTCCCACA
23	790967	729450	733451	OBD154_125	TACTCTTCAAAAGCACAGCCAACGGG
24	69930519	69847512	69851513	OBD154_133	GGTGGAAGTCGTCTGCCAAGATG
25	110783525	110816886	110820887	OBD154_137	TGGCTAACTGTCTCCTCAAAATCCTA
26	29759643	29820061	29824062	OBD154_141	CGTAACACCCGAATCAGTGGAAGGAA
27	7697820	7673458	7677459	OBD154_149	GCCTCCTCTCCCTATCTCTGGAT
28	17641147	17623423	17627424	OBD154_153	CAGATGCTGGGTTTTGCCCTCAGG
29	45862762	45775880	45779881	OBD154_157	TGACTCTGCTGTAGATGTCCTGGCTC
30	76755869	76724347	76728348	OBD154_161	GGGTGAGGTTCTTTCCCTGTAGG
31	64193405	64339228	64343229	OBD154_165	GGTAGAAAGCGTTTAGCCCTGTATTT
32	104394567	104318188	104322189	OBD154_169	CACCTTCATCCTTCACCAAGTCCTGC
33	85949922	85987651	85991652	OBD154_177	CCCTCAACCCATTTCCTTCACTTGCC
34	5315708	5202402	5206403	OBD154_185	TGAGGATGGTCAGTGAGACTCGTAAA
35	24910177	25028150	25032151	OBD154_201	ACAGTAGACAGACAGCACAGGGTTTA
36	18616544	18648509	18652510	OBD154_205	AAAGGTGGTGGGCAGGACTCCAG
37	41705256	41786781	41790782	OBD154_209	ATGTAGGGCATCACCACAGCGTG
38	44083169	44118479	44122480	OBD154_213	TCCCCACTTCTCCTCCACAAGGC
39	18616544	18641258	18645259	OBD154_217	AAAGGTGGTGGGCAGGACTCCAG

40	84540820	84582113	84586114	OBD154_229	ACTCGGCTAACCCTCTACTTCAAGGT
41	55291596	55153174	55157175	OBD154_237	GGCGGCTGTGTGAGTTTTGCCAA
42	100801373	100747636	100751637	OBD154_245	ACCATTAGTTGGCTCATCTCCTTGCC

Table 24.d

No.	PCR-Primer2_ID	PCR_Primer2	GLMNET
1	OBD154_003	GGAGGCAAGGCTGTGATGAAAGTCAA	0.044648292
2	OBD154_011	GTGAGTGGGTTTCCCTGCTGAAC	0.077266514
3	OBD154_015	GCTGCTGTGGGTTTCTGCGACAT	0.10805769
4	OBD154_035	GCCTGGAACAGTTGAGCAAACGC	0.052504077
5	OBD154_039	CCAGTGCCTCTCTTCAGCATCCC	0.016550856
6	OBD154_043	CTCACACAGAGAGGAGGAGAGGA	0.033835679
7	OBD154_047	CCCCAGGTTTGGAAGTTCTCAGC	-0.031914355
8	OBD154_051	CGGAGCAGAACATTCGCCTAAGC	0.073432502
9	OBD154_055	GCAGTGTGACAAGGAAGCAGCAG	0.034421206
10	OBD154_059	ACCCTCAGAAATCCCTCCCAGGC	0.014137586
11	OBD154_063	TCTTCACCATTTTCTTGAGCACTGTG	-0.034009396
12	OBD154_071	GCCAGCCACTGTCCCAAGGAGAT	0.046480779
13	OBD154_075	CGCAGGGCTAATCTTCCTCAACC	-0.092997789
14	OBD154_079	TTTTGAGGGAGAGTCCGTGAAGC	0.018460556
15	OBD154_087	ATCACGGACAGGCACCTACGGCT	0.105247988
16	OBD154_095	ATCAAACTCCAGCAATCTGACTCCAG	0.067222042
17	OBD154_099	GCCAGGCTCACTCCTTTCCCTTTTAG	0.069540888
18	OBD154_107	GCCCTGAGACAAGCATTTTCCTCGTC	0.072250245
19	OBD154_111	CGGAGTCTCGTCCCGACATTTAC	-0.021487184
20	OBD154_115	ACTGTGTGGGAGGAAGGTGGAGG	-0.089547447
21	OBD154_119	CACCCACCTTTGTTCACCCGCTC	0.053341863
22	OBD154_123	CCCAGGTAGTCGTGGAAACGGAT	-0.009481999
23	OBD154_127	CCCCTGGCTTTAGGCTTAGATTCTCT	0.184254198
24	OBD154_135	TTCTCGCCTGCTTCCTGCCTGTG	0.013549498
25	OBD154_139	GCCATTCGGTGACATCAGGGTGA	-0.029260042
26	OBD154_143	AGAGTCACGGTTTCTGCCTATCAAGA	0.040466078
27	OBD154_151	CCTCTCGCTGAAGTCCCTGCCAT	-0.026044566
28	OBD154_155	CAGGGAAGGGAGAATAGTCAGGG	0.05560739
29	OBD154_159	GGAGAGAAGATAGGCTGGCAATAGAT	-0.111847127
30	OBD154_163	CACCTCCTCCCTCAACCCCTAAG	-0.011075719
31	OBD154_167	ATTTAGGCACTTGGGAGAGGAGAGCC	0.052703232
32	OBD154_171	CTGATGATAGTTAGGGAGAGGTGAGT	0.072817076
33	OBD154_179	AAGGTTTGTGGCTCTTGAACATACCA	0.023527
34	OBD154_187	AATGGCACATCCTCCAACCCCAAACC	-0.028512982
35	OBD154_203	TGTGTGTCTACTGCCAACTCTGCCCT	-0.076839662
36	OBD154_207	CCTCAGGTCAGGTTTTGTCACGG	0.101263033
37	OBD154_211	CCGCCCGCATTGGCATCCGAATA	0.048686754
38	OBD154_215	CCGAGCCTTCTCCCTTTTCTCCA	-0.060839024
39	OBD154_219	CAGAACTCCTCAGGCTCAGACAC	0.01900231
40	OBD154_231	CTGGCTCAATAAGAGTGCTTTCCTTG	0.10786072
41	OBD154_239	TGGCAGGGAAAGACTCGGAGGTC	-0.04345676
42	OBD154_247	CCTCTTCCCTAACTGCGAAACAAAAC	0.059641358

Table 24.e

No.	Marker	GLMNET
1	OBD154_001/OBD154_003_1:2x	0.044648292
2	OBD154_009/OBD154_011_1:2x	0.077266514
3	OBD154_013/OBD154_015_1x	0.10805769
4	OBD154_033/OBD154_035_1:4x	0.052504077
5	OBD154_037/OBD154_039_1:8x	0.016550856

6	OBD154_041/OBD154_043_1x	0.033835679
7	OBD154_045/OBD154_047_1x	-0.031914355
8	OBD154_049/OBD154_051_1:4x	0.073432502
9	OBD154_053/OBD154_055_1:2x	0.034421206
10	OBD154_057/OBD154_059_1:2x	0.014137586
11	OBD154_061/OBD154_063_1x	-0.034009396
12	OBD154_069/OBD154_071_1x	0.046480779
13	OBD154_073/OBD154_075_1x	-0.092997789
14	OBD154_077/OBD154_079_1x	0.018460556
15	OBD154_085/OBD154_087_1:2x	0.105247988
16	OBD154_093/OBD154_095_1:2x	0.067222042
17	OBD154_097/OBD154_099_1x	0.069540888
18	OBD154_105/OBD154_107_1:2x	0.072250245
19	OBD154_109/OBD154_111_1:2x	-0.021487184
20	OBD154_113/OBD154_115_1:4x	-0.089547447
21	OBD154_117/OBD154_119_1x	0.053341863
22	OBD154_121/OBD154_123_1x	-0.009481999
23	OBD154_125/OBD154_127_1:2x	0.184254198
24	OBD154_133/OBD154_135_1:2x	0.013549498
25	OBD154_137/OBD154_139_1x	-0.029260042
26	OBD154_141/OBD154_143_1x	0.040466078
27	OBD154_149/OBD154_151_1:2x	-0.026044566
28	OBD154_153/OBD154_155_1:8x	0.05560739
29	OBD154_157/OBD154_159_1:2x	-0.111847127
30	OBD154_161/OBD154_163_1:2x	-0.011075719
31	OBD154_165/OBD154_167_1x	0.052703232
32	OBD154_169/OBD154_171_1:4x	0.072817076
33	OBD154_177/OBD154_179_1x	0.023527
34	OBD154_185/OBD154_187_1x	-0.028512982
35	OBD154_201/OBD154_203_1x	-0.076839662
36	OBD154_205/OBD154_207_1:2x	0.101263033
37	OBD154_209/OBD154_211_1:2x	0.048686754
38	OBD154_213/OBD154_215_1:2x	-0.060839024
39	OBD154_217/OBD154_219_1x	0.01900231
40	OBD154_229/OBD154_231_1x	0.10786072
41	OBD154_237/OBD154_239_1x	-0.04345676
42	OBD154_245/OBD154_247_1x	0.059641358

Table 24.f

No.	Probe	Loci	Probe_Count_Total	Probe_Count_Sig
1	CBL_11_119249760_119252653_119294588_119299643_RF	CBL	24	19
2	DKK3_11_11956071_11968035_11984245_11993733_FR	DKK3	54	36
3	DKK3_11_11956071_11968035_12048403_12051930_FR	DKK3	54	36
4	FBXO32_8_123526212_123527874_123555254_123559065_FR	FBXO32	41	26
5	KDM1A_1_23064655_23070269_23096951_23098159_FR	KDM1A	25	18
6	EYA1_8_71216399_71218728_71261816_71267769_RR	EYA1	139	80
7	PCK1_20_57527297_57530814_57579772_57583521_RR	PCK1	36	26
8	PIK3C3_18_42070009_42072187_42088671_42094691_FF	PIK3C3	141	89
9	ALDH1A2_15_58053198_58062371_58157807_58162832_RR	ALDH1A2	185	100
10	CD36_7_80539507_80544315_80679651_80687690_FR	CD36	169	96
11	DKK3_11_11956071_11968035_12010923_12019458_FF	DKK3	54	36
12	IL1RAP_3_190489665_190498302_190560851_190563356_FR	IL1RAP	160	82
13	RUNX3_1_24920810_24923822_24973522_24976037_RF	RUNX3	51	24
14	PPARA_22_46101029_46102611_46241078_46244347_FR	PPARA	44	26
15	SLC25A13_7_96209525_96214524_96295606_96302029_FF	SLC25A13	143	99

16	PCK1_20_57527297_57530814_57551578_57557205_RR	PCK1	36	26
17	MYL1_2_210288997_210291732_210359762_210362293_FF	MYL1	9	5
18	C1GALT1_7_7113076_7114831_7258228_7260668_FF	C1GALT1	89	4
19	COL25A1_4_109024771_109031337_109090838_109104305_RR	COL25A1	134	3
20	COL5A1_9_134738485_134741113_134811418_134816113_RR	COL5A1	180	0
21	DIAPH3_13_59818047_59823591_59854837_59860534_RR	DIAPH3	167	1
22	FBLN2_3_13512352_13515076_13582406_13590343_RF	FBLN2	93	1
23	GPC6_13_94121445_94133208_94296633_94304225_FF	GPC6	166	7
24	GSN_9_121177548_121180410_121268506_121274144_FR	GSN	156	6
25	GSN_9_121227501_121232628_121268506_121274144_FR	GSN	156	6
26	GSN_9_121239116_121243347_121268506_121274144_FR	GSN	156	6
27	LCK_1_32214585_32217213_32237144_32241139_RF	LCK	24	1
28	LMO4_1_87315524_87318670_87343110_87349940_FF	LMO4	105	0
29	MAPK10_4_86572598_86581486_86617317_86621940_FF	MAPK10	172	2
30	MBNL1_3_152229500_152234786_152281057_152285843_FR	MBNL1	144	2
31	NCAM1_11_113019160_113028536_113163748_113168132_FR	NCAM1	198	3
32	PCK1_20_57527297_57530814_57570220_57572870_RR	PCK1	36	0
33	PDK3_X_24441637_24447950_24480152_24481252_FR	PDK3	22	0
34	PDK3_X_24441637_24447950_24490440_24491541_FR	PDK3	22	0
35	PTPRC_1_198595771_198598296_198659753_198666156_RF	PTPRC	184	14
36	PTPRC_1_198659753_198666156_198721093_198724578_FF	PTPRC	184	14
37	RYR1_19_38410632_38413089_38495982_38499305_RR	RYR1	41	6
38	THNSL2_2_88139809_88146295_88161717_88164554_FR	THNSL2	29	2
39	UACA_15_70715123_70719636_70780754_70784668_RF	UACA	132	1
40	ZEB1_10_31273317_31275631_31507470_31524442_FF	ZEB1	163	11
41	ZFHX3_16_73147488_73153243_73182254_73184585_FF	ZFHX3	170	1
42	ADRB3_8_37962724_37965269_37987735_37989039_FR	ADRB3	18	0
43	AGT_1_230724515_230729957_230752057_230757333_RF	AGT	45	3
44	HTR2A_13_46860092_46866824_46904346_46907815_RF	HTR2A	60	5
45	SOS1_2_38982199_38993639_39061418_39066028_FF	SOS1	126	0
46	ACBD6_1_180431719_180434683_180541491_180549122_RR	ACBD6	173	4
47	MYH1_17_10502067_10505465_10533547_10534931_RF	MYH1	103	2
48	MYOD1_11_17685862_17689487_17729653_17733608_FR	MYOD1	15	1
49	NECTIN3_3_111028574_111034204_111209684_111210764_FR	NECTIN3	85	4
50	ACACB_12_109146008_109150083_109236052_109237242_RR	ACACB	133	2
51	ACACB_12_109236052_109237242_109268078_109273323_RR	ACACB	133	2
52	IGF1R_15_98652565_98657862_98731539_98737034_RF	IGF1R	176	2
53	SOCS7_17_38347510_38348776_38360864_38363420_FR	SOCS7	31	1
54	STXBP4_17_55035186_55042800_55117598_55123347_RR	STXBP4	141	4
55	SVEP1_9_110397951_110405969_110503630_110509758_FF	SVEP1	177	7
56	EMCN_4_100636305_100649860_100744427_100745788_RR	EMCN	178	2
57	ACACB_12_109146008_109150083_109185066_109187324_RR	ACACB	133	2
58	FOXO1_13_40524349_40526124_40688580_40690771_RR	FOXO1	89	0
59	FOXO3_6_108603215_108604436_108629992_108635481_FR	FOXO3	159	2
60	FTO_16_53844989_53854574_54045378_54052319_RF	FTO	153	1
61	GPC6_13_94054831_94060621_94121445_94133208_RF	GPC6	166	7
62	PPP3CA_4_101055418_101067369_101247819_101259416_RR	PPP3CA	153	2
63	SMAD7_18_48917335_48920290_48969505_48974578_RF	SMAD7	42	0
64	SYK_9_90816328_90822228_90832284_90836084_RR	SYK	160	12
65	SYK_9_90816328_90822228_90872966_90875740_RR	SYK	160	12
66	TGFB2_1_218317687_218325587_218386401_218389011_FR	TGFB2	130	2
67	TGFBR2_3_30566144_30567439_30694718_30698514_RR	TGFBR2	191	4
68	TLR2_4_153659613_153661830_153693586_153700349_RF	TLR2	32	1
69	SVEP1_9_110493529_110499578_110527410_110532406_FR	SVEP1	177	7
70	MTFR1_8_65658401_65661888_65780891_65782535_RF	MTFR1	91	2
71	GSN_9_121182946_121189020_121323589_121328431_FF	GSN	156	6

72	MUSK_9_110648469_110652659_110747866_110751903_FR	MUSK	125	1
73	PPARA_22_46128634_46134707_46231440_46235124_FR	PPARA	44	0
74	PPP1R9A_7_94903925_94908776_94951930_94967018_RF	PPP1R9A	166	1
75	PLCXD2_3_111633890_111638317_111672672_111677327_FR	PLCXD2	144	2
76	SGCZ_8_14631157_14642508_14778176_14785491_FF	SGCZ	191	11
77	SRI_7_88199682_88203042_88229166_88237101_RF	SRI	57	2

Table 25.a

No.	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr	t
1	0.023815147	0.261918121	79.17	-0.426375519	-0.426375519	-4.618561579
2	0.113222201	0.567553327	66.67	-0.452190179	-0.452190179	-4.498338722
3	0.113222201	0.567553327	66.67	-0.473931719	-0.473931719	-4.801248921
4	0.279504208	0.898561555	63.41	-0.428908404	-0.428908404	-11.06651685
5	0.103914483	0.548863748	72	0.450982494	0.450982494	11.74211542
6	0.544172978	1	57.55	-0.420279402	-0.420279402	-6.888734462
7	0.052274012	0.438252195	72.22	-0.454377101	-0.454377101	-3.146677782
8	0.108139211	0.559937306	63.12	0.349058418	0.349058418	10.19574365
9	0.85625995	1	54.05	-0.42054833	-0.42054833	-8.812988665
10	0.618616868	1	56.8	0.355814357	0.355814357	4.033543511
11	0.113222201	0.567553327	66.67	-0.474435884	-0.474435884	-4.565896539
12	0.956664907	1	51.25	0.348466077	0.348466077	11.56470451
13	0.95196413	1	47.06	0.364233402	0.364233402	10.30993314
14	0.486340587	1	59.09	-0.447624697	-0.447624697	-6.45833793
15	0.00284877	0.08241485	69.23	0.351229127	0.351229127	5.941886473
16	0.052274012	0.438252195	72.22	-0.427795857	-0.427795857	-2.904768228
17	0.682316487	1	55.56	-0.389190141	-0.389190141	-13.74123239
18	0.024327419	0.687064234	4.49	-0.555546218	-0.555546218	-11.0417245
19	0.228355538	1	2.24	0.335547043	0.335547043	5.207330156
20	1	1	0	-0.481446393	-0.481446393	-3.82029126
21	0.873903179	1	0.6	0.405185839	0.405185839	2.998972245
22	0.684023987	1	1.08	-0.422325738	-0.422325738	-8.04265312
23	0.004639027	0.223094969	4.22	0.395980197	0.395980197	1.793119535
24	0.013014007	0.465546506	3.85	-0.435924362	-0.435924362	-4.024149814
25	0.013014007	0.465546506	3.85	-0.489846734	-0.489846734	-3.901621745
26	0.013014007	0.465546506	3.85	-0.490566516	-0.490566516	-4.064123806
27	0.257000004	1	4.17	0.404856809	0.404856809	4.029112137
28	1	1	0	-0.425303631	-0.425303631	-4.334227249
29	0.626639375	1	1.16	0.369477889	0.369477889	10.62330419
30	0.530285478	1	1.39	-0.423225201	-0.423225201	-5.762419013
31	0.440361719	1	1.52	-0.473418522	-0.473418522	-5.252061333
32	1	1	0	-0.443750376	-0.443750376	-3.069308332
33	1	1	0	-0.516209141	-0.516209141	-2.912953295
34	1	1	0	-0.482956676	-0.482956676	-2.845644248
35	7.93E-08	3.12E-05	7.61	0.342871898	0.342871898	12.24688433
36	7.93E-08	3.12E-05	7.61	0.353200746	0.353200746	12.71706109
37	1.05E-05	0.00164927	14.63	0.379845454	0.379845454	3.091066536
38	0.049255392	1	6.9	0.348303621	0.348303621	5.482854907
39	0.805245253	1	0.76	-0.452444827	-0.452444827	-6.645114759
40	6.24E-06	0.00122739	6.75	0.341402554	0.341402554	8.358154799
41	0.878517137	1	0.59	-0.437339546	-0.437339546	-7.571199723
42	1	1	0	-0.431801011	-0.431801011	-3.395119054
43	0.017905795	0.612689599	6.67	-0.462997504	-0.462997504	-4.192393926
44	0.000863162	0.056609039	8.33	-0.450665703	-0.450665703	-8.327533972
45	1	1	0	-0.483305844	-0.483305844	-11.1896848
46	0.165185813	1	2.31	-0.438627353	-0.438627353	-7.215605041
47	0.362024499	1	1.94	-0.433949544	-0.433949544	-7.773631426

48	0.169428566	1	6.67	-0.44490366	-0.44490366	-11.70445784
49	0.020952195	0.683779761	4.71	-0.367763769	-0.367763769	-7.284235112
50	0.488070766	1	1.5	0.37639594	0.37639594	5.784183467
51	0.488070766	1	1.5	0.361980641	0.361980641	6.812052569
52	0.63908073	1	1.14	0.376793177	0.376793177	3.580450098
53	0.318687894	1	3.23	0.325631694	0.325631694	8.979749407
54	0.096791402	1	2.84	0.347975579	0.347975579	7.974747337
55	0.006539151	0.270858531	3.95	0.328480984	0.328480984	4.835157675
56	0.645178258	1	1.12	0.319852241	0.319852241	5.68627836
57	0.488070766	1	1.5	-0.639467523	-0.639467523	-7.69815267
58	1	1	0	0.393248671	0.393248671	6.480891366
59	0.583919721	1	1.26	0.365259231	0.365259231	6.804140703
60	0.849949517	1	0.65	-0.434234901	-0.434234901	-9.879188206
61	0.004639027	0.223094969	4.22	0.528815395	0.528815395	2.192030297
62	0.563021006	1	1.31	-0.462324823	-0.462324823	-10.32420109
63	1	1	0	0.40277223	0.40277223	2.549597378
64	7.81E-07	0.000204861	7.5	0.454881152	0.454881152	6.892290381
65	7.81E-07	0.000204861	7.5	0.491854549	0.491854549	7.332798069
66	0.476152064	1	1.54	-0.427835042	-0.427835042	-9.631799551
67	0.209498358	1	2.09	0.713766505	0.713766505	5.020955434
68	0.327072861	1	3.12	0.370613279	0.370613279	12.69019114
69	0.006539151	0.270858531	3.95	-0.425150058	-0.425150058	-9.267584464
70	0.308264448	1	2.2	-0.373414166	-0.373414166	-11.79966649
71	0.013014007	0.465546506	3.85	0.360333931	0.360333931	7.597970849
72	0.787565452	1	0.8	0.386657089	0.386657089	7.586923373
73	1	1	0	0.362541486	0.362541486	2.971365926
74	0.872326654	1	0.6	0.363099567	0.363099567	3.977705912
75	0.530285478	1	1.39	0.371871445	0.371871445	9.143459938
76	2.76E-05	0.00285196	5.76	0.351857885	0.351857885	12.4599802
77	0.155413907	1	3.51	0.345097648	0.345097648	6.863477929

Table 25.b

No.	P.Value	adj.P.Val	B	FC
1	0.000204351	0.001696324	0.420007759	0.744128913
2	0.000266954	0.002046882	0.154483715	0.730932365
3	0.000136422	0.001270248	0.822155807	0.719999735
4	0.00000000106	0.000000159	12.50758304	0.742823621
5	0.00000000057763115753262	0.000000240382974465845	13.11880883	1.366970864
6	0.00000174500366992146	0.0000602085318700566	5.184417423	0.747279887
7	0.005488024	0.018949968	-2.809655881	0.729825214
8	0.00000000406	0.000000379	11.17917387	1.27372905
9	0.000000519795383109141	0.00000495299418442526	8.693472403	0.747140602
10	0.000716034	0.003059888	-0.936521584	1.279707733
11	0.000229703	0.001841162	0.303764249	0.719748167
12	0.000000000513	0.0000000948	13.22969486	1.273206191
13	0.00000000464664280056321	0.000000961862645683259	11.08156058	1.287197476
14	0.00000409787235536200	0.000109374	4.328897959	0.733249101
15	0.0000118	0.000224511	3.269636273	1.275646972
16	0.00932387	0.028011446	-3.317120561	0.743396676
17	0.0000000000274	0.0000000141	16.09554078	0.763558109
18	0.00000000111	0.000000163	12.47094565	0.680399404
19	0.0000510	0.000371158	1.696824449	1.26185579
20	0.001219666	0.006253664	-1.346303854	0.716259169
21	0.007408583	0.020028642	-3.214800278	1.324259482
22	0.000000161	0.00000491	7.493520599	0.746220688
23	0.089475491	0.154086604	-5.389247882	1.315836464

24	0.000771506	0.004457333	-0.895719572	0.739219971
25	0.001015971	0.005458351	-1.166748282	0.712100745
26	0.000705273	0.004168565	-0.807203494	0.711745556
27	0.0007233	0.003084781	-0.946498319	1.323957498
28	0.000385015	0.002678159	-0.20873374	0.744681988
29	0.00000000289295572819759	0.000000681985048919552	11.54687815	1.291885213
30	0.0000171628795759885	0.000292745	2.893666517	0.745755594
31	0.0000462	0.000343634	1.795697	0.7202559
32	0.006507463	0.021473733	-2.97336687	0.73522087
33	0.009159444	0.027632407	-3.300175166	0.699206673
34	0.010599052	0.030783445	-3.439002954	0.715509746
35	0.000000000196	0.0000000539	14.17658691	1.26827878
36	0.000000000104	0.0000000375	14.80248355	1.277391491
37	0.006203474	0.020718718	-2.927451691	1.301202459
38	0.0000279	0.000231594	2.302943346	1.273062829
39	0.00000241	0.0000352	4.766915889	0.73080336
40	0.0000000904	0.00000323	8.071768487	1.266987731
41	0.000000474476333843650	0.0000231189585700664	6.488080595	0.738495203
42	0.003161948	0.012613791	-2.27662634	0.741335749
43	0.00052891	0.00336987	-0.523006115	0.725477359
44	0.000000120499326458705	0.00000908377824577704	7.856562067	0.731705139
45	0.0000000012603812609386	0.000000406018047073111	12.35960543	0.715336596
46	0.000000773	0.0000152	5.912515816	0.737836287
47	0.000000265	0.00000692	6.989653482	0.740232537
48	0.000000000420	0.0000000817	13.42754235	0.734633372
49	0.000000676	0.0000139	6.047319254	0.774982819
50	0.0000163956845883121	0.000282973	2.939466958	1.298094974
51	0.0000202795176244020	0.0000670770127555545	5.033860861	1.285189092
52	0.002089314	0.00927894	-1.873258731	1.298452444
53	0.0000000302	0.00000149	9.171680821	1.253213047
54	0.000000182	0.00000536	7.367278195	1.27277339
55	0.000116599	0.000719355	0.868191804	1.25569056
56	0.0000179	0.000164182	2.745641844	1.248202703
57	0.000000306	0.00000769	6.846486395	0.641949839
58	0.0000391616567926034	0.000106263	4.374356285	1.313347482
59	0.0000205973252071508	0.0000679202407840129	5.018280323	1.288113063
60	0.00000000906782907573557	0.00000142181714589480	10.42301097	0.740086138
61	0.041519144	0.085450094	-4.70897528	1.442744064
62	0.00000000454643610867096	0.000000946006652142489	11.10299558	0.725815704
63	0.019933628	0.04923408	-4.033722222	1.322045866
64	0.00000146	0.0000245	5.268722172	1.370669886
65	0.000000615	0.0000130	6.142312649	1.406251416
66	0.0000000101	0.000000678	10.2711503	0.743376485
67	0.0000842245621504624	0.000906383	1.302982598	1.640080359
68	0.000000000161476307566624	0.000000940784035927087	14.34965814	1.292902317
69	0.000000242868020514695	0.0000282996756590024	9.44872473	0.744761263
70	0.000000000367	0.0000000760	13.56117136	0.771953491
71	0.000000451423921266660	0.0000224517338792905	6.53788422	1.283722998
72	0.000000460792529508426	0.0000227787899768996	6.517344279	1.307360568
73	0.008064742	0.025126002	-3.178757551	1.285688803
74	0.000856336	0.004819753	-0.998511342	1.286186246
75	0.0000000228	0.00000120	9.452862589	1.294030342
76	0.000000000146	0.0000000458	14.46288268	1.276203048
77	0.00000155	0.0000255	5.210654526	1.270236955

Table 25.c

				Probe sequence
No.	FC_1	LS	Loop detected	60 mer
1	-1.343853172	-1	Str_train	ACCGCCTCACCTCAGCTCTCCAGTGAGATCGATCCTCCCACCTAAGCTTCCCAAGTTGCT
2	-1.36811564	-1	Str_train	GACACCTCCTCTCCCTTCCCTCCCCTTCTCGAGTTATCAAAATATTTTGAGAGACAGTAT
3	-1.3888894	-1	Str_train	GACACCTCCTCTCCCTTCCCTCCCCTTCTCGATGGCCACATGTGGCCAGTGGCTCTCATG
4	-1.346214596	-1	End_train	TGCAGAAAGTACTACAAAAAAAGAAGCTTCGAAAATGTTGGAGATGAGAGTTTCTTCACC
5	1.366970864	1	Str_control	GGCAGGTGGATCATTTGAGGTCAAGAGCTCGACAGAGCAAGACACCATCTCCAAAAAGAA
6	-1.338186692	-1	Str_train	TGTCCTTTCAAGGAAGGATTAGCATCCTTCGAAAGACCTATCAGGATTTCATTTGTAATG
7	-1.370191083	-1	Str_train	CCTCGTCGTCCCCTCTCTTCCTCGTTCCTCGAACATCTCCAAGTCAGATAATCATAACAA
8	1.27372905	1	End_control	ATCTATTATAATGATGCAATATTGTTAATCGATTCAAAGATCAAATTAATTATTAAAGCT
9	-1.338436162	-1	Str_train	ATTTTAAATGTGGCATTTTAGGTTTATTTCGATTTTGCATAAATTGAAAAAGCTGGAGAT
10	1.279707733	1	End_control	TGCTGAAAGAAAACACAATTTATTTAAGTCGAAATTTTGGAAAAGCCCTGATTTAAGTCA
11	-1.389374847	-1	Str_train	GACACCTCCTCTCCCTTCCCTCCCCTTCTCGATCACTTTGCAAAGCTTTGTTGGCTAGGC
12	1.273206191	1	End_control	TAAATAAAATTGTCTTTTTTTGTCTTTCTCGATTACAGAGAACTAAGTACATTTTAAATC
13	1.287197476	1	Str_control	CTTAATTTTTTTTCTTTGAATGCCTCTATCGACAGTCTTCTCTCTACTTTCTACAGTGAA
14	-1.363793011	-1	Str_train	ACACCTCACCCACCCAGCTGGGCTGGCCTCGATGCCATTAAATCATCCCGTGACCTTCCT
15	1.275646972	1	Str_control	GGCAGGCGGATCATTTCAGGTCAGGAGTTCGACCTGAAATTTCCATACTAAATTTAAATA
16	-1.345176851	-1	Str_train	CCTCGTCGTCCCCTCTCTTCCTCGTTCCTCGACAGGAAAGCATACGGAAAAAGTTAAAGA
17	-1.309658019	-1	End-Train	AATTTCACATTGATACATTGATAGACATTCGAAATCATACACAGCATACTCTCAAACCAT
18	-1.469724979	-1	END_Train	AAATGTATAAGAACAGAAGAGAATTATCTCGACATGTCTGAAAAGTATTATCAGCCCTCT
19	1.26185579	1	END_Control	AAAACACCCTGAATTGGAAGAAAGAAACTCGAGGGATGAGTGTGTATCATCAAAGTCAAA
20	-1.396142686	-1	Str_Train	CGCGGGGCCTTCTGGGCCAGGCGGGCCCTCGAAAAGCCCCACGCCCCCCCAGAGCTGCTG
21	1.324259482	1	END_Control	AATACGTGGTCAATCTAAGGATTATAGTTCGAAAAGATTAATGATGTATTGATGACACTT
22	-1.340086139	-1	END_Train	CTTGCCTAGTCTTTAATTTATTTATTTATCGACATTTTTTTCTTATCAACGAGACGATGT
23	1.315836464	1	Str_Control	AATTAGACAACGACTATATGACTCTGTCTCGAGATTGGTCTTAACACACTATTGATTATT
24	-1.352777305	-1	Str_Train	AAAAAGAGAAAAGCAGGTTAGCACATTGTCGACCCCGCCCCCGGGATGGGGGAACTGGCC
25	-1.404295681	-1	Str_Train	AAATTTTCAAGTGTACGATATGGTATCATCGACCCCGCCCCCGGGATGGGGGAACTGGCC
26	-1.40499648	-1	Str_Train	AAACTTACGATTACATTTAGAGATCACTTCGACCCCGCCCCCGGGATGGGGGAACTGGCC
27	1.323957498	1	END_Control	AAGGGCTCGGGAGCTCCCTCGGCACACCTCGAGGAGTGCCAGGCATCTACTGCTCTGTCC
28	-1.342855092	-1	Str_Train	CCCCTGGCTCACCTACACAAAATTGTGCTCGACTCTACTCTTAGCCCTGCTAAATAAGTA
29	1.291885213	1	Str_Control	ATTATATTAGTGCTGTAATAAAATTAAGTCGACACATTTGATACTGCTTATTGGGTTATT
30	-1.34092189	-1	Str_Train	TACCTTGAAAAGCTCTTCAGTATGATTATCGAGCTTTAGCCATTCTAGTAATTATTAAAA
31	-1.38839543	-1	END_Train	ATGAATTAATGTTTCCTAGAAAGTTGTCTCGAAAGAAGAAAGTGTCAGGGTTCAACTGCC
32	-1.360135493	-1	Str_Train	CCTCGTCGTCCCCTCTCTTCCTCGTTCCTCGATGCGGGACTGATTGTTACAGAACTGTTT
33	-1.4301923	-1	Str_Train	GGGGATGGGGCCGAAATATGATTGCACTTCGAGTTTGTTTAGTTTTTATCTTCCCCATTT
34	-1.397605002	-1	Str_Train	GGGGATGGGGCCGAAATATGATTGCACTTCGAACTTCAGCACCTGACCTTTGTCATCAAC
35	1.26827878	1	END_Control	AGAGGCTGAGGTGAAAAGATTGTTTGAGTCGAAGATCATTGTCTCATTTTTTTACTTGTT
36	1.277391491	1	END_Control	AGAGGCTGAGGTGAAAAGATTGTTTGAGTCGATACACTGAACAAGTGCCAGAGCAGAATA
37	1.301202459	1	Str_Control	GGTGGGAGGATCACTTGAGGTCAGAAGTTCGATCTCCTGACCTCAAGTGATCCTCTAGCT
38	1.273062829	1	END_Control	TATCAAGTTAAACATTCAGACGTCTAGGTCGACTTGAAGTTCACCTAAAGTTTTCCAGTC
39	-1.368357145	-1	END_Train	ATAGTATAGAATGACAGCATGCTGGTTATCGACAAGAGTTCTTAAAAAGCCTAAATGTCA
40	1.266987731	1	END_Control	ATTCCACAAATATTTGTGAGCACCATCTTCGAGCTCATTAGTTCAAGACCAGCCTGGGCA
41	-1.354104937	-1	Str_Train	CTCTCAACTTTGGATGTAAGAATCATCTTCGAGATTTTGACTCTCCACCTGCCCCACAGG
42	-1.348916468	-1	Str_Train	CGGTCCCTCTGCCCCGGTTACCTACCCGTCGACATGACACTTGGGTGGGGATACAGGGCC
43	-1.378402768	-1	Str_Train	TCCCCCTCTTCCTCTGCCTCCCTTCCCCTCGAAAACTGATTAAAAAGAATATTGCTGGCT
44	-1.366670735	-1	Str_Train	TCACTTTTATTTATCTTACTCACTTTTCTCGAGGAATTCTCAGAATTCTCCTCAACCCAC
45	-1.397943297	-1	Str_Train	TTTCTTCCAACTGAGAGAATCTTAAAAATCGAAATTGGATAAGGAAAAAAGTGAAATGTG
46	-1.355314205	-1	END_Train	TTTTAGTTTTATTTATTTAGTTATCATCTCGAAAAACAAACAACAATAACAGCAACCCTC
47	-1.350926837	-1	END_train	GCAAGACTTTGTCTCAAAACAAAAGTGTTCGAAAAAGTCATCGTTTAAAAGGTAAAATGT
48	-1.361223214	-1	END_Train	TCCATTAGCTCTGCTTTCAAATACTATATCGATGTAGCTTATGTAAAATAAATGTATTAA
49	-1.290351187	-1	END_Train	TCAAAGTTACAGTTTATATAATTAGAAATCGATCTAACCTCAATTCCAGTCCCACAAATG
50	1.298094974	1	Str_Control	TCAAGAAAAAATAATAATAATTTTTTTTTCGAACTTATGGCTCAAGCGATTCTCTTGCTT
51	1.285189092	1	Str_Control	AAGCAAGAGAATCGCTTGAGCCATAAGTTCGATGCTGCTTTGGGAACTGAAGGTTTTTCT
52	1.298452444	1	Str_Control	CGTAGAACTAAGATGTATTCAAAGTCAGTCGAAAAAGATTAGAAAAGTTCAACTCTAAGA
53	1.253213047	1	END_Control	AGGCAGGCAGATCAATGAGGTTGGGAGATCGACAAGTTCAGTAATTCTGAGGTGAGTTTT

54	1.27277339	1	END_Control	GTTGTTATAACTATATCATGAGACTAAGTCGAAAAAAAAAAACAATAATTTCAGCTGTAT
55	1.25569056	1	END_Control	TATATTAGAAACATGTCTGAAAAAAGTATCGATAAATGTATACGTTGATGTACATTGATA
56	1.248202703	1	END_Ctrl	GGTATTACCTTGATGGCCTTAAAGAAGATCGAGCCAGAGGGCCTCTGTTCATGTTTGGGC
57	-1.55775411	-1	END_train	TCAAGAAAAAATAATAATAATTTTTTTTTCGATTCCTGCTACACATTTTGGCAGAATACT
58	1.313347482	1	STR_Ctrl	CATGGTTTATAATCCTTTTTATACATTGTCGACACTGTATTTTCACAGATCACTCTGGAG
59	1.288113063	1	STR_Ctrl	AGAACTTCCTGATATATTTTTTTTCTTTTCGAAGGTCTTAAAATGTTTTTAAACATGACC
60	-1.351194069	-1	STR_train	GACTCTTAAAACAATAATATCAAACAACTCGACTTGTCATTTAGTTCTTTGGGAAGCAGT
61	1.442744064	1	STR_Ctrl	AATTAGACAACGACTATATGACTCTGTCTCGACTTTAAAGCAAGTACTTCTTGTATGCTC
62	-1.377760215	-1	STR_train	TCTTTGTTTCCTGTTTCCACTTCTTATTTCGATATTTATTGAGTGCTACTATATATATGC
63	1.322045866	1	STR_Ctrl	TATGAATCCCTAAATGTCACACATCAAGTCGAATTATATAAGATACCCTGAAATTTAAGG
64	1.370669886	1	END_Ctrl	ATGACTGTGGAAGGTTCTGATGTCTCTGTCGATGAAATGGAGAGAGGAGAAAGAAAAGAA
65	1.406251416	1	END_Ctrl	ATGACTGTGGAAGGTTCTGATGTCTCTGTCGACATCATTTTTACAAATAAGACCAGATGT
66	-1.345213388	-1	END_train	AATATTGCTACTGGAAAATCTGAATCTTTCGAAGAAAGCCCTTTGTAAGTTGTTTTCAAA
67	1.640080359	1	STR_Ctrl	AACTATGTGACTTTTAGCTATACGAGTTTCGACTGGGTTCTAAATAGTTAATGTCATAGT
68	1.292902317	1	STR_Ctrl	TAAAACTATTTTAAATGTTTTTAAAGTATCGATGTGTACTTTGACATCTGTGATGATGAT
69	-1.342712154	-1	STR_train	TTATGGCTTAGAAGTAGAAAGTCATAAATCGATTCCTAAAAATTAATGAGGTGAATAGTA
70	-1.29541483	-1	END_train	TTTCTATGAAGAATGTTCAAGATGCAATTCGAGCTACATACTATTATATATTTTCACAGT
71	1.283722998	1	STR_Ctrl	CTCTATAAATTTACCAGAATATAAATTCTCGACTAAAAGTTCAGTTCTTCATTCCCACTA
72	1.307360568	1	STR_Ctrl	ATCTTACAAAGAATAATTCTAAGAAAAGTCGAGCATTGGAGAAAATCTCCCTTTTCTTTT
73	1.285688803	1	STR_Ctrl	TGTTTTTATTTTCATGTTTTAATTTTGTTCGAACTCTTGACCTCAGGTAAACCACCCACC
74	1.286186246	1	STR_Ctrl	AGAACTGGTTATTGATCTATTCAGGGATTCGAAATAATAGATTATGAATAAATTATTCTG
75	1.294030342	1	END_Ctrl	CTTTTTGAAGATTATAATCTATTAGTGATCGAGGCTTTTTTGCTTTTTTTTTTTTGAGAT
76	1.276203048	1	END_Ctrl	CTATATGTAAGTTACAATATGTAAGGTATCGATAGTCACTGAGACTAATTTAATGTTATA
77	1.270236955	1	END_Ctrl	TGTAGGCAGATTACCTGAAGTTAGGAGTTCGATTAGGAATAACCTATCATTAGAGTTGTT

Table 25.d

	Probe Location					4 kb Sequence Location		
No.	Chr	Start1	End1	Start2	End2	Chr	Start1	End1
1	11	119249760	119249791	119299612	119299643	11	119249760	119253761
2	11	11968004	11968035	11984245	11984276	11	11964034	11968035
3	11	11968004	11968035	12048403	12048434	11	11964034	11968035
4	8	123527843	123527874	123555254	123555285	8	123523873	123527874
5	1	23070238	23070269	23096951	23096982	1	23066268	23070269
6	8	71216399	71216430	71261816	71261847	8	71216399	71220400
7	20	57527297	57527328	57579772	57579803	20	57527297	57531298
8	18	42072156	42072187	42094660	42094691	18	42068186	42072187
9	15	58053198	58053229	58157807	58157838	15	58053198	58057199
10	7	80544284	80544315	80679651	80679682	7	80540314	80544315
11	11	11968004	11968035	12019427	12019458	11	11964034	11968035
12	3	190498271	190498302	190560851	190560882	3	190494301	190498302
13	1	24920810	24920841	24976006	24976037	1	24920810	24924811
14	22	46102580	46102611	46241078	46241109	22	46098610	46102611
15	7	96214493	96214524	96301998	96302029	7	96210523	96214524
16	20	57527297	57527328	57551578	57551609	20	57527297	57531298
17	2	210291701	210291732	210362262	210362293	2	210287731	210291732
18	7	7114800	7114831	7260637	7260668	7	7110830	7114831
19	4	109024771	109024802	109090838	109090869	4	109024771	109028772
20	9	134738485	134738516	134811418	134811449	9	134738485	134742486
21	13	59818047	59818078	59854837	59854868	13	59818047	59822048
22	3	13512352	13512383	13590312	13590343	3	13512352	13516353
23	13	94133177	94133208	94304194	94304225	13	94129207	94133208
24	9	121180379	121180410	121268506	121268537	9	121176409	121180410
25	9	121232597	121232628	121268506	121268537	9	121228627	121232628
26	9	121243316	121243347	121268506	121268537	9	121239346	121243347
27	1	32214585	32214616	32241108	32241139	1	32214585	32218586
28	1	87318639	87318670	87349909	87349940	1	87314669	87318670

29	4	86581455	86581486	86621909	86621940	4	86577485	86581486
30	3	152234755	152234786	152281057	152281088	3	152230785	152234786
31	11	113028505	113028536	113163748	113163779	11	113024535	113028536
32	20	57527297	57527328	57570220	57570251	20	57527297	57531298
33	X	24447919	24447950	24480152	24480183	X	24443949	24447950
34	X	24447919	24447950	24490440	24490471	X	24443949	24447950
35	1	198595771	198595802	198666125	198666156	1	198595771	198599772
36	1	198666125	198666156	198724547	198724578	1	198662155	198666156
37	19	38410632	38410663	38495982	38496013	19	38410632	38414633
38	2	88146264	88146295	88161717	88161748	2	88142294	88146295
39	15	70715123	70715154	70784637	70784668	15	70715123	70719124
40	10	31275600	31275631	31524411	31524442	10	31271630	31275631
41	16	73153212	73153243	73184554	73184585	16	73149242	73153243
42	8	37965238	37965269	37987735	37987766	8	37961268	37965269
43	1	230724515	230724546	230757302	230757333	1	230724515	230728516
44	13	46860092	46860123	46907784	46907815	13	46860092	46864093
45	2	38993608	38993639	39065997	39066028	2	38989638	38993639
46	1	180431719	180431750	180541491	180541522	1	180431719	180435720
47	17	10502067	10502098	10534900	10534931	17	10502067	10506068
48	11	17689456	17689487	17729653	17729684	11	17685486	17689487
49	3	111034173	111034204	111209684	111209715	3	111030203	111034204
50	12	109146008	109146039	109236052	109236083	12	109146008	109150009
51	12	109236052	109236083	109268078	109268109	12	109236052	109240053
52	15	98652565	98652596	98737003	98737034	15	98652565	98656566
53	17	38348745	38348776	38360864	38360895	17	38344775	38348776
54	17	55035186	55035217	55117598	55117629	17	55035186	55039187
55	9	110405938	110405969	110509727	110509758	9	110401968	110405969
56	4	100636305	100636336	100744427	100744458	4	100636305	100640306
57	12	109146008	109146039	109185066	109185097	12	109146008	109150009
58	13	40524349	40524380	40688580	40688611	13	40524349	40528350
59	6	108604405	108604436	108629992	108630023	6	108600435	108604436
60	16	53844989	53845020	54052288	54052319	16	53844989	53848990
61	13	94054831	94054862	94133177	94133208	13	94054831	94058832
62	4	101055418	101055449	101247819	101247850	4	101055418	101059419
63	18	48917335	48917366	48974547	48974578	18	48917335	48921336
64	9	90816328	90816359	90832284	90832315	9	90816328	90820329
65	9	90816328	90816359	90872966	90872997	9	90816328	90820329
66	1	218325556	218325587	218386401	218386432	1	218321586	218325587
67	3	30566144	30566175	30694718	30694749	3	30566144	30570145
68	4	153659613	153659644	153700318	153700349	4	153659613	153663614
69	9	110499547	110499578	110527410	110527441	9	110495577	110499578
70	8	65658401	65658432	65782504	65782535	8	65658401	65662402
71	9	121188989	121189020	121328400	121328431	9	121185019	121189020
72	9	110652628	110652659	110747866	110747897	9	110648658	110652659
73	22	46134676	46134707	46231440	46231471	22	46130706	46134707
74	7	94903925	94903956	94966987	94967018	7	94903925	94907926
75	3	111638286	111638317	111672672	111672703	3	111634316	111638317
76	8	14642477	14642508	14785460	14785491	8	14638507	14642508
77	7	88199682	88199713	88237070	88237101	7	88199682	88203683

Table 25.e

	4 kb Sequence Location			
No.	**Start2**	**End2**	**PCR-Primer1_ID**	**PCR_Primer1**
1	119295642	119299643	OBD142_029	ACTGAAGGTTCCCAAGTTCCCGAGAG
2	11984245	11988246	OBD142_061	GCTCCACATTTCCCAATCTAACCTGC
3	12048403	12052404	OBD142_069	GTCCCTCTGCCCTCTCTTATTGGC

4	123555254	123559255	OBD142_089	AATCTCTGTCCCCAACTGTATCTGGC
5	23096951	23100952	OBD142_137	CCCAGTCTCAGGCTTTGTCACTC
6	71261816	71265817	OBD142_081	GGCAAGTTTCCTGACCTCTCTGACAT
7	57579772	57583773	OBD142_189	TTCTCCCTCGGACGCTCATCCTC
8	42090690	42094691	OBD142_213	CTGGAACTTGTTTAGGCACTGAAGCA
9	58157807	58161808	OBD142_017	GCTGTCATTTTCAGTGATAGGCACAC
10	80679651	80683652	OBD142_037	GCTGGTTTCCTGAGAAGGTAACTC
11	12015457	12019458	OBD142_065	TTCTTGCCCTGTCCCTCTGCCCT
12	190560851	190564852	OBD142_133	AGATGCTGGCAGTCTCCCTCTTGAG
13	24972036	24976037	OBD142_253	CTGAAATCCCATAGTGAGATGCCTTC
14	46241078	46245079	OBD142_353	GCCCTTCTCCAAAAACACCTCAC
15	96298028	96302029	OBD142_477	CAGGCGGATCATTTCAGGTC
16	57551578	57555579	OBD142_181	TCATCCTCCTCCACACCCGCCTA
17	210358292	210362293	OBD142_397	CAGGCGGATCATTTCAGGTC
18	7256667	7260668	OBD142_025	CACCTCAAAAGACAACCCCAGACCCA
19	109090838	109094839	OBD142_041	CTGCCCCTTTCTTTATTCCTACTTCC
20	134811418	134815419	OBD142_045	ACCCCACCAAGAGCACCTTCTGC
21	59854837	59858838	OBD142_057	CAGTCTCTGTGGCAACTCTCGTG
22	13586342	13590343	OBD142_085	CCCCATCGCTGCTGGAAACCATT
23	94300224	94304225	OBD142_113	GAGTATTTACGATGGTCAGGTGCTGC
24	121268506	121272507	OBD142_117	GACCTGTGGTTCTGACTGTCCAG
25	121268506	121272507	OBD142_121	GGGCTGGTTAGTCAGTTATCCCTTTT
26	121268506	121272507	OBD142_125	CCACTTCCCTGCCTTTTCTGGCT
27	32237138	32241139	OBD142_141	GCGGAGCCTCTTTGAACAGAAGC
28	87345939	87349940	OBD142_145	GCAACCTGGTCTCCTACCTGCTTCTA
29	86617939	86621940	OBD142_153	TAGCAGACAATCAGAGGGTTTTGC
30	152281057	152285058	OBD142_157	GCTGGTAGTTGGCTTTTGGGAAGAAC
31	113163748	113167749	OBD142_165	CAGGAGGTGTGGATTTGACTCATACT
32	57570220	57574221	OBD142_185	TCATCCTCCTCCACACCCGCCTA
33	24480152	24484153	OBD142_197	GGGAGTAGGGAGCAGAACCAGGA
34	24490440	24494441	OBD142_201	CAACAAGGAGGGAGTGACCACAAGAT
35	198662155	198666156	OBD142_233	GCAAAGGGCAGGTCATCATCATTCAA
36	198720577	198724578	OBD142_241	AAGACATAGGCACTTTGAGAGGC
37	38495982	38499983	OBD142_257	GGACAGATTTGGAGACCCATAGAAAG
38	88161717	88165718	OBD142_297	GTAACACAGGTAGGAAGGAGTGGAGC
39	70780667	70784668	OBD142_309	GTGAGGAAGGTGTAGAAGAACAGACT
40	31520441	31524442	OBD142_321	CTTGTCGTAGAGGATGCTCAGGC
41	73180584	73184585	OBD142_325	CCTGGATGTTCATTCCCACCTGG
42	37987735	37991736	OBD142_329	TACTCCTCGTTCCCTTTTCTCTC
43	230753332	230757333	OBD142_337	GCAGATTCCACAGGGCTTAC
44	46903814	46907815	OBD142_349	TTTGTCATGTTGTCCAGGCTG
45	39062027	39066028	OBD142_357	GCTGGTCTCAAAGTCCTGGC
46	180541491	180545492	OBD142_373	GCTGGTCTCAAACTCCTGGC
47	10530930	10534931	OBD142_393	AGTATTTGAGGCTGGGCATG
48	17729653	17733654	OBD142_401	TTCTTTGTCTCCCCTCTCTACTCCT
49	111209684	111213685	OBD142_405	ACAGGAAATCCAGTATCTTGGGGAAA
50	109236052	109240053	OBD142_413	ACGGTTAGAAGATTTGCCAGAGGAT
51	109268078	109272079	OBD142_417	GAATATCAAAGATGCCAGGGAGCTG
52	98733033	98737034	OBD142_445	GACGTTTCACCATGTTGCCC
53	38360864	38364865	OBD142_509	GAATGAAACTCTGAGGCCGG
54	55117598	55121599	OBD142_517	TGTGTTATCAGGATAAGATTCCAGGT
55	110505757	110509758	OBD142_521	AGGATCTTGCTGTTTGTTTCACG
56	100744427	100748428	OBD142_005	CCCTAAACCCAGTAATCCTGTGCTTC
57	109185066	109189067	OBD142_009	GCAGAAACAGGACCTCAAACGGTTAG
58	40688580	40692581	OBD142_093	AGTTTCTCTCTGTTCCCAGTTTGCTG
59	108629992	108633993	OBD142_097	GTTCCTTTGCCCTCTTCAGTGGC

60	54048318	54052319	OBD142_101	TAGCATCCTGCCTTGACTGAGGGTGA
61	94129207	94133208	OBD142_109	GAGTATTTACGATGGTCAGGTGCTGC
62	101247819	101251820	OBD142_225	GGCTCACACAGGCTTCTGGATAGGAA
63	48970577	48974578	OBD142_261	ATTACTCAGCCCCTCGGAGCCAT
64	90832284	90836285	OBD142_265	GACTCAGGGCTGGCAGTGAACGA
65	90872966	90876967	OBD142_273	GACTCAGGGCTGGCAGTGAACGA
66	218386401	218390402	OBD142_277	TTATGGAGAACATCCTCAGTGTCCTG
67	30694718	30698719	OBD142_285	CAAGAACTGACCCCAAGTCCCTG
68	153696348	153700349	OBD142_313	GGCAGCCACTTCATCCATCCAGAATC
69	110527410	110531411	OBD142_361	TGTGTTCCCACAAATTGGAAATGCC
70	65778534	65782535	OBD142_389	CCATGCTGGCATTCATCTATTTGGT
71	121324430	121328431	OBD142_433	TAGAAGTCACTCACTCCCATCCTCT
72	110747866	110751867	OBD142_449	ACAGTCAGTGATTGGCACAGAGTAA
73	46231440	46235441	OBD142_457	ACACTTTAGACAGAGTGACAGGGTC
74	94963017	94967018	OBD142_461	AGGAATGGTTACTGCTCCTCTTTGT
75	111672672	111676673	OBD142_497	AGTCCCCACAACTGCCAATG
76	14781490	14785491	OBD142_501	AGTCTAAGAGATGGTCACACCCATT
77	88233100	88237101	OBD142_513	GTTTGGGAGGCCAATGTAGG

Table 25.f

No.	PCR-Primer2_ID	PCR_Primer2	GLMNET	Marker
1	OBD142_031	TTAGTCTGTATGGTAGTGTGTGCCTG	0.027324192	OBD142_029.031_1x
2	OBD142_063	GTCAGAGTTGCCGATAGGTCTTGCTA	0.066643802	OBD142_061.063_1.8x
3	OBD142_071	GGTGGGTCTGACTGCCTTTCTCA	-0.093076823	OBD142_069.071_1.2x
4	OBD142_091	ACATCTATCTTGCCCCTCACTCAGGT	0.004873633	OBD142_089.091_1x
5	OBD142_139	GCCTGAGGGAGCAAGTTCAACCC	-0.019817526	OBD142_137.139_1.2x
6	OBD142_083	GAAGGAGGGAGGTAGGAGAGTCATTA	0.030332059	OBD142_081.083_1.4x
7	OBD142_191	GAGGAGGAGAAACTCAGAAGCCC	0.03066036	OBD142_189.191_1x
8	OBD142_215	GCACAAGACCTCACATTCTGATGGGC	0.006242977	OBD142_213.215_1.4x
9	OBD142_019	CAAAGAGAAAGGGCTGAGGATGAAGC	0.017005669	OBD142_017.019_1.2x
10	OBD142_039	CCCCTCATCTCAGTATGTTTATGTCC	0.014942824	OBD142_037.039_1x
11	OBD142_067	GCCTGGCAAGGAGTAAGCATTCG	0.067763605	OBD142_065.067_1x
12	OBD142_135	ATGCTCCCTCCCTTATCTTTTGGTA	0.006222197	OBD142_133.135_1x
13	OBD142_255	CCCCAAACTCCCAGACACATCAGAGA	0.066746082	OBD142_253.255_1.2x
14	OBD142_355	TGCTGTCAAAATGGTGCCTGAAAAT	-0.026372512	OBD142_353.355_1x
15	OBD142_479	CTTACTGCAGCCTCACACTC	0.015126312	OBD142_477.479_1x
16	OBD142_183	GACAGTAAACACACCCACTCCCC	0.04064456	OBD142_181.183_1.4x
17	OBD142_399	CTTACTGCAGCCTCACACTC	0.006805912	OBD142_397.399_1x
18	OBD142_027	CCCTCACTTTCCTTCTACTCTTCAAG	0.000572834	OBD142_025.027_1/2X
19	OBD142_043	TGTTCCCTTTGTTCAACCCAGGCTAT	0.003754206	OBD142_041.043_1/2X
20	OBD142_047	ATGGGTGAGGATGCTGGCAATGC	0.002011981	OBD142_045.047_1/2X
21	OBD142_059	CCTGAATCTGCTGTGGCTTGGGC	-0.003337259	OBD142_057.059_1/4X
22	OBD142_087	CCAGTAGGAGGGAAGACACGGTC	0.007164008	OBD142_085.087_1/4X
23	OBD142_115	GATTTAGGCACTACGGAGAAAAGGGC	-0.005249258	OBD142_113.115_1/2X
24	OBD142_119	TATCGTCCAGGAGGCAAGGGTCC	-0.001120031	OBD142_117.119_1/2X
25	OBD142_123	AGAGGAGAGCAGGCACAGGTATCGT	0.003244236	OBD142_121.123_1/8X
26	OBD142_127	TATCGTCCAGGAGGCAAGGGTCC	-0.007783392	OBD142_125.127_1/2X
27	OBD142_143	GCCTCTTCCCACCAGCCTGACTT	-0.005778408	OBD142_141.143_1/4X
28	OBD142_147	GATGAGGTAACCAAAGTTCAGGGAGA	-0.005269663	OBD142_145.147_1/2X
29	OBD142_155	CTCTCTCCTCATCCTCCCTCCTAATA	0.003978216	OBD142_153.155_1/2X
30	OBD142_159	GGGAGCCAGAAAGATAGCAATGCCTA	-0.003656603	OBD142_157.159_1/4X
31	OBD142_167	TCACTCCCTCTCTTCTCCCCTTCACT	-0.005244916	OBD142_165.167_1X
32	OBD142_187	CTCTGTGGCATCCCTAAATCCCG	-0.005243145	OBD142_185.187_1/4X
33	OBD142_199	ACTCCTCAAGCCCAGACAATGGC	-0.000856647	OBD142_197.199_1/4X
34	OBD142_203	GTCAGTTCAGGTCTGGTTTTGCCACA	-0.005241372	OBD142_201.203_1/4X

35	OBD142_235	CTCTCCTTTATCCCCTACCCTGCTCA	-0.003634106	OBD142_233.235_1/2X
36	OBD142_243	GGGACCCTTTCTTCTTGCTCTGAT	-0.002467172	OBD142_241.243_1X
37	OBD142_259	CATTCTTGACCCTCTCACTCTGTGCC	-0.009961655	OBD142_257.259_1/2X
38	OBD142_299	CACCATAAAATAGGGCAAGGTCAGCA	0.004963311	OBD142_297.299_1/2X
39	OBD142_311	GGATAGAAGGCACAGTGACCCTCCT	0.002101178	OBD142_309.311_1/2X
40	OBD142_323	GGCACGCAATCTCAATCTCGGCTC	-0.005202079	OBD142_321.323_1X
41	OBD142_327	AGAGGGAAAGGCAGGTCGTGAGC	-0.003264119	OBD142_325.327_1/4
42	OBD142_331	TGTGTGCTAGGCTGATATGGTTTG	0.001018411	OBD142_329.331_1X
43	OBD142_339	AGTCTAAAGCCCATGTGAGCC	-0.000807541	OBD142_337.339_1X
44	OBD142_351	CTCAGCACCAGAACTAGGGC	-0.005203446	OBD142_349.351_1X
45	OBD142_359	GCTCTAGGTGCTGATGATTCAAC	-0.003795912	OBD142_357.359_1/4X
46	OBD142_375	GGTCCCCACATTACATTTTGGC	-0.006643376	OBD142_373.375_1X
47	OBD142_395	AGGGTGTTCTAAGAAGGCAGC	-0.006900338	OBD142_393.395_1/2X
48	OBD142_403	TTTTTATTAACTGCACGGCACACCT	-0.001296151	OBD142_401.403_1X
49	OBD142_407	ACTAAGAATGGATGGGGCCAATTAT	-0.00075487	OBD142_405.407_1X
50	OBD142_415	GAATATCAAAGATGCCAGGGAGCTG	-0.005201838	OBD142_413.415_1/2X
51	OBD142_419	CTGCACATTTCCTAGTAGGCTCTCT	-0.000282666	OBD142_417.419_1X
52	OBD142_447	GTCACTCCCCATTCCATCCG	0.001436473	OBD142_445.447_1/2X
53	OBD142_511	CCCATTCGTCTCTCTGAGCTG	-0.001530558	OBD142_509.511_1/8X
54	OBD142_519	TTGGTGAAAGGAAGGGAGTAGAAGT	0.005722578	OBD142_517.519_1X, 1/2X
55	OBD142_523	TGCCATCACACCCATGCATG	-0.005188075	OBD142_521.523_1/4X
56	OBD142_007	ATTGCTGTGGAGGGAATGGTGTGC	-0.003614434	OBD142_005.007_1X
57	OBD142_011	TTTTGTAAAGGGCACCCGAAGGG	0.00909588	OBD142_009.011_1/4X
58	OBD142_095	AGCATCACCTTCGTATCTTCCCCAAG	-0.002626343	OBD142_093.095_1X
59	OBD142_099	GCCTGCTCTTCCCTGTTTCTGCC	0.003599622	OBD142_097.099_1/8X
60	OBD142_103	AAACAAAGCCTCACAAACTCCACAGC	-0.005544516	OBD142_101.103_1X
61	OBD142_111	ATCCAAACACAGGACGAGAATAAAGC	-0.010787892	OBD142_109.111_1/2X
62	OBD142_227	TTTTGTCCCTCTTCAGGCAGTGC	-0.004657708	OBD142_225.227_1/2X
63	OBD142_263	GCAGAGGAGGTGGGACTTTCAGC	-0.003808119	OBD142_261.263_1/X
64	OBD142_267	CTGCCTCACCCTGGCTTCTTTCA	0.005232196	OBD142_265.267_1/4X
65	OBD142_275	CCGCCACTCAGCCATTGTTTCCA	-0.003175937	OBD142_273.275_1/4X
66	OBD142_279	GCTACACAAAGAGACTTCCAGTGATT	0.00931825	OBD142_277.279_1/2X
67	OBD142_287	GGTGGAGGCGAGGGATACTGCTA	-0.004573651	OBD142_285.287_1/4X
68	OBD142_315	GCAAATGCTTAGGACCCAAACCCTTT	0.004668104	OBD142_313.315_1X
69	OBD142_363	CACTTGCACCCCTAAAGCTATTGAAA	-0.006335271	OBD142_361.363_1/2X
70	OBD142_391	AATTTTGGTTGGCAGCTGGTAGAAG	0.008864459	OBD142_389.391_1X
71	OBD142_435	CTTGAAATGCGACCAGTGGGAATTA	-0.002735702	OBD142_433.435_1X
72	OBD142_451	AGGAAATAGCCCAAATGCAACTGAA	-0.004744695	OBD142_449.451_1X
73	OBD142_459	CTCAACTTCAAAATCGGTTGGGGAA	-0.006822261	OBD142_457.459_1X
74	OBD142_463	TTTCTGTCTGCAAATCCTCCACCTA	-0.002268338	OBD142_461.463_1/4X
75	OBD142_499	CGAGAAGGGTGGCTCATGAG	-0.00572004	OBD142_497.499_1/2X
76	OBD142_503	ATGGAAACCCAAGTTTGCAAGGAA	-0.004756155	OBD142_501.503_1X
77	OBD142_515	GCCACAAGAGATCTGGGAC	-0.005511591	OBD142_513.515_1/2X

Table 25.g

No.	Location	Training	Odds Ratio	Glmnet
1	CBL	Any	7.2	0.027324192
2	DKK3	Any	8.2	0.066643802
3	DKK3	Any	8	-0.093076823
4	FBXO32	Any	2.9	0.004873633
5	KDM1A	Any	8	-0.019817526
6	EYA1	Endurance	6	0.030332059
7	PCK1	Endurance	4.5	0.03066036
8	PIK3C3	Endurance	2.25	0.006242977
9	ALDH1A2	Strength	4	0.017005669
10	CD36	Strength	12	0.014942824

11	DKK3	Strength	5	0.067763605
12	IL1RAP	Strength	4	0.006222197
13	RUNX3	Strength	12	0.066746082
14	ADRB3	Strength	9	-0.026372512
15	PLCXD2	Strength	9	0.015126312
16	PCK1	Strength	2	0.04064456
17	SLC25A13	Strength	2	0.006805912
18	C1GALT1	Any	n/a	0.000572834
19	COL25A1	Any	n/a	0.003754206
20	COL5A1	Any	n/a	0.002011981
21	DIAPH3	Any	n/a	-0.003337259
22	FBLN2	Any	n/a	0.007164008
23	GPC6	Any	n/a	-0.005249258
24	GSN	Any	n/a	-0.001120031
25	GSN	Any	n/a	0.003244236
26	GSN	Strength	n/a	-0.007783392
27	LCK	Endurance	n/a	-0.005778408
28	LMO4	Any	n/a	-0.005269663
29	MAPK10	Any	n/a	0.003978216
30	MBNL1	Any	n/a	-0.003656603
31	NCAM1	Endurance	n/a	-0.005244916
32	PCK1	Any	n/a	-0.005243145
33	PDK3	Any	n/a	-0.000856647
34	PDK3	Any	n/a	-0.005241372
35	PTPRC	Any	n/a	-0.003634106
36	PTPRC	Any	n/a	-0.002467172
37	RYR1	Any	n/a	-0.009961655
38	THNSL2	Endurance	n/a	0.004963311
39	UACA	Any	n/a	0.002101178
40	ZEB1	Any	n/a	-0.005202079
41	ZFHX3	Any	n/a	-0.003264119
42	ADRB3	Any	n/a	0.001018411
43	AGT	Endurance	n/a	-0.000807541
44	HTR2A	Any	n/a	-0.005203446
45	SOS1	Endurance	n/a	-0.003795912
46	ACBD6	Any	n/a	-0.006643376
47	MYH1	Any	n/a	-0.006900338
48	MYOD1	Endurance	n/a	-0.001296151
49	NECTIN3	Endurance	n/a	-0.00075487
50	ACACB	Endurance	n/a	-0.005201838
51	ACACB	Strength	n/a	-0.000282666
52	IGF1R	Any	n/a	0.001436473
53	SOCS7	Any	n/a	-0.001530558
54	STXBP4	Any	n/a	0.005722578
55	SVEP1	Any	n/a	-0.005188075
56	EMCN	Endurance	n/a	-0.003614434
57	ACACB	Endurance	n/a	0.00909588
58	FOXO1	Strength	n/a	-0.002626343
59	FOXO3	Endurance	n/a	0.003599622
60	FTO	Any	n/a	-0.005544516
61	GPC6	Endurance	n/a	-0.010787892
62	PPP3CA	Any	n/a	-0.004657708
63	SMAD7	Any	n/a	-0.003808119
64	SYK	Endurance	n/a	0.005232196
65	SYK	Any	n/a	-0.003175937
66	TGFB2	Endurance	n/a	0.00931825

67	TGFBR2	Strength	n/a	-0.004573651
68	TLR2	Endurance	n/a	0.004668104
69	SVEP1	Any	n/a	-0.006335271
70	MTFR1	Any	n/a	0.008864459
71	GSN	Any	n/a	-0.002735702
72	MUSK	Strength	n/a	-0.004744695
73	PPARA	Endurance	n/a	-0.006822261
74	PPP1R9A	Any	n/a	-0.002268338
75	PLCXD2	Any	n/a	-0.00572004
76	SGCZ	Endurance	n/a	-0.004756155
77	SRI	Strength	n/a	-0.005511591

Table 25.h

Gene	Gene name	Function
CBL	Cbl Proto-Oncogene	Pretein coding, associated with noonan syndrome-like disorder with or without juvenile myelomonocytic leukemia and juvenile myelomonocytic leukemia, related to immune response Fc epsilon RI pathway and EGF/EGFR signaling pathway
DKK3	Dickkopf WNT Signaling Pathway Inhibitor 3	Pretein coding, associated with oral submucous fibrosis disease, related to regulation of Wnt/B-catenin signaling pathways
FBXO32	F-Box Protein 32	Protein coding, accociated with muscle hypertrophy and muscle tissue disease, related to class I MHC mediated antigen processing and presentation and FoxO signaling pathway
KDM1A	Lysine Demethylase 1A	Proteing coding; Associated with cleft palate, psychomotor retardation, and distinctive facial features and Kbg syndrome; Related to signaling by Rho GTPases and coregulation of androgen receptor activity
EYA1	EYA Transcriptional Coactivator And Phosphatase 1	Protein coding, associated with otofaciocervical syndrome 1 and branchiootorenal syndrome 1, related to transcriptional misregulation in cancer and DNA double-strand break repair
PCK1	Phosphoenolpyruvate Carboxykinase 1	Protein coding; Associated with phosphoenolpyruvate carboxykinase deficiency, cytosolic and pepck 1 deficiency; Related to adipogenesis and AMP-activated protein kinase (AMPK) signaling
PIK3C3	Phosphatidylinositol 3-Kinase Catalytic Subunit Type 3	Protein coding, associated with amyotrophic lateral sclerosis 1 disease, related to mTOR and MAPK Pathway, involved in regulation of degradative endocytic trafficking and required for the abcission step in cytokinesis, involved in trasport from early to late endosomes
ALDH1A2	Aldehyde Dehydrogenase 1 Family Member A2	Protein coding, associated with diaphragm disease and neural tube defects, related to drug metabolism cytochrome P450 and vitamin A and carotenoid metabolism
CD36	CD36 Molecule	Protein coding, associated with platelet glycoprotein Iv deficiency and coronary heart disease 7, related to activated TLR4 signaling and hematopoietic stem cell differentiation pathways and lineage-specific markers
IL1RAP	Interleukin 1 Receptor Accessory Protein	Protein coding, associated with chromosome Xp21 deletion syndrome and stromal keratitis, relared to bacterial infections in CF airways and IL-1 family signaling pathways
RUNX3	Runt Related Transcription Factor 3	Protein coding, associated with testicular yolk sac tumor and cleidocranial dysplasia, related to sudden infant death syndrome (SIDS) susceptibility pathways and Wnt / Hedgehog / Notch
PPARA	Peroxisome Proliferator Activated Receptor Alpha	Protein coding, associated with fatty liver disease and alcoholic cardiomyopathy, related to gene expression and regulation of cholesterol biosynthesis by SREBP

SLC25A13	Solute Carrier Family 25 Member 13	Protein coding, related to metabolism and protein metabolism pathways, associated with Citrullinemia, Type Ii, Neonatal-Onset and Citrullinemia, Type Ii, Adult-Onset
MYL1	Myosin Light Chain 1	Protein coding, related to ERK signaling and cytoskeleton remodeling regulation of actin cytoskeleton by Rho GTPases

Table 26

GeneSet	Number Of Protein In Gene Set	Protein From Network	FDR	Nodes
Th17 cell differentiation(K)	107	14	1.52E-10	RORA,FOXP3,GATA3,SMAD3,NFATC3,NFATC2,NFKB1,NFKBIE,LAT,IKBKB,PPP3CA,TGFBR2,CD247,IL17A
T cell receptor signaling pathway(K)	105	12	1.99E-08	GRAP2,PIK3R1,NFATC3,NFATC2,NFKB1,NFKBIE,LAT,IKBKB,PPP3CA,LCP2,CBL,CD247
Pathways in cancer(K)	397	19	7.44E-08	RB1,ETS1,IGF1R,RASSF1,CDH1,COL4A1,PIK3R1,TGFB2,SMAD3,NFKB1,BCL2,ITGB1,IKBKB,TGFBR2,LAMA2,LAMA4,CBL,TCF7L2,APC
T cell activation(P)	81	10	2.03E-07	GRAP2,PIK3R1,NFATC3,NFATC2,NFKB1,LAT,IKBKB,PPP3CA,LCP2,CD247
Th1 and Th2 cell differentiation(K)	92	10	4.55E-07	GATA3,NFATC3,NFATC2,NFKB1,NFKBIE,LAT,IKBKB,PPP3CA,DLL1,CD247
TCR signaling in naïve CD4+ T cells(N)	67	9	4.55E-07	GRAP2,PRKCE,STIM1,LAT,IKBKB,LCP2,CBL,PTPN11,CD247
Chronic myeloid leukemia(K)	73	9	8.09E-07	RB1,PIK3R1,TGFB2,SMAD3,NFKB1,IKBKB,TGFBR2,CBL,PTPN11
TCR signaling in naïve CD8+ T cells(N)	54	8	1.21E-06	GRAP2,PRKCE,STIM1,LAT,IKBKB,LCP2,CBL,CD247
Small cell lung cancer(K)	86	9	2.54E-06	RB1,COL4A1,PIK3R1,NFKB1,BCL2,ITGB1,IKBKB,LAMA2,LAMA4
Fc-epsilon receptor I signaling in mast cells(N)	62	8	2.74E-06	PIK3R1,NFATC2,NFKB1,LAT,IKBKB,LCP2,CBL,PTPN11
Inflammatory bowel disease (IBD)(K)	65	8	3.58E-06	RORA,IL18RAP,FOXP3,GATA3,TGFB2,SMAD3,NFKB1,IL17A
Adherens junction(K)	72	8	7.15E-06	IGF1R,CDH1,LMO7,SMAD3,WASL,TGFBR2,TCF7L2,NECTIN3
Hepatitis B(K)	146	10	1.47E-05	RB1,PIK3R1,TGFB2,SMAD3,EGR3,NFATC3,NFATC2,NFKB1,BCL2,IKBKB
TGF-beta signaling pathway(K)	84	8	1.94E-05	ACVR1,TGFB2,SMAD3,SMAD9,BMPR1B,BMPR1A,DCN,TGFBR2

Neurotrophin signaling pathway(K)	121	9	2.59E-05	PIK3R1,FOXO3,NFKB1,BCL2,NFKBIE,IKBKB,IRAK3,NTRK2,PTPN11
Colorectal cancer(K)	62	7	2.85E-05	PIK3R1,TGFB2,SMAD3,BCL2,TGFBR2,TCF7L2,APC
Signaling by Interleukins(R)	460	16	2.85E-05	RORA,IL18RAP,PIK3R1,GATA3,FOXO3,NFKB1,BCL2,LAT,ITGB1,IKBKB,IRAK3,ZEB1,CBL,NCAM1,PTPN11,IL17A
HTLV-I infection(K)	258	12	3.78E-05	RB1,ETS1,PIK3R1,TGFB2,SMAD3,NFATC3,NFATC2,NFKB1,IKBKB,PPP3CA,TGFBR2,APC
Pancreatic cancer(K)	66	7	3.78E-05	RB1,PIK3R1,TGFB2,SMAD3,NFKB1,IKBKB,TGFBR2
Osteoclast differentiation(K)	132	9	3.88E-05	PIK3R1,TGFB2,NFATC2,NFKB1,IKBKB,PPP3CA,FCGR3A,TGFBR2,LCP2
Natural killer cell mediated cytotoxicity(K)	135	9	4.44E-05	PIK3R1,NFATC2,KLRD1,LAT,PPP3CA,FCGR3A,LCP2,PTPN11,CD247
AGE-RAGE signaling pathway in diabetic complications(K)	101	8	4.44E-05	PRKCE,COL4A1,PIK3R1,TGFB2,SMAD3,NFKB1,BCL2,TGFBR2
AP-1 transcription factor network(N)	70	7	4.44E-05	ETS1,BCL2L11,NFATC3,NFATC2,ELF1,TCF7L2,AGT
CDC42 signaling events(N)	70	7	4.44E-05	CDH1,PRKCE,PIK3R1,WASL,PAX6,CBL,APC
ras-independent pathway in nk cell-mediated cytotoxicity(B)	25	5	4.95E-05	PIK3R1,KLRD1,LAT,FCGR3A,PTPN11
B cell receptor signaling pathway(K)	73	7	5.26E-05	PIK3R1,NFATC3,NFATC2,NFKB1,NFKBIE,IKBKB,PPP3CA
Signaling pathways regulating pluripotency of stem cells(K)	142	9	5.26E-05	IGF1R,ACVR1,PIK3R1,SMAD3,SMAD9,BMPR1B,BMPR1A,PAX6,APC
Angiopoietin receptor Tie2-mediated signaling(N)	50	6	7.08E-05	ETS1,PIK3R1,NFKB1,ITGB1,ELF1,PTPN11
IL2 signaling events mediated by STAT5(N)	28	5	7.08E-05	FOXP3,PIK3R1,BCL2,ELF1,PTPN11
TGF-beta signaling pathway(P)	80	7	7.95E-05	ACVR1,TGFB2,SMAD3,SMAD9,BMPR1B,BMPR1A,TGFBR2
Signaling events mediated by Hepatocyte Growth Factor Receptor (c-Met)(N)	80	7	7.95E-05	ETS1,CDH1,PIK3R1,WASL,CBL,PTPN11,APC
Signaling events mediated by Stem cell factor receptor (c-Kit)(N)	52	6	8.17E-05	GRAP2,PIK3R1,FOXO3,BCL2,CBL,PTPN11

Hippo signaling pathway(K)	154	9	8.17E-05	RASSF1,CDH1,TGFB2,SMAD3,BMPR1B,BMPR1A,TGFBR2,TCF7L2,APC
Toxoplasmosis(K)	118	8	9.76E-05	PIK3R1,TGFB2,NFKB1,BCL2,ITGB1,IKBKB,LAMA2,LAMA4
EPO signaling pathway(N)	33	5	1.31E-04	PIK3R1,NFKB1,BCL2,CBL,PTPN11
Prostate cancer(K)	89	7	1.41E-04	RB1,IGF1R,PIK3R1,NFKB1,BCL2,IKBKB,TCF7L2
IL2 signaling events mediated by PI3K(N)	35	5	1.63E-04	PIK3R1,FOXO3,NFKB1,BCL2,PTPN11
FoxO signaling pathway(K)	134	8	2.14E-04	IGF1R,PIK3R1,FOXO3,BCL2L11,TGFB2,SMAD3,IKBKB,TGFBR2
Chagas disease (American trypanosomiasis)(K)	104	7	3.32E-04	PIK3R1,TGFB2,SMAD3,NFKB1,IKBKB,TGFBR2,CD247
Adipocytokine signaling pathway(K)	70	6	3.45E-04	ACACB,PPARGC1A,NFKB1,NFKBIE,IKBKB,PTPN11
sumoylation as a mechanism to modulate ctbp-dependent gene responses(B)	7	3	3.94E-04	UBE3A,CDH1,ZEB1
Insulin resistance(K)	109	7	4.15E-04	PRKCE,PIK3R1,ACACB,PPARGC1A,NFKB1,IKBKB,PTPN11
Calcineurin-regulated NFAT-dependent transcription in lymphocytes(N)	46	5	5.17E-04	FOXP3,GATA3,EGR3,NFATC3,NFATC2
MAPK signaling pathway(K)	255	10	5.28E-04	CACNB1,DDIT3,CACNA1E,TGFB2,NFATC3,NFKB1,IKBKB,PPP3CA,TGFBR2,NTRK2
FGF signaling pathway(N)	47	5	5.28E-04	CDH1,PIK3R1,CBL,NCAM1,PTPN11
Integrins in angiogenesis(N)	47	5	5.28E-04	IGF1R,PIK3R1,TGFBR2,CBL,PTPN11
TCR signaling(R)	123	7	8.14E-04	GRAP2,PIK3R1,NFKB1,LAT,IKBKB,LCP2,CD247
Endometrial cancer(K)	52	5	8.48E-04	CDH1,PIK3R1,FOXO3,TCF7L2,APC
PI3K-Akt signaling pathway(K)	341	11	1.10E-03	IGF1R,COL4A1,PIK3R1,FOXO3,BCL2L11,NFKB1,BCL2,ITGB1,IKBKB,LAMA2,LAMA4
Fc epsilon receptor (FCERI) signaling(R)	405	12	1.16E-03	GRAP2,PIK3R1,FOXO3,NFATC3,NFATC2,NFKB1,LAT,IKBKB,PPP3CA,LCP2,NCAM1,PTPN11
Transcriptional misregulation in cancer(K)	180	8	1.17E-03	IGF1R,DDIT3,NFKB1,NR4A3,TGFBR2,ZEB1,PAX7,EYA1
Fc gamma R-mediated phagocytosis(K)	93	6	1.17E-03	PRKCE,PIK3R1,LAT,WASL,FCGR3A,GSN

ATF-2 transcription factor network(N)	58	5	1.17E-03	RB1,DDIT3,PPARGC1A,TGFB2,BCL2
Validated targets of C-MYC transcriptional repression(N)	60	5	1.37E-03	DDIT3,FOXO3,SMAD3,BCL2,ITGB1
Amoebiasis(K)	98	6	1.55E-03	COL4A1,PIK3R1,TGFB2,NFKB1,LAMA2,LAMA4
IL1-mediated signaling events(N)	34	4	1.81E-03	PIK3R1,NFKB1,IKBKB,IRAK3
BCR signaling pathway(N)	65	5	1.95E-03	ETS1,PIK3R1,NFKB1,IKBKB,PPP3CA
JNK signaling in the CD4+ TCR pathway(N)	14	3	1.95E-03	GRAP2,LAT,LCP2
Atypical NF-kappaB pathway(N)	14	3	1.95E-03	PIK3R1,NFKB1,IKBKB
Extracellular matrix organization(R)	255	9	2.09E-03	CDH1,COL4A1,TGFB2,ITGB1,DCN,LAMA2,LAMA4,NRXN1,NCAM1
IL23-mediated signaling events(N)	37	4	2.25E-03	IL18RAP,PIK3R1,NFKB1,IL17A
Proteoglycans in cancer(K)	205	8	2.43E-03	IGF1R,PIK3R1,TGFB2,ITGB1,DCN,CBL,GPC1,PTPN11
Wnt signaling pathway(P)	268	9	3.00E-03	CDH1,PRKCE,NFATC3,NFATC2,BMPR1B,BMPR1A,PPP3CA,TCF7L2,APC
FOXM1 transcription factor network(N)	40	4	3.01E-03	RB1,NFATC3,LAMA4,CENPF
Bacterial invasion of epithelial cells(K)	78	5	3.64E-03	CDH1,PIK3R1,ITGB1,WASL,CBL
il-2 receptor beta chain in t cell activation(B)	44	4	3.82E-03	RB1,PIK3R1,CBL,PTPN11
Axon guidance mediated by netrin(P)	4	2	4.06E-03	NFATC3,NFATC2
Insulin Pathway(N)	45	4	4.16E-03	PIK3R1,FOXO3,CBL,PTPN11
AMPK signaling pathway(K)	124	6	4.26E-03	IGF1R,PIK3R1,FOXO3,ACACB,ACACA,PPARGC1A
EGFR tyrosine kinase inhibitor resistance(K)	81	5	4.26E-03	IGF1R,PIK3R1,FOXO3,BCL2L11,BCL2
Ras signaling pathway(K)	229	8	4.26E-03	ETS1,IGF1R,RASSF1,PIK3R1,NFKB1,LAT,IKBKB,PTPN11
Hypertrophic cardiomyopathy (HCM)(K)	83	5	4.26E-03	CACNB1,TGFB2,ITGB1,LAMA2,TTN
the co-stimulatory signal during t-cell activation(B)	20	3	4.26E-03	PIK3R1,PTPN11,CD247
Axon guidance(K)	177	7	4.27E-03	PIK3R1,NFATC3,NFATC2,BMPR1B,ITGB1,PPP3CA,PTPN11
Type II diabetes mellitus(K)	48	4	4.62E-03	PRKCE,PIK3R1,CACNA1E,IKBKB

t cell receptor signaling pathway(B)	48	4	4.62E-03	PIK3R1,LAT,PTPN11,CD247
GPVI-mediated activation cascade(R)	49	4	4.99E-03	PIK3R1,LAT,LCP2,PTPN11
MicroRNAs in cancer(K)	299	9	5.10E-03	RASSF1,PRKCE,BCL2L11,TGFB2,NFKB1,BCL2,IKBKB,ZEB1,APC
influence of ras and rho proteins on g1 to s transition(B)	22	3	5.46E-03	RB1,PIK3R1,IKBKB
Dilated cardiomyopathy(K)	90	5	5.46E-03	CACNB1,TGFB2,ITGB1,LAMA2,TTN
Role of Calcineurin-dependent NFAT signaling in lymphocytes(N)	52	4	5.46E-03	PRKCE,NFATC3,NFATC2,BCL2
Signaling by MET(R)	52	4	5.46E-03	PIK3R1,ITGB1,CBL,PTPN11
Signaling by BMP(R)	23	3	5.46E-03	SMAD9,BMPR1B,BMPR1A
role of mef2d in t-cell apoptosis(B)	23	3	5.46E-03	LAT,PTPN11,CD247
Apoptosis(K)	140	6	6.04E-03	DDIT3,PIK3R1,BCL2L11,NFKB1,BCL2,IKBKB
Insulin signaling pathway(K)	140	6	6.04E-03	PIK3R1,ACACB,ACACA,PPARGC1A,IKBKB,CBL
IL2-mediated signaling events(N)	54	4	6.12E-03	PRKCE,PIK3R1,BCL2,PTPN11
Longevity regulating pathway(K)	94	5	6.28E-03	IGF1R,PIK3R1,FOXO3,PPARGC1A,NFKB1
Wnt signaling pathway(K)	143	6	6.46E-03	SMAD3,NFATC3,NFATC2,PPP3CA,TCF7L2,APC
Non-small cell lung cancer(K)	56	4	6.46E-03	RB1,RASSF1,PIK3R1,FOXO3
Cell adhesion molecules (CAMs)(K)	145	6	6.46E-03	CDH1,CD226,ITGB1,NRXN1,NCAM1,NECTIN3
Acute myeloid leukemia(K)	57	4	6.46E-03	PIK3R1,NFKB1,IKBKB,TCF7L2
Breast cancer(K)	146	6	6.46E-03	RB1,IGF1R,PIK3R1,DLL1,TCF7L2,APC
DAP12 interactions(R)	323	9	6.46E-03	GRAP2,PRKCE,PIK3R1,FOXO3,KLRD1,LAT,LCP2,NCAM1,PTPN11
Endocrine resistance(K)	98	5	6.46E-03	RB1,IGF1R,PIK3R1,BCL2,DLL1
Focal adhesion(K)	201	7	6.46E-03	IGF1R,COL4A1,PIK3R1,BCL2,ITGB1,LAMA2,LAMA4
ALK1 signaling events(N)	26	3	6.46E-03	ACVR1,SMAD9,TGFBR2
Apoptosis signaling pathway(P)	26	3	6.46E-03	PRKCE,BCL2L11,BCL2
B cell activation(P)	59	4	7.05E-03	NFATC3,NFATC2,IKBKB,PPP3CA

Cytokine-cytokine receptor interaction(K)	265	8	7.11E-03	IL18RAP,ACVR1,TGFB2,BMPR1B,BMPR1A,TGFBR2,TNFRSF25,IL17A
VEGFR1 specific signals(N)	27	3	7.19E-03	PIK3R1,CBL,PTPN11
Signaling events mediated by focal adhesion kinase(N)	60	4	7.49E-03	ETS1,PIK3R1,ITGB1,WASL
Signaling by the B Cell Receptor (BCR)(R)	270	8	7.99E-03	STIM1,PIK3R1,FOXO3,NFKB1,NFKBIE,IKBKB,CBL,PTPN11
Rap1 signaling pathway(K)	212	7	8.61E-03	IGF1R,CDH1,PIK3R1,DRD2,LAT,ITGB1,LCP2
EGF receptor (ErbB1) signaling pathway(N)	29	3	8.80E-03	WASL,GSN,PTPN11
Osteopontin-mediated events(N)	29	3	8.80E-03	PIK3R1,NFKB1,GSN
Costimulation by the CD28 family(R)	63	4	8.94E-03	GRAP2,PIK3R1,PTPN11,CD247
Downstream signaling in naïve CD8+ T cells(N)	64	4	9.47E-03	PRKCE,NFATC3,NFATC2,CD247
IGF1 pathway(N)	30	3	9.69E-03	IGF1R,PIK3R1,PTPN11
Nectin adhesion pathway(N)	30	3	9.69E-03	CDH1,PIK3R1,NECTIN3
Shigellosis(K)	65	4	0.01	NFKB1,ITGB1,WASL,IKBKB
Beta1 integrin cell surface interactions(N)	66	4	0.0101	COL4A1,ITGB1,LAMA2,LAMA4
Signalling by NGF(R)	421	10	0.0101	PRKCE,PIK3R1,FOXO3,BCL2L11,NFKB1,LAT,IKBKB,NCAM1,NTRK2,PTPN11
Renal cell carcinoma(K)	67	4	0.0101	ETS1,PIK3R1,TGFB2,PTPN11
N-cadherin signaling events(N)	33	3	0.0101	PIK3R1,GSN,PTPN11
HIV-1 Nef: Negative effector of Fas and TNF-alpha(N)	33	3	0.0101	NFKB1,BCL2,CD247
Melanoma(K)	71	4	0.011	RB1,IGF1R,CDH1,PIK3R1
Arrhythmogenic right ventricular cardiomyopathy (ARVC)(K)	72	4	0.0116	CACNB1,ITGB1,LAMA2,TCF7L2
a6b1 and a6b4 Integrin signaling(N)	35	3	0.012	CDH1,PIK3R1,ITGB1
Leishmaniasis(K)	73	4	0.0121	TGFB2,NFKB1,ITGB1,FCGR3A
Validated transcriptional targets of AP1 family members Fra1 and Fra2(N)	37	3	0.014	NFATC3,NFATC2,DCN
GMCSF-mediated signaling events(N)	37	3	0.014	PIK3R1,IKBKB,PTPN11

ALK2 signaling events(N)	11	2	0.0148	ACVR1,SMAD9
lck and fyn tyrosine kinases in initiation of tcr activation(B)	11	2	0.0148	PTPN11,CD247
Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell(R)	187	6	0.0169	CDH1,CD226,KLRD1,ITGB1,FCGR3A,CD247
IFN-gamma pathway(N)	40	3	0.0173	PIK3R1,CBL,PTPN11
Signaling by FGFR3(R)	40	3	0.0173	PIK3R1,CBL,PTPN11
insulin signaling pathway(B)	12	2	0.0175	PIK3R1,PTPN11
C-MYB transcription factor network(N)	82	4	0.0183	ETS1,GATA3,BCL2,PPP3CA
ECM-receptor interaction(K)	82	4	0.0183	COL4A1,ITGB1,LAMA2,LAMA4
Bladder cancer(K)	41	3	0.0186	RB1,RASSF1,CDH1
Signaling by FGFR4(R)	41	3	0.0186	PIK3R1,CBL,PTPN11
BMP receptor signaling(N)	41	3	0.0186	SMAD9,BMPR1B,BMPR1A
human cytomegalovirus and map kinase pathways(B)	13	2	0.0205	RB1,PIK3R1
Metabolism of Angiotensinogen to Angiotensins(R)	13	2	0.0205	ACE2,AGT
Fatty acid biosynthesis(K)	13	2	0.0205	ACACB,ACACA
b cell survival pathway(B)	13	2	0.0205	PIK3R1,ITGB1
Beta3 integrin cell surface interactions(N)	43	3	0.0212	COL4A1,TGFBR2,LAMA4
C-type lectin receptors (CLRs)(R)	139	5	0.0215	NFATC3,NFATC2,NFKB1,IKBKB,PPP3CA
IL5-mediated signaling events(N)	14	2	0.0215	PIK3R1,PTPN11
Viral carcinogenesis(K)	203	6	0.0215	RB1,UBE3A,PIK3R1,EGR3,NFKB1,GSN
Epstein-Barr virus infection(K)	204	6	0.0215	RB1,PIK3R1,NFKB1,BCL2,NFKBIE,IKBKB
keratinocyte differentiation(B)	47	3	0.0215	ETS1,PRKCE,IKBKB
Apoptotic execution phase(R)	47	3	0.0215	CDH1,GSN,APC
Ceramide signaling pathway(N)	48	3	0.0215	RB1,NFKB1,BCL2

Posttranslational regulation of adherens junction stability and dissassembly(N)	48	3	0.0215	IGF1R,CDH1,NTRK2
FoxO family signaling(N)	48	3	0.0215	FOXO3,BCL2L11,IKBKB
Signaling by FGFR1(R)	49	3	0.0227	PIK3R1,CBL,PTPN11
NF-kappa B signaling pathway(K)	95	4	0.0228	NFKB1,BCL2,LAT,IKBKB
role of pi3k subunit p85 in regulation of actin organization and cell migration(B)	16	2	0.0229	PIK3R1,WASL
Non-alcoholic fatty liver disease (NAFLD)(K)	151	5	0.0235	DDIT3,PIK3R1,BCL2L11,NFKB1,IKBKB
SHP2 signaling(N)	51	3	0.0253	IGF1R,PIK3R1,PTPN11
pten dependent cell cycle arrest and apoptosis(B)	17	2	0.0257	PIK3R1,ITGB1
Signaling by SCF-KIT(R)	290	7	0.028	GRAP2,PIK3R1,FOXO3,LAT,CBL,NCAM1,PTPN11
Fcgamma receptor (FCGR) dependent phagocytosis(R)	159	5	0.0289	PRKCE,PIK3R1,WASL,FCGR3A,CD247
Oxytocin signaling pathway(K)	159	5	0.0289	CACNB1,PIK3R1,NFATC3,NFATC2,PPP3CA
Glucagon signaling pathway(K)	103	4	0.0301	ACACB,ACACA,PPARGC1A,PPP3CA
HIF-1 signaling pathway(K)	103	4	0.0301	IGF1R,PIK3R1,NFKB1,BCL2
Pathogenic Escherichia coli infection(K)	55	3	0.031	CDH1,ITGB1,WASL
cyclins and cell cycle regulation(B)	19	2	0.0318	RB1,PTPN11
tgf beta signaling pathway(B)	19	2	0.0318	CDH1,TGFB2
Signaling by NODAL(R)	19	2	0.0318	FOXO3,SMAD3
fas signaling pathway (cd95)(B)	19	2	0.0318	RB1,PTPN11
tumor suppressor arf inhibits ribosomal biogenesis(B)	19	2	0.0318	RB1,PIK3R1
cGMP-PKG signaling pathway(K)	168	5	0.0346	PRKCE,PIK3R1,NFATC3,NFATC2,PPP3CA
cell cycle: g1/s check point(B)	21	2	0.0346	RB1,PTPN11
growth hormone signaling pathway(B)	21	2	0.0346	PIK3R1,PTPN11
E-cadherin signaling in keratinocytes(N)	21	2	0.0346	CDH1,PIK3R1

igf-1 signaling pathway(B)	21	2	0.0346	PIK3R1,PTPN11
nf-kb signaling pathway(B)	21	2	0.0346	NFKB1,IKBKB
Neurotrophic factor-mediated Trk receptor signaling(N)	60	3	0.0346	PIK3R1,NTRK2,PTPN11
IL12-mediated signaling events(N)	61	3	0.0346	IL18RAP,NFKB1,CD247
VEGF signaling pathway(K)	61	3	0.0346	PIK3R1,NFATC2,PPP3CA
ctcf: first multivalent nuclear factor(B)	22	2	0.0346	PIK3R1,TGFB2
Nephrin interactions(R)	22	2	0.0346	PIK3R1,WASL
Incretin synthesis, secretion, and inactivation(R)	22	2	0.0346	PAX6,TCF7L2
Signaling by EGFR(R)	317	7	0.0346	PRKCE,PIK3R1,FOXO3,LAT,CBL,NCAM1,PTPN11
IL4-mediated signaling events(N)	63	3	0.0346	ETS1,PIK3R1,CBL
Signaling events mediated by VEGFR1 and VEGFR2(N)	63	3	0.0346	PIK3R1,CBL,PTPN11
LPA receptor mediated events(N)	63	3	0.0346	PRKCE,PIK3R1,NFKB1
Canonical NF-kappaB pathway(N)	23	2	0.0346	NFKB1,IKBKB
Signaling events mediated by the Hedgehog family(N)	23	2	0.0346	PIK3R1,TGFB2
Renin-angiotensin system(K)	23	2	0.0346	ACE2,AGT
Signaling events mediated by PRL(N)	23	2	0.0346	ITGB1,AGT
Tuberculosis(K)	179	5	0.0346	TGFB2,NFKB1,BCL2,PPP3CA,FCGR3A
Longevity regulating pathway - multiple species(K)	64	3	0.0346	IGF1R,PIK3R1,FOXO3
Regulation of retinoblastoma protein(N)	64	3	0.0346	RB1,TGFB2,ELF1
HIF-1-alpha transcription factor network(N)	65	3	0.0346	RORA,ETS1,SMAD3
nfkb activation by nontypeable hemophilus influenzae(B)	24	2	0.0346	TGFB2,IKBKB

PDGFR-beta signaling pathway(N)	120	4	0.0346	PRKCE,WASL,CBL,PTPN11
Sphingolipid signaling pathway(K)	120	4	0.0346	PRKCE,PIK3R1,NFKB1,BCL2
Glioma(K)	66	3	0.0346	RB1,IGF1R,PIK3R1
Angiogenesis(P)	66	3	0.0346	ETS1,TCF7L2,APC
Signaling by PDGF(R)	328	7	0.0346	PRKCE,COL4A1,PIK3R1,FOXO 3,LAT,NCAM1,PTPN11
Platelet activation(K)	122	4	0.0352	STIM1,PIK3R1,ITGB1,LCP2
VEGFR3 signaling in lymphatic endothelium(N)	25	2	0.0355	PIK3R1,ITGB1
Glypican 1 network(N)	25	2	0.0355	TGFBR2,GPC1
Epithelial cell signaling in Helicobacter pylori infection(K)	68	3	0.0362	NFKB1,IKBKB,PTPN11
Regulation of Telomerase(N)	68	3	0.0362	UBE3A,SMAD3,NFKB1
Chemokine signaling pathway(K)	187	5	0.0365	PIK3R1,FOXO3,NFKB1,WASL, IKBKB
p75(NTR)-mediated signaling(N)	69	3	0.0377	PIK3R1,BCL2L11,IKBKB
IL3-mediated signaling events(N)	26	2	0.0382	PIK3R1,PTPN11
IL27-mediated signaling events(N)	26	2	0.0382	GATA3,IL17A
Signaling events mediated by HDAC Class III(N)	26	2	0.0382	FOXO3,PPARGC1A
Endocytosis(K)	260	6	0.0384	IGF1R,TGFB2,SMAD3,WASL,T GFBR2,CBL
Fc epsilon RI signaling pathway(K)	70	3	0.0391	PIK3R1,LAT,LCP2
Cell junction organization(R)	70	3	0.0391	CDH1,ITGB1,NECTIN3
Signaling by FGFR2(R)	71	3	0.0406	PIK3R1,CBL,PTPN11
Calcium signaling in the CD4+ TCR pathway(N)	27	2	0.041	NFATC3,NFATC2
Prolactin signaling pathway(K)	72	3	0.0421	PIK3R1,FOXO3,NFKB1
Signaling by TGF-beta Receptor Complex(R)	73	3	0.0436	SMAD3,TGFBR2,CBL
Reelin signaling pathway(N)	28	2	0.0439	PIK3R1,ITGB1
IL8- and CXCR1-mediated signaling events(N)	28	2	0.0439	PRKCE,CBL
p73 transcription factor network(N)	75	3	0.0467	RB1,FOXO3,BCL2L11
Thyroid cancer(K)	29	2	0.0468	CDH1,TCF7L2

AlphaE beta7 integrin cell surface interactions(N)	3	1	0.048	CDH1
erk and pi-3 kinase are necessary for collagen binding in corneal epithelia(B)	30	2	0.0499	PIK3R1,ITGB1
Regulation of nuclear SMAD2/3 signaling(N)	77	3	0.05	GATA3,FOXO3,SMAD3
IL12 signaling mediated by STAT4(N)	31	2	0.053	IL18RAP,CD247
Antifolate resistance(K)	31	2	0.053	NFKB1,IKBKB
trefoil factors initiate mucosal healing(B)	31	2	0.053	PIK3R1,IKBKB
Regulation of nuclear beta catenin signaling and target gene transcription(N)	80	3	0.0551	CDH1,TCF7L2,APC
Toll-Like Receptors Cascades(R)	141	4	0.056	NFKB1,IKBKB,IRAK3,PTPN11
Netrin-mediated signaling events(N)	32	2	0.0562	PIK3R1,WASL
Propanoate metabolism(K)	32	2	0.0562	ACACB,ACACA
L1CAM interactions(R)	82	3	0.0587	ITGB1,CHL1,NCAM1
Apoptosis - multiple species(K)	33	2	0.0594	BCL2L11,BCL2
Regulation of actin cytoskeleton(K)	214	5	0.0605	PIK3R1,ITGB1,WASL,GSN,APC
phospholipase c signaling pathway(B)	4	1	0.0638	PIK3R1
signal transduction through il1r(B)	35	2	0.0662	TGFB2,IKBKB
Signaling mediated by p38-alpha and p38-beta(N)	35	2	0.0662	DDIT3,PPARGC1A
Salmonella infection(K)	86	3	0.0662	NFKB1,WASL,DYNC1I1
Trk receptor signaling mediated by PI3K and PLC-gamma(N)	36	2	0.0696	PIK3R1,FOXO3
mechanism of gene regulation by peroxisome proliferators via ppara(B)	36	2	0.0696	RB1,PPARGC1A
inactivation of gsk3 by akt causes accumulation of b-catenin in alveolar macrophages(B)	36	2	0.0696	PIK3R1,IKBKB

E-cadherin signaling in the nascent adherens junction(N)	36	2	0.0696	CDH1,PIK3R1
Retinoid metabolism and transport(R)	38	2	0.0768	GPC1,GPC6
Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways(R)	38	2	0.0768	BCL2,IKBKB
EPHB forward signaling(N)	38	2	0.0768	PIK3R1,WASL
Integration of energy metabolism(R)	92	3	0.0783	ACACB,CACNA1E,ACACA
cyclin e destruction pathway(B)	5	1	0.0794	RB1
Signaling events regulated by Ret tyrosine kinase(N)	39	2	0.0805	PIK3R1,PTPN11
Pyruvate metabolism(K)	39	2	0.0805	ACACB,ACACA
Oxidative stress response(P)	40	2	0.0842	DDIT3,BCL2
Class I PI3K signaling events(N)	40	2	0.0842	FOXO3,LAT
Intrinsic Pathway for Apoptosis(R)	41	2	0.0849	BCL2L11,BCL2
Netrin-1 signaling(R)	42	2	0.0849	WASL,PTPN11
Stabilization and expansion of the E-cadherin adherens junction(N)	42	2	0.0849	IGF1R,CDH1
Plasma membrane estrogen receptor signaling(N)	42	2	0.0849	IGF1R,PIK3R1
Inflammatory mediator regulation of TRP channels(K)	99	3	0.0849	PRKCE,PIK3R1,HTR2A
proteolysis and signaling pathway of notch(B)	6	1	0.0849	DLL1
overview of telomerase rna component gene hterc transcriptional regulation(B)	6	1	0.0849	RB1
e2f1 destruction pathway(B)	6	1	0.0849	RB1
regulation of p27 phosphorylation during cell cycle progression(B)	6	1	0.0849	RB1

cell to cell adhesion signaling(B)	6	1	0.0849	PTPN11
Alternative NF-kappaB pathway(N)	6	1	0.0849	NFKB1
Presenilin action in Notch and Wnt signaling(N)	45	2	0.0849	DLL1,APC
TNF receptor signaling pathway(N)	46	2	0.0849	NFKB1,IKBKB
cbl mediated ligand-induced downregulation of egf receptors pathway(B)	7	1	0.0849	CBL
Depolarization of the Presynaptic Terminal Triggers the Opening of Calcium Channels(R)	7	1	0.0849	CACNA1E
Toll-like receptor signaling pathway(K)	106	3	0.0849	PIK3R1,NFKB1,IKBKB
IL6-mediated signaling events(N)	47	2	0.0849	PIK3R1,PTPN11
TGF-beta receptor signaling(N)	47	2	0.0849	SMAD3,TGFBR2
Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R)(R)	255	5	0.0849	IGF1R,PIK3R1,LAT,NCAM1,PTPN11
Cardiac conduction(R)	107	3	0.0849	CACNB1,STIM1,TRDN
Heterotrimeric G-protein signaling pathway-Gq alpha and Go alpha mediated pathway(P)	108	3	0.0849	PRKCE,CACNA1E,DRD2
Cocaine addiction(K)	49	2	0.0849	DRD2,NFKB1
TNF signaling pathway(K)	110	3	0.0849	PIK3R1,NFKB1,IKBKB
Calcium signaling pathway(K)	182	4	0.0849	STIM1,CACNA1E,HTR2A,PPP3CA
PIP3 activates AKT signaling(R)	111	3	0.0849	PIK3R1,FOXO3,PTPN11
chaperones modulate interferon signaling pathway(B)	8	1	0.0849	RB1
a4b7 Integrin signaling(N)	8	1	0.0849	ITGB1
Amyotrophic lateral sclerosis (ALS)(K)	51	2	0.0849	BCL2,PPP3CA
Signaling events mediated by PTP1B(N)	52	2	0.0849	PIK3R1,LAT
Caspase cascade in apoptosis(N)	52	2	0.0849	BCL2,GSN

Notch signaling pathway(N)	52	2	0.0849	GATA3,DLL1
Leukocyte transendothelial migration(K)	116	3	0.0849	PIK3R1,ITGB1,PTPN11
Regulation of cholesterol biosynthesis by SREBP (SREBF)(R)	53	2	0.0849	ACACB,ACACA
btg family proteins and cell cycle regulation(B)	9	1	0.0849	RB1
proteasome complex(B)	9	1	0.0849	UBE3A
Interleukin signaling pathway(P)	55	2	0.0849	FOXO3,IKBKB
Basal cell carcinoma(K)	55	2	0.0849	TCF7L2,APC
Fatty acid, triacylglycerol, and ketone body metabolism(R)	195	4	0.0849	RORA,ACACA,PPARGC1A,AGT
GP1b-IX-V activation signalling(R)	10	1	0.0849	PIK3R1
cxcr4 signaling pathway(B)	10	1	0.0849	PIK3R1
cardiac protection against ros(B)	10	1	0.0849	PRKCE
Cell cycle(K)	124	3	0.0849	RB1,TGFB2,SMAD3
Platelet homeostasis(R)	59	2	0.0849	STIM1,PTPN11
PI Metabolism(R)	59	2	0.0849	PIK3R1,MTMR7
Gastrin-CREB signalling pathway via PKC and MAPK(R)	376	6	0.0849	PRKCE,PIK3R1,LAT,HTR2A,NCAM1,AGT
il-7 signal transduction(B)	11	1	0.0853	PIK3R1
Signaling by NOTCH4(R)	11	1	0.0853	DLL1
Signaling by NOTCH3(R)	11	1	0.0853	DLL1
protein kinase a at the centrosome(B)	11	1	0.0853	PRKCE
rb tumor suppressor/checkpoint signaling in response to dna damage(B)	11	1	0.0853	RB1
regulation of transcriptional activity by pml(B)	11	1	0.0853	RB1
Alpha6 beta4 integrin-ligand interactions(N)	11	1	0.0853	LAMA2

how does salmonella hijack a cell(B)	11	1	0.0853	WASL
Coregulation of Androgen receptor activity(N)	60	2	0.0855	UBE3A,GSN
Cell surface interactions at the vascular wall(R)	208	4	0.089	PIK3R1,ITGB1,GPC1,PTPN11
Direct p53 effectors(N)	132	3	0.0923	RB1,BCL2,APC
epo signaling pathway(B)	12	1	0.0927	PTPN11
trka receptor signaling pathway(B)	12	1	0.0927	PIK3R1
Signal regulatory protein (SIRP) family interactions(R)	12	1	0.0927	PTPN11
p53 signaling pathway(B)	12	1	0.0927	RB1
Hepatitis C(K)	133	3	0.0939	PIK3R1,NFKB1,IKBKB
Cytosolic DNA-sensing pathway(K)	64	2	0.0954	NFKB1,IKBKB
mTOR signaling pathway(N)	64	2	0.0954	PPARGC1A,IKBKB
Renin secretion(K)	65	2	0.0979	PPP3CA,AGT
il 6 signaling pathway(B)	13	1	0.1	PTPN11
il 3 signaling pathway(B)	13	1	0.1	PTPN11
Platelet Adhesion to exposed collagen(R)	13	1	0.1	ITGB1
Signaling by Activin(R)	13	1	0.1	SMAD3
double stranded rna induced gene expression(B)	13	1	0.1	IKBKB
multiple antiapoptotic pathways from igf-1r signaling lead to bad phosphorylation(B)	13	1	0.1	PIK3R1
Circadian Clock(R)	67	2	0.1029	RORA,PPARGC1A
Cytosolic sensors of pathogen-associated DNA (R)	67	2	0.1029	NFKB1,IKBKB
RET signaling(R)	222	4	0.1063	PIK3R1,LAT,NCAM1,PTPN11
Degradation of beta-catenin by the destruction complex(R)	70	2	0.1107	TCF7L2,APC
RIG-I-like receptor signaling pathway(K)	70	2	0.1107	NFKB1,IKBKB
Deubiquitination(R)	226	4	0.1116	GATA3,SMAD3,TGFBR2,APC

Inflammation mediated by chemokine and cytokine signaling pathway(P)	71	2	0.1133	PRKCE,IKBKB
telomeres telomerase cellular aging and immortality(B)	15	1	0.1145	RB1
Prolactin receptor signaling(R)	15	1	0.1145	PTPN11
ucalpain and friends in cell spread(B)	15	1	0.1145	ITGB1
Interferon-gamma signaling pathway(P)	15	1	0.1145	PTPN11
NCAM signaling for neurite out-growth(R)	231	4	0.1183	CACNB1,COL4A1,LAT,NCAM1
Interferon gamma signaling(R)	73	2	0.1185	NCAM1,PTPN11
Metabolism of water-soluble vitamins and cofactors(R)	73	2	0.1185	ACACB,ACACA
Adrenergic signaling in cardiomyocytes(K)	149	3	0.1207	CACNB1,PIK3R1,BCL2
bone remodeling(B)	16	1	0.1216	IKBKB
nerve growth factor pathway (ngf)(B)	16	1	0.1216	PIK3R1
LPA4-mediated signaling events(N)	16	1	0.1216	PRKCE
RAF-independent MAPK1/3 activation(R)	16	1	0.1216	PTPN11
downregulated of mta-3 in er-negative breast tumors(B)	16	1	0.1216	CDH1
y branching of actin filaments(B)	16	1	0.1216	WASL
akt signaling pathway(B)	16	1	0.1216	PIK3R1
the igf-1 receptor and longevity(B)	16	1	0.1216	PIK3R1
role of nicotinic acetylcholine receptors in the regulation of apoptosis(B)	16	1	0.1216	PIK3R1
Platinum drug resistance(K)	75	2	0.1239	PIK3R1,BCL2
Pertussis(K)	76	2	0.1266	NFKB1,ITGB1
control of skeletal myogenesis by hdac and calcium/calmodulin-dependent kinase (camk)(B)	17	1	0.1287	PIK3R1

phosphoinositides and their downstream targets(B)	17	1	0.1287	PRKCE
Peroxisomal lipid metabolism(R)	17	1	0.1287	AGPS
gata3 participate in activating the th2 cytokine genes expression(B)	17	1	0.1287	GATA3
RIG-I/MDA5 mediated induction of IFN-alpha/beta pathways(R)	77	2	0.1293	NFKB1,IKBKB
Phagosome(K)	154	3	0.1297	ITGB1,FCGR3A,DYNC1I1
mTOR signaling pathway(K)	154	3	0.1297	IGF1R,PIK3R1,IKBKB
Glucocorticoid receptor regulatory network(N)	78	2	0.132	GATA3,NFKB1
EPHA2 forward signaling(N)	18	1	0.1357	PIK3R1
Metabolism of nitric oxide(R)	18	1	0.1357	WASL
Degradation of beta catenin(N)	18	1	0.1357	APC
Regulation of cytoplasmic and nuclear SMAD2/3 signaling(N)	18	1	0.1357	SMAD3
mets affect on macrophage differentiation(B)	18	1	0.1357	ETS1
VEGF signaling pathway(P)	18	1	0.1357	ETS1
regulation of pgc-1a(B)	18	1	0.1357	PPARGC1A
Integrin signalling pathway(P)	158	3	0.137	COL4A1,PIK3R1,ITGB1
Jak-STAT signaling pathway(K)	158	3	0.137	PIK3R1,BCL2,PTPN11
CXCR4-mediated signaling events(N)	80	2	0.1374	PTPN11,CD247
sprouty regulation of tyrosine kinase signals(B)	19	1	0.1427	CBL
EGF receptor signaling pathway(P)	82	2	0.143	PRKCE,CBL
Visual phototransduction(R)	83	2	0.1457	GPC1,GPC6
Transcriptional regulation of white adipocyte differentiation(R)	84	2	0.1485	PPARGC1A,NFKB1

Canonical Wnt signaling pathway(N)	20	1	0.1497	APC
tnf/stress related signaling(B)	20	1	0.1497	IKBKB
regulation of bad phosphorylation(B)	20	1	0.1497	PIK3R1
egf signaling pathway(B)	21	1	0.1565	PIK3R1
erk1/erk2 mapk signaling pathway(B)	21	1	0.1565	PTPN11
segmentation clock(B)	21	1	0.1565	DLL1
PDGFR-alpha signaling pathway(N)	21	1	0.1565	PIK3R1
how progesterone initiates the oocyte maturation(B)	21	1	0.1565	PTPN11
regulation of ck1/cdk5 by type 1 glutamate receptors(B)	21	1	0.1565	DRD2
NOD-like receptor signaling pathway(K)	170	3	0.1597	NFKB1,BCL2,IKBKB
ErbB signaling pathway(K)	88	2	0.1598	PIK3R1,CBL
Gap junction(K)	88	2	0.1598	DRD2,HTR2A
stathmin and breast cancer resistance to antimicrotubule agents(B)	22	1	0.1633	CD247
ras signaling pathway(B)	22	1	0.1633	PIK3R1
inhibition of cellular proliferation by gleevec(B)	22	1	0.1633	PIK3R1
Other types of O-glycan biosynthesis(K)	22	1	0.1633	COLGALT2
TRAIL signaling pathway(N)	22	1	0.1633	IKBKB
Protein digestion and absorption(K)	90	2	0.1655	ACE2,COL4A1
Rheumatoid arthritis(K)	90	2	0.1655	TGFB2,IL17A
Influenza A(K)	175	3	0.1695	PIK3R1,NFKB1,IKBKB
Signaling by Robo receptor(R)	23	1	0.1701	GPC1
Effects of PIP2 hydrolysis(R)	23	1	0.1701	PRKCE
alk in cardiac myocytes(B)	23	1	0.1701	TGFB2
regulation of eif-4e and p70s6 kinase(B)	23	1	0.1701	PIK3R1

role of erk5 in neuronal survival pathway(B)	23	1	0.1701	PIK3R1
FGF signaling pathway(P)	92	2	0.1712	PRKCE,PTPN11
corticosteroids and cardioprotection(B)	24	1	0.1768	PIK3R1
mtor signaling pathway(B)	24	1	0.1768	PIK3R1
Hypoxia response via HIF activation(P)	24	1	0.1768	PIK3R1
transcription factor creb and its extracellular signals(B)	24	1	0.1768	PIK3R1
Ephrin B reverse signaling(N)	24	1	0.1768	PIK3R1
skeletal muscle hypertrophy is regulated via akt-mtor pathway(B)	24	1	0.1768	PIK3R1
Alpha9 beta1 integrin signaling events(N)	24	1	0.1768	ITGB1
Nongenotropic Androgen signaling(N)	25	1	0.1835	PIK3R1
Endogenous TLR signaling(N)	25	1	0.1835	IKBKB
fc epsilon receptor i signaling in mast cells(B)	25	1	0.1835	PIK3R1
Nephrin/Neph1 signaling in the kidney podocyte(N)	25	1	0.1835	WASL
tpo signaling pathway(B)	25	1	0.1835	PIK3R1
Signaling by Insulin receptor(R)	277	4	0.1872	PIK3R1,LAT,NCAM1,PTPN11
Progesterone-mediated oocyte maturation(K)	98	2	0.1886	IGF1R,PIK3R1
Herpes simplex infection(K)	185	3	0.1896	NFKB1,IKBKB,PTPN11
S1P2 pathway(N)	26	1	0.1901	PIK3R1
mcalpain and friends in cell motility(B)	26	1	0.1901	ITGB1
Maturity onset diabetes of the young(K)	26	1	0.1901	PAX6
bioactive peptide induced signaling pathway(B)	26	1	0.1901	PIK3R1

RXR and RAR heterodimerization with other nuclear receptor(N)	26	1	0.1901	BCL2
pdgf signaling pathway(B)	26	1	0.1901	PIK3R1
PI3 kinase pathway(P)	26	1	0.1901	FOXO3
Phosphatidylinositol signaling system(K)	99	2	0.1915	PIK3R1,MTMR7
DNA Damage/Telomere Stress Induced Senescence(R)	27	1	0.1966	RB1
thrombin signaling and protease-activated receptors(B)	27	1	0.1966	PIK3R1
Choline metabolism in cancer(K)	101	2	0.1973	PIK3R1,WASL
Signaling by NOTCH2(R)	28	1	0.2031	DLL1
role of erbb2 in signal transduction and oncology(B)	28	1	0.2031	PIK3R1
vegf hypoxia and angiogenesis(B)	28	1	0.2031	PIK3R1
Dorso-ventral axis formation(K)	28	1	0.2031	ETS1
Hippo signaling pathway -multiple species(K)	29	1	0.2096	RASSF1
CD40/CD40L signaling(N)	29	1	0.2096	NFKB1
Response to elevated platelet cytosolic Ca2+(R)	106	2	0.2121	TGFB2,TTN
ceramide signaling pathway(B)	30	1	0.2159	IKBKB
Regulation of CDC42 activity(N)	30	1	0.2159	APC
cAMP signaling pathway(K)	200	3	0.2208	PIK3R1,DRD2,NFKB1
Circadian rhythm(K)	31	1	0.2223	RORA
amb2 Integrin signaling(N)	31	1	0.2223	NFKB1
Striated Muscle Contraction(R)	31	1	0.2223	TTN
Detoxification of Reactive Oxygen Species(R)	31	1	0.2223	PRDX6
phospholipids as signalling intermediaries(B)	31	1	0.2223	PIK3R1

Regulation of beta-cell development(R)	31	1	0.2223	PAX6
Mucin type O-glycan biosynthesis(K)	31	1	0.2223	C1GALT1
p38 mapk signaling pathway(B)	31	1	0.2223	DDIT3
role of egf receptor transactivation by gpcrs in cardiac hypertrophy(B)	31	1	0.2223	IKBKB
EPHA forward signaling(N)	31	1	0.2223	CBL
Alzheimer disease-presenilin pathway(P)	111	2	0.2269	CDH1,TCF7L2
Cholinergic synapse(K)	111	2	0.2269	PIK3R1,BCL2
Oncogene Induced Senescence(R)	32	1	0.2286	ETS1
HIF-2-alpha transcription factor network(N)	32	1	0.2286	ETS1
Syndecan-4-mediated signaling events(N)	32	1	0.2286	ITGB1
FAS (CD95) signaling pathway(N)	32	1	0.2286	IKBKB
DAG and IP3 signaling(R)	32	1	0.2286	PRKCE
toll-like receptor pathway(B)	32	1	0.2286	IKBKB
Syndecan-2-mediated signaling events(N)	32	1	0.2286	ITGB1
Noncanonical Wnt signaling pathway(N)	32	1	0.2286	NFATC2
Beta-catenin independent WNT signaling(R)	112	2	0.2299	PPP3CA,TCF7L2
Alpha4 beta1 integrin signaling events(N)	33	1	0.2348	ITGB1
integrin signaling pathway(B)	33	1	0.2348	ITGB1
FAS signaling pathway(P)	33	1	0.2348	GSN
Signaling by Leptin(R)	209	3	0.24	LAT,NCAM1,PTPN11
IL8- and CXCR2-mediated signaling events(N)	34	1	0.241	CBL
actions of nitric oxide in the heart(B)	34	1	0.241	PIK3R1
Arf6 trafficking events(N)	34	1	0.241	CDH1
Clathrin-mediated endocytosis(R)	117	2	0.2448	WASL,CBL
Prion diseases(K)	35	1	0.2471	NCAM1

Internalization of ErbB1(N)	35	1	0.2471	CBL
Class I PI3K signaling events mediated by Akt(N)	35	1	0.2471	FOXO3
African trypanosomiasis(K)	35	1	0.2471	LAMA4
Signaling events mediated by TCPTP(N)	35	1	0.2471	ITGB1

Table 27

GeneSet	Number Of Protein In Gene Set	Protein From Network	FDR	Nodes
BCR signaling pathway(N)	65	7	1.04E-05	ETS1,SYK,CARD11,PIK3R1,PAG1,NFKB1,PTPRC
Pathways in cancer(K)	397	13	1.04E-05	GSK3B,ETS1,FGF2,IGF1R,CASP9,TGFBR2,COL4A2,COL4A1,LAMA2,CXCR4,PIK3R1,TGFB2,NFKB1
T cell receptor signaling pathway(K)	105	7	1.16E-04	GSK3B,PRKCQ,CARD11,PIK3R1,NFATC2,NFKB1,PTPRC
TCR signaling in naïve CD4+ T cells(N)	67	6	1.16E-04	STIM1,PRKCQ,CARD11,STK39,PAG1,PTPRC
B cell receptor signaling pathway(K)	73	6	1.51E-04	GSK3B,SYK,CARD11,PIK3R1,NFATC2,NFKB1
Extracellular matrix organization(R)	255	9	2.72E-04	FGF2,DCN,COL4A2,COL4A1,LAMA2,COL13A1,FBLN2,NCAM1,TGFB2
Small cell lung cancer(K)	86	6	2.72E-04	CASP9,COL4A2,COL4A1,LAMA2,PIK3R1,NFKB1
Angiopoietin receptor Tie2-mediated signaling(N)	50	5	2.72E-04	ETS1,FGF2,ELF1,PIK3R1,NFKB1
PI3K-Akt signaling pathway(K)	341	10	2.72E-04	GSK3B,FGF2,IGF1R,CASP9,SYK,COL4A2,COL4A1,LAMA2,PIK3R1,NFKB1
TCR signaling in naïve CD8+ T cells(N)	54	5	3.35E-04	STIM1,PRKCQ,CARD11,PAG1,PTPRC
Amoebiasis(K)	98	6	3.61E-04	COL4A2,COL4A1,LAMA2,PIK3R1,TGFB2,NFKB1
AGE-RAGE signaling pathway in diabetic complications(K)	101	6	3.97E-04	TGFBR2,COL4A2,COL4A1,PIK3R1,TGFB2,NFKB1
Colorectal cancer(K)	62	5	4.64E-04	GSK3B,CASP9,TGFBR2,PIK3R1,TGFB2
Th17 cell differentiation(K)	107	6	4.64E-04	RORA,IL1RAP,TGFBR2,PRKCQ,NFATC2,NFKB1
Insulin resistance(K)	109	6	4.84E-04	GSK3B,PYGM,PRKCQ,PIK3R1,ACACB,NFKB1
Pancreatic cancer(K)	66	5	5.40E-04	CASP9,TGFBR2,PIK3R1,TGFB2,NFKB1

Fc epsilon receptor (FCERI) signaling(R)	405	10	6.24E-04	GSK3B,FGF2,CASP9,SYK,PRKCQ,CARD11,PIK3R1,NCAM1,NFATC2,NFKB1
TCR signaling(R)	123	6	7.96E-04	PRKCQ,CARD11,PIK3R1,PAG1,NFKB1,PTPRC
Osteoclast differentiation(K)	132	6	1.03E-03	SYK,TGFBR2,PIK3R1,TGFB2,NFATC2,NFKB1
Signaling by the B Cell Receptor (BCR)(R)	270	8	1.03E-03	GSK3B,FGF2,CASP9,SYK,STIM1,CARD11,PIK3R1,NFKB1
Atypical NF-kappaB pathway(N)	14	3	1.03E-03	SYK,PIK3R1,NFKB1
T cell activation(P)	81	5	1.03E-03	PRKCQ,PIK3R1,NFATC2,NFKB1,PTPRC
Prostate cancer(K)	89	5	1.49E-03	GSK3B,IGF1R,CASP9,PIK3R1,NFKB1
Hepatitis B(K)	146	6	1.49E-03	CASP9,PIK3R1,TGFB2,EGR3,NFATC2,NFKB1
Integrins in angiogenesis(N)	47	4	1.56E-03	FGF2,IGF1R,TGFBR2,PIK3R1
Fc-epsilon receptor I signaling in mast cells(N)	62	4	4.28E-03	SYK,PIK3R1,NFATC2,NFKB1
HTLV-I infection(K)	258	7	4.28E-03	GSK3B,ETS1,TGFBR2,PIK3R1,TGFB2,NFATC2,NFKB1
Regulation of retinoblastoma protein(N)	64	4	4.48E-03	ELF1,MYL1,MYOD1,TGFB2
Toxoplasmosis(K)	118	5	4.49E-03	CASP9,LAMA2,PIK3R1,TGFB2,NFKB1
Osteopontin-mediated events(N)	29	3	5.96E-03	SYK,PIK3R1,NFKB1
Adherens junction(K)	72	4	5.96E-03	WASL,IGF1R,TGFBR2,NECTIN3
Focal adhesion(K)	201	6	5.96E-03	GSK3B,IGF1R,COL4A2,COL4A1,LAMA2,PIK3R1
IGF1 pathway(N)	30	3	5.96E-03	IGF1R,GRB10,PIK3R1
Chronic myeloid leukemia(K)	73	4	5.96E-03	TGFBR2,PIK3R1,TGFB2,NFKB1
FoxO signaling pathway(K)	134	5	6.50E-03	IGF1R,TGFBR2,PIK3R1,TGFB2,FBXO32
IL1-mediated signaling events(N)	34	3	7.79E-03	IL1RAP,PIK3R1,NFKB1
Signaling pathways regulating pluripotency of stem cells(K)	142	5	7.79E-03	GSK3B,FGF2,IGF1R,PIK3R1,BMPR1B
EGFR tyrosine kinase inhibitor resistance(K)	81	4	8.11E-03	GSK3B,FGF2,IGF1R,PIK3R1
TGF-beta signaling pathway(K)	84	4	9.27E-03	DCN,TGFBR2,TGFB2,BMPR1B
Signaling by PDGF(R)	328	7	0.0113	GSK3B,FGF2,CASP9,COL4A2,COL4A1,PIK3R1,NCAM1
Th1 and Th2 cell differentiation(K)	92	4	0.0113	MAML2,PRKCQ,NFATC2,NFKB1

Fc gamma R-mediated phagocytosis(K)	93	4	0.0113	WASL,SYK,PIK3R1,PTPRC
cxcr4 signaling pathway(B)	10	2	0.0113	CXCR4,PIK3R1
NF-kappa B signaling pathway(K)	95	4	0.0122	SYK,PRKCQ,CARD11,NFKB1
Calcineurin-regulated NFAT-dependent transcription in lymphocytes(N)	46	3	0.0152	PRKCQ,EGR3,NFATC2
Endocytosis(K)	260	6	0.0155	WASL,IGF1R,TGFBR2,CXCR4,TGFB2,EHD1
Chagas disease (American trypanosomiasis)(K)	104	4	0.0155	TGFBR2,PIK3R1,TGFB2,NFKB1
Axon guidance(K)	177	5	0.0155	GSK3B,CXCR4,PIK3R1,NFATC2,BMPR1B
SHP2 signaling(N)	51	3	0.0172	IGF1R,PIK3R1,PAG1
PIP3 activates AKT signaling(R)	111	4	0.0172	GSK3B,FGF2,CASP9,PIK3R1
Role of Calcineurin-dependent NFAT signaling in lymphocytes(N)	52	3	0.0172	GSK3B,PRKCQ,NFATC2
Signaling events mediated by Stem cell factor receptor (c-Kit)(N)	52	3	0.0172	GSK3B,GRB10,PIK3R1
Endometrial cancer(K)	52	3	0.0172	GSK3B,CASP9,PIK3R1
Chemokine signaling pathway(K)	187	5	0.0174	GSK3B,WASL,CXCR4,PIK3R1,NFKB1
Signaling by SCF-KIT(R)	290	6	0.0224	GSK3B,FGF2,CASP9,GRB10,PIK3R1,NCAM1
role of pi3k subunit p85 in regulation of actin organization and cell migration(B)	16	2	0.0224	WASL,PIK3R1
B cell activation(P)	59	3	0.0224	SYK,NFATC2,PTPRC
Viral carcinogenesis(K)	203	5	0.0224	SYK,HDAC4,PIK3R1,EGR3,NFKB1
Epstein-Barr virus infection(K)	204	5	0.0224	GSK3B,SYK,HDAC4,PIK3R1,NFKB1
control of skeletal myogenesis by hdac and calcium/calmodulin-dependent kinase (camk)(B)	17	2	0.0224	MYOD1,PIK3R1
Signaling events mediated by focal adhesion kinase(N)	60	3	0.0225	WASL,ETS1,PIK3R1
Proteoglycans in cancer(K)	205	5	0.0226	FGF2,IGF1R,DCN,PIK3R1,TGFB2

VEGF signaling pathway(K)	61	3	0.0235	CASP9,PIK3R1,NFATC2
VEGF signaling pathway(P)	18	2	0.025	ETS1,CASP9
LPA receptor mediated events(N)	63	3	0.0251	GSK3B,PIK3R1,NFKB1
Inflammatory bowel disease (IBD)(K)	65	3	0.0251	RORA,TGFB2,NFKB1
HIF-1-alpha transcription factor network(N)	65	3	0.0251	RORA,ETS1,CXCR4
Angiogenesis(P)	66	3	0.0251	GSK3B,ETS1,CASP9
Renal cell carcinoma(K)	67	3	0.0258	ETS1,PIK3R1,TGFB2
Signaling by EGFR(R)	317	6	0.0258	GSK3B,FGF2,CASP9,PIK3R1,NCAM 1,PAG1
Measles(K)	136	4	0.0258	GSK3B,PRKCQ,PIK3R1,NFKB1
C-type lectin receptors (CLRs)(R)	139	4	0.0258	SYK,CARD11,NFATC2,NFKB1
DAP12 interactions(R)	323	6	0.0258	GSK3B,FGF2,CASP9,SYK,PIK3R1,N CAM1
Insulin signaling pathway(K)	140	4	0.0258	GSK3B,PYGM,PIK3R1,ACACB
AP-1 transcription factor network(N)	70	3	0.0258	ETS1,ELF1,NFATC2
CDC42 signaling events(N)	70	3	0.0258	GSK3B,WASL,PIK3R1
Adipocytokine signaling pathway(K)	70	3	0.0258	PRKCQ,ACACB,NFKB1
Melanoma(K)	71	3	0.0258	FGF2,IGF1R,PIK3R1
Ras signaling pathway(K)	229	5	0.0258	ETS1,FGF2,IGF1R,PIK3R1,NFKB1
ctcf: first multivalent nuclear factor(B)	22	2	0.0264	PIK3R1,TGFB2
Nephrin interactions(R)	22	2	0.0264	WASL,PIK3R1
Prolactin signaling pathway(K)	72	3	0.0266	GSK3B,PIK3R1,NFKB1
Breast cancer(K)	146	4	0.0283	GSK3B,FGF2,IGF1R,PIK3R1
Effects of PIP2 hydrolysis(R)	23	2	0.0287	PRKCQ,DGKH
Signaling events mediated by the Hedgehog family(N)	23	2	0.0287	PIK3R1,TGFB2
Glypican 1 network(N)	25	2	0.0304	FGF2,TGFBR2
Signaling by Interleukins(R)	460	7	0.0304	RORA,IL1RAP,FGF2,SYK,PIK3R1,N CAM1,NFKB1
Hippo signaling pathway(K)	154	4	0.0304	GSK3B,TGFBR2,TGFB2,BMPR1B
mTOR signaling pathway(K)	154	4	0.0304	GSK3B,IGF1R,GRB10,PIK3R1
TGF-beta signaling pathway(P)	80	3	0.0304	TGFBR2,TGFB2,BMPR1B

CXCR4-mediated signaling events(N)	80	3	0.0304	CXCR4,PAG1,PTPRC
Signaling events mediated by Hepatocyte Growth Factor Receptor (c-Met)(N)	80	3	0.0304	WASL,ETS1,PIK3R1
Signaling events mediated by HDAC Class III(N)	26	2	0.0304	MYOD1,HDAC4
Integrin signalling pathway(P)	158	4	0.0304	COL4A2,COL4A1,COL13A1,PIK3R1
ECM-receptor interaction(K)	82	3	0.0304	COL4A2,COL4A1,LAMA2
Insulin-mediated glucose transport(N)	27	2	0.0313	GSK3B,STXBP4
Reelin signaling pathway(N)	28	2	0.0335	GSK3B,PIK3R1
IL2 signaling events mediated by STAT5(N)	28	2	0.0335	ELF1,PIK3R1
Cytokine-cytokine receptor interaction(K)	265	5	0.0375	IL1RAP,TGFBR2,CXCR4,TGFB2,BMPR1B
Nectin adhesion pathway(N)	30	2	0.0383	PIK3R1,NECTIN3
Protein digestion and absorption(K)	90	3	0.0391	COL4A2,COL4A1,COL13A1
Wnt signaling pathway(P)	268	5	0.0392	GSK3B,MYH1,PRKCQ,NFATC2,BMPR1B
Striated Muscle Contraction(R)	31	2	0.0407	MYBPC1,MYL1
Influenza A(K)	175	4	0.0421	GSK3B,CASP9,PIK3R1,NFKB1
Syndecan-4-mediated signaling events(N)	32	2	0.0427	FGF2,CXCR4
Netrin-mediated signaling events(N)	32	2	0.0427	WASL,PIK3R1
Propanoate metabolism(K)	32	2	0.0427	HADHA,ACACB
Longevity regulating pathway(K)	94	3	0.0427	IGF1R,PIK3R1,NFKB1
Tuberculosis(K)	179	4	0.0427	CASP9,SYK,TGFB2,NFKB1
EPO signaling pathway(N)	33	2	0.0427	PIK3R1,NFKB1
HIV-1 Nef: Negative effector of Fas and TNF-alpha(N)	33	2	0.0427	CASP9,NFKB1
Inflammatory mediator regulation of TRP channels(K)	99	3	0.0427	IL1RAP,PRKCQ,PIK3R1
IL2 signaling events mediated by PI3K(N)	35	2	0.0427	PIK3R1,NFKB1
signal transduction through il1r(B)	35	2	0.0427	IL1RAP,TGFB2

Class I PI3K signaling events mediated by Akt(N)	35	2	0.0427	GSK3B,CASP9
Choline metabolism in cancer(K)	101	3	0.0427	WASL,DGKH,PIK3R1
Trk receptor signaling mediated by PI3K and PLC-gamma(N)	36	2	0.0427	GSK3B,PIK3R1
HIF-1 signaling pathway(K)	103	3	0.0427	IGF1R,PIK3R1,NFKB1
Validated transcriptional targets of AP1 family members Fra1 and Fra2(N)	37	2	0.0427	DCN,NFATC2
IL23-mediated signaling events(N)	37	2	0.0427	PIK3R1,NFKB1
GMCSF-mediated signaling events(N)	37	2	0.0427	SYK,PIK3R1
hiv-1 defeats host-mediated resistance by cem15(B)	3	1	0.0436	CXCR4
EPHB forward signaling(N)	38	2	0.0449	WASL,PIK3R1
Signaling events regulated by Ret tyrosine kinase(N)	39	2	0.0472	GRB10,PIK3R1
Signalling by NGF(R)	421	6	0.049	GSK3B,FGF2,CASP9,PIK3R1,NCAM 1,NFKB1
Signaling by FGFR3(R)	40	2	0.0495	FGF2,PIK3R1
activation of csk by camp-dependent protein kinase inhibits signaling through the t cell receptor(B)	41	2	0.0518	CXCR4,PTPRC
Signaling by FGFR4(R)	41	2	0.0518	FGF2,PIK3R1
Netrin-1 signaling(R)	42	2	0.0542	WASL,PRKCQ
Plasma membrane estrogen receptor signaling(N)	42	2	0.0542	IGF1R,PIK3R1
Beta3 integrin cell surface interactions(N)	43	2	0.0566	TGFBR2,COL4A1
Axon guidance mediated by netrin(P)	4	1	0.058	NFATC2
phospholipase c signaling pathway(B)	4	1	0.058	PIK3R1
Thyroid hormone signaling pathway(K)	118	3	0.0601	GSK3B,CASP9,PIK3R1
Validated transcriptional targets of deltaNp63 isoforms(N)	45	2	0.0616	GSK3B,STXBP4
Insulin Pathway(N)	45	2	0.0616	GRB10,PIK3R1

PDGFR-beta signaling pathway(N)	120	3	0.0628	WASL,GRB10,PAG1
Neurotrophin signaling pathway(K)	121	3	0.0642	GSK3B,PIK3R1,NFKB1
Platelet activation(K)	122	3	0.0656	SYK,STIM1,PIK3R1
FGF signaling pathway(N)	47	2	0.0667	PIK3R1,NCAM1
Notch-mediated HES/HEY network(N)	47	2	0.0667	MAML2,MYOD1
keratinocyte differentiation(B)	47	2	0.0667	ETS1,PRKCQ
AMPK signaling pathway(K)	124	3	0.0667	IGF1R,PIK3R1,ACACB
RET signaling(R)	222	4	0.0667	FGF2,GRB10,PIK3R1,NCAM1
GPVI-mediated activation cascade(R)	49	2	0.0667	SYK,PIK3R1
Signaling by FGFR1(R)	49	2	0.0667	FGF2,PIK3R1
NCAM signaling for neurite out-growth(R)	231	4	0.0667	FGF2,COL4A2,COL4A1,NCAM1
Metabolism of carbohydrates(R)	233	4	0.0667	PYGM,DCN,GPC5,B3GAT2
Hepatitis C(K)	133	3	0.0667	GSK3B,PIK3R1,NFKB1
Natural killer cell mediated cytotoxicity(K)	135	3	0.0667	SYK,PIK3R1,NFATC2
Thromboxane A2 receptor signaling(N)	54	2	0.0667	SYK,PRKCQ
IL2-mediated signaling events(N)	54	2	0.0667	SYK,PIK3R1
Alternative NF-kappaB pathway(N)	6	1	0.0667	NFKB1
Legionellosis(K)	55	2	0.0667	CASP9,NFKB1
Non-small cell lung cancer(K)	56	2	0.0667	CASP9,PIK3R1
Apoptosis(K)	140	3	0.0667	CASP9,PIK3R1,NFKB1
Acute myeloid leukemia(K)	57	2	0.0667	PIK3R1,NFKB1
Phospholipase D signaling pathway(K)	144	3	0.0667	SYK,DGKH,PIK3R1
Viral myocarditis(K)	59	2	0.0677	CASP9,LAMA2
Cell adhesion molecules (CAMs)(K)	145	3	0.0679	NCAM1,PTPRC,NECTIN3
MAPK signaling pathway(K)	255	4	0.0715	FGF2,TGFBR2,TGFB2,NFKB1
Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R)(R)	255	4	0.0715	FGF2,IGF1R,PIK3R1,NCAM1
Gastrin-CREB signalling pathway via PKC and MAPK(R)	376	5	0.0721	FGF2,PRKCQ,DGKH,PIK3R1,NCAM 1
Non-alcoholic fatty liver disease (NAFLD)(K)	151	3	0.0751	GSK3B,PIK3R1,NFKB1

IL4-mediated signaling events(N)	63	2	0.0762	ETS1,PIK3R1
Ras Pathway(P)	63	2	0.0762	GSK3B,ETS1
Ligand-independent caspase activation via DCC(R)	8	1	0.0766	CASP9
pertussis toxin-insensitive ccr5 signaling in macrophage(B)	8	1	0.0766	CXCR4
signal dependent regulation of myogenesis by corepressor mitr(B)	8	1	0.0766	MYOD1
Downstream signaling in naïve CD8+ T cells(N)	64	2	0.0784	PRKCQ,NFATC2
Longevity regulating pathway - multiple species(K)	64	2	0.0784	IGF1R,PIK3R1
Semaphorin interactions(R)	65	2	0.0806	GSK3B,PTPRC
Shigellosis(K)	65	2	0.0806	WASL,NFKB1
Glioma(K)	66	2	0.0829	IGF1R,PIK3R1
Beta1 integrin cell surface interactions(N)	66	2	0.0829	COL4A1,LAMA2
Fcgamma receptor (FCGR) dependent phagocytosis(R)	159	3	0.0854	WASL,SYK,PIK3R1
regulators of bone mineralization(B)	9	1	0.0859	COL4A2
5-Hydroxytryptamine degredation(P)	9	1	0.0859	ALDH1A2
p75(NTR)-mediated signaling(N)	69	2	0.0898	CASP9,PIK3R1
Fc epsilon RI signaling pathway(K)	70	2	0.0921	SYK,PIK3R1
Signaling by Insulin receptor(R)	277	4	0.0922	FGF2,GRB10,PIK3R1,NCAM1
Signaling by FGFR2(R)	71	2	0.0945	FGF2,PIK3R1
GP1b-IX-V activation signalling(R)	10	1	0.0952	PIK3R1
Leishmaniasis(K)	73	2	0.0992	TGFB2,NFKB1
Platinum drug resistance(K)	75	2	0.1007	CASP9,PIK3R1
il-7 signal transduction(B)	11	1	0.1007	PIK3R1
Alpha6 beta4 integrin-ligand interactions(N)	11	1	0.1007	LAMA2
how does salmonella hijack a cell(B)	11	1	0.1007	WASL
Glucocorticoid receptor regulatory network(N)	78	2	0.1007	GSK3B,NFKB1

Bacterial invasion of epithelial cells(K)	78	2	0.1007	WASL,PIK3R1
insulin signaling pathway(B)	12	1	0.1007	PIK3R1
trka receptor signaling pathway(B)	12	1	0.1007	PIK3R1
Transcriptional misregulation in cancer(K)	180	3	0.1007	IGF1R,TGFBR2,NFKB1
C-MYB transcription factor network(N)	82	2	0.1007	ETS1,MYOD1
human cytomegalovirus and map kinase pathways(B)	13	1	0.1007	PIK3R1
Fatty acid biosynthesis(K)	13	1	0.1007	ACACB
b cell survival pathway(B)	13	1	0.1007	PIK3R1
multiple antiapoptotic pathways from igf-1r signaling lead to bad phosphorylation(B)	13	1	0.1007	PIK3R1
Visual phototransduction(R)	83	2	0.1007	PRKCQ,GPC5
Hypertrophic cardiomyopathy (HCM)(K)	83	2	0.1007	LAMA2,TGFB2
IL5-mediated signaling events(N)	14	1	0.1007	PIK3R1
Salmonella infection(K)	86	2	0.1007	WASL,NFKB1
ErbB signaling pathway(K)	88	2	0.1007	GSK3B,PIK3R1
Sumoylation by RanBP2 regulates transcriptional repression(N)	15	1	0.1007	HDAC4
Dilated cardiomyopathy(K)	90	2	0.1007	LAMA2,TGFB2
FGF signaling pathway(P)	92	2	0.1007	FGF2,PRKCQ
nerve growth factor pathway (ngf)(B)	16	1	0.1007	PIK3R1
y branching of actin filaments(B)	16	1	0.1007	WASL
akt signaling pathway(B)	16	1	0.1007	PIK3R1
the igf-1 receptor and longevity(B)	16	1	0.1007	PIK3R1
role of nicotinic acetylcholine receptors in the regulation of apoptosis(B)	16	1	0.1007	PIK3R1

pten dependent cell cycle arrest and apoptosis(B)	17	1	0.1007	PIK3R1
Endocrine resistance(K)	98	2	0.1007	IGF1R,PIK3R1
Progesterone-mediated oocyte maturation(K)	98	2	0.1007	IGF1R,PIK3R1
EPHA2 forward signaling(N)	18	1	0.1007	PIK3R1
Metabolism of nitric oxide(R)	18	1	0.1007	WASL
Degradation of beta catenin(N)	18	1	0.1007	GSK3B
mets affect on macrophage differentiation(B)	18	1	0.1007	ETS1
Phosphatidylinositol signaling system(K)	99	2	0.1007	DGKH,PIK3R1
Rap1 signaling pathway(K)	212	3	0.1007	FGF2,IGF1R,PIK3R1
Regulation of actin cytoskeleton(K)	214	3	0.1007	WASL,FGF2,PIK3R1
sprouty regulation of tyrosine kinase signals(B)	19	1	0.1007	PTPRC
tgf beta signaling pathway(B)	19	1	0.1007	TGFB2
tumor suppressor arf inhibits ribosomal biogenesis(B)	19	1	0.1007	PIK3R1
Glucagon signaling pathway(K)	103	2	0.1007	PYGM,ACACB
Canonical Wnt signaling pathway(N)	20	1	0.1007	GSK3B
the co-stimulatory signal during t-cell activation(B)	20	1	0.1007	PIK3R1
regulation of bad phosphorylation(B)	20	1	0.1007	PIK3R1
Toll-like receptor signaling pathway(K)	106	2	0.1007	PIK3R1,NFKB1
Cardiac conduction(R)	107	2	0.1007	TRDN,STIM1
egf signaling pathway(B)	21	1	0.1007	PIK3R1
growth hormone signaling pathway(B)	21	1	0.1007	PIK3R1
E-cadherin signaling in keratinocytes(N)	21	1	0.1007	PIK3R1
igf-1 signaling pathway(B)	21	1	0.1007	PIK3R1
PDGFR-alpha signaling pathway(N)	21	1	0.1007	PIK3R1
nf-kb signaling pathway(B)	21	1	0.1007	NFKB1

TNF signaling pathway(K)	110	2	0.1007	PIK3R1,NFKB1
intrinsic prothrombin activation pathway(B)	22	1	0.1018	COL4A2
ras signaling pathway(B)	22	1	0.1018	PIK3R1
inhibition of cellular proliferation by gleevec(B)	22	1	0.1018	PIK3R1
influence of ras and rho proteins on g1 to s transition(B)	22	1	0.1018	PIK3R1
Nicotinic acetylcholine receptor signaling pathway(P)	22	1	0.1018	MYH1
alk in cardiac myocytes(B)	23	1	0.1062	TGFB2
Signaling by BMP(R)	23	1	0.1062	BMPR1B
Canonical NF-kappaB pathway(N)	23	1	0.1062	NFKB1
Biosynthesis of unsaturated fatty acids(K)	23	1	0.1062	HADHA
regulation of eif-4e and p70s6 kinase(B)	23	1	0.1062	PIK3R1
role of erk5 in neuronal survival pathway(B)	23	1	0.1062	PIK3R1
Mannose type O-glycan biosynthesis(K)	23	1	0.1062	B3GAT2
Leukocyte transendothelial migration(K)	116	2	0.11	CXCR4,PIK3R1
corticosteroids and cardioprotection(B)	24	1	0.1106	PIK3R1
mtor signaling pathway(B)	24	1	0.1106	PIK3R1
nfkb activation by nontypeable hemophilus influenzae(B)	24	1	0.1106	TGFB2
Hypoxia response via HIF activation(P)	24	1	0.1106	PIK3R1
transcription factor creb and its extracellular signals(B)	24	1	0.1106	PIK3R1
Myogenesis(R)	24	1	0.1106	MYOD1
Ephrin B reverse signaling(N)	24	1	0.1106	PIK3R1
skeletal muscle hypertrophy is regulated via akt-mtor pathway(B)	24	1	0.1106	PIK3R1

VEGFR3 signaling in lymphatic endothelium(N)	25	1	0.1149	PIK3R1
Fatty acid elongation(K)	25	1	0.1149	HADHA
Nongenotropic Androgen signaling(N)	25	1	0.1149	PIK3R1
ras-independent pathway in nk cell-mediated cytotoxicity(B)	25	1	0.1149	PIK3R1
S1P3 pathway(N)	25	1	0.1149	CXCR4
C-MYC pathway(N)	25	1	0.1149	GSK3B
fc epsilon receptor i signaling in mast cells(B)	25	1	0.1149	PIK3R1
Nephrin/Neph1 signaling in the kidney podocyte(N)	25	1	0.1149	WASL
tpo signaling pathway(B)	25	1	0.1149	PIK3R1
Sphingolipid signaling pathway(K)	120	2	0.1163	PIK3R1,NFKB1
S1P2 pathway(N)	26	1	0.1192	PIK3R1
IL3-mediated signaling events(N)	26	1	0.1192	PIK3R1
bioactive peptide induced signaling pathway(B)	26	1	0.1192	PIK3R1
pdgf signaling pathway(B)	26	1	0.1192	PIK3R1
PI3 kinase pathway(P)	26	1	0.1192	GSK3B
ALK1 signaling events(N)	26	1	0.1192	TGFBR2
Apoptosis signaling pathway(P)	26	1	0.1192	PRKCQ
activation of camp-dependent protein kinase pka(B)	26	1	0.1192	CXCR4
ß-arrestins in gpcr desensitization(B)	26	1	0.1192	CXCR4
Binding and Uptake of Ligands by Scavenger Receptors(R)	124	2	0.1227	COL4A2,COL4A1
Cell cycle(K)	124	2	0.1227	GSK3B,TGFB2
Calcium signaling in the CD4+ TCR pathway(N)	27	1	0.1235	NFATC2
thrombin signaling and protease-activated receptors(B)	27	1	0.1235	PIK3R1
VEGFR1 specific signals(N)	27	1	0.1235	PIK3R1
Integrin alphaIIb beta3 signaling(R)	27	1	0.1235	SYK

role of ß-arrestins in the activation and targeting of map kinases(B)	28	1	0.1278	CXCR4
Signaling by NOTCH2(R)	28	1	0.1278	MAML2
role of erbb2 in signal transduction and oncology(B)	28	1	0.1278	PIK3R1
Butanoate metabolism(K)	28	1	0.1278	HADHA
vegf hypoxia and angiogenesis(B)	28	1	0.1278	PIK3R1
Dorso-ventral axis formation(K)	28	1	0.1278	ETS1
EGF receptor (ErbB1) signaling pathway(N)	29	1	0.1321	WASL
CD40/CD40L signaling(N)	29	1	0.1321	NFKB1
erk and pi-3 kinase are necessary for collagen binding in corneal epithelia(B)	30	1	0.1363	PIK3R1
Alpha-synuclein signaling(N)	30	1	0.1363	SYK
Circadian rhythm(K)	31	1	0.1405	RORA
Aurora A signaling(N)	31	1	0.1405	GSK3B
beta-Alanine metabolism(K)	31	1	0.1405	HADHA
amb2 Integrin signaling(N)	31	1	0.1405	NFKB1
Detoxification of Reactive Oxygen Species(R)	31	1	0.1405	PRDX6
phospholipids as signalling intermediaries(B)	31	1	0.1405	PIK3R1
Mucin type O-glycan biosynthesis(K)	31	1	0.1405	C1GALT1
Antifolate resistance(K)	31	1	0.1405	NFKB1
trefoil factors initiate mucosal healing(B)	31	1	0.1405	PIK3R1
Tight junction(K)	137	2	0.1441	MYH1,PRKCQ
Oncogene Induced Senescence(R)	32	1	0.1447	ETS1
HIF-2-alpha transcription factor network(N)	32	1	0.1447	ETS1
roles of ß arrestin dependent recruitment of src kinases in gpcr signaling(B)	32	1	0.1447	CXCR4
FAS (CD95) signaling pathway(N)	32	1	0.1447	SYK

Noncanonical Wnt signaling pathway(N)	32	1	0.1447	NFATC2
N-cadherin signaling events(N)	33	1	0.1489	PIK3R1
Apoptosis - multiple species(K)	33	1	0.1489	CASP9
FAS signaling pathway(P)	33	1	0.1489	CASP9
actions of nitric oxide in the heart(B)	34	1	0.153	PIK3R1
Signaling by Retinoic Acid(R)	34	1	0.153	ALDH1A2
Wnt signaling pathway(K)	143	2	0.1542	GSK3B,NFATC2
a6b1 and a6b4 Integrin signaling(N)	35	1	0.1572	PIK3R1
B-WICH complex positively regulates rRNA expression(R)	35	1	0.1572	GSK3B
Prion diseases(K)	35	1	0.1572	NCAM1
Metabolic pathways(K)	1266	9	0.1586	PYGM,HADHA,ALDH1A2,DGKH,PON1,ACACB,B3GAT2,C1GALT1,PRDX6
Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated pathway(P)	147	2	0.161	GSK3B,PYGM
Transcriptional regulation of pluripotent stem cells(R)	36	1	0.1613	FGF2
chrebp regulation by carbohydrates and camp(B)	36	1	0.1613	CXCR4
Arachidonic acid metabolism(R)	36	1	0.1613	PON1
Starch and sucrose metabolism(K)	36	1	0.1613	PYGM
inactivation of gsk3 by akt causes accumulation of b-catenin in alveolar macrophages(B)	36	1	0.1613	PIK3R1
E-cadherin signaling in the nascent adherens junction(N)	36	1	0.1613	PIK3R1
Signaling by VEGF(R)	287	3	0.1645	FGF2,PIK3R1,NCAM1
Primary immunodeficiency(K)	37	1	0.1654	PTPRC
Platelet Aggregation (Plug Formation)(R)	37	1	0.1654	SYK

rac1 cell motility signaling pathway(B)	37	1	0.1654	PIK3R1
nfat and hypertrophy of the heart (B)	37	1	0.1654	PIK3R1
Retinoid metabolism and transport(R)	38	1	0.1694	GPC5
Pre-NOTCH Expression and Processing(R)	38	1	0.1694	MAML2
Signaling events mediated by HDAC Class II(N)	38	1	0.1694	HDAC4
Aldosterone-regulated sodium reabsorption(K)	39	1	0.1735	PIK3R1
Pyruvate metabolism(K)	39	1	0.1735	ACACB
IFN-gamma pathway(N)	40	1	0.1775	PIK3R1
Tryptophan metabolism(K)	40	1	0.1775	HADHA
Class I PI3K signaling events(N)	40	1	0.1775	SYK
MicroRNAs in cancer(K)	299	3	0.1788	HDAC4,TGFB2,NFKB1
Intrinsic Pathway for Apoptosis(R)	41	1	0.1815	CASP9
BMP receptor signaling(N)	41	1	0.1815	BMPR1B
Oxytocin signaling pathway(K)	159	2	0.1818	PIK3R1,NFATC2
Stabilization and expansion of the E-cadherin adherens junction(N)	42	1	0.1855	IGF1R
Signaling by ERBB4(R)	42	1	0.1855	PIK3R1
ion channels and their functional role in vascular endothelium(B)	43	1	0.1895	CXCR4
Signaling by ERBB2(R)	43	1	0.1895	PIK3R1
PAR1-mediated thrombin signaling events(N)	43	1	0.1895	PIK3R1
LKB1 signaling events(N)	43	1	0.1895	GSK3B
Fatty acid degradation(K)	44	1	0.1935	HADHA
il-2 receptor beta chain in t cell activation(B)	44	1	0.1935	PIK3R1
Integrin-linked kinase signaling(N)	45	1	0.1974	GSK3B
Presenilin action in Notch and Wnt signaling(N)	45	1	0.1974	GSK3B
cGMP-PKG signaling pathway(K)	168	2	0.1977	PIK3R1,NFATC2
Carbohydrate digestion and absorption(K)	46	1	0.2013	PIK3R1

TNF receptor signaling pathway(N)	46	1	0.2013	NFKB1
Alzheimer's disease(K)	171	2	0.203	GSK3B,CASP9
Hedgehog signaling pathway(K)	47	1	0.2052	GSK3B
IL6-mediated signaling events(N)	47	1	0.2052	PIK3R1
TGF-beta receptor signaling(N)	47	1	0.2052	TGFBR2
Apoptotic execution phase(R)	47	1	0.2052	PRKCQ
Hedgehog signaling events mediated by Gli proteins(N)	48	1	0.2091	GSK3B
Ceramide signaling pathway(N)	48	1	0.2091	NFKB1
Fatty acid metabolism(K)	48	1	0.2091	HADHA
Posttranslational regulation of adherens junction stability and dissassembly(N)	48	1	0.2091	IGF1R
Type II diabetes mellitus(K)	48	1	0.2091	PIK3R1
t cell receptor signaling pathway(B)	48	1	0.2091	PIK3R1
FoxO family signaling(N)	48	1	0.2091	FBXO32
Valine, leucine and isoleucine degradation(K)	48	1	0.2091	HADHA
Notch signaling pathway(K)	48	1	0.2091	MAML2
Cocaine addiction(K)	49	1	0.213	NFKB1
Regulation of Androgen receptor activity(N)	49	1	0.213	GSK3B
Malaria(K)	49	1	0.213	TGFB2
Intestinal immune network for IgA production(K)	49	1	0.213	CXCR4
Ovarian steroidogenesis(K)	50	1	0.2168	IGF1R
Amyotrophic lateral sclerosis (ALS)(K)	51	1	0.2207	CASP9
Senescence-Associated Secretory Phenotype (SASP)(R)	52	1	0.2245	NFKB1
Signaling events mediated by PTP1B(N)	52	1	0.2245	PIK3R1
Caspase cascade in apoptosis(N)	52	1	0.2245	CASP9
Notch signaling pathway(N)	52	1	0.2245	MAML2

Signaling by MET(R)	52	1	0.2245	PIK3R1
Regulation of cholesterol biosynthesis by SREBP (SREBF)(R)	53	1	0.2283	ACACB
Interleukin signaling pathway(P)	55	1	0.2358	GSK3B
Endothelin signaling pathway(P)	55	1	0.2358	PRKCQ
Basal cell carcinoma(K)	55	1	0.2358	GSK3B
Pathogenic Escherichia coli infection(K)	55	1	0.2358	WASL
Regulation of lipolysis in adipocytes(K)	56	1	0.2395	PIK3R1
Signaling events mediated by HDAC Class I(N)	56	1	0.2395	NFKB1
p53 pathway(N)	57	1	0.2433	GSK3B
Fatty acid, triacylglycerol, and ketone body metabolism(R)	195	2	0.2461	RORA,HADHA
ATF-2 transcription factor network(N)	58	1	0.247	TGFB2

Table 28

GeneSet	Number Of Protein In Gene Set	Protein From Network	FDR	Nodes
T cell receptor signaling pathway(K)	105	6	1.54E-04	PIK3R1,CBL,PPP3CA,PPP3CC,PLCG1,SOS1
Th17 cell differentiation(K)	107	6	1.54E-04	PPP3CA,PPP3CC,TBX21,PLCG1,IRF4,IL17A
BCR signaling pathway(N)	65	5	2.02E-04	PIK3R1,PPP3CA,PPP3CC,TRAF6,SOS1
EPO signaling pathway(N)	33	4	3.11E-04	PIK3R1,CBL,PLCG1,SOS1
T cell activation(P)	81	5	3.49E-04	PIK3R1,PPP3CA,PPP3CC,PLCG1,SOS1
Signaling by FGFR3(R)	40	4	4.10E-04	PIK3R1,CBL,PLCG1,SOS1
Signaling by FGFR4(R)	41	4	4.10E-04	PIK3R1,CBL,PLCG1,SOS1
FGF signaling pathway(N)	47	4	6.22E-04	PIK3R1,CBL,PLCG1,SOS1
Signaling by FGFR1(R)	49	4	6.40E-04	PIK3R1,CBL,PLCG1,SOS1
TCR signaling in naïve CD8+ T cells(N)	54	4	8.45E-04	CBL,PLCG1,TRAF6,SOS1
VEGF signaling pathway(K)	61	4	1.10E-03	PIK3R1,PPP3CA,PPP3CC,PLCG1
PDGFR-alpha signaling pathway(N)	21	3	1.10E-03	PIK3R1,PLCG1,SOS1
Fc-epsilon receptor I signaling in mast cells(N)	62	4	1.10E-03	PIK3R1,CBL,PLCG1,SOS1

Renin secretion(K)	65	4	1.23E-03	PPP3CA,PPP3CC,AGT,ADRB3
TCR signaling in naïve CD4+ T cells(N)	67	4	1.26E-03	CBL,PLCG1,TRAF6,SOS1
Natural killer cell mediated cytotoxicity(K)	135	5	1.26E-03	PIK3R1,PPP3CA,PPP3CC,PLCG1,SOS1
Signaling by FGFR2(R)	71	4	1.41E-03	PIK3R1,CBL,PLCG1,SOS1
B cell receptor signaling pathway(K)	73	4	1.50E-03	PIK3R1,PPP3CA,PPP3CC,SOS1
VEGFR1 specific signals(N)	27	3	1.58E-03	PIK3R1,CBL,PLCG1
EGF receptor (ErbB1) signaling pathway(N)	29	3	1.82E-03	PLCG1,GSN,SOS1
Signaling events mediated by Hepatocyte Growth Factor Receptor (c-Met)(N)	80	4	1.82E-03	PIK3R1,CBL,PLCG1,SOS1
N-cadherin signaling events(N)	33	3	2.33E-03	PIK3R1,PLCG1,GSN
ErbB signaling pathway(K)	88	4	2.33E-03	PIK3R1,CBL,PLCG1,SOS1
Th1 and Th2 cell differentiation(K)	92	4	2.60E-03	PPP3CA,PPP3CC,TBX21,PLCG1
Trk receptor signaling mediated by PI3K and PLC-gamma(N)	36	3	2.60E-03	PIK3R1,PLCG1,SOS1
Axon guidance(K)	177	5	2.60E-03	PIK3R1,PPP3CA,PPP3CC,PLCG1,BMPR1B
Calcium signaling pathway(K)	182	5	2.96E-03	HTR2A,PPP3CA,PPP3CC,PLCG1,ADRB3
Glucagon signaling pathway(K)	103	4	3.45E-03	PPP3CA,PPP3CC,PCK1,PPARA
Signaling by ERBB2(R)	43	3	4.02E-03	PIK3R1,PLCG1,SOS1
Insulin Pathway(N)	45	3	4.24E-03	PIK3R1,CBL,SOS1
IL6-mediated signaling events(N)	47	3	4.81E-03	PIK3R1,LMO4,SOS1
Neurotrophin signaling pathway(K)	121	4	5.37E-03	PIK3R1,PLCG1,TRAF6,SOS1
SHP2 signaling(N)	51	3	5.37E-03	PIK3R1,LMO4,SOS1
Signaling events mediated by Stem cell factor receptor (c-Kit)(N)	52	3	5.37E-03	PIK3R1,CBL,SOS1
Signaling by MET(R)	52	3	5.37E-03	PIK3R1,CBL,SOS1
Non-small cell lung cancer(K)	56	3	6.65E-03	PIK3R1,PLCG1,SOS1
Osteoclast differentiation(K)	132	4	6.72E-03	PIK3R1,PPP3CA,PPP3CC,TRAF6
Hepatitis C(K)	133	4	6.91E-03	PIK3R1,TRAF6,SOS1,PPARA

Neurotrophic factor-mediated Trk receptor signaling(N)	60	3	7.30E-03	PIK3R1,PLCG1,SOS1
Signaling events mediated by focal adhesion kinase(N)	60	3	7.30E-03	PIK3R1,PLCG1,SOS1
Insulin signaling pathway(K)	140	4	7.47E-03	PIK3R1,CBL,PCK1,SOS1
Signaling pathways regulating pluripotency of stem cells(K)	142	4	7.47E-03	PIK3R1,ZFHX3,BMPR1B,BMPR1A
IL4-mediated signaling events(N)	63	3	7.47E-03	PIK3R1,CBL,IRF4
Signaling events mediated by VEGFR1 and VEGFR2(N)	63	3	7.47E-03	PIK3R1,CBL,PLCG1
MAPK signaling pathway(K)	255	5	7.81E-03	PPP3CA,PPP3CC,NR4A1,TRAF6,SOS1
Glioma(K)	66	3	8.53E-03	PIK3R1,PLCG1,SOS1
Wnt signaling pathway(P)	268	5	8.80E-03	PPP3CA,PPP3CC,MYH1,BMPR1B,BMPR1A
Fc epsilon receptor (FCERI) signaling(R)	405	6	8.80E-03	PIK3R1,PPP3CA,PLCG1,NR4A1,TRAF6,SOS1
Signaling by the B Cell Receptor (BCR)(R)	270	5	8.80E-03	PIK3R1,CBL,PLCG1,NR4A1,SOS1
Fc epsilon RI signaling pathway(K)	70	3	8.83E-03	PIK3R1,PLCG1,SOS1
Chronic myeloid leukemia(K)	73	3	9.96E-03	PIK3R1,CBL,SOS1
cGMP-PKG signaling pathway(K)	168	4	0.0114	PIK3R1,PPP3CA,PPP3CC,ADRB3
E-cadherin signaling in keratinocytes(N)	21	2	0.0119	PIK3R1,PLCG1
EGFR tyrosine kinase inhibitor resistance(K)	81	3	0.0119	PIK3R1,PLCG1,SOS1
EGF receptor signaling pathway(P)	82	3	0.0119	CBL,PLCG1,SOS1
Signaling by BMP(R)	23	2	0.0136	BMPR1B,BMPR1A
Signaling by Interleukins(R)	460	6	0.0143	PIK3R1,CBL,IRF4,TRAF6,SOS1,IL17A
Signaling by EGFR(R)	317	5	0.0152	PIK3R1,CBL,PLCG1,NR4A1,SOS1
VEGFR3 signaling in lymphatic endothelium(N)	25	2	0.016	PIK3R1,SOS1
Fc gamma R-mediated phagocytosis(K)	93	3	0.0168	PIK3R1,PLCG1,GSN
IL27-mediated signaling events(N)	26	2	0.0168	TBX21,IL17A

RXR and RAR heterodimerization with other nuclear receptor(N)	26	2	0.0168	NR4A1,PPARA
IL2 signaling events mediated by STAT5(N)	28	2	0.0168	PIK3R1,SOS1
Proteoglycans in cancer(K)	205	4	0.0168	PIK3R1,CBL,PLCG1,SOS1
Inflammatory mediator regulation of TRP channels(K)	99	3	0.0168	PIK3R1,HTR2A,PLCG1
Choline metabolism in cancer(K)	101	3	0.0178	PIK3R1,PLCG1,SOS1
Osteopontin-mediated events(N)	29	2	0.0178	PIK3R1,GSN
IGF1 pathway(N)	30	2	0.019	PIK3R1,SOS1
EPHA forward signaling(N)	31	2	0.0203	CBL,PLCG1
Netrin-mediated signaling events(N)	32	2	0.0215	PIK3R1,PLCG1
toll-like receptor pathway(B)	32	2	0.0215	TRAF6,PPARA
Insulin resistance(K)	109	3	0.022	PIK3R1,PCK1,PPARA
Signaling by Retinoic Acid(R)	34	2	0.0228	PDK3,ALDH1A2
IL1-mediated signaling events(N)	34	2	0.0228	PIK3R1,TRAF6
Internalization of ErbB1(N)	35	2	0.0228	CBL,SOS1
IL2 signaling events mediated by PI3K(N)	35	2	0.0228	PIK3R1,SOS1
GMCSF-mediated signaling events(N)	37	2	0.0228	PIK3R1,SOS1
IL23-mediated signaling events(N)	37	2	0.0228	PIK3R1,IL17A
PDGFR-beta signaling pathway(N)	120	3	0.0229	CBL,PLCG1,SOS1
TCR signaling(R)	123	3	0.0246	PIK3R1,PLCG1,TRAF6
Signaling events regulated by Ret tyrosine kinase(N)	39	2	0.0253	PIK3R1,SOS1
Pathways in cancer(K)	397	5	0.0263	PIK3R1,CBL,PLCG1,TRAF6,SOS1
FOXA2 and FOXA3 transcription factor networks(N)	40	2	0.0265	PCK1,DLK1
IFN-gamma pathway(N)	40	2	0.0265	PIK3R1,CBL
BMP receptor signaling(N)	41	2	0.0278	BMPR1B,BMPR1A
Plasma membrane estrogen receptor signaling(N)	42	2	0.0291	PIK3R1,SOS1

Signaling by ERBB4(R)	42	2	0.0291	PIK3R1,SOS1
FoxO signaling pathway(K)	134	3	0.031	PIK3R1,PCK1,SOS1
il-2 receptor beta chain in t cell activation(B)	44	2	0.0319	PIK3R1,CBL
Cytokine-cytokine receptor interaction(K)	265	4	0.0329	TNFRSF25,BMPR1B,IL17A,BMPR1A
Ubiquitin mediated proteolysis(K)	137	3	0.0329	UBE3A,CBL,TRAF6
Signalling by NGF(R)	421	5	0.0329	PIK3R1,PLCG1,NR4A1,TRAF6,SOS1
Calcineurin-regulated NFAT-dependent transcription in lymphocytes(N)	46	2	0.0329	TBX21,IRF4
Integrins in angiogenesis(N)	47	2	0.0329	PIK3R1,CBL
Phospholipase D signaling pathway(K)	144	3	0.0329	PIK3R1,PLCG1,SOS1
Amyotrophic lateral sclerosis (ALS)(K)	51	2	0.0329	PPP3CA,PPP3CC
Endometrial cancer(K)	52	2	0.0329	PIK3R1,SOS1
Signaling by SCF-KIT(R)	290	4	0.0336	PIK3R1,CBL,NR4A1,SOS1
IL2-mediated signaling events(N)	54	2	0.0353	PIK3R1,SOS1
phospholipase c signaling pathway(B)	4	1	0.0362	PIK3R1
Integrin signalling pathway(P)	158	3	0.0363	PIK3R1,COL5A1,SOS1
Oxytocin signaling pathway(K)	159	3	0.037	PIK3R1,PPP3CA,PPP3CC
Regulation of lipolysis in adipocytes(K)	56	2	0.0378	PIK3R1,ADRB3
Acute myeloid leukemia(K)	57	2	0.0391	PIK3R1,SOS1
B cell activation(P)	59	2	0.0418	PPP3CA,SOS1
Coregulation of Androgen receptor activity(N)	60	2	0.0431	UBE3A,GSN
basic mechanism of action of ppara pparb(d) and pparg and effects on gene expression(B)	5	1	0.0452	PPARA
Opioid Signalling(R)	62	2	0.0459	PPP3CA,PPP3CC
LPA receptor mediated events(N)	63	2	0.0469	PIK3R1,PLCG1
DAP12 interactions(R)	323	4	0.0469	PIK3R1,PLCG1,NR4A1,SOS1
Inflammatory bowel disease (IBD)(K)	65	2	0.0469	TBX21,IL17A

Tuberculosis(K)	179	3	0.0469	PPP3CA,PPP3CC,TRAF6
Signaling by PDGF(R)	328	4	0.0469	PIK3R1,PLCG1,NR4A1,SOS1
Angiogenesis(P)	66	2	0.0469	PLCG1,SOS1
Renal cell carcinoma(K)	67	2	0.0469	PIK3R1,SOS1
Long-term potentiation(K)	67	2	0.0469	PPP3CA,PPP3CC
cd40l signaling pathway(B)	6	1	0.0469	TRAF6
Amphetamine addiction(K)	68	2	0.0469	PPP3CA,PPP3CC
p75(NTR)-mediated signaling(N)	69	2	0.0469	PIK3R1,TRAF6
CDC42 signaling events(N)	70	2	0.0469	PIK3R1,CBL
Adipocytokine signaling pathway(K)	70	2	0.0469	PCK1,PPARA
PI3K-Akt signaling pathway(K)	341	4	0.0469	PIK3R1,PCK1,NR4A1,SOS1
Inflammation mediated by chemokine and cytokine signaling pathway(P)	71	2	0.0469	PLCG1,SOS1
PPAR signaling pathway(K)	72	2	0.0469	PCK1,PPARA
Prolactin signaling pathway(K)	72	2	0.0469	PIK3R1,SOS1
sumoylation as a mechanism to modulate ctbp-dependent gene responses(B)	7	1	0.0469	UBE3A
Abacavir transport and metabolism(R)	7	1	0.0469	PCK1
cbl mediated ligand-induced downregulation of egf receptors pathway(B)	7	1	0.0469	CBL
Viral carcinogenesis(K)	203	3	0.0469	UBE3A,PIK3R1,GSN
Glucocorticoid receptor regulatory network(N)	78	2	0.047	TBX21,NR4A1
Bacterial invasion of epithelial cells(K)	78	2	0.047	PIK3R1,CBL
Epstein-Barr virus infection(K)	204	3	0.0475	PIK3R1,PLCG1,TRAF6
yaci and bcma stimulation of b cell immune responses(B)	8	1	0.048	TRAF6
TGF-beta signaling pathway(P)	80	2	0.0492	BMPR1B,BMPR1A

Cell surface interactions at the vascular wall(R)	208	3	0.0499	PIK3R1,PLCG1,SOS1
C-MYB transcription factor network(N)	82	2	0.0515	PPP3CA,ZFHX3
Gastrin-CREB signalling pathway via PKC and MAPK(R)	376	4	0.0527	PIK3R1,HTR2A,AGT,SOS1
Regulation of actin cytoskeleton(K)	214	3	0.0537	PIK3R1,GSN,SOS1
TGF-beta signaling pathway(K)	84	2	0.0538	BMPR1B,BMPR1A
Transcriptional regulation of white adipocyte differentiation(R)	84	2	0.0538	PCK1,PPARA
EGFR-dependent Endothelin signaling events(N)	9	1	0.0539	SOS1
proteasome complex(B)	9	1	0.0539	UBE3A
5-Hydroxytryptamine degredation(P)	9	1	0.0539	ALDH1A2
Small cell lung cancer(K)	86	2	0.0561	PIK3R1,TRAF6
Gap junction(K)	88	2	0.0561	HTR2A,SOS1
RET signaling(R)	222	3	0.0561	PIK3R1,PLCG1,SOS1
GP1b-IX-V activation signalling(R)	10	1	0.0561	PIK3R1
cxcr4 signaling pathway(B)	10	1	0.0561	PIK3R1
Prostate cancer(K)	89	2	0.0561	PIK3R1,SOS1
FGF signaling pathway(P)	92	2	0.0561	PLCG1,SOS1
Ras signaling pathway(K)	229	3	0.0561	PIK3R1,PLCG1,SOS1
il-7 signal transduction(B)	11	1	0.0561	PIK3R1
Metabolism of carbohydrates(R)	233	3	0.0561	PCK1,GPC6,B3GAT1
NF-kappa B signaling pathway(K)	95	2	0.0561	PLCG1,TRAF6
Endocrine resistance(K)	98	2	0.0561	PIK3R1,SOS1
insulin signaling pathway(B)	12	1	0.0561	PIK3R1
trka receptor signaling pathway(B)	12	1	0.0561	PIK3R1
Phosphatidylinositol signaling system(K)	99	2	0.0561	PIK3R1,PLCG1
Estrogen signaling pathway(K)	100	2	0.0561	PIK3R1,SOS1

AGE-RAGE signaling pathway in diabetic complications(K)	101	2	0.0561	PIK3R1,PLCG1
human cytomegalovirus and map kinase pathways(B)	13	1	0.0561	PIK3R1
Metabolism of Angiotensinogen to Angiotensins(R)	13	1	0.0561	AGT
b cell survival pathway(B)	13	1	0.0561	PIK3R1
multiple antiapoptotic pathways from igf-1r signaling lead to bad phosphorylation(B)	13	1	0.0561	PIK3R1
HIF-1 signaling pathway(K)	103	2	0.0561	PIK3R1,PLCG1
Chagas disease (American trypanosomiasis)(K)	104	2	0.0561	PIK3R1,TRAF6
Toll-like receptor signaling pathway(K)	106	2	0.0561	PIK3R1,TRAF6
S1P4 pathway(N)	14	1	0.0561	PLCG1
Atypical NF-kappaB pathway(N)	14	1	0.0561	PIK3R1
IL5-mediated signaling events(N)	14	1	0.0561	PIK3R1
HTLV-I infection(K)	258	3	0.0561	PIK3R1,PPP3CA,PPP3CC
Endocytosis(K)	260	3	0.0561	CBL,ADRB3,TRAF6
PIP3 activates AKT signaling(R)	111	2	0.0561	PIK3R1,NR4A1
Glutamatergic synapse(K)	114	2	0.0561	PPP3CA,PPP3CC
bone remodeling(B)	16	1	0.0561	TRAF6
akt signaling pathway(B)	16	1	0.0561	PIK3R1
the igf-1 receptor and longevity(B)	16	1	0.0561	PIK3R1
nerve growth factor pathway (ngf)(B)	16	1	0.0561	PIK3R1
role of nicotinic acetylcholine receptors in the regulation of apoptosis(B)	16	1	0.0561	PIK3R1
role of pi3k subunit p85 in regulation of actin organization and cell migration(B)	16	1	0.0561	PIK3R1

Leukocyte transendothelial migration(K)	116	2	0.0561	PIK3R1,PLCG1
Toxoplasmosis(K)	118	2	0.0561	PIK3R1,TRAF6
Thyroid hormone signaling pathway(K)	118	2	0.0561	PIK3R1,PLCG1
control of skeletal myogenesis by hdac and calcium/calmodulin-dependent kinase (camk)(B)	17	1	0.0561	PIK3R1
pten dependent cell cycle arrest and apoptosis(B)	17	1	0.0561	PIK3R1
EPHA2 forward signaling(N)	18	1	0.0561	PIK3R1
S1P1 pathway(N)	18	1	0.0561	PLCG1
VEGF signaling pathway(P)	18	1	0.0561	PLCG1
regulation of pgc-1a(B)	18	1	0.0561	PPARA
AMPK signaling pathway(K)	124	2	0.0561	PIK3R1,PCK1
Oocyte meiosis(K)	124	2	0.0561	PPP3CA,PPP3CC
Signaling by VEGF(R)	287	3	0.0561	PIK3R1,PLCG1,SOS1
sprouty regulation of tyrosine kinase signals(B)	19	1	0.0561	CBL
tumor suppressor arf inhibits ribosomal biogenesis(B)	19	1	0.0561	PIK3R1
the co-stimulatory signal during t-cell activation(B)	20	1	0.059	PIK3R1
regulation of bad phosphorylation(B)	20	1	0.059	PIK3R1
Dopaminergic synapse(K)	130	2	0.0592	PPP3CA,PPP3CC
egf signaling pathway(B)	21	1	0.0618	PIK3R1
growth hormone signaling pathway(B)	21	1	0.0618	PIK3R1
nf-kb signaling pathway(B)	21	1	0.0618	TRAF6
igf-1 signaling pathway(B)	21	1	0.0618	PIK3R1
Measles(K)	136	2	0.064	PIK3R1,TRAF6
ctcf: first multivalent nuclear factor(B)	22	1	0.0647	PIK3R1
ras signaling pathway(B)	22	1	0.0647	PIK3R1

inhibition of cellular proliferation by gleevec(B)	22	1	0.0647	PIK3R1
Nephrin interactions(R)	22	1	0.0647	PIK3R1
influence of ras and rho proteins on g1 to s transition(B)	22	1	0.0647	PIK3R1
Nicotinic acetylcholine receptor signaling pathway(P)	22	1	0.0647	MYH1
C-type lectin receptors (CLRs)(R)	139	2	0.0665	PPP3CA,TRAF6
Renin-angiotensin system(K)	23	1	0.0675	AGT
Signaling by Robo receptor(R)	23	1	0.0675	SOS1
regulation of eif-4e and p70s6 kinase(B)	23	1	0.0675	PIK3R1
Canonical NF-kappaB pathway(N)	23	1	0.0675	TRAF6
Signaling events mediated by PRL(N)	23	1	0.0675	AGT
role of erk5 in neuronal survival pathway(B)	23	1	0.0675	PIK3R1
Mannose type O-glycan biosynthesis(K)	23	1	0.0675	B3GAT1
Proximal tubule bicarbonate reclamation(K)	23	1	0.0675	PCK1
Signaling events mediated by the Hedgehog family(N)	23	1	0.0675	PIK3R1
Wnt signaling pathway(K)	143	2	0.0699	PPP3CA,PPP3CC
corticosteroids and cardioprotection(B)	24	1	0.0704	PIK3R1
Ephrin B reverse signaling(N)	24	1	0.0704	PIK3R1
skeletal muscle hypertrophy is regulated via akt-mtor pathway(B)	24	1	0.0704	PIK3R1
mtor signaling pathway(B)	24	1	0.0704	PIK3R1
Hypoxia response via HIF activation(P)	24	1	0.0704	PIK3R1
transcription factor creb and its extracellular signals(B)	24	1	0.0704	PIK3R1
Breast cancer(K)	146	2	0.0725	PIK3R1,SOS1

fc epsilon receptor i signaling in mast cells(B)	25	1	0.0732	PIK3R1
Nephrin/Neph1 signaling in the kidney podocyte(N)	25	1	0.0732	PLCG1
tpo signaling pathway(B)	25	1	0.0732	PIK3R1
Nongenotropic Androgen signaling(N)	25	1	0.0732	PIK3R1
ras-independent pathway in nk cell-mediated cytotoxicity(B)	25	1	0.0732	PIK3R1
Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated pathway(P)	147	2	0.0733	HTR2A,ADRB3
S1P2 pathway(N)	26	1	0.076	PIK3R1
IL3-mediated signaling events(N)	26	1	0.076	PIK3R1
bioactive peptide induced signaling pathway(B)	26	1	0.076	PIK3R1
ß-arrestins in gpcr desensitization(B)	26	1	0.076	PPARA
pdgf signaling pathway(B)	26	1	0.076	PIK3R1
Non-alcoholic fatty liver disease (NAFLD)(K)	151	2	0.0768	PIK3R1,PPARA
thrombin signaling and protease-activated receptors(B)	27	1	0.0788	PIK3R1
Integrin alphaIIb beta3 signaling(R)	27	1	0.0788	SOS1
p38 MAPK signaling pathway(N)	27	1	0.0788	TRAF6
Hippo signaling pathway(K)	154	2	0.0794	BMPR1B,BMPR1A
mTOR signaling pathway(K)	154	2	0.0794	PIK3R1,SOS1
role of erbb2 in signal transduction and oncology(B)	28	1	0.0816	PIK3R1
IL8- and CXCR1-mediated signaling events(N)	28	1	0.0816	CBL
Reelin signaling pathway(N)	28	1	0.0816	PIK3R1
Dorso-ventral axis formation(K)	28	1	0.0816	SOS1

vegf hypoxia and angiogenesis(B)	28	1	0.0816	PIK3R1
Jak-STAT signaling pathway(K)	158	2	0.083	PIK3R1,SOS1
Fcgamma receptor (FCGR) dependent phagocytosis(R)	159	2	0.0839	PIK3R1,PLCG1
CD40/CD40L signaling(N)	29	1	0.0844	TRAF6
Regulation of CDC42 activity(N)	30	1	0.0872	PLCG1
Nectin adhesion pathway(N)	30	1	0.0872	PIK3R1
erk and pi-3 kinase are necessary for collagen binding in corneal epithelia(B)	30	1	0.0872	PIK3R1
Citrate cycle (TCA cycle)(K)	30	1	0.0872	PCK1
IL12 signaling mediated by STAT4(N)	31	1	0.09	TBX21
Detoxification of Reactive Oxygen Species(R)	31	1	0.09	PRDX6
phospholipids as signalling intermediaries(B)	31	1	0.09	PIK3R1
Regulation of p38-alpha and p38-beta(N)	31	1	0.09	TRAF6
trefoil factors initiate mucosal healing(B)	31	1	0.09	PIK3R1
DAG and IP3 signaling(R)	32	1	0.0927	PLCG1
Alzheimer's disease(K)	171	2	0.0949	PPP3CA,PPP3CC
FAS signaling pathway(P)	33	1	0.0955	GSN
IL8- and CXCR2-mediated signaling events(N)	34	1	0.0982	CBL
actions of nitric oxide in the heart(B)	34	1	0.0982	PIK3R1
a6b1 and a6b4 Integrin signaling(N)	35	1	0.101	PIK3R1
signal transduction through il1r(B)	35	1	0.101	TRAF6
Signaling events mediated by TCPTP(N)	35	1	0.101	SOS1
inactivation of gsk3 by akt causes accumulation of b-catenin in alveolar macrophages(B)	36	1	0.1037	PIK3R1

mechanism of gene regulation by peroxisome proliferators via ppara(B)	36	1	0.1037	PPARA
E-cadherin signaling in the nascent adherens junction(N)	36	1	0.1037	PIK3R1
rac1 cell motility signaling pathway(B)	37	1	0.1064	PIK3R1
ErbB2/ErbB3 signaling events(N)	37	1	0.1064	SOS1
Inositol phosphate metabolism(R)	37	1	0.1064	PLCG1
Platelet Aggregation (Plug Formation)(R)	37	1	0.1064	SOS1
nfat and hypertrophy of the heart (B)	37	1	0.1064	PIK3R1
Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways(R)	38	1	0.1092	TRAF6
Retinoid metabolism and transport(R)	38	1	0.1092	GPC6
EPHB forward signaling(N)	38	1	0.1092	PIK3R1
Regulation of RAC1 activity(N)	38	1	0.1092	SOS1
Chemokine signaling pathway(K)	187	2	0.1102	PIK3R1,SOS1
Aldosterone-regulated sodium reabsorption(K)	39	1	0.1119	PIK3R1
Pyruvate metabolism(K)	39	1	0.1119	PCK1
Class I PI3K signaling events(N)	40	1	0.1146	PLCG1
GPCR ligand binding(R)	395	3	0.1171	HTR2A,AGT,ADRB3
Intrinsic Pathway for Apoptosis(R)	41	1	0.1173	PPP3CC
Fatty acid, triacylglycerol, and ketone body metabolism(R)	195	2	0.1181	AGT,PPARA
Netrin-1 signaling(R)	42	1	0.12	PLCG1
PAR1-mediated thrombin signaling events(N)	43	1	0.1226	PIK3R1
cAMP signaling pathway(K)	200	2	0.1231	PIK3R1,PPARA

Focal adhesion(K)	201	2	0.1241	PIK3R1,SOS1
Validated transcriptional targets of deltaNp63 isoforms(N)	45	1	0.128	COL5A1
DNA Double Strand Break Response(R)	45	1	0.128	EYA1
Carbohydrate digestion and absorption(K)	46	1	0.1306	PIK3R1
Amyloid fiber formation(R)	47	1	0.1333	GSN
TGF-beta receptor signaling(N)	47	1	0.1333	SOS1
Apoptotic execution phase(R)	47	1	0.1333	GSN
Rap1 signaling pathway(K)	212	2	0.1353	PIK3R1,PLCG1
t cell receptor signaling pathway(B)	48	1	0.1359	PIK3R1
Type II diabetes mellitus(K)	48	1	0.1359	PIK3R1
GPVI-mediated activation cascade(R)	49	1	0.1385	PIK3R1
GPCR downstream signaling(R)	915	5	0.1405	PIK3R1,HTR2A,AGT,ADRB3,SOS1
Angiopoietin receptor Tie2-mediated signaling(N)	50	1	0.1412	PIK3R1
Vibrio cholerae infection(K)	51	1	0.1438	PLCG1
Caspase cascade in apoptosis(N)	52	1	0.1464	GSN
Notch signaling pathway(N)	52	1	0.1464	DLK1
Role of Calcineurin-dependent NFAT signaling in lymphocytes(N)	52	1	0.1464	NR4A1
Mitochondrial biogenesis(R)	52	1	0.1464	PPARA
Signaling events mediated by PTP1B(N)	52	1	0.1464	PIK3R1
Regulation of cholesterol biosynthesis by SREBP (SREBF)(R)	53	1	0.149	PPARA
Interleukin signaling pathway(P)	55	1	0.1542	SOS1
Signaling by NOTCH1(R)	59	1	0.1644	DLK1
PI Metabolism(R)	59	1	0.1644	PIK3R1

Signaling by PTK6(R)	61	1	0.1695	CBL
IL12-mediated signaling events(N)	61	1	0.1695	TBX21
Colorectal cancer(K)	62	1	0.1721	PIK3R1
Validated nuclear estrogen receptor alpha network(N)	62	1	0.1721	LMO4
Costimulation by the CD28 family(R)	63	1	0.1746	PIK3R1
Ras Pathway(P)	63	1	0.1746	SOS1
Longevity regulating pathway - multiple species(K)	64	1	0.1771	PIK3R1
Retinol metabolism(K)	65	1	0.1796	ALDH1A2
Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R)(R)	255	2	0.181	PIK3R1,SOS1
Pancreatic cancer(K)	66	1	0.1821	PIK3R1
Beta1 integrin cell surface interactions(N)	66	1	0.1821	COL5A1
ISG15 antiviral mechanism(R)	67	1	0.1846	PLCG1
Circadian Clock(R)	67	1	0.1846	PPARA
Central carbon metabolism in cancer(K)	67	1	0.1846	PIK3R1
Glycolysis / Gluconeogenesis(K)	67	1	0.1846	PCK1
Interferon alpha/beta signaling(R)	68	1	0.1871	IRF4
Epithelial cell signaling in Helicobacter pylori infection(K)	68	1	0.1871	PLCG1
Regulation of Telomerase(N)	68	1	0.1871	UBE3A
AP-1 transcription factor network(N)	70	1	0.1921	AGT
RIG-I-like receptor signaling pathway(K)	70	1	0.1921	TRAF6
Inositol phosphate metabolism(K)	71	1	0.1945	PLCG1
Melanoma(K)	71	1	0.1945	PIK3R1
Signaling by TGF-beta Receptor Complex(R)	73	1	0.1994	CBL
Leishmaniasis(K)	73	1	0.1994	TRAF6
Interferon gamma signaling(R)	73	1	0.1994	IRF4
Platinum drug resistance(K)	75	1	0.2043	PIK3R1
Signaling by Insulin receptor(R)	277	2	0.2053	PIK3R1,SOS1

Neuroactive ligand-receptor interaction(K)	278	2	0.2064	HTR2A,ADRB3
Pertussis(K)	76	1	0.2067	TRAF6
RIG-I/MDA5 mediated induction of IFN-alpha/beta pathways(R)	77	1	0.2092	TRAF6
Aldosterone synthesis and secretion(K)	82	1	0.2212	NR4A1
Visual phototransduction(R)	83	1	0.2235	GPC6
MicroRNAs in cancer(K)	299	2	0.2299	PLCG1,SOS1
Rheumatoid arthritis(K)	90	1	0.24	IL17A
Salivary secretion(K)	90	1	0.24	ADRB3
Protein digestion and absorption(K)	90	1	0.24	COL5A1
GnRH signaling pathway(K)	92	1	0.2446	SOS1
Longevity regulating pathway(K)	94	1	0.2493	PIK3R1

Table 29

	probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig	HyperG_Stats	FDR_HyperG
1	ACACB_12_109146008_109150083_109185066_109187324_RR	ACACB	191	87	0.388279548	1
2	ACBD6_1_180269638_180272765_180371571_180375410_RR	ACBD6	200	111	0.00091339	0.014340227
3	ACBD6_1_180337907_180340909_180371571_180375410_FR	ACBD6	200	111	0.00091339	0.014340227
4	ADRB3_8_37962724_37965269_37984580_37986052_FF	ADRB3	29	12	0.689607935	1
5	ADRB3_8_37962724_37965269_37996522_37999233_FR	ADRB3	29	12	0.689607935	1
6	ALDH1A2_15_58053198_58062371_58157807_58162832_RR	ALDH1A2	200	111	0.00091339	0.014340227
7	ALDH1A2_15_58053198_58062371_58229591_58234474_RF	ALDH1A2	200	111	0.00091339	0.014340227
8	ANO2_12_5767708_5775129_5922387_5930466_RR	ANO2	200	111	0.00091339	0.014340227
9	ANO2_12_5872622_5877860_5922387_5930466_RR	ANO2	200	111	0.00091339	0.014340227
10	B3GAT1_11_134376219_134382136_134419343_134423366_FF	B3GAT1	110	65	0.001249162	0.018857547
11	B3GAT2_6_70837358_70839856_70855194_70857991_FR	B3GAT2	97	39	0.81848692	1
12	B3GAT2_6_70837358_70839856_70933019_70941366_FF	B3GAT2	97	39	0.81848692	1
13	BMP7_20_57274840_57277666_57290751_57294583_RF	BMP7	79	37	0.363905679	1
14	C1GALT1_7_7113076_7114831_7258228_7260668_FF	C1GALT1	109	57	0.056359167	0.291065435
15	CALCR_7_93553156_93563952_93593898_93597071_RF	CALCR	45	37	1.92096E-07	1.37086E-05
16	CARD11_7_2966372_2970772_3066095_3073017_RR	CARD11	122	41	0.993686632	1
17	CASP9_1_15526774_15533191_15569002_15572579_FR	CASP9	49	22	0.520298425	1
18	CBL_11_119249760_119252653_119294588_119299643_RF	CBL	76	20	0.999603201	1
19	CD36_7_80539507_80544315_80603212_80611693_FR	CD36	200	101	0.044617305	0.247106631
20	CD36_7_80539507_80544315_80679651_80687690_FR	CD36	200	101	0.044617305	0.247106631
21	COL13A1_10_69769669_69775141_69840301_69843474_RF	COL13A1	200	73	0.989437228	1
22	COL25A1_4_109024771_109031337_109090838_109104305_RR	COL25A1	200	73	0.989437228	1
23	COL25A1_4_109090838_109104305_109307411_109309712_RF	COL25A1	200	73	0.989437228	1
24	COL4A2_13_110272408_110277108_110487749_110493325_FR	COL4A2	47	26	0.08460057	0.378025067
25	COL5A1_9_134738485_134741113_134811418_134816113_RR	COL5A1	200	94	0.240043966	0.795082334
26	CYGB_17_76511049_76513649_76555120_76557454_RF	CYGB	33	21	0.01973308	0.135639073
27	CYGB_17_76533052_76534398_76555120_76557454_RF	CYGB	33	21	0.01973308	0.135639073
28	CYGB_17_76555120_76557454_76593886_76595265_FF	CYGB	33	21	0.01973308	0.135639073
29	CYGB_17_76555120_76557454_76593886_76595265_FR	CYGB	33	21	0.01973308	0.135639073

Table 30.A1

	Percent_Sig	logFC	AveExpr	t	P.Value	adj.P.Val	B	FC	FC_1	LS	Loop detected
1	45.55	-0.63947	-0.63947	-7.69815	3.1E-07	7.7E-06	6.84649	0.64195	-1.55775	-1	E_Trn
2	55.5	-0.40863	-0.40863	-8.71959	4.8E-08	2E-06	8.7176	0.75334	-1.32742	-1	E_Trn
3	55.5	-0.37204	-0.37204	-4.7404	0.00014	0.00085	0.65579	0.77269	-1.29418	-1	E_Trn
4	41.38	-0.43258	-0.43258	-3.39837	0.00314	0.01255	-2.26959	0.74093	-1.34965	-1	Str_Trn
5	41.38	-0.41009	-0.41009	-3.34476	0.00354	0.0137	-2.38547	0.75257	-1.32877	-1	Str_Trn
6	55.5	-0.42055	-0.42055	-8.81299	5.2E-08	5E-06	8.69347	0.74714	-1.33844	-1	Str_Trn
7	55.5	-0.38345	-0.38345	-10.298	3.5E-09	3.4E-07	11.3398	0.7666	-1.30445	-1	E_Trn
8	55.5	-0.41242	-0.41242	-5.49229	3E-05	0.00044	2.3207	0.75136	-1.33092	-1	Str_Trn
9	55.5	-0.41127	-0.41127	-5.12273	6.7E-05	0.00077	1.52446	0.75196	-1.32986	-1	Str_Trn
10	59.09	-0.41969	-0.41969	-10.1091	6.3E-09	1.1E-06	10.7772	0.74758	-1.33764	-1	Str_Trn
11	40.21	-0.37049	-0.37049	-9.68101	9.3E-09	6.4E-07	10.3519	0.77352	-1.29279	-1	E_Trn
12	40.21	0.37079	0.37079	12.5019	2.1E-10	1.1E-07	14.1122	1.29306	1.29306	1	Str_Ctrl
13	46.84	0.32369	0.32369	7.23249	7.5E-07	1.5E-05	5.94574	1.25153	1.25153	1	E_Ctrl
14	52.29	-0.55555	-0.55555	-11.0417	1.1E-09	1.6E-07	12.4709	0.6804	-1.46972	-1	E_Trn
15	82.22	0.32372	0.32372	7.81516	2.5E-07	6.6E-06	7.06808	1.25156	1.25156	1	E_Ctrl
16	33.61	-0.37618	-0.37618	-8.25898	1.1E-07	3.7E-06	7.89147	0.77047	-1.2979	-1	E_Trn
17	44.9	-0.3658	-0.3658	-7.08702	9.9E-07	1.8E-05	5.6582	0.77604	-1.28859	-1	E_Trn
18	26.32	-0.42638	-0.42638	-4.61856	0.0002	0.0017	0.42001	0.74413	-1.34385	-1	Str_Trn
19	50.5	0.36751	0.36751	3.11685	0.0057	0.01625	-2.96367	1.29012	1.29012	1	E_Ctrl
20	50.5	0.35581	0.35581	4.03354	0.00072	0.00306	-0.93652	1.27971	1.27971	1	E_Ctrl
21	36.5	-0.39187	-0.39187	-7.41112	5.3E-07	1.2E-05	6.29483	0.76214	-1.31209	-1	E_Trn
22	36.5	0.33555	0.33555	5.20733	5.1E-05	0.00037	1.69682	1.26186	1.26186	1	E_Ctrl
23	36.5	0.32915	0.32915	4.61978	0.00019	0.00106	0.38479	1.25627	1.25627	1	E_Ctrl
24	55.32	-0.36515	-0.36515	-5.22977	4.9E-05	0.00036	1.74644	0.77639	-1.28802	-1	E_Trn
25	47	-0.48145	-0.48145	-3.82029	0.00122	0.00625	-1.3463	0.71626	-1.39614	-1	Str_Trn
26	63.64	-0.47142	-0.47142	-3.45234	0.00278	0.01148	-2.15253	0.72126	-1.38647	-1	Str_Trn
27	63.64	-0.48149	-0.48149	-3.45927	0.00274	0.01134	-2.13747	0.71624	-1.39618	-1	Str_Trn
28	63.64	-0.41585	-0.41585	-2.94096	0.00862	0.02643	-3.24207	0.74958	-1.33409	-1	Str_Trn
29	63.64	-0.41368	-0.41368	-2.8539	0.01041	0.03037	-3.42204	0.75071	-1.33208	-1	Str_Trn

Table 30.A2

	Probe sequence	Probe Location				
	60 mer	Chr	Start1	End1	Start2	End2
1	TCAAGAAAAAATAATAATAATTTTTTTTTCGATTCCTGCTACACATTTTGGCAGAATACT	12	109146008	109146039	109185066	109185097
2	ATGCAATCACCAAAAATGTTTTAATTTCTCGACTCTTGGTGATCCAGGTTTCAGAACTTC	1	180269638	180269669	180371571	180371602
3	GGTCACCAGCACAGAATGATGATGAGGATCGACTCTTGGTGATCCAGGTTTCAGAACTTC	1	180340878	180340909	180371571	180371602
4	CGGTCCCTCTGCCCCGGTTACCTACCCGTCGACATTGGAATCACTTTCTAATCCGGGACA	8	37965238	37965269	37986021	37986052
5	CGGTCCCTCTGCCCCGGTTACCTACCCGTCGAGGACATTCCGGCTACCCCTTCCCATCAC	8	37965238	37965269	37996522	37996553
6	ATTTTAAATGTGGCATTTTAGGTTTATTTCGATTTTGCATAAATTGAAAAAGCTGGAGAT	15	58053198	58053229	58157807	58157838
7	CCTTGTCTATGAAGTAAGAGATTAAATCTCGAAATAAACCTAAAATGCCACATTTAAAAT	15	58053198	58053229	58234443	58234474
8	GGGGGAAGGGCCCATGCGGACAAGTAGCTCGACTGGCCTCCCACGCCTCCTCCTTTCCTG	12	5767708	5767739	5922387	5922418
9	ATATTTAAAAAAAATTAAGATGTAATTTTCGACTGGCCTCCCACGCCTCCTCCTTTCCTG	12	5872622	5872653	5922387	5922418
10	AAACATTTCTCCTGCCCCTCCTTTTCCTTCGAGCAGCAGCGAACTGTGATTGCTGTGAGT	11	134382105	134382136	134423335	134423366
11	TTTAAAAAAGCTATGTTTCAGCATAAAATCGATTAGATGCTCTGCAGCTTCCTGAAGTGT	6	70839825	70839856	70855194	70855225
12	TTTAAAAAAGCTATGTTTCAGCATAAAATCGAGTGATTGTTTTAAGTGCTCTAGGCAAGT	6	70839825	70839856	70941335	70941366
13	TTATAGTGAGAATATATGACTTTTGTAATCGAGTTTTATCTTTATTCCCTCCCCATTGGT	20	57274840	57274871	57294552	57294583
14	AAATGTATAAGAACAGAAGAGAATTATCTCGACATGTCTGAAAAGTATTATCAGCCCTCT	7	7114800	7114831	7260637	7260668
15	TATAAAGGTGGTTAGGGACAGATTTTCATCGAATTTCACCCATGGTGGAGATATTTCACT	7	93553156	93553187	93597040	93597071
16	CTAGGAAAAAAGAATGGGAAGGAATAGATCGATATAGAATCTCAGTTATTCCTCAGGAAA	7	2966372	2966403	3066095	3066126
17	TTCAAGGAATTAAACCTAGCCCTTACTATCGATTTTAGGGTATGGATATTAGGAGCCATA	1	15533160	15533191	15569002	15569033
18	ACCGCCTCACCTCAGCTCTCCAGTGAGATCGATCCTCCCACCTAAGCTTCCCAAGTTGCT	11	119249760	119249791	119299612	119299643
19	TGCTGAAAGAAAACACAATTTATTTAAGTCGAGACACAATTAAGGTTGATACAAAAAAAG	7	80544284	80544315	80603212	80603243
20	TGCTGAAAGAAAACACAATTTATTTAAGTCGAAATTTTGGAAAAGCCCTGATTTAAGTCA	7	80544284	80544315	80679651	80679682
21	CCACACATGACTGTATATTTAAATTAATTCGATGCCCAAAGGACTGTCATAATCACTCAG	10	69769669	69769700	69843443	69843474
22	AAAACACCCTGAATTGGAAGAAAGAAACTCGAGGGATGAGTGTGTATCATCAAAGTCAAA	4	109024771	109024802	109090838	109090869
23	CATGTTTTGAAAAAACTATGCATGGATTTCGAGGGATGAGTGTGTATCATCAAAGTCAAA	4	109090838	109090869	109309681	109309712
24	TTTAGATAACCAATGTATAGTACGTTAATCGATGTGAAGTTCAAGAACTGACAAGGCTGT	13	110277077	110277108	110487749	110487780
25	CGCGGGGCCTTCTGGGCCAGGCGGGCCCTCGAAAAGCCCCACGCCCCCCCAGAGCTGCTG	9	134738485	134738516	134811418	134811449
26	CCCGGTTTCCTCATCTGTCCCTGCCCCCTCGAGACTTGACTGGGGGACAATCCACTTTGA	17	76511049	76511080	76557423	76557454
27	CCCGGTTTCCTCATCTGTCCCTGCCCCCTCGAGTCTCAGATGTGAGGGCTGGAACAGATG	17	76533052	76533083	76557423	76557454
28	CCCGGTTTCCTCATCTGTCCCTGCCCCCTCGAACAATCTTGAGCATAGAGAACCAGACCC	17	76557423	76557454	76595234	76595265
29	CCCGGTTTCCTCATCTGTCCCTGCCCCCTCGAAGTATGGAGGTAAATGCCAAAGGCTCAG	17	76557423	76557454	76593886	76593917

Table 30.A3

	4 kb Sequence Location				
	Chr.1	Start1.1	End1.1	Start2.1	End2.1
1	12	109146008	109150009	1.1E+08	109189067
2	1	180269638	180273639	1.8E+08	180375572
3	1	180336908	180340909	1.8E+08	180375572
4	8	37961268	37965269	3.8E+07	37986052
5	8	37961268	37965269	3.8E+07	38000523
6	15	58053198	58057199	5.8E+07	58161808
7	15	58053198	58057199	5.8E+07	58234474
8	12	5767708	5771709	5922387	5926388
9	12	5872622	5876623	5922387	5926388
10	11	134378135	134382136	1.3E+08	134423366
11	6	70835855	70839856	7.1E+07	70859195
12	6	70835855	70839856	7.1E+07	70941366
13	20	57274840	57278841	5.7E+07	57294583
14	7	7110830	7114831	7256667	7260668
15	7	93553156	93557157	9.4E+07	93597071
16	7	2966372	2970373	3066095	3070096
17	1	15529190	15533191	1.6E+07	15573003
18	11	119249760	119253761	1.2E+08	119299643
19	7	80540314	80544315	8.1E+07	80607213
20	7	80540314	80544315	8.1E+07	80683652
21	10	69769669	69773670	7E+07	69843474
22	4	109024771	109028772	1.1E+08	109094839
23	4	109090838	109094839	1.1E+08	109309712
24	13	110273107	110277108	1.1E+08	110491750
25	9	134738485	134742486	1.3E+08	134815419
26	17	76511049	76515050	7.7E+07	76557454
27	17	76533052	76537053	7.7E+07	76557454
28	17	76553453	76557454	7.7E+07	76595265
29	17	76553453	76557454	7.7E+07	76597887

Table 30.A4

30	DGKH_13_42011104_42015078_42235825_42240914_RR	DGKH	200	99	0.078405901	0.370774891
31	DIAPH3_13_59818047_59823591_59854837_59860534_RR	DIAPH3	200	91	0.389926943	1
32	DKK3_11_11956071_11968035_11984245_11993733_FR	DKK3	62	37	0.010531285	0.08702167
33	DKK3_11_11956071_11968035_12010923_12019458_FF	DKK3	62	37	0.010531285	0.08702167
34	DKK3_11_11956071_11968035_12010923_12019458_FR	DKK3	62	37	0.010531285	0.08702167
35	DKK3_11_11956071_11968035_12048403_12051930_FR	DKK3	62	37	0.010531285	0.08702167
36	DLK1_14_100687837_100692867_100749541_100751577_RF	DLK1	47	28	0.025050129	0.159872776
37	DOK5_20_54466479_54470848_54572383_54577350_RF	DOK5	200	107	0.005388757	0.052676227
38	EGR3_8_22681793_22682820_22737091_22739184_FF	EGR3	33	16	0.375730688	1
39	EHD1_11_64868178_64874017_64914431_64916090_RF	EHD1	47	8	0.999981792	1
40	EMCN_4_100525710_100532027_100732651_100738720_RR	EMCN	200	121	2.82028E-06	0.000158137
41	ETS1_11_128476761_128480323_128561632_128566579_RR	ETS1	200	112	0.000559145	0.010705579
42	EYA1_8_71216399_71218728_71261816_71267769_RR	EYA1	139	89	2.12839E-06	0.000128522
43	FBLN2_3_13512352_13515076_13582406_13590343_RF	FBLN2	193	61	0.999882361	1
44	FBXO32_8_123526212_123527874_123555254_123559065_FR	FBXO32	48	27	0.06408635	0.316104415
45	FOXO1_13_40524349_40526124_40688580_40690771_RR	FOXO1	199	76	0.964953638	1
46	FOXO3_6_108603215_108604436_108629992_108635481_FR	FOXO3	200	94	0.240043966	0.795082334
47	FTO_16_53844989_53854574_54045378_54052319_RF	FTO	200	100	0.059654823	0.302381977
48	GPC5_13_91724432_91728749_91910388_91925040_FR	GPC5	200	102	0.032796361	0.195038964
49	GPC5_13_91794062_91815301_91953115_91957441_RR	GPC5	200	102	0.032796361	0.195038964
50	GPC6_13_94054831_94060621_94121445_94133208_RF	GPC6	200	109	0.002303017	0.026200987
51	GPC6_13_94121445_94133208_94296633_94304225_FF	GPC6	200	109	0.002303017	0.026200987
52	GRB10_7_50706363_50709345_50775503_50780905_RF	GRB10	200	95	0.198157163	0.697548759
53	GSN_9_121177548_121180410_121268506_121274144_FR	GSN	200	80	0.902128149	1
54	GSN_9_121182946_121189020_121239116_121243347_FF	GSN	200	80	0.902128149	1
55	GSN_9_121227501_121232628_121268506_121274144_FR	GSN	200	80	0.902128149	1
56	GSN_9_121239116_121243347_121268506_121274144_FR	GSN	200	80	0.902128149	1
57	GSN_9_121253564_121256485_121268506_121274144_RR	GSN	200	80	0.902128149	1
58	HDAC9_7_18055950_18064786_18135886_18142010_RF	HDAC9	200	75	0.9780749	1
59	HOXC6_12_53956382_53960014_53992251_53994278_FF	HOXC6	120	71	0.000728297	0.012823129

Table 30.B1

30	49.5	-0.40058	-0.40058	-5.54747	2.4E-05	0.00021	2.44404	0.75755	-1.32004	-1	E_Trn
31	45.5	0.40519	0.40519	2.99897	0.00741	0.02003	-3.2148	1.32426	1.32426	1	E_Ctrl
32	59.68	-0.45219	-0.45219	-4.49834	0.00027	0.00205	0.15448	0.73093	-1.36812	-1	Str_Trn
33	59.68	-0.47444	-0.47444	-4.5659	0.00023	0.00184	0.30376	0.71975	-1.38937	-1	Str_Trn
34	59.68	-0.43473	-0.43473	-4.56246	0.00023	0.00185	0.29618	0.73983	-1.35166	-1	Str_Trn
35	59.68	-0.47393	-0.47393	-4.80125	0.00014	0.00127	0.82216	0.72	-1.38889	-1	Str_Trn
36	59.57	-0.4092	-0.4092	-4.72064	0.00016	0.00144	0.64495	0.75304	-1.32794	-1	Str_Trn
37	53.5	0.363	0.363	12.7216	1.5E-10	9.4E-08	14.389	1.28609	1.28609	1	Str_Ctrl
38	48.48	-0.37008	-0.37008	-9.47862	1.3E-08	8.1E-07	10.0177	0.77374	-1.29242	-1	E_Trn
39	17.02	-0.39552	-0.39552	-9.28016	1.8E-08	1E-06	9.68498	0.76022	-1.31541	-1	E_Trn
40	60.5	0.37461	0.37461	6.40303	4.6E-06	0.00012	4.21714	1.29649	1.29649	1	Str_Ctrl
41	56	-0.37402	-0.37402	-9.59542	1.1E-08	7.1E-07	10.2112	0.77163	-1.29596	-1	E_Trn
42	64.03	-0.42028	-0.42028	-6.88873	1.7E-06	6E-05	5.18442	0.74728	-1.33819	-1	Str_Trn
43	31.61	-0.42233	-0.42233	-8.04265	1.6E-07	4.9E-06	7.49352	0.74622	-1.34009	-1	E_Trn
44	56.25	-0.42891	-0.42891	-11.0665	1.1E-09	1.6E-07	12.5076	0.74282	-1.34621	-1	E_Trn
45	38.19	0.39325	0.39325	6.48089	3.9E-06	0.00011	4.37436	1.31335	1.31335	1	Str_Ctrl
46	47	0.36526	0.36526	6.80414	2.1E-06	6.8E-05	5.01828	1.28811	1.28811	1	Str_Ctrl
47	50	-0.43423	-0.43423	-9.87919	9.1E-09	1.4E-06	10.423	0.74009	-1.35119	-1	Str_Trn
48	51	-0.46546	-0.46546	-5.10325	6.4E-05	0.00045	1.46612	0.72424	-1.38075	-1	E_Trn
49	51	-0.36364	-0.36364	-5.17542	5.5E-05	0.00039	1.62618	0.7772	-1.28667	-1	E_Trn
50	54.5	0.52882	0.52882	2.19203	0.04152	0.08545	-4.70898	1.44274	1.44274	1	Str_Ctrl
51	54.5	0.39598	0.39598	1.79312	0.08948	0.15409	-5.38925	1.31584	1.31584	1	Str_Ctrl
52	47.5	-0.3813	-0.3813	-6.54839	2.9E-06	4.1E-05	4.56832	0.76775	-1.30252	-1	E_Trn
53	40	-0.43592	-0.43592	-4.02415	0.00077	0.00446	-0.89572	0.73922	-1.35278	-1	Str_Trn
54	40	0.38727	0.38727	10.2623	5E-09	1E-06	11.0098	1.30792	1.30792	1	Str_Ctrl
55	40	-0.48985	-0.48985	-3.90162	0.00102	0.00546	-1.16675	0.7121	-1.4043	-1	Str_Trn
56	40	-0.49057	-0.49057	-4.06412	0.00071	0.00417	-0.8072	0.71175	-1.405	-1	Str_Trn
57	40	-0.46894	-0.46894	-3.75332	0.00142	0.00697	-1.49388	0.72249	-1.3841	-1	Str_Trn
58	37.5	0.32134	0.32134	2.04678	0.05484	0.10013	-5.07725	1.24949	1.24949	1	E_Ctrl
59	59.17	-0.41983	-0.41983	-3.39948	0.00313	0.01253	-2.26719	0.74751	-1.33777	-1	Str_Trn

Table 30.B2

30	AGAAACCACAAAGCTAGGAATTAAATTTTCGAATGTTTTTCTTCCTCTTAAGTGAGATAA	13	42011104	42011135	42235825	42235856
31	AATACGTGGTCAATCTAAGGATTATAGTTCGAAAAGATTAATGATGTATTGATGACACTT	13	59818047	59818078	59854837	59854868
32	GACACCTCCTCTCCCTTCCCTCCCCTTCTCGAGTTATCAAAATATTTTGAGAGACAGTAT	11	11968004	11968035	11984245	11984276
33	GACACCTCCTCTCCCTTCCCTCCCCTTCTCGATCACTTTGCAAAGCTTTGTTGGCTAGGC	11	11968004	11968035	12019427	12019458
34	GACACCTCCTCTCCCTTCCCTCCCCTTCTCGAAGGAAAAGCCCTGGGGCCAGCTGTAGAG	11	11968004	11968035	12010923	12010954
35	GACACCTCCTCTCCCTTCCCTCCCCTTCTCGATGGCCACATGTGGCCAGTGGCTCTCATG	11	11968004	11968035	12048403	12048434
36	CCGCTCTGCTATGGACCCCGGCTCGCTCTCGACTTGGCCCCCAGCATGTCCTCAGCCACC	14	100687837	100687868	100751546	100751577
37	TTATAATTGTTACTATTGGGAAGAGGATTCGACACAGAAACTAAGTTTTCAAAATAAAAA	20	54466479	54466510	54577319	54577350
38	GCCAAGAGGGGAAAGGACTCATGTTCTCTCGACTGCCTCCTCTCCCACCTCTGCTCGGAT	8	22682789	22682820	22739153	22739184
39	CCACCCCTGCTGCTCTGGACCTGGTGGATCGACTTTTGTTTCCTGTCATTCAAGCTGCGT	11	64868178	64868209	64916059	64916090
40	TTTGGTGATGAAATGAAAATAATTTATTTCGAAGAGCTCCTTATTCCAGTAGAAACACAA	4	100525710	100525741	100732651	100732682
41	ACCATCAGAAAGCTCCATTTTCTTTTGTTCGACATGATTTTATGACTGATTGGTCATAGG	11	128476761	128476792	128561632	128561663
42	TGTCCTTTCAAGGAAGGATTAGCATCCTTCGAAAGACCTATCAGGATTTCATTTGTAATG	8	71216399	71216430	71261816	71261847
43	CTTGCCTAGTCTTTAATTTATTTATTTATCGACATTTTTTTCTTATCAACGAGACGATGT	3	13512352	13512383	13590312	13590343
44	TGCAGAAAGTACTACAAAAAAAGAAGCTTCGAAAATGTTGGAGATGAGAGTTTCTTCACC	8	123527843	123527874	123555254	123555285
45	CATGGTTTATAATCCTTTTTATACATTGTCGACACTGTATTTTCACAGATCACTCTGGAG	13	40524349	40524380	40688580	40688611
46	AGAACTTCCTGATATATTTTTTTTCTTTTCGAAGGTCTTAAAATGTTTTTAAACATGACC	6	108604405	108604436	108629992	108630023
47	GACTCTTAAAACAATAATATCAAACAACTCGACTTGTCATTTAGTTCTTTGGGAAGCAGT	16	53844989	53845020	54052288	54052319
48	ACAACAGAATAGAACATATTCAATTAAATCGACATAGGAATAGGTTTCAGATCCTAGTCT	13	91728718	91728749	91910388	91910419
49	TAATAATTTTATATAATAGAATTTTGACTCGAAGTTGATGTCAAGATTTATGGCTTACAT	13	91794062	91794093	91953115	91953146
50	AATTAGACAACGACTATATGACTCTGTCTCGACTTTAAAGCAAGTACTTCTTGTATGCTC	13	94054831	94054862	94133177	94133208
51	AATTAGACAACGACTATATGACTCTGTCTCGAGATTGGTCTTAACACACTATTGATTATT	13	94133177	94133208	94304194	94304225
52	GCAAATTTTGGAGCCTAACCTCCAAAATTCGAGCACAAAACTTTGTCCACATTTCTGATT	7	50706363	50706394	50780874	50780905
53	AAAAAGAGAAAAGCAGGTTAGCACATTGTCGACCCCGCCCCCGGGATGGGGGAACTGGCC	9	121180379	121180410	121268506	121268537
54	CTCTATAAATTTACCAGAATATAAATTCTCGAAGTGATCTCTAAATGTAATCGTAAGTTT	9	121188989	121189020	121243316	121243347
55	AAATTTTCAAGTGTACGATATGGTATCATCGACCCCGCCCCCGGGATGGGGGAACTGGCC	9	121232597	121232628	121268506	121268537
56	AAACTTACGATTACATTTAGAGATCACTTCGACCCCGCCCCCGGGATGGGGGAACTGGCC	9	121243316	121243347	121268506	121268537
57	GAGAGATGCCCACTCATACCATATAACTTCGACCCCGCCCCCGGGATGGGGGAACTGGCC	9	121253564	121253595	121268506	121268537
58	CCACATAAAACCTTGGGTTCTTAATTTATCGAAGTTGAGTTACGTGTTTAAAAAAAGAAA	7	18055950	18055981	18141979	18142010
59	TCATATAAATGCCCCACAGAGTGCAGCATCGAACCTCGCCCCCTGCACGACCCACACAAA	12	53959983	53960014	53994247	53994278

Table 30.B3

30	13	42011104	42015105	4.2E+07	42239826
31	13	59818047	59822048	6E+07	59858838
32	11	11964034	11968035	1.2E+07	11988246
33	11	11964034	11968035	1.2E+07	12019458
34	11	11964034	11968035	1.2E+07	12014924
35	11	11964034	11968035	1.2E+07	12052404
36	14	100687837	100691838	1E+08	100751577
37	20	54466479	54470480	5.5E+07	54577350
38	8	22678819	22682820	2.3E+07	22739184
39	11	64868178	64872179	6.5E+07	64916090
40	4	100525710	100529711	1E+08	100736652
41	11	128476761	128480762	1.3E+08	128565633
42	8	71216399	71220400	7.1E+07	71265817
43	3	13512352	13516353	1.4E+07	13590343
44	8	123523873	123527874	1.2E+08	123559255
45	13	40524349	40528350	4.1E+07	40692581
46	6	108600435	108604436	1.1E+08	108633993
47	16	53844989	53848990	5.4E+07	54052319
48	13	91724748	91728749	9.2E+07	91914389
49	13	91794062	91798063	9.2E+07	91957116
50	13	94054831	94058832	9.4E+07	94133208
51	13	94129207	94133208	9.4E+07	94304225
52	7	50706363	50710364	5.1E+07	50780905
53	9	121176409	121180410	1.2E+08	121272507
54	9	121185019	121189020	1.2E+08	121243347
55	9	121228627	121232628	1.2E+08	121272507
56	9	121239346	121243347	1.2E+08	121272507
57	9	121253564	121257565	1.2E+08	121272507
58	7	18055950	18059951	1.8E+07	18142010
59	12	53956013	53960014	5.4E+07	53994278

Table 30.B4

60	IGF1R_15_98659065_98662585_98893484_98899517_FR	IGF1R	200	106	0.008018013	0.06952724
61	IL1RAP_3_190465562_190469171_190489665_190498302_RF	IL1RAP	200	89	0.502149894	1
62	IL1RAP_3_190489665_190498302_190560851_190563356_FR	IL1RAP	200	89	0.502149894	1
63	KDM1A_1_23064655_23070269_23096951_23098159_FR	KDM1A	47	20	0.647904687	1
64	LAMA2_6_128920996_128927003_129105731_129113311_FF	LAMA2	200	150	9.1067E-19	7.14876E-16
65	LAMA2_6_129342029_129351351_129383008_129389769_FR	LAMA2	200	150	9.1067E-19	7.14876E-16
66	LCK_1_32214585_32217213_32237144_32241139_RF	LCK	47	19	0.750202183	1
67	LDB2_4_16489298_16494220_16535160_16542582_RR	LDB2	200	108	0.003555653	0.038235451
68	LMO4_1_87315524_87318670_87343110_87349940_FF	LMO4	106	81	1.57736E-11	3.09557E-09
69	LMO4_1_87315524_87318670_87355277_87360229_FR	LMO4	106	81	1.57736E-11	3.09557E-09
70	MAPK10_4_86572598_86581486_86617317_86621940_FF	MAPK10	200	114	0.000197862	0.005547208
71	MBNL1_3_152229500_152234786_152252961_152257281_FR	MBNL1	200	91	0.389926943	1
72	MBNL1_3_152229500_152234786_152281057_152285843_FR	MBNL1	200	91	0.389926943	1
73	MYBPC1_12_101527342_101530065_101646571_101655128_RF	MYBPC1	186	94	0.05009075	0.263900932
74	MYH1_17_10491098_10496051_10520297_10523271_RR	MYH1	103	52	0.121185055	0.485358512
75	MYH1_17_10523271_10524567_10560779_10565755_FF	MYH1	103	52	0.121185055	0.485358512
76	MYO18B_22_26004818_26009467_26030914_26037279_FF	MYO18B	200	73	0.989437228	1
77	NCAM1_11_113019160_113028536_113163748_113168132_FR	NCAM1	200	111	0.00091339	0.014340227
78	NECTIN2_19_44815042_44816736_44827160_44828776_RR	NECTIN2	47	12	0.997525539	1
79	NFKB1_4_102504137_102509238_102557818_102560252_FF	NFKB1	120	73	0.00019192	0.005547208
80	NFKB1_4_102557818_102560252_102627099_102634363_FR	NFKB1	120	73	0.00019192	0.005547208
81	NFKB1_4_102599188_102601960_102627099_102634363_FR	NFKB1	120	73	0.00019192	0.005547208
82	NR4A1_12_51995149_51997631_52041793_52046779_RR	NR4A1	47	13	0.993704481	1
83	NRXN1_2_50580957_50583587_50867546_50884047_RF	NRXN1	200	110	0.00146407	0.020081546
84	NTRK2_9_84804816_84814325_84917519_84924935_FR	NTRK2	200	108	0.003555653	0.038235451
85	NTRK2_9_84804816_84814325_84934592_84942655_RF	NTRK2	200	108	0.003555653	0.038235451
86	PAG1_8_81007411_81018107_81069439_81070856_FR	PAG1	200	126	7.40996E-08	5.81682E-06
87	PAG1_8_81007411_81018107_81126745_81129448_FR	PAG1	200	126	7.40996E-08	5.81682E-06
88	PCK1_20_57527297_57530814_57551578_57557205_RR	PCK1	47	27	0.047791071	0.253486424
89	PCK1_20_57527297_57530814_57570220_57572870_RR	PCK1	47	27	0.047791071	0.253486424

Table 30.C1

60	53	-0.3995	-0.3995	-9.07793	2.6E-08	1.3E-06	9.34074	0.75812	-1.31905	-1	E_Trn
61	44.5	-0.37779	-0.37779	-9.55782	1.1E-08	7.4E-07	10.1491	0.76962	-1.29935	-1	E_Trn
62	44.5	0.34847	0.34847	11.5647	5.1E-10	9.5E-08	13.2297	1.27321	1.27321	1	E_Ctrl
63	42.55	0.45098	0.45098	11.7421	5.8E-10	2.4E-07	13.1188	1.36697	1.36697	1	Str_Ctrl
64	75	-0.38825	-0.38825	-5.36236	3.6E-05	0.00028	2.03874	0.76406	-1.3088	-1	E_Trn
65	75	-0.40794	-0.40794	-12.0446	2.6E-10	6.4E-08	13.9006	0.7537	-1.32679	-1	E_Trn
66	40.43	0.40486	0.40486	4.02911	0.00072	0.00308	-0.9465	1.32396	1.32396	1	E_Ctrl
67	54	0.33023	0.33023	5.78958	1.4E-05	0.00014	2.96874	1.25721	1.25721	1	E_Ctrl
68	76.42	-0.4253	-0.4253	-4.33423	0.00039	0.00268	-0.20873	0.74468	-1.34286	-1	Str_Trn
69	76.42	-0.45509	-0.45509	-5.12331	6.7E-05	0.00077	1.52571	0.72946	-1.37087	-1	Str_Trn
70	57	0.36948	0.36948	10.6233	2.9E-09	6.8E-07	11.5469	1.29189	1.29189	1	Str_Ctrl
71	45.5	-0.38329	-0.38329	-8.65576	5.3E-08	2.2E-06	8.60483	0.76669	-1.30431	-1	E_Trn
72	45.5	-0.42323	-0.42323	-5.76242	1.7E-05	0.00029	2.89367	0.74576	-1.34092	-1	Str_Trn
73	50.54	0.38033	0.38033	2.20515	0.04044	0.08374	-4.68518	1.30164	1.30164	1	Str_Ctrl
74	50.49	-0.41206	-0.41206	-6.14494	7.8E-06	0.00017	3.69022	0.75155	-1.33058	-1	Str_Trn
75	50.49	0.32004	0.32004	7.50348	4.4E-07	1E-05	6.47359	1.24836	1.24836	1	E_Ctrl
76	36.5	-0.36797	-0.36797	-5.42926	3.1E-05	0.00025	2.18559	0.77487	-1.29054	-1	E_Trn
77	55.5	-0.47342	-0.47342	-5.25206	4.6E-05	0.00034	1.7957	0.72026	-1.3884	-1	E_Trn
78	25.53	0.32241	0.32241	8.11688	1.4E-07	4.5E-06	7.63079	1.25042	1.25042	1	E_Ctrl
79	60.83	0.35343	0.35343	7.56553	4.8E-07	2.3E-05	6.47751	1.2776	1.2776	1	Str_Ctrl
80	60.83	-0.40158	-0.40158	-7.53437	4.2E-07	9.8E-06	6.5331	0.75703	-1.32096	-1	E_Trn
81	60.83	-0.41977	-0.41977	-16.809	8E-13	1.4E-09	19.4697	0.74754	-1.33772	-1	E_Trn
82	27.66	-0.40863	-0.40863	-6.84429	1.9E-06	6.4E-05	5.09725	0.75334	-1.32742	-1	Str_Trn
83	55	0.32026	0.32026	5.92682	1.1E-05	0.00011	3.26326	1.24856	1.24856	1	E_Ctrl
84	54	0.37084	0.37084	6.52335	3.1E-06	4.3E-05	4.5167	1.2931	1.2931	1	E_Ctrl
85	54	0.35785	0.35785	10.4559	2.7E-09	2.9E-07	11.5853	1.28152	1.28152	1	E_Ctrl
86	63	-0.38914	-0.38914	-8.8407	3.9E-08	1.8E-06	8.93009	0.76359	-1.30961	-1	E_Trn
87	63	-0.38118	-0.38118	-6.54771	2.9E-06	4.1E-05	4.56692	0.76781	-1.30241	-1	E_Trn
88	57.45	-0.4278	-0.4278	-2.90477	0.00932	0.02801	-3.31712	0.7434	-1.34518	-1	Str_Trn
89	57.45	-0.44375	-0.44375	-3.06931	0.00651	0.02147	-2.97337	0.73522	-1.36014	-1	Str_Trn

Table 30.C2

60	ATGAAAGAATATGATTTTTTTTTTTTACTCGAGTGTAAAAGGGCTTTTACTGGTGCACAC	15	98662554	98662585	98893484	98893515
61	TAAATAAAATTGTCTTTTTTTGTCTTTCTCGAGATTTTGAAACACCTTCAGTTTGAAGAC	3	190465562	190465593	190498271	190498302
62	TAAATAAAATTGTCTTTTTTTGTCTTTCTCGATTACAGAGAACTAAGTACATTTTAAATC	3	190498271	190498302	190560851	190560882
63	GGCAGGTGGATCATTTGAGGTCAAGAGCTCGACAGAGCAAGACACCATCTCCAAAAAGAA	1	23070238	23070269	23096951	23096982
64	TCTAAGGTATAGTTTTGGGTATAAACCATCGAACATTACCCCCGATTGTTTTGGAAATTA	6	128926972	128927003	129113280	129113311
65	TTATTTGTTAATATCCAGTAGTATTTAATCGATTGCCGTTGGCTCAAAGTAATATTTGAA	6	129351320	129351351	129383008	129383039
66	AAGGGCTCGGGAGCTCCCTCGGCACACCTCGAGGAGTGCCAGGCATCTACTGCTCTGTCC	1	32214585	32214616	32241108	32241139
67	AGGAATCCATTTTCAGATCACACCCCAGTCGAAAGAAAACCATTTGGATGACCGTGGAAG	4	16489298	16489329	16535160	16535191
68	CCCCTGGCTCACCTACACAAAATTGTGCTCGACTCTACTCTTAGCCCTGCTAAATAAGTA	1	87318639	87318670	87349909	87349940
69	CCCCTGGCTCACCTACACAAAATTGTGCTCGAATGTCTGAACAAGTGAATGAACAAATGA	1	87318639	87318670	87355277	87355308
70	ATTATATTAGTGCTGTAATAAAATTAAGTCGACACATTTGATACTGCTTATTGGGTTATT	4	86581455	86581486	86621909	86621940
71	TACCTTGAAAAGCTCTTCAGTATGATTATCGAAAGATTCATTTTCATGTTCCGTTTTATC	3	152234755	152234786	152252961	152252992
72	TACCTTGAAAAGCTCTTCAGTATGATTATCGAGCTTTAGCCATTCTAGTAATTATTAAAA	3	152234755	152234786	152281057	152281088
73	AGATCTCACATGTAAATTAGAATAGCAGTCGACTAAATATAAAGACTCAATAACCACCAT	12	101527342	101527373	101655097	101655128
74	TTTTCTCCCAAAGTTTATATCCTAATATTCGAGGAAGGTTATATTTTTGGCTATGCATCT	17	10491098	10491129	10520297	10520328
75	TGTCTGTTCCAGAGTGGCCCGCAGCTCCTCGAGGAGCTGGCACTCTTATACACCTCTGGG	17	10524536	10524567	10565724	10565755
76	TGAGTTACTGTTTTTCCTTCCTTTTGATTCGAGAAGAAACCAAGAATTAGAGGGATTTAA	22	26009436	26009467	26037248	26037279
77	ATGAATTAATGTTTCCTAGAAAGTTGTCTCGAAAGAAGAAAGTGTCAGGGTTCAACTGCC	11	113028505	113028536	113163748	113163779
78	GGTCAGGTCTGTGCTATGGAAAGAGCTCTCGACCTCCAGTCTTTCCTCTCGCATAAATGG	19	44815042	44815073	44827160	44827191
79	TCTTTATGGTGTCTCTTTATATATTTACTCGAGAAAGAAGTAACACACTATTGCTAATTC	4	102509207	102509238	102560221	102560252
80	GAATTAGCAATAGTGTGTTACTTCTTTCTCGATATTTTACATGGAATCTTTCCCTTTTTA	4	102560221	102560252	102627099	102627130
81	TACCTTTCCATTTGTCTCCTTCCCTTCATCGATATTTTACATGGAATCTTTCCCTTTTTA	4	102601929	102601960	102627099	102627130
82	ATCTGGCTTCACATTCCTCGGCCCTTCCTCGACTCTCCCTCTGTAGGCCTCCACCATGGA	12	51995149	51995180	52041793	52041824
83	ATTCATTTATCTGTATTCTTAGTATGCTTCGAAGGTAATATAACCTTGAAAATGTAACAA	2	50580957	50580988	50884016	50884047
84	CTCTTCAGGGGTGTGTGGAGTAAATAGCTCGAGTTTGTCCACAGCCCTCACAGCCCTTGG	9	84814294	84814325	84917519	84917550
85	TAAAAAGAAACATATGAAACTTATTTTATCGACCCTATAGATTTTTCAATATATGTTTAT	9	84804816	84804847	84942624	84942655
86	TCAGATAAGTAACTTCCTGATAATTAACTCGAAGTCCAGGATTCATTATAAACACTGATA	8	81018076	81018107	81069439	81069470
87	TCAGATAAGTAACTTCCTGATAATTAACTCGAGAAACATTTATTGGTTGTCCAATTGTTT	8	81018076	81018107	81126745	81126776
88	CCTCGTCGTCCCCTCTCTTCCTCGTTCCTCGACAGGAAAGCATACGGAAAAAGTTAAAGA	20	57527297	57527328	57551578	57551609
89	CCTCGTCGTCCCCTCTCTTCCTCGTTCCTCGATGCGGGACTGATTGTTACAGAACTGTTT	20	57527297	57527328	57570220	57570251

Table 30.C3

60	15	98658584	98662585	9.9E+07	98897485
61	3	190465562	190469563	1.9E+08	190498302
62	3	190494301	190498302	1.9E+08	190564852
63	1	23066268	23070269	2.3E+07	23100952
64	6	128923002	128927003	1.3E+08	129113311
65	6	129347350	129351351	1.3E+08	129387009
66	1	32214585	32218586	3.2E+07	32241139
67	4	16489298	16493299	1.7E+07	16539161
68	1	87314669	87318670	8.7E+07	87349940
69	1	87314669	87318670	8.7E+07	87359278
70	4	86577485	86581486	8.7E+07	86621940
71	3	152230785	152234786	1.5E+08	152256962
72	3	152230785	152234786	1.5E+08	152285058
73	12	101527342	101531343	1E+08	101655128
74	17	10491098	10495099	1.1E+07	10524298
75	17	10520566	10524567	1.1E+07	10565755
76	22	26005466	26009467	2.6E+07	26037279
77	11	113024535	113028536	1.1E+08	113167749
78	19	44815042	44819043	4.5E+07	44831161
79	4	102505237	102509238	1E+08	102560252
80	4	102556251	102560252	1E+08	102631100
81	4	102597959	102601960	1E+08	102631100
82	12	51995149	51999150	5.2E+07	52045794
83	2	50580957	50584958	5.1E+07	50884047
84	9	84810324	84814325	8.5E+07	84921520
85	9	84804816	84808817	8.5E+07	84942655
86	8	81014106	81018107	8.1E+07	81073440
87	8	81014106	81018107	8.1E+07	81130746
88	20	57527297	57531298	5.8E+07	57555579
89	20	57527297	57531298	5.8E+07	57574221

Table 30.C4

90	PCK1_20_57527297_57530814_57579772_57583521_RR	PCK1	47	27	0.047791071	0.253486424
91	PCK1_20_57527297_57530814_57583521_57585923_RR	PCK1	47	27	0.047791071	0.253486424
92	PDK3_X_24441637_24447950_24480152_24481252_FR	PDK3	42	14	0.945004612	1
93	PDK3_X_24441637_24447950_24490440_24491541_FR	PDK3	42	14	0.945004612	1
94	PHTF2_7_77800747_77805972_77956111_77960107_RR	PHTF2	200	99	0.078405901	0.370774891
95	PHTF2_7_77846910_77851576_77956111_77960107_RR	PHTF2	200	99	0.078405901	0.370774891
96	PIK3C3_18_42033052_42039159_42070009_42072187_RF	PIK3C3	174	92	0.013813418	0.105277024
97	PIK3C3_18_42070009_42072187_42088671_42094691_FF	PIK3C3	174	92	0.013813418	0.105277024
98	PIK3R1_5_68187850_68194388_68237549_68241297_FF	PIK3R1	146	71	0.164362225	0.605748107
99	PIK3R1_5_68203536_68213336_68237549_68241297_FR	PIK3R1	146	71	0.164362225	0.605748107
100	PLCXD2_3_111719030_111722119_111809065_111815838_RR	PLCXD2	200	76	0.969310539	1
101	PPARGC1A_4_23871872_23880181_23925180_23932379_FF	PPARGC1A	200	109	0.002303017	0.026200987
102	PPP3CA_4_101055418_101067369_101247819_101259416_RR	PPP3CA	200	95	0.198157163	0.697548759
103	PRDX6_1_173434669_173438537_173475099_173476805_FR	PRDX6	38	21	0.115306099	0.474801595
104	PRDX6_1_173434669_173438537_173477717_173485417_FR	PRDX6	38	21	0.115306099	0.474801595
105	PRDX6_1_173450908_173452763_173477717_173485417_FR	PRDX6	38	21	0.115306099	0.474801595
106	PRKCQ_10_6432893_6439235_6488207_6489596_FF	PRKCQ	200	106	0.008018013	0.06952724
107	PTPRC_1_198595771_198598296_198659753_198666156_RF	PTPRC	200	98	0.101325207	0.434758425
108	PTPRC_1_198631562_198634915_198659753_198666156_RF	PTPRC	200	98	0.101325207	0.434758425
109	PTPRC_1_198659753_198666156_198697386_198704777_FR	PTPRC	200	98	0.101325207	0.434758425
110	PTPRC_1_198659753_198666156_198704777_198709653_FR	PTPRC	200	98	0.101325207	0.434758425
111	PTPRC_1_198659753_198666156_198721093_198724578_FF	PTPRC	200	98	0.101325207	0.434758425
112	PTPRC_1_198659753_198666156_198768850_198775826_FF	PTPRC	200	98	0.101325207	0.434758425
113	PYGM_11_64747174_64749438_64762879_64765587_RF	PYGM	16	8	0.413940883	1
114	RGS6_14_72139099_72144564_72213251_72222544_FR	RGS6	200	110	0.00146407	0.020081546
115	RORA_15_60902137_60909221_61019417_61030714_RR	RORA	200	102	0.032796361	0.195038964
116	RUNX3_1_24920810_24923822_24973522_24976037_RF	RUNX3	94	25	0.999868187	1
117	RYR1_19_38410632_38413089_38495982_38499305_RR	RYR1	75	31	0.734667715	1
118	SGCZ_8_14631157_14642508_14656955_14664444_RF	SGCZ	200	131	1.15564E-09	1.13397E-07
119	SLC35B1_17_49700402_49702340_49724264_49725934_RR	SLC35B1	34	9	0.989799814	1

Table 30.D1

90	57.45	-0.45438	-0.45438	-3.14668	0.00549	0.01895	-2.80966	0.72983	-1.37019	-1	Str_Trn
91	57.45	-0.46711	-0.46711	-3.5423	0.00228	0.00989	-1.95661	0.72341	-1.38233	-1	Str_Trn
92	33.33	-0.51621	-0.51621	-2.91295	0.00916	0.02763	-3.30018	0.69921	-1.43019	-1	Str_Trn
93	33.33	-0.48296	-0.48296	-2.84564	0.0106	0.03078	-3.439	0.71551	-1.39761	-1	Str_Trn
94	49.5	-0.37906	-0.37906	-7.13828	9E-07	1.7E-05	5.75985	0.76894	-1.3005	-1	E_Trn
95	49.5	0.40917	0.40917	9.25447	2.5E-08	2.9E-06	9.42731	1.32792	1.32792	1	Str_Ctrl
96	52.87	0.36058	0.36058	10.1197	6.2E-09	1.1E-06	10.7935	1.28394	1.28394	1	Str_Ctrl
97	52.87	0.34906	0.34906	10.1957	4.1E-09	3.8E-07	11.1792	1.27373	1.27373	1	E_Ctrl
98	48.63	-0.40001	-0.40001	-7.21891	7.7E-07	1.5E-05	5.91903	0.75785	-1.31952	-1	E_Trn
99	48.63	-0.37383	-0.37383	-6.77717	1.8E-06	2.9E-05	5.03603	0.77173	-1.29578	-1	E_Trn
100	38	0.36966	0.36966	10.925	1.3E-09	1.8E-07	12.2976	1.29205	1.29205	1	E_Ctrl
101	54.5	0.3467	0.3467	10.5435	2.4E-09	2.6E-07	11.7202	1.27165	1.27165	1	E_Ctrl
102	47.5	-0.46232	-0.46232	-10.3242	4.5E-09	9.5E-07	11.103	0.72582	-1.37776	-1	Str_Trn
103	55.26	-0.37846	-0.37846	-6.54322	3E-06	4.2E-05	4.55767	0.76926	-1.29995	-1	E_Trn
104	55.26	-0.36712	-0.36712	-9.7319	8.6E-09	6E-07	10.4352	0.77533	-1.28977	-1	E_Trn
105	55.26	-0.43334	-0.43334	-6.62265	2.9E-06	8.8E-05	4.6585	0.74054	-1.35036	-1	Str_Trn
106	53	-0.39208	-0.39208	-8.21682	1.2E-07	3.9E-06	7.81442	0.76203	-1.31228	-1	E_Trn
107	49	0.34287	0.34287	12.2469	2E-10	5.4E-08	14.1766	1.26828	1.26828	1	E_Ctrl
108	49	0.3635	0.3635	12.1633	2.2E-10	5.8E-08	14.0631	1.28654	1.28654	1	E_Ctrl
109	49	0.32003	0.32003	11.7784	3.8E-10	7.8E-08	13.5313	1.24836	1.24836	1	E_Ctrl
110	49	0.33346	0.33346	13.2487	5.1E-11	2.3E-08	15.4853	1.26003	1.26003	1	E_Ctrl
111	49	0.3532	0.3532	12.7171	1E-10	3.8E-08	14.8025	1.27739	1.27739	1	E_Ctrl
112	49	0.33194	0.33194	12.0445	2.6E-10	6.4E-08	13.9006	1.25871	1.25871	1	E_Ctrl
113	50	-0.38806	-0.38806	-9.61961	1E-08	6.9E-07	10.2511	0.76415	-1.30864	-1	E_Trn
114	55	0.37355	0.37355	9.04986	3.5E-08	3.6E-06	9.09037	1.29554	1.29554	1	Str_Ctrl
115	51	-0.47031	-0.47031	-3.83332	0.00113	0.00442	-1.38642	0.72181	-1.38541	-1	E_Trn
116	26.6	0.36423	0.36423	10.3099	4.6E-09	9.6E-07	11.0816	1.2872	1.2872	1	Str_Ctrl
117	41.33	0.37985	0.37985	3.09107	0.0062	0.02072	-2.92745	1.3012	1.3012	1	Str_Ctrl
118	65.5	-0.39071	-0.39071	-7.31446	6.4E-07	1.3E-05	6.10649	0.76275	-1.31104	-1	E_Trn
119	26.47	-0.41926	-0.41926	-4.89024	0.00011	0.00111	1.01732	0.74781	-1.33724	-1	Str_Trn

Table 30.D2

90	CCTCGTCGTCCCCTCTCTTCCTCGTTCCTCGAACATCTCCAAGTCAGATAATCATAACAA	20	57527297	57527328	57579772	57579803
91	CCTCGTCGTCCCCTCTCTTCCTCGTTCCTCGAGCCTCTGTCCCAATGTCACCTCTTCAGA	20	57527297	57527328	57583521	57583552
92	GGGGATGGGGCCGAAATATGATTGCACTTCGAGTTTGTTTAGTTTTTATCTTCCCCATTT	X	24447919	24447950	24480152	24480183
93	GGGGATGGGGCCGAAATATGATTGCACTTCGAACTTCAGCACCTGACCTTTGTCATCAAC	X	24447919	24447950	24490440	24490471
94	AAATAATATACAAGTAGTCCAACTATTTTCGAGTATTTTAGAAATTACATGAAACATGAA	7	77800747	77800778	77956111	77956142
95	TCAGGCTTGCAGGCTCATGCCTGCAATGTCGAGTATTTTAGAAATTACATGAAACATGAA	7	77846910	77846941	77956111	77956142
96	ATCTATTATAATGATGCAATATTGTTAATCGAGTTTTCCTTCTTAAAGAACAAACTCACC	18	42033052	42033083	42072156	42072187
97	ATCTATTATAATGATGCAATATTGTTAATCGATTCAAAGATCAAATTAATTATTAAAGCT	18	42072156	42072187	42094660	42094691
98	CTGAGTCTTCATTACCAAAAAAAAAAGTTCGAACATGCACTGGGGTTTTACTAAAACTAT	5	68194357	68194388	68241266	68241297
99	CGTTGCAAATTGTACATCTTCTGCTATTTCGAATGCGAAGTTGAGAAATTTTACTTATTT	5	68213305	68213336	68237549	68237580
100	TACTTTTTTCATATGGATATACAGTTATTCGAGGAGGAATAGTCACATAAATAAATTATT	3	111719030	111719061	111809065	111809096
101	TACATGAATATACAGTCTTGTATTGTTTTCGATCTATAGAATGGAAGGATAGCATTAGCT	4	23880150	23880181	23932348	23932379
102	TCTTTGTTTCCTGTTTCCACTTCTTATTTCGATATTTATTGAGTGCTACTATATATATGC	4	101055418	101055449	101247819	101247850
103	ACTGTATCTTTTGCTTATTTTCTATACTTCGAGGCATAGAACCTTTCCTTAAACTTATTT	1	173438506	173438537	173475099	173475130
104	ACTGTATCTTTTGCTTATTTTCTATACTTCGATCCCTCCTGGCCTCCCCGCCTCCGGCGT	1	173438506	173438537	173477717	173477748
105	TAATGCTGGAGCAAGACAAAGATAGACTTCGATCCCTCCTGGCCTCCCCGCCTCCGGCGT	1	173452732	173452763	173477717	173477748
106	TTCCACCTGTAATACTGTGCCTGTATTCTCGACTCTTCTCGCCCTCTTCTCCAGCTCTCT	10	6439204	6439235	6489565	6489596
107	AGAGGCTGAGGTGAAAAGATTGTTTGAGTCGAAGATCATTGTCTCATTTTTTTACTTGTT	1	198595771	198595802	198666125	198666156
108	AGAGGCTGAGGTGAAAAGATTGTTTGAGTCGACAAATGTTATACATGGCTTGTAACACTG	1	198631562	198631593	198666125	198666156
109	AGAGGCTGAGGTGAAAAGATTGTTTGAGTCGACAACCCAATTTTGTTATTTGAGTTTCTT	1	198666125	198666156	198697386	198697417
110	AGAGGCTGAGGTGAAAAGATTGTTTGAGTCGAATTCAATTTTACTGCAAACCTCAGCATC	1	198666125	198666156	198704777	198704808
111	AGAGGCTGAGGTGAAAAGATTGTTTGAGTCGATACACTGAACAAGTGCCAGAGCAGAATA	1	198666125	198666156	198724547	198724578
112	AGAGGCTGAGGTGAAAAGATTGTTTGAGTCGAGTCACATGATCAAGCGCTCATTTCTGTT	1	198666125	198666156	198775795	198775826
113	GAGGAGAGAAAGAAGACAAAGAAGACACTCGATCTGCCCTGCGGCCCCACCTGAGTGATT	11	64747174	64747205	64765556	64765587
114	AATGGCATTCTCCATTTATTCGTATTTATCGAGACTTTCTATGAAAGCTTTTTTGATGTT	14	72144533	72144564	72213251	72213282
115	GGCTGAAGAATGGAATTGAAGTAGAAAATCGATGATTATCAAGTATATACCAAACATTAT	15	60902137	60902168	61019417	61019448
116	CTTAATTTTTTTTCTTTGAATGCCTCTATCGACAGTCTTCTCTCTACTTTCTACAGTGAA	1	24920810	24920841	24976006	24976037
117	GGTGGGAGGATCACTTGAGGTCAGAAGTTCGATCTCCTGACCTCAAGTGATCCTCTAGCT	19	38410632	38410663	38495982	38496013
118	ATGAAAGAAATACCAATATTTGTTTAATTCGAATCTCCAACACGTTATTTACCACTGGGA	8	14631157	14631188	14664413	14664444
119	TGGTGGCTGAGTCCTGGCACAGCCACTGTCGAAGCTGGGCCCCGCACCCCCCACACAAAC	17	49700402	49700433	49724264	49724295

Table 30.D3

90	20	57527297	57531298	5.8E+07	57583773
91	20	57527297	57531298	5.8E+07	57587522
92	X	24443949	24447950	2.4E+07	24484153
93	X	24443949	24447950	2.4E+07	24494441
94	7	77800747	77804748	7.8E+07	77960112
95	7	77846910	77850911	7.8E+07	77960112
96	18	42033052	42037053	4.2E+07	42072187
97	18	42068186	42072187	4.2E+07	42094691
98	5	68190387	68194388	6.8E+07	68241297
99	5	68209335	68213336	6.8E+07	68241550
100	3	111719030	111723031	1.1E+08	111813066
101	4	23876180	23880181	2.4E+07	23932379
102	4	101055418	101059419	1E+08	101251820
103	1	173434536	173438537	1.7E+08	173479100
104	1	173434536	173438537	1.7E+08	173481718
105	1	173448762	173452763	1.7E+08	173481718
106	10	6435234	6439235	6485595	6489596
107	1	198595771	198599772	2E+08	198666156
108	1	198631562	198635563	2E+08	198666156
109	1	198662155	198666156	2E+08	198701387
110	1	198662155	198666156	2E+08	198708778
111	1	198662155	198666156	2E+08	198724578
112	1	198662155	198666156	2E+08	198775826
113	11	64747174	64751175	6.5E+07	64765587
114	14	72140563	72144564	7.2E+07	72217252
115	15	60902137	60906138	6.1E+07	61023418
116	1	24920810	24924811	2.5E+07	24976037
117	19	38410632	38414633	3.8E+07	38499983
118	8	14631157	14635158	1.5E+07	14664444
119	17	49700402	49704403	5E+07	49728265

Table 30.D4

120	SLC35D1_1_66998822_67004850_67070417_67074223_FR	SLC35D1	83	35	0.689428445	1
121	SMAD7_18_48917335_48920290_48969505_48974578_RF	SMAD7	49	21	0.632626918	1
122	STIM1_11_4071215_4074242_4084365_4091420_FR	STIM1	200	71	0.99529685	1
123	STK39_2_167959346_167965882_168109573_168114525_FF	STK39	200	95	0.198157163	0.697548759
124	STK39_2_168057412_168062336_168109573_168114525_FF	STK39	200	95	0.198157163	0.697548759
125	STXBP4_17_55035186_55042800_55142272_55149288_FR	STXBP4	178	72	0.865724188	1
126	SULF2_20_47663998_47665865_47797013_47801718_FR	SULF2	200	95	0.198157163	0.697548759
127	SYK_9_90789107_90793598_90876350_90879196_RF	SYK	189	111	4.46333E-05	0.001946506
128	SYK_9_90816328_90822228_90832284_90836084_RR	SYK	189	111	4.46333E-05	0.001946506
129	SYK_9_90816328_90822228_90836573_90843345_FR	SYK	189	111	4.46333E-05	0.001946506
130	SYK_9_90816328_90822228_90836573_90843345_RR	SYK	189	111	4.46333E-05	0.001946506
131	SYK_9_90816328_90822228_90872966_90875740_RR	SYK	189	111	4.46333E-05	0.001946506
132	TBX21_17_47685438_47687129_47704291_47707744_FR	TBX21	2	0	1	1
133	TGFB2_1_218317687_218325587_218386401_218389011_FR	TGFB2	132	81	5.75498E-05	0.002258828
134	TGFBR2_3_30563062_30565548_30608158_30611268_FF	TGFBR2	200	116	6.4811E-05	0.002312575
135	TGFBR2_3_30566144_30567439_30633318_30636860_RR	TGFBR2	200	116	6.4811E-05	0.002312575
136	TGFBR2_3_30566144_30567439_30694718_30698514_RR	TGFBR2	200	116	6.4811E-05	0.002312575
137	TGFBR2_3_30641481_30645057_30688470_30694718_FF	TGFBR2	200	116	6.4811E-05	0.002312575
138	THADA_2_43260154_43263093_43324949_43335508_FF	THADA	200	116	6.4811E-05	0.002312575
139	THADA_2_43260154_43263093_43415062_43421910_FF	THADA	200	116	6.4811E-05	0.002312575
140	THNSL2_2_88139809_88146295_88161717_88164554_FF	THNSL2	29	22	0.000554527	0.010705579
141	THNSL2_2_88139809_88146295_88161717_88164554_FR	THNSL2	29	22	0.000554527	0.010705579
142	TLR2_4_153659613_153661830_153693586_153700349_RF	TLR2	35	27	7.79458E-05	0.002581174
143	TNFRSF25_1_6481328_6484248_6494588_6498048_FR	TNFRSF25	23	9	0.758494992	1
144	TTN_2_178554164_178555670_178788193_178796485_FR	TTN	200	105	0.011714369	0.093834484
145	UACA_15_70715123_70719636_70780754_70784668_RF	UACA	171	86	0.066058747	0.322087682
146	WASL_7_123664155_123666896_123763390_123768284_RF	WASL	117	46	0.880312179	1
147	ZEB1_10_31273317_31275631_31437913_31439545_RF	ZEB1	181	122	2.83212E-10	3.70535E-08
148	ZEB1_10_31273317_31275631_31507470_31524442_FF	ZEB1	181	122	2.83212E-10	3.70535E-08
149	ZEB1_10_31437913_31439545_31458964_31462037_FR	ZEB1	181	122	2.83212E-10	3.70535E-08

Table 30.E1

120	42.17	0.32021	0.32021	6.5647	2.8E-06	4E-05	4.60189	1.24851	1.24851	1	E_Ctrl
121	42.86	0.40277	0.40277	2.5496	0.01993	0.04923	-4.03372	1.32205	1.32205	1	Str_Ctrl
122	35.5	-0.38567	-0.38567	-6.19747	6.1E-06	7.2E-05	3.83751	0.76542	-1.30647	-1	E_Trn
123	47.5	-0.38658	-0.38658	-6.41859	3.8E-06	5.1E-05	4.29985	0.76494	-1.30729	-1	E_Trn
124	47.5	-0.38862	-0.38862	-6.08691	7.6E-06	8.6E-05	3.60402	0.76386	-1.30914	-1	E_Trn
125	40.45	-0.39909	-0.39909	-8.20964	1.2E-07	4E-06	7.80127	0.75834	-1.31868	-1	E_Trn
126	47.5	-0.41472	-0.41472	-4.62876	0.0002	0.00167	0.44251	0.75016	-1.33304	-1	Str_Trn
127	58.73	-0.40056	-0.40056	-15.082	5.4E-12	5.3E-09	17.6554	0.75756	-1.32002	-1	E_Trn
128	58.73	0.45488	0.45488	6.89229	1.5E-06	2.5E-05	5.26872	1.37067	1.37067	1	E_Ctrl
129	58.73	-0.41655	-0.41655	-6.92127	1.4E-06	2.3E-05	5.32701	0.74922	-1.33473	-1	E_Trn
130	58.73	0.43262	0.43262	6.95618	1.3E-06	2.2E-05	5.39709	1.34968	1.34968	1	E_Ctrl
131	58.73	0.49185	0.49185	7.3328	6.2E-07	1.3E-05	6.14231	1.40625	1.40625	1	E_Ctrl
132	0	-0.40849	-0.40849	-1.91206	0.07163	0.12978	-5.19571	0.75341	-1.32729	-1	Str_Trn
133	61.36	-0.42784	-0.42784	-9.6318	1E-08	6.8E-07	10.2712	0.74338	-1.34521	-1	E_Trn
134	58	-0.38523	-0.38523	-10.9424	1.3E-09	1.8E-07	12.3234	0.76566	-1.30607	-1	E_Trn
135	58	0.62646	0.62646	4.01916	0.00078	0.00449	-0.90676	1.54377	1.54377	1	Str_Ctrl
136	58	0.71377	0.71377	5.02096	8.4E-05	0.00091	1.30298	1.64008	1.64008	1	Str_Ctrl
137	58	-0.38301	-0.38301	-6.46184	3.5E-06	4.7E-05	4.38955	0.76684	-1.30406	-1	E_Trn
138	58	-0.44624	-0.44624	-2.33673	0.03099	0.06849	-4.44221	0.73395	-1.36248	-1	Str_Trn
139	58	-0.49656	-0.49656	-2.6351	0.01664	0.04305	-3.86485	0.7088	-1.41084	-1	Str_Trn
140	75.86	0.33309	0.33309	6.66784	2.3E-06	3.4E-05	4.81339	1.25971	1.25971	1	E_Ctrl
141	75.86	0.3483	0.3483	5.48285	2.8E-05	0.00023	2.30294	1.27306	1.27306	1	E_Ctrl
142	77.14	0.37061	0.37061	12.6902	1.6E-10	9.4E-08	14.3497	1.2929	1.2929	1	Str_Ctrl
143	39.13	-0.421	-0.421	-2.51835	0.02128	0.05168	-4.09478	0.74691	-1.33885	-1	Str_Trn
144	52.5	0.32765	0.32765	14.3916	1.2E-11	8.6E-09	16.8699	1.25496	1.25496	1	E_Ctrl
145	50.29	-0.45244	-0.45244	-6.64511	2.4E-06	3.5E-05	4.76692	0.7308	-1.36836	-1	E_Trn
146	39.32	-0.54064	-0.54064	-8.60372	5.8E-08	2.4E-06	8.51248	0.68746	-1.45462	-1	E_Trn
147	67.4	0.3798	0.3798	3.26917	0.00406	0.01232	-2.63478	1.30116	1.30116	1	E_Ctrl
148	67.4	0.3414	0.3414	8.35815	9E-08	3.2E-06	8.07177	1.26699	1.26699	1	E_Ctrl
149	67.4	0.35465	0.35465	3.41727	0.00291	0.00948	-2.31101	1.27867	1.27867	1	E_Ctrl

Table 30.E2

120	TAAATTTTTACTTGTATTTTTTTGCATTTCGAGTACTGTTTCCTTATTGGTCTTCTATAT	1	67004819	67004850	67070417	67070448
121	TATGAATCCCTAAATGTCACACATCAAGTCGAATTATATAAGATACCCTGAAATTTAAGG	18	48917335	48917366	48974547	48974578
122	CTTGTTATGATTTTAGTATGAGATAGTTTCGAGACAGAATTTATTTGTAATTTTATCAAT	11	4074211	4074242	4084365	4084396
123	TCTGCGCAAGTTTTAATTTTCTCTAAGGTCGATTTCCCCACCTTCCCAACCTCCAAGGGT	2	167965851	167965882	168114494	168114525
124	TAAAATATAAATGAAAGAAGTACCTCGTTTCGATTTCCCCACCTTCCCAACCTCCAAGGGT	2	168062305	168062336	168114494	168114525
125	TTTCATTTAGTTAAAACCAGATACATAATCGAGAGCACACAAAGGGGAATCCCAACAGACTC	17	55042769	55042800	55142272	55142303
126	CCTCTCCCGCTCTCCACTCACCTCGTGGTCGAAGTGTTGTCCCTGGACTGGCAGCATCTG	20	47665834	47665865	47797013	47797044
127	AAATTATGTTTCATGGAATGATCAGGAATCGAAACTCTCTCCAATGAAACAATTCTTTGA	9	90789107	90789138	90879165	90879196
128	ATGACTGTGGAAGGTTCTGATGTCTCTGTCGATGAAATGGAGAGAGGAGAAAGAAAAGAA	9	90816328	90816359	90832284	90832315
129	TTTTACTGTTTTTGTAAGAGATATGTTTTCGAGAGTTGCAAGTACCTGCCTAAATCACTG	9	90822197	90822228	90836573	90836604
130	ATGACTGTGGAAGGTTCTGATGTCTCTGTCGAGAGTTGCAAGTACCTGCCTAAATCACTG	9	90816328	90816359	90836573	90836604
131	ATGACTGTGGAAGGTTCTGATGTCTCTGTCGACATCATTTTTACAAATAAGACCAGATGT	9	90816328	90816359	90872966	90872997
132	GAGAGAGCGCCTGACATATAGTAGACCTTCGAGGAGAGAGAAGGGGCTCAAGGCGCCCGA	17	47687098	47687129	47704291	47704322
133	AATATTGCTACTGGAAAATCTGAATCTTTCGAAGAAAGCCCTTTGTAAGTTGTTTTCAAA	1	218325556	218325587	218386401	218386432
134	TTAATTTTCAAAAATTCATTTCCAACATTCGACCTCAGTTGCATTAGATACAGTAGGATG	3	30565517	30565548	30611237	30611268
135	AACTATGTGACTTTTAGCTATACGAGTTTCGATAAATCATGATCATGGTAATAATAATTA	3	30566144	30566175	30633318	30633349
136	AACTATGTGACTTTTAGCTATACGAGTTTCGACTGGGTTCTAAATAGTTAATGTCATAGT	3	30566144	30566175	30694718	30694749
137	TTTCCCTTTCCTTTAGACCATCTCTCTTTCGATAACTAAGAAGAAGCTACAGAATCTCTC	3	30645026	30645057	30694687	30694718
138	GTTTGTCCTTCTCCCACCCTACCCCAACTCGAATCATTGACCTAGAATTTTAGAACTGGA	2	43263062	43263093	43335477	43335508
139	GTTTGTCCTTCTCCCACCCTACCCCAACTCGATCTCTCAAAGAAAAGAAGTTGGGATGCC	2	43263062	43263093	43421879	43421910
140	TATCAAGTTAAACATTCAGACGTCTAGGTCGAGTAGTATTTAGCTTTCTTCCTTTCTAAC	2	88146264	88146295	88164523	88164554
141	TATCAAGTTAAACATTCAGACGTCTAGGTCGACTTGAAGTTCACCTAAAGTTTTCCAGTC	2	88146264	88146295	88161717	88161748
142	TAAAACTATTTTAAATGTTTTTTAAAGTATCGATGTGTACTTTGACATCTGTGATGATGAT	4	153659613	153659644	153700318	153700349
143	GCACCCCACCCTGGATCCCTTGAAAGCCTCGACAATGTTATTCTTTGTTTCTCTTACCAA	1	6484217	6484248	6494588	6494619
144	TTGGAATTATCAAGAAAGATAACTAAATTCGAAAAAGATGTATTTGTTTTTGTTTAATAG	2	178555639	178555670	178788193	178788224
145	ATAGTATAGAATGACAGCATGCTGGTTATCGACAAGAGTTCTTAAAAAGCCTAAATGTCA	15	70715123	70715154	70784637	70784668
146	GCCATTATTAAAATAAAAACCAAACAATTCGATAAATGTGTATTGAAGTTTTTTCCCTTT	7	123664155	123664186	123768253	123768284
147	GTGTTCTAGATGAGGGGAACAGTGGTGATCGAAGTATACTAACTGAAGGAGAATAAAAAA	10	31273317	31273348	31439514	31439545
148	ATTCCACAAATATTTGTGAGCACCATCTTCGAGCTCATTAGTTCAAGACCAGCCTGGGCA	10	31275600	31275631	31524411	31524442
149	GTGTTCTAGATGAGGGGAACAGTGGTGATCGAAAATGCATTTAATATACTTAACCTATCA	10	31439514	31439545	31458964	31458995

Table 30.E3

120	1	67000849	67004850	6.7E+07	67074418
121	18	48917335	48921336	4.9E+07	48974578
122	11	4070241	4074242	4084365	4088366
123	2	167961881	167965882	1.7E+08	168114525
124	2	168058335	168062336	1.7E+08	168114525
125	17	55038799	55042800	5.5E+07	55146273
126	20	47661864	47665865	4.8E+07	47801014
127	9	90789107	90793108	9.1E+07	90879196
128	9	90816328	90820329	9.1E+07	90836285
129	9	90818227	90822228	9.1E+07	90840574
130	9	90816328	90820329	9.1E+07	90840574
131	9	90816328	90820329	9.1E+07	90876967
132	17	47683128	47687129	4.8E+07	47708292
133	1	218321586	218325587	2.2E+08	218390402
134	3	30561547	30565548	3.1E+07	30611268
135	3	30566144	30570145	3.1E+07	30637319
136	3	30566144	30570145	3.1E+07	30698719
137	3	30641056	30645057	3.1E+07	30694718
138	2	43259092	43263093	4.3E+07	43335508
139	2	43259092	43263093	4.3E+07	43421910
140	2	88142294	88146295	8.8E+07	88164554
141	2	88142294	88146295	8.8E+07	88165718
142	4	153659613	153663614	1.5E+08	153700349
143	1	6480247	6484248	6494588	6498589
144	2	178551669	178555670	1.8E+08	178792194
145	15	70715123	70719124	7.1E+07	70784668
146	7	123664155	123668156	1.2E+08	123768284
147	10	31273317	31277318	3.1E+07	31439545
148	10	31271630	31275631	3.2E+07	31524442
149	10	31435544	31439545	3.1E+07	31462965

Table 30.E4

150	ZEB1_10_31437913_31439545_31463562_31470397_FR	ZEB1	181	122	2.83212E-10	3.70535E-08
151	ZFHX3_16_73147488_73153243_73182254_73184585_FF	ZFHX3	200	131	1.15564E-09	1.13397E-07
152	ADRB3_8_37962724_37965269_37987735_37989039_FR	ADRB3	29	12	0.689607935	1
153	ADRB3_8_37962724_37965269_38014799_38016599_FR	ADRB3	29	12	0.689607935	1
154	AGT_1_230717799_230719628_230752057_230757333_RF	AGT	47	33	0.000290665	0.006914309
155	AGT_1_230724515_230729957_230752057_230757333_RF	AGT	47	33	0.000290665	0.006914309
156	BMPR1B_4_94967703_94973952_95026184_95035151_FR	BMPR1B	200	87	0.614370341	1
157	HTR2A_13_46860092_46866824_46904346_46907815_RF	HTR2A	87	42	0.259371991	0.827670783
158	PPARA_22_46101029_46102611_46241078_46244347_FR	PPARA	47	28	0.025050129	0.159872776
159	SOS1_2_38982199_38993639_39061418_39066028_FF	SOS1	200	83	0.805923582	1
160	SVEP1_9_110493529_110499578_110527410_110532406_FR	SVEP1	189	101	0.006989682	0.066107233
161	UBE3A_15_25355032_25368345_25399797_25404434_FF	UBE3A	154	109	2.51446E-11	3.9477E-09
162	UBE3A_15_25355032_25368345_25457129_25464700_FR	UBE3A	154	109	2.51446E-11	3.9477E-09
163	ACBD6_1_180431719_180434683_180541491_180549122_RR	ACBD6	200	111	0.00091339	0.014340227
164	BMPR1B_4_94821712_94826817_94866803_94871889_FF	BMPR1B	200	87	0.614370341	1
165	HADHA_2_26188355_26191067_26247231_26249308_FR	HADHA	47	27	0.047791071	0.253486424
166	HADHA_2_26188355_26191067_26280650_26284864_FF	HADHA	47	27	0.047791071	0.253486424
167	MTFR1_8_65658401_65661888_65780891_65782535_RF	MTFR1	184	76	0.812499278	1
168	MYBPC1_12_101567479_101571538_101655128_101656342_RF	MYBPC1	186	94	0.05009075	0.263900932
169	MYH1_17_10502067_10505465_10533547_10534931_RF	MYH1	103	52	0.121185055	0.485358512
170	MYL1_2_210288997_210291732_210359762_210362293_FF	MYL1	10	5	0.476822977	1
171	MYOD1_11_17685862_17689487_17729653_17733608_FR	MYOD1	17	6	0.838751191	1
172	NECTIN3_3_111028574_111034204_111209684_111210764_FR	NECTIN3	97	52	0.040549948	0.23579044
173	PON1_7_95303795_95305644_95332254_95337348_RF	PON1	21	14	0.032634239	0.195038964
174	ACACB_12_109146008_109150083_109236052_109237242_RR	ACACB	191	87	0.388279548	1
175	ACACB_12_109236052_109237242_109268078_109273323_RR	ACACB	191	87	0.388279548	1
176	COL1A2_7_94359704_94366215_94394399_94397338_RF	COL1A2	47	26	0.08460057	0.378025067
177	COX6A1_12_120397017_120399520_120449180_120450939_RF	COX6A1	22	5	0.990048121	1
178	GGPS1_1_235284158_235288561_235306299_235310474_FR	GGPS1	29	5	0.999501849	1
179	GSN_9_121182946_121189020_121323589_121328431_FF	GSN	200	80	0.902128149	1

Table 30.F1

150	67.4	0.32502	0.32502	3.52284	0.00229	0.00784	-2.07823	1.25268	1.25268	1	E_Ctrl
151	65.5	-0.43734	-0.43734	-7.5712	4.7E-07	2.3E-05	6.48808	0.7385	-1.3541	-1	Str_Trn
152	41.38	-0.4318	-0.4318	-3.39512	0.00316	0.01261	-2.27663	0.74134	-1.34892	-1	Str_Trn
153	41.38	-0.32388	-0.32388	-4.68737	0.00016	0.00094	0.53671	0.79892	-1.25169	-1	Str_Trn
154	70.21	-0.43415	-0.43415	-3.86294	0.00111	0.00583	-1.25218	0.74013	-1.35111	-1	Str_Trn
155	70.21	-0.463	-0.463	-4.19239	0.00053	0.00337	-0.52301	0.72548	-1.3784	-1	Str_Trn
156	43.5	-0.46141	-0.46141	-4.19386	0.00053	0.00336	-0.51977	0.72628	-1.37689	-1	Str_Trn
157	48.28	-0.45067	-0.45067	-8.32753	1.2E-07	9.1E-06	7.85656	0.73171	-1.36667	-1	Str_Trn
158	59.57	-0.33358	-0.33358	-9.83579	7.2E-09	5.5E-07	10.6041	0.79356	-1.26014	-1	Str_Trn
159	41.5	-0.31318	-0.31318	-6.096	7.5E-06	8.5E-05	3.62327	0.80487	-1.24244	-1	Str_Trn
160	53.44	-0.42515	-0.42515	-9.26758	2.4E-08	2.8E-06	9.44872	0.74476	-1.34271	-1	Str_Trn
161	70.78	-0.20195	-0.20195	-3.01457	0.00716	0.01948	-3.18176	0.86938	-1.15025	-1	Str_Trn
162	70.78	-0.24775	-0.24775	-2.82758	0.01079	0.02719	-3.57372	0.84221	-1.18735	-1	Str_Trn
163	55.5	-0.43863	-0.43863	-7.21561	7.7E-07	1.5E-05	5.91252	0.73784	-1.35531	-1	Str_Trn
164	43.5	-0.40597	-0.40597	-5.58481	2.2E-05	0.00019	2.52537	0.75473	-1.32498	-1	Str_Trn
165	57.45	-0.39201	-0.39201	-14.4017	1.9E-11	2.6E-08	16.364	0.76207	-1.31222	-1	Str_Trn
166	57.45	-0.19239	-0.19239	-1.68433	0.10907	0.18026	-5.55862	0.87515	-1.14266	-1	Str_Trn
167	41.3	-0.37341	-0.37341	-11.7997	3.7E-10	7.6E-08	13.5612	0.77195	-1.29541	-1	Str_Trn
168	50.54	-0.42597	-0.42597	-4.76806	0.00014	0.00081	0.71784	0.74434	-1.34348	-1	Str_Trn
169	50.49	-0.43395	-0.43395	-7.77363	2.7E-07	6.9E-06	6.98965	0.74023	-1.35093	-1	Str_Trn
170	50	-0.38919	-0.38919	-13.7412	2.7E-11	1.4E-08	16.0955	0.76356	-1.30966	-1	Str_Trn
171	35.29	-0.4449	-0.4449	-11.7045	4.2E-10	8.2E-08	13.4275	0.73463	-1.36122	-1	Str_Trn
172	53.61	-0.36776	-0.36776	-7.28424	6.8E-07	1.4E-05	6.04732	0.77498	-1.29035	-1	Str_Trn
173	66.67	-0.39554	-0.39554	-9.56195	1.1E-08	7.4E-07	10.156	0.76021	-1.31543	-1	Str_Trn
174	45.55	0.3764	0.3764	5.78418	1.6E-05	0.00028	2.93947	1.29809	1.29809	1	E_Ctrl
175	45.55	0.36198	0.36198	6.81205	2E-06	6.7E-05	5.03386	1.28519	1.28519	1	E_Ctrl
176	55.32	0.2558	0.2558	5.00789	7.9E-05	0.00053	1.254	1.194	1.194	1	E_Ctrl
177	22.73	0.30181	0.30181	5.45361	3E-05	0.00024	2.23895	1.23269	1.23269	1	E_Ctrl
178	17.24	0.29388	0.29388	2.41607	0.02598	0.05481	-4.39757	1.22593	1.22593	1	E_Ctrl
179	40	0.2534	0.2534	3.85238	0.00108	0.00427	-1.34367	1.19202	1.19202	1	E_Ctrl

Table 30.F2

150	GTGTTCTAGATGAGGGGAACAGTGGTGATCGACTGTGAGGATGAACTAAAAGCAAACCAT	10	31439514	31439545	31463562	31463593
151	CTCTCAACTTTGGATGTAAGAATCATCTTCGAGATTTTGACTCTCCACCTGCCCCACAGG	16	73153212	73153243	73184554	73184585
152	CGGTCCCTCTGCCCCGGTTACCTACCCGTCGACATGACACTTGGGTGGGGATACAGGGCC	8	37965238	37965269	37987735	37987766
153	CGGTCCCTCTGCCCCGGTTACCTACCCGTCGAAGTGGAATGAAGGAGCTTCTAAGTCATA	8	37965238	37965269	38014799	38014830
154	TCCCCCTCTTCCTCTGCCTCCCTTCCCCTCGATTTGTAAAATGGGCTCATTAGGGAAAAG	1	230717799	230717830	230757302	230757333
155	TCCCCCTCTTCCTCTGCCTCCCTTCCCCTCGAAAACTGATTAAAAAGAATATTGCTGGCT	1	230724515	230724546	230757302	230757333
156	AATTACTAAGAAAAAAGTGGTTACAATGTCGAAGAACATAAATATTATGTGGAGACTTAT	4	94973921	94973952	95026184	95026215
157	TCACTTTTATTTATCTTACTCACTTTTCTCGAGGAATTCTCAGAATTCTCCTCAACCCAC	13	46860092	46860123	46907784	46907815
158	ACACCTCACCCACCCAGCTGGGCTGGCCTCGATGCCATTAAATCATCCCGTGACCTTCCT	22	46102580	46102611	46241078	46241109
159	TTTCTTCCAACTGAGAGAATCTTAAAAATCGAAATTGGATAAGGAAAAAAGTGAAATGTG	2	38993608	38993639	39065997	39066028
160	TTATGGCTTAGAAGTAGAAAGTCATAAATCGATTCCTAAAAATTAATGAGGTGAATAGTA	9	110499547	110499578	110527410	110527441
161	GTTATCAATTTTACTTATAAGACCTATTTCGAGGTATTAAGGGTTGGAATGAAAAATACA	15	25368314	25368345	25404403	25404434
162	GTTATCAATTTTACTTATAAGACCTATTTCGATGCAAAAGACACAACAAAGTAGGATTTTCA	15	25368314	25368345	25457129	25457160
163	TTTTAGTTTTATTTATTTAGTTATCATCTCGAAAAACAAACAACAATAACAGCAACCCTC	1	180431719	180431750	180541491	180541522
164	TGAAATCAATAGTTTTATATTAGTCGTATCGAGCATTCTAGAATCAAACCTTGGGGTATT	4	94826786	94826817	94871858	94871889
165	TACCTTCCAACAGGAAGTGCAAACTAATTCGATCCTACCCTACCCTGGAGTTTCC	2	26191036	26191067	26247231	26247262
166	TACCTTCCAACAGGAAGTGCAAACTAATTCGAATAAGAACCTCGTTATTCATGTTCCTCT	2	26191036	26191067	26284833	26284864
167	TTTCTATGAAGAATGTTCAAGATGCAATTCGAGCTACATACTATTATATATTTTCACAGT	8	65658401	65658432	65782504	65782535
168	AAATAATAACAAATATGACAGATATTGATCGATGTCTTAACTTGCCACAGAGATATTTTC	12	101567479	101567510	101656311	101656342
169	GCAAGACTTTGTCTCAAAACAAAAGTGTTCGAAAAAGTCATCGTTTAAAAGGTAAAATGT	17	10502067	10502098	10534900	10534931
170	AATTTCACATTGATACATTGATAGACATTCGAAATCATACACAGCATACTCTCAAACCAT	2	210291701	210291732	210362262	210362293
171	TCCATTAGCTCTGCTTTCAAATACTATATCGATGTAGCTTATGTAAAATAAATGTATTAA	11	17689456	17689487	17729653	17729684
172	TCAAAGTTACAGTTTATATAAATTAGAAATCGATCTAACCTCAATTCCAGTCCCACAAATG	3	111034173	111034204	111209684	111209715
173	TAGAATTATAATACATTCCAAGCTCTTTTCGAAAAATTCGCATTCCTTGGTCAAGAAAAC	7	95303795	95303826	95337317	95337348
174	TCAAGAAAAAAATAATAATTTTTTTTTCGAACTTATGGCTCAAGCGATTCTCTTGCTT	12	109146008	109146039	109236052	109236083
175	AAGCAAGAGAATCGCTTGAGCCATAAGTTCGATGCTGCTTTGGGAACTGAAGGTTTTTCT	12	109236052	109236083	109268078	109268109
176	AACATACTTTCCTAAATTTTTACCTTTTTTCGAGAAAACATGGACATAAAGATGGCAACAA	7	94359704	94359735	94397307	94397338
177	GGCAGGCAGATCACTTTAGGTCAGGAGTTCGAACTCCTGACTTCAAGTGATTCGCCCACC	12	120397017	120397048	120450908	120450939
178	ATCTTTCTACATCAGTAAACACAAACTGTCGAGACCATCCTGGCTAAGACAGTGAAACCC	1	235288530	235288561	235306299	235306330
179	CTCTATAAATTTACCAGAATATAAATTCTCGACTAAAAGTTCAGTTCTTCATTCCCACTA	9	121188989	121189020	121328400	121328431

Table 30.F3

10	31435544	31439545	3.1E+07	31467563		
16	73149242	73153243	7.3E+07	73184585		
8	37961268	37965269	3.8E+07	37991736		
8	37961268	37965269	3.8E+07	38018800		
1	230717799	230721800	2.3E+08	230757333		
1	230724515	230728516	2.3E+08	230757333		
4	94969951	94973952	9.5E+07	95030185		
13	46860092	46864093	4.7E+07	46907815		
22	46098610	46102611	4.6E+07	46245079		
2	38989638	38993639	3.9E+07	39066028		
9	110495577	110499578	1.1E+08	110531411		
15	25364344	25368345	2.5E+07	25404434		
15	25364344	25368345	2.5E+07	25461130		
1	180431719	180435720	1.8E+08	180545492		
4	94822816	94826817	9.5E+07	94871889		
2	26187066	26191067	2.6E+07	26251232		
2	26187066	26191067	2.6E+07	26284864		
8	65658401	65662402	6.6E+07	65782535		
12	101567479	101571480	1E+08	101656342		
17	10502067	10506068	1.1E+07	10534931		
2	210287731	210291732	2.1E+08	210362293		
11	17685486	17689487	1.8E+07	17733654		
3	111030203	111034204	1.1E+08	111213685		
7	95303795	95307796	9.5E+07	95337348		
12	109146008	109150009	1.1E+08	109240053		
12	109236052	109240053	1.1E+08	109272079		
7	94359704	94363705	9.4E+07	94397338		
12	120397017	120401018	1.2E+08	120450939		
1	235284560	235288561	2.4E+08	235310300		
9	121185019	121189020	1.2E+08	121328431		

Table 30.F4

180	HTR2A_13_46847106_46857832_46938758_46942222_RF	HTR2A	87	42	0.259371991	0.827670783
181	HTR2A_13_46877712_46880636_46938758_46942222_FF	HTR2A	87	42	0.259371991	0.827670783
182	IGF1R_15_98652565_98657862_98731539_98737034_RF	IGF1R	200	106	0.008018013	0.06952724
183	MUSK_9_110648469_110652659_110747866_110751903_FR	MUSK	154	75	0.152643976	0.578867253
184	MYOT_5_137829466_137834410_137882068_137884626_RR	MYOT	75	20	0.999459925	1
185	PPARA_22_46128634_46134707_46231440_46235124_FR	PPARA	47	28	0.025050129	0.159872776
186	PPP1R9A_7_94903925_94908776_94951930_94967018_RF	PPP1R9A	200	113	0.000335824	0.007753573
187	PPP1R9A_7_94951930_94967018_95061734_95065150_FR	PPP1R9A	200	113	0.000335824	0.007753573
188	PPP1R9A_7_94951930_94967018_95258927_95267729_FF	PPP1R9A	200	113	0.000335824	0.007753573
189	RB1_13_48378062_48381344_48486008_48495146_FF	RB1	189	84	0.509778071	1
190	SLC25A13_7_96209525_96214524_96295606_96302029_FF	SLC25A13	200	105	0.011714369	0.093834484
191	ACE2_X_15558483_15561359_15624288_15632375_RR	ACE2	34	23	0.005085953	0.051850296
192	DNAH5_5_13907228_13913186_13947622_13950495_FR	DNAH5	200	106	0.008018013	0.06952724
193	EMCN_4_100636305_100649860_100744427_100745788_RR	EMCN	200	121	2.82028E-06	0.000158137
194	ITGAV_2_186622411_186639782_186682119_186696186_RR	ITGAV	38	16	0.665375941	1
195	MSTN_2_190044593_190053476_190068550_190073029_FR	MSTN	11	5	0.58381774	1
196	PLCXD2_3_111633890_111638317_111672672_111677327_FR	PLCXD2	200	76	0.969310539	1
197	SGCZ_8_14631157_14642508_14778176_14785491_FF	SGCZ	200	131	1.15564E-09	1.13397E-07
198	SLC25A13_7_96178122_96182739_96295606_96302029_RF	SLC25A13	200	105	0.011714369	0.093834484
199	SOCS7_17_38347510_38348776_38360864_38363420_FR	SOCS7	47	25	0.139363472	0.533660124
200	SRI_7_88199682_88203042_88229166_88237101_RF	SRI	61	34	0.047542529	0.253486424
201	STXBP4_17_55035186_55042800_55117598_55123347_RR	STXBP4	178	72	0.865724188	1
202	SVEP1_9_110397951_110405969_110503630_110509758_FF	SVEP1	189	101	0.006989682	0.066107233

Table 30.G1

180	48.28	0.23347	0.23347	2.92357	0.00875	0.02288	-3.37367	1.17566	1.17566	1	E_Ctrl
181	48.28	0.31362	0.31362	5.2027	5.2E-05	0.00037	1.68658	1.24282	1.24282	1	E_Ctrl
182	53	0.23289	0.23289	2.56313	0.01907	0.04289	-4.11013	1.17519	1.17519	1	E_Ctrl
183	48.7	0.30041	0.30041	3.63015	0.00179	0.00643	-1.84018	1.23149	1.23149	1	E_Ctrl
184	26.67	0.26883	0.26883	6.70047	2.2E-06	3.3E-05	4.88	1.20483	1.20483	1	E_Ctrl
185	59.57	0.29923	0.29923	2.46766	0.02333	0.05033	-4.29772	1.23049	1.23049	1	E_Ctrl
186	56.5	0.29403	0.29403	4.70344	0.00016	0.00091	0.57281	1.22606	1.22606	1	E_Ctrl
187	56.5	0.28471	0.28471	4.35389	0.00035	0.00171	-0.21427	1.21816	1.21816	1	E_Ctrl
188	56.5	0.2709	0.2709	3.54424	0.00218	0.00753	-2.03086	1.20656	1.20656	1	E_Ctrl
189	44.44	0.30464	0.30464	6.97933	1.2E-06	2.2E-05	5.44345	1.23511	1.23511	1	E_Ctrl
190	52.5	0.31224	0.31224	5.62896	2E-05	0.00018	2.62135	1.24163	1.24163	1	E_Ctrl
191	67.65	0.32899	0.32899	9.15537	2.2E-08	1.2E-06	9.47318	1.25614	1.25614	1	E_Ctrl
192	53	0.3725	0.3725	11.9417	3E-10	6.9E-08	13.7588	1.2946	1.2946	1	E_Ctrl
193	60.5	0.31985	0.31985	5.68628	1.8E-05	0.00016	2.74564	1.2482	1.2482	1	E_Ctrl
194	42.11	0.35248	0.35248	2.33791	0.03054	0.06245	-4.54674	1.27675	1.27675	1	E_Ctrl
195	45.45	0.22853	0.22853	2.5176	0.021	0.04632	-4.20002	1.17164	1.17164	1	E_Ctrl
196	38	0.37187	0.37187	9.14346	2.3E-08	1.2E-06	9.45286	1.29403	1.29403	1	E_Ctrl
197	65.5	0.35186	0.35186	12.46	1.5E-10	4.6E-08	14.4629	1.2762	1.2762	1	E_Ctrl
198	52.5	0.3227	0.3227	8.1037	1.4E-07	4.6E-06	7.60648	1.25067	1.25067	1	E_Ctrl
199	53.19	0.32563	0.32563	8.97975	3E-08	1.5E-06	9.17168	1.25321	1.25321	1	E_Ctrl
200	55.74	0.3451	0.3451	6.86348	1.6E-06	2.6E-05	5.21065	1.27024	1.27024	1	E_Ctrl
201	40.45	0.34798	0.34798	7.97475	1.8E-07	5.4E-06	7.36728	1.27277	1.27277	1	E_Ctrl
202	53.44	0.32848	0.32848	4.83516	0.00012	0.00072	0.86819	1.25569	1.25569	1	E_Ctrl

Table 30.G2

180	CCAAAAGTAATGGCAACAAAAGTCAAAATCGATTCTTGGGAATTTCCCAAAATACTGAAA	13	46847106	46847137	46942191	46942222
181	GGCAGGCGGATCTCCTGAGGTCAGGAGATCGATTTTGACTTTTGTTGCCATTACTTTTGG	13	46880605	46880636	46942191	46942222
182	CGTAGAACTAAGATGTATTCAAAGTCAGTCGAAAAAGATTAGAAAAGTTCAACTCTAAGA	15	98652565	98652596	98737003	98737034
183	ATCTTACAAAGAATAATTCTAAGAAAAAGTCGAGCATTGGAGAAAATCTCCCTTTTCTTTT	9	110652628	110652659	110747866	110747897
184	CAAAACAATGTGTTAACTTTTTTTTTTTTCGATTGATGAAGGAAGATTCTGCAGAATGGA	5	137829466	137829497	137882068	137882099
185	TGTTTTTATTTTCATGTTTTTAATTTTGTTCGAACTCTTGACCTCAGGTAAACCACCCACC	22	46134676	46134707	46231440	46231471
186	AGAACTGGTTATTGATCTATTCAGGGATTCGAAATAATAGATTATGAATAAATTATTCTG	7	94903925	94903956	94966987	94967018
187	AGAACTGGTTATTGATCTATTCAGGGATTCGAATGAATGAAATAAAGAGCCATGG	7	94966987	94967018	95061734	95061765
188	AGAACTGGTTATTGATCTATTCAGGGATTCGAAGGGTAAATACTTAAGTCTTTAAATAAA	7	94966987	94967018	95267698	95267729
189	TTAAAAGCCTTTGATTTTTTACAAAGTGATCGAGTCAGTTTCCTTTTGGTATAAGGATATC	13	48381313	48381344	48495115	48495146
190	GGCAGGCGGATCATTTCAGGTCAGGAGTTCGACCTGAAATTTCCATACTAAATTTAAATA	7	96214493	96214524	96301998	96302029
191	AAATAAGAAGAAGAAAGGAAAAAAAATCTTCGAAAGAGCGTAAGATAGAGAATAATTATTT	X	15558483	15558514	15624288	15624319
192	TTGTTTGTAAATTGTTTTTTCTAAAATCTTCGAGAGCTGGTTGAAAATTTTGCTCTCAATT	5	13913155	13913186	13947622	13947653
193	GGTATTACCTTGATGGCCTTAAAGAAGATCGAGCCAGAGGGCCTCTGTTCATGTTTGGGC	4	100636305	100636336	100744427	100744458
194	AGAAGACTCACCAAAATTTTTATCCTGTTTCGAACCTTATAATGGTGATAAATCATTAATG	2	186622411	186622442	186682119	186682150
195	TTCCAAATACTTCCTCTGCAAAATGCCATCGAACTCCTGGCCTCAAGTCATCCATCCGCC	2	190053445	190053476	190068550	190068581
196	CTTTTTGAAGATTATAATCTATTAGTGATCGAGGCTTTTTTTGCTTTTTTTTTTTTTGAGAT	3	111638286	111638317	111672672	111672703
197	CTATATGTAAGTTACAATATGTAAGGTATCGATAGTCACTGAGACTAATTTAATGTTATA	8	14642477	14642508	14785460	14785491
198	TATTTAAATTTAGTATGGAAATTTCAGGTCGAAGGCACTGAATGTCAGAGCCAAGCTGTA	7	96178122	96178153	96301998	96302029
199	AGGCAGGCAGATCAATGAGGTTGGGAGATCGACAAGTTCAGTAATTCTGAGGTGAGTTTT	17	38348745	38348776	38360864	38360895
200	TGTAGGCAGATTACCTGAAGTTAGGAGTTCGATTAGGAATAACCTATCATTAGAGTTGTT	7	88199682	88199713	88237070	88237101
201	GTTGTTATAACTATATCATGAGACTAAGTCGAAAAAAAAAAAACAATAATTTCAGCTGTAT	17	55035186	55035217	55117598	55117629
202	TATATTAGAAACATGTCTGAAAAAAGTATCGATAAATGTATACGTTGATGTACATTGATA	9	110405938	110405969	110509727	110509758

Table 30.G3

180	13	46847106	46851107	4.7E+07	46942222
181	13	46876635	46880636	4.7E+07	46942222
182	15	98652565	98656566	9.9E+07	98737034
183	9	110648658	110652659	1.1E+08	110751867
184	5	137829466	137833467	1.4E+08	137886069
185	22	46130706	46134707	4.6E+07	46235441
186	7	94903925	94907926	9.5E+07	94967018
187	7	94963017	94967018	9.5E+07	95065735
188	7	94963017	94967018	9.5E+07	95267729
189	13	48377343	48381344	4.8E+07	48495146
190	7	96210523	96214524	9.6E+07	96302029
191	X	15558483	15562484	1.6E+07	15628289
192	5	13909185	13913186	1.4E+07	13951623
193	4	100636305	100640306	1E+08	100748428
194	2	186622411	186626412	1.9E+08	186686120
195	2	190049475	190053476	1.9E+08	190072551
196	3	111634316	111638317	1.1E+08	111676673
197	8	14638507	14642508	1.5E+07	14785491
198	7	96178122	96182123	9.6E+07	96302029
199	17	38344775	38348776	3.8E+07	38364865
200	7	88199682	88203683	8.8E+07	88237101
201	17	55035186	55039187	5.5E+07	55121599
202	9	110401968	110405969	1.1E+08	110509758

Table 30.G4

	Probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig
1	C1GALT1_7_7113076_7114831_7258228_7260668_FF	C1GALT1	89	52
2	DKK3_11_11956071_11968035_11984245_11993733_FR	DKK3	54	36
3	FBXO32_8_123526212_123527874_123555254_123559065_FR	FBXO32	41	26
4	GPC6_13_94054831_94060621_94121445_94133208_RF	GPC6	166	105
5	GSN_9_121177548_121180410_121268506_121274144_FR	GSN	156	76
6	LMO4_1_87315524_87318670_87343110_87349940_FF	LMO4	105	75
7	MAPK10_4_86572598_86581486_86617317_86621940_FF	MAPK10	172	107
8	MBNL1_3_152229500_152234786_152281057_152285843_FR	MBNL1	145	85
9	PCK1_20_57527297_57530814_57579772_57583521_RR	PCK1	36	26
10	PIK3C3_18_42070009_42072187_42088671_42094691_FF	PIK3C3	141	89
11	PTPRC_1_198595771_198598296_198659753_198666156_RF	PTPRC	185	91
12	RGS6_14_72139099_72144564_72213251_72222544_FR	RGS6	174	104
13	RUNX3_1_24920810_24923822_24973522_24976037_RF	RUNX3	51	24
14	ZFHX3_16_73147488_73153243_73182254_73184585_FF	ZFHX3	171	123
15	MYOT_5_137829466_137834410_137882068_137884626_RR	MYOT	35	20
16	AGT_1_230724515_230729957_230752057_230757333_RF	AGT	47	31
17	MYL1_2_210288997_210291732_210359762_210362293_FF	MYL1	9	5
18	SRI_7_88199682_88203042_88229166_88237101_RF	SRI	57	30

Table 31.a

	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr
1	0.485083555	1	58.43	-0.555546218	-0.555546218
2	0.113222201	0.567553327	66.67	-0.452190179	-0.452190179
3	0.279504208	0.898561555	63.41	-0.428908404	-0.428908404
4	0.081947099	0.503453115	63.25	0.528815395	0.528815395
5	0.990051008	1	48.72	-0.435924362	-0.435924362
6	0.002438643	0.079967184	71.43	-0.425303631	-0.425303631
7	0.127316337	0.601206787	62.21	0.369477889	0.369477889
8	0.440065203	1	58.62	-0.423225201	-0.423225201
9	0.052274012	0.438252195	72.22	-0.454377101	-0.454377101
10	0.108139211	0.559937306	63.12	0.349058418	0.349058418
11	0.991656906	1	49.19	0.342871898	0.342871898
12	0.312185766	0.950015156	59.77	0.373553959	0.373553959
13	0.95196413	1	47.06	0.364233402	0.364233402
14	7.53E-05	0.010367006	71.93	-0.437339546	-0.437339546
15	0.594268263	1	57.14	0.377641822	0.377641822
16	0.156967939	0.666487236	65.96	-0.462997504	-0.462997504
17	0.682316487	1	55.56	-0.356584057	-0.356584057
18	0.816232021	1	52.63	0.347423032	0.347423032

Table 31.b

	t	P.Value	adj.P.Val	B
1	-11.0417245	0.00000000111	0.000000163	12.47094565
2	-4.498338722	0.000266954	0.002046882	0.154483715
3	-11.06651685	0.00000000106	0.000000159	12.50758304
4	2.192030297	0.041519144	0.085450094	-4.70897528
5	-4.024149814	0.000771506	0.004457333	-0.895719572
6	-4.334227249	0.000385015	0.002678159	-0.20873374
7	10.62330419	0.00000000289295572819759	0.000000681985048919552	11.54687815
8	-5.762419013	0.000017162879575988 5	0.000292745	2.893666517
9	-3.146677782	0.005488024	0.018949968	-2.809655881
10	10.19574365	0.00000000406	0.000000379	11.17917387
11	12.24688433	0.000000000196	0.0000000539	14.17658691
12	9.049855001	0.000000034856893346579	0.000003626450717738 6	9.09037332
13	10.30993314	0.000000004646642800563 21	0.000009611862645683259	11.08156058
14	-7.571199723	0.000000474476333843650	0.000023118958570066 4	6.488080595
15	10.49506981	0.000000003507627360653 39	0.000007777454166573518	11.35784279
16	-4.192393926	0.00052891	0.00336987	-0.523006115
17	-7.810248605	0.000003053171587917033	0.000016979280859509 3	6.929231219
18	5.646538925	0.000021915796810150 7	0.000348185	2.648883369

Table 31.c

	FC	FC_1	LS	Loop Detected
1	0.680399404	-1.469724979	-1	E_Trn
2	0.730932365	-1.36811564	-1	Str_Trn
3	0.742823621	-1.346214596	-1	E_Trn
4	1.442744064	1.442744064	1	Str_Ctrl
5	0.739219971	-1.352777305	-1	Str_Trn
6	0.744681988	-1.342855092	-1	Str_Trn
7	1.291885213	1.291885213	1	Str_Ctrl
8	0.745755594	-1.34092189	-1	Str_Trn

9	0.729825214	-1.370191083	-1	Str_Trn
10	1.27372905	1.27372905	1	E_Ctrl
11	1.26827878	1.26827878	1	E_Ctrl
12	1.295540359	1.295540359	1	Str_Ctrl
13	1.287197476	1.287197476	1	Str_Ctrl
14	0.738495203	-1.354104937	-1	Str_Trn
15	1.299216466	1.299216466	1	Str_Ctrl
16	0.725477359	-1.378402768	-1	Str_Trn
17	0.781011633	-1.280390659	-1	Str_Trn
18	1.272286016	1.272286016	1	Str_Ctrl

Table 31.d

	Probe sequence	Probe Location	
	60 mer	**Chr**	**Start1**
1	AAATGTATAAGAACAGAAGAGAATTATCTCGACATGTCTGAAAAGTATTATCAGCCCTCT	7	7114800
2	GACACCTCCTCTCCCTTCCCTCCCCTTCTCGAGTTATCAAAATATTTTGAGAGACAGTAT	11	11968004
3	TGCAGAAAGTACTACAAAAAAAGAAGCTTCGAAAATGTTGGAGATGAGAGTTTCTTCACC	8	123527843
4	AATTAGACAACGACTATATGACTCTGTCTCGACTTTAAAGCAAGTACTTCTTGTATGCTC	13	94054831
5	AAAAAGAGAAAAGCAGGTTAGCACATTGTCGACCCCGCCCCCGGGATGGGGGAACTGGCC	9	121180379
6	CCCCTGGCTCACCTACACAAAATTGTGCTCGACTCTACTCTTAGCCCTGCTAAATAAGTA	1	87318639
7	ATTATATTAGTGCTGTAATAAAATTAAGTCGACACATTTGATACTGCTTATTGGGTTATT	4	86581455
8	TACCTTGAAAAGCTCTTCAGTATGATTATCGAGCTTTAGCCATTCTAGTAATTATTAAAA	3	152234755
9	CCTCGTCGTCCCCTCTCTTCCTCGTTCCTCGAACATCTCCAAGTCAGATAATCATAACAA	20	57527297
10	ATCTATTATAATGATGCAATATTGTTAATCGATTCAAAGATCAAATTAATTATTAAAGCT	18	42072156
11	AGAGGCTGAGGTGAAAAGATTGTTTGAGTCGAAGATCATTGTCTCATTTTTTTACTTGTT	1	198595771
12	AATGGCATTCTCCATTTATTCGTATTTATCGAGACTTTCTATGAAAGCTTTTTTGATGTT	14	72144533
13	CTTAATTTTTTTTCTTTGAATGCCTCTATCGACAGTCTTCTCTCTACTTTCTACAGTGAA	1	24920810
14	CTCTCAACTTTGGATGTAAGAATCATCTTCGAGATTTTGACTCTCCACCTGCCCCACAGG	16	73153212
15	CAAAACAATGTGTTAACTTTTTTTTTTTTTCGATTGATGAAGGAAGATTCTGCAGAATGGA	5	137829466
16	TCCCCCTCTTCCTCTGCCTCCCTTCCCCTCGAAAACTGATTAAAAAGAATATTGCTGGCT	1	230724515
17	AATTTCACATTGATACATTGATAGACATTCGAAATCATACACAGCATACTCTCAAACCAT	2	210291701
18	TGTAGGCAGATTACCTGAAGTTAGGAGTTCGATTAGGAATAACCTATCATTAGAGTTGTT	7	88199682

Table 31.e

	Probe Location			4 kb Sequence Location				
	End1	**Start2**	**End2**	**Chr**	**Start1**	**End1**	**Start2**	**End2**
1	7114831	7260637	7260668	7	7110830	7114831	7256667	7260668
2	11968035	11984245	11984276	11	11964034	11968035	11984245	11988246
3	123527874	123555254	123555285	8	123523873	123527874	123555254	123559255
4	94054862	94133177	94133208	13	94054831	94058832	94129207	94133208
5	121180410	121268506	121268537	9	121176409	121180410	121268506	121272507
6	87318670	87349909	87349940	1	87314669	87318670	87345939	87349940
7	86581486	86621909	86621940	4	86577485	86581486	86617939	86621940
8	152234786	152281057	152281088	3	152230785	152234786	152281057	152285058
9	57527328	57579772	57579803	20	57527297	57531298	57579772	57583773
10	42072187	42094660	42094691	18	42068186	42072187	42090690	42094691
11	198595802	198666125	198666156	1	198595771	198599772	198662155	198666156
12	72144564	72213251	72213282	14	72140563	72144564	72213251	72217252
13	24920841	24976006	24976037	1	24920810	24924811	24972036	24976037
14	73153243	73184554	73184585	16	73149242	73153243	73180584	73184585
15	137829497	137882068	137882099	5	137829466	137833467	137882068	137886069
16	230724546	230757302	230757333	1	230724515	230728516	230753332	230757333
17	210291732	210362262	210362293	2	210287731	210291732	210358292	210362293

18	88199713	88237070	88237101	7	88199682	88203683	88233100	88237101

Table 31.f

		Inner_primers
	Probe	**PCR-Primer1_ID**
1	C1GALT1_7_7113076_7114831_7258228_7260668_FF	OBD142_025
2	DKK3_11_11956071_11968035_11984245_11993733_FR	OBD142_061
3	FBXO32_8_123526212_123527874_123555254_123559065_FR	OBD142_089
4	GPC6_13_94054831_94060621_94121445_94133208_RF	OBD142_109
5	GSN_9_121177548_121180410_121268506_121274144_FR	OBD142_117
6	LMO4_1_87315524_87318670_87343110_87349940_FF	OBD142_145
7	MAPK10_4_86572598_86581486_86617317_86621940_FF	OBD142_153
8	MBNL1_3_152229500_152234786_152281057_152285843_FR	OBD142_157
9	PCK1_20_57527297_57530814_57579772_57583521_RR	OBD142_189
10	PIK3C3_18_42070009_42072187_42088671_42094691_FF	OBD142_213
11	PTPRC_1_198595771_198598296_198659753_198666156_RF	OBD142_233
12	RGS6_14_72139099_72144564_72213251_72222544_FR	OBD142_245
13	RUNX3_1_24920810_24923822_24973522_24976037_RF	OBD142_253
14	ZFHX3_16_73147488_73153243_73182254_73184585_FF	OBD142_325
15	MYOT_5_137829466_137834410_137882068_137884626_RR	OBD142_341
16	AGT_1_230724515_230729957_230752057_230757333_RF	OBD142_365
17	MYL1_2_210288997_210291732_210359762_210362293_FF	OBD142_449
18	SRI_7_88199682_88203042_88229166_88237101_RF	OBD142_509

Table 31.g

	Inner_primers			Category
	PCR_Primer1	**PCR-Primer2_ID**	**PCR_Primer2**	**High or Low Responder**
1	CACCTCAAAAGACAACCCCAGACCCA	OBD142_027	CCCTCACTTTCCTTCTACTCTTCAAG	High
2	GCTCCACATTTCCCAATCTAACCTGC	OBD142_063	GTCAGAGTTGCCGATAGGTCTTGCTA	High
3	AATCTCTGTCCCCAACTGTATCTGGC	OBD142_091	ACATCTATCTTGCCCCTCACTCAGGT	High
4	GAGTATTTACGATGGTCAGGTGCTGC	OBD142_111	ATCCAAACACAGGACGAGAATAAAGC	High
5	GACCTGTGGTTCTGACTGTCCAG	OBD142_119	TATCGTCCAGGAGGCAAGGGTCC	High
6	GCAACCTGGTCTCCTACCTGCTTCTA	OBD142_147	GATGAGGTAACCAAAGTTCAGGGAGA	High
7	TAGCAGACAATCAGAGGGTTTTGC	OBD142_155	CTCTCTCCTCATCCTCCCTCCTAATA	High
8	GCTGGTAGTTGGCTTTTGGGAAGAAC	OBD142_159	GGGAGCCAGAAAGATAGCAATGCCTA	High
9	TTCTCCCTCGGACGCTCATCCTC	OBD142_191	GAGGAGGAGAAACTCAGAAGCCC	High
10	CTGGAACTTGTTTAGGCACTGAAGCA	OBD142_215	GCACAAGACCTCACATTCTGATGGGC	High
11	GCAAAGGGCAGGTCATCATCATTCAA	OBD142_235	CTCTCCTTTATCCCCTACCCTGCTCA	High
12	CCCCGATGAATGTTACCCTGTCCC	OBD142_247	CAGAGAAAGGGAGTTTGGAGGGC	High
13	CTGAAATCCCATAGTGAGATGCCTTC	OBD142_255	CCCCAAACTCCCAGACACATCAGAGA	High
14	CCTGGATGTTCATTCCCACCTGG	OBD142_327	AGAGGGAAAGGCAGGTCGTGAGC	Low
15	GCAGATTCCACAGGGCTTAC	OBD142_343	GCTGGTCTCAAACTCCTGGG	Low
16	ACCCAACCCTGCTATACAATTCCA	OBD142_367	GGGCATCTTTCCTCTTATTCAAGGT	Low
17	ACAGTCAGTGATTGGCACAGAGTAA	OBD142_451	AGGAAATAGCCCAAATGCAACTGAA	High
18	GAATGAAACTCTGAGGCCGG	OBD142_511	CCCATTCGTCTCTCTGAGCTG	High

Table 31.h

	Gene	Marker	GLMNET
1	C1GALT1	OBD142_025.027	0.242638274

2	DKK3	OBD142_061.063	0.147262728
3	FBXO32	OBD142_089.091	-0.087251896
4	GPC6	OBD142_109.111	0.233745002
5	GSN	OBD142_117.119	0.294663423
6	LMO4	OBD142_145.147	-0.118956396
7	MAPK10	OBD142_153.155	-0.17796692
8	MBNL1	OBD142_157.159	-0.161065194
9	PCK1	OBD142_189.191	0.196530289
10	PIK3C3	OBD142_213.215	-0.083748281
11	PTPRC	OBD142_233.235	0.30236596
12	RGS6	OBD142_245.247	0.078658478
13	RUNX3	OBD142_253.255	0.06399744
14	ZFHX3	OBD142_325.327	0.115886108
15	MYOT	OBD142_341.343	-0.049119122
16	AGT	OBD142_365.367	0.199239865
17	MYL1	OBD142_449.451	-0.16982619
18	SRI	OBD142_509.511	0.129049402

Table 31.i

	Probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig
1	THNSL2_2_88139809_88146295_88161717_88164554_FR	THNSL2	29	20
2	IGF1R_15_98652565_98657862_98731539_98737034_RF	IGF1R	177	96
3	DKK3_11_11956071_11968035_11984245_11993733_FR	DKK3	54	36
4	CBL_11_119249760_119252653_119294588_119299643_RF	CBL	24	19
5	EYA1_8_71216399_71218728_71261816_71267769_RR	EYA1	139	80
6	ACACB_12_109236052_109237242_109268078_109273323_RR	ACACB	133	81
7	PTPRC_1_198595771_198598296_198659753_198666156_RF	PTPRC	185	91

Table 32.a

	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr	t
1	0.147351557	0.651492557	68.97	0.348303621	0.348303621	5.482854907
2	0.840040511	1	54.24	0.376793177	0.376793177	3.580450098
3	0.113222201	0.567553327	66.67	-0.452190179	-0.452190179	-4.498338722
4	0.023815147	0.261918121	79.17	-0.426375519	-0.426375519	-4.618561579
5	0.544172978	1	57.55	-0.420279402	-0.420279402	-6.888734462
6	0.250820309	0.854526334	60.9	0.361980641	0.361980641	6.812052569
7	0.991656906	1	49.19	0.342871898	0.342871898	12.24688433

Table 32.b

	P.Value	adj.P.Val	B	FC	FC_1
1	0.0000279	0.000231594	2.302943346	1.273062829	1.273062829
2	0.002089314	0.00927894	-1.873258731	1.298452444	1.298452444
3	0.000266954	0.002046882	0.154483715	0.730932365	-1.36811564
4	0.000204351	0.001696324	0.420007759	0.744128913	-1.343853172
5	0.00000174500366992146	0.0000602085318700566	5.184417423	0.747279887	-1.338186692
6	0.00000202795176244020	0.0000670770127555545	5.033860861	1.285189092	1.285189092
7	0.000000000196	0.0000000539	14.17658691	1.26827878	1.26827878

Table 32.c

			Probe sequence
	LS	Loop Detected	60 mer
1	1	E_Ctrl	TATCAAGTTAAACATTCAGACGTCTAGGTCGACTTGAAGTTCACCTAAAGTTTTCCAGTC
2	1	E_Ctrl	CGTAGAACTAAGATGTATTCAAAGTCAGTCGAAAAAGATTAGAAAAGTTCAACTCTAAGA
3	-1	Str_Trn	GACACCTCCTCTCCCTTCCCTCCCCTTCTCGAGTTATCAAAATATTTTGAGAGACAGTAT
4	-1	Str_Trn	ACCGCCTCACCTCAGCTCTCCAGTGAGATCGATCCTCCCACCTAAGCTTCCCAAGTTGCT
5	-1	Str_Trn	TGTCCTTTCAAGGAAGGATTAGCATCCTTCGAAAGACCTATCAGGATTTCATTTGTAATG
6	1	E_Ctrl	AAGCAAGAGAATCGCTTGAGCCATAAGTTCGATGCTGCTTTGGGAACTGAAGGTTTTTCT
7	1	E_Ctrl	AGAGGCTGAGGTGAAAAGATTGTTTGAGTCGAAGATCATTGTCTCATTTTTTTACTTGTT

Table 32.d

	Probe Location				
	Chr	**Start1**	**End1**	**Start2**	**End2**
1	2	88146264	88146295	88161717	88161748
2	15	98652565	98652596	98737003	98737034
3	11	11968004	11968035	11984245	11984276
4	11	119249760	119249791	119299612	119299643
5	8	71216399	71216430	71261816	71261847
6	12	109236052	109236083	109268078	109268109
7	1	198595771	198595802	198666125	198666156

Table 32.e

	4 kb Sequence Location				
	Chr	**Start1**	**End1**	**Start2**	**End2**
1	2	88142294	88146295	88161717	88165718
2	15	98652565	98656566	98733033	98737034
3	11	11964034	11968035	11984245	11988246
4	11	119249760	119253761	119295642	119299643
5	8	71216399	71220400	71261816	71265817
6	12	109236052	109240053	109268078	109272079
7	1	198595771	198599772	198662155	198666156

Table 32.f

		Inner_primers
	Probe	**PCR-Primer1_ID**
1	THNSL2_2_88139809_88146295_88161717_88164554_FR	OBD142_297
2	IGF1R_15_98652565_98657862_98731539_98737034_RF	OBD142_329
3	DKK3_11_11956071_11968035_11984245_11993733_FR	OBD142_061
4	CBL_11_119249760_119252653_119294588_119299643_RF	OBD142_029
5	EYA1_8_71216399_71218728_71261816_71267769_RR	OBD142_081
6	ACACB_12_109236052_109237242_109268078_109273323_RR	OBD142_469
7	PTPRC_1_198595771_198598296_198659753_198666156_RF	OBD142_233

Table 32.g

	Inner_primers			Category
	PCR_Primer1	**PCR-Primer2_ID**	**PCR_Primer2**	**High or Low Responder**
1	GTAACACAGGTAGGAAGGAGTGGAGC	OBD142_299	CACCATAAAATAGGGCAAGGTCAGCA	High
2	TACTCCTCGTTCCCTTTTCTCTC	OBD142_331	TGTGTGCTAGGCTGATATGGTTTG	High
3	GCTCCACATTTCCCAATCTAACCTGC	OBD142_063	GTCAGAGTTGCCGATAGGTCTTGCTA	High
4	ACTGAAGGTTCCCAAGTTCCCGAGAG	OBD142_031	TTAGTCTGTATGGTAGTGTGTGCCTG	High
5	GGCAAGTTTCCTGACCTCTCTGACAT	OBD142_083	GAAGGAGGGAGGTAGGAGAGTCATTA	High
6	AGGAATGGTTACTGCTCCTCTTTGT	OBD142_471	ATTGAATTCTCTCTGTGGCCTTTGC	High

7	GCAAAGGGCAGGTCATCATCATTCAA	OBD142_235	CTCTCCTTTATCCCCTACCCTGCTCA	High

Table 32.h

	Gene	Marker	GLMNET
1	THNSL2	OBD142_297.299	0.379691192
2	IGF1R	OBD142_329.331	0.248382918
3	DKK3	OBD142_061.063	-0.259421345
4	CBL	OBD142_029.031	0.125293919
5	EYA1	OBD142_081.083	-0.165674931
6	ACACB	OBD142_469.471	-0.229960031
7	PTPRC	OBD142_233.235	-0.066564639

Table 32.i

N	Probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig
1	ABCC9_6_47915416_47925286_48134697_48137569_RF	ABCC9	1	53
2	ACACA_11_36333514_36339214_36350786_36357493_RR	ACACA	4	219
3	ACACA_11_36333514_36339214_36436048_36448276_RR	ACACA	4	219
4	ACACA_11_36333514_36339214_36541652_36552356_RF	ACACA	4	219
5	ACACA_11_36436048_36448276_36626441_36631346_FF	ACACA	4	219
6	ACACB_8_11863063_11867350_11908667_11911946_RR	ACACB	1	31
7	ACBD6_5_17677182_17680294_17812085_17822701_FR	ACBD6	3	206
8	ACBD6_5_17677182_17680294_17952666_17962707_FF	ACBD6	3	206
9	ACBD6_5_17677182_17680294_17952666_17962707_FR	ACBD6	3	206
10	AHCYL2_4_84035626_84046686_84262207_84266431_FR	AHCYL2	2	209
11	AHCYL2_4_84081753_84093856_84262207_84266431_FR	AHCYL2	2	209
12	ANGPTL1_5_13716369_13718618_13770118_13781369_FR	ANGPTL1	2	41
13	ANGPTL1_5_13716369_13718618_13770118_13781369_RR	ANGPTL1	2	41
14	APC_14_59179179_59182887_59237657_59248555_FF	APC	2	76
15	APC_14_59179179_59182887_59237657_59248555_FR	APC	2	76
16	APOA2_5_35820030_35830912_35848600_35852478_RF	APOA2	3	65
17	APOA2_5_35820030_35830912_35866091_35873759_RR	APOA2	3	65
18	APOA2_5_35848600_35852478_35900637_35912475_FR	APOA2	3	65
19	BECN1_11_20175502_20184049_20243179_20248279_RF	BECN1	3	28
20	BECN1_11_20175502_20184049_20320840_20322495_RF	BECN1	3	28
21	BECN1_11_20243179_20248279_20281555_20289129_FR	BECN1	3	28
22	BTN1A1_20_24591764_24605263_24706408_24710466_FR	BTN1A1	1	122
23	BTNL2_20_32536895_32543196_32585002_32592656_RF	BTNL2	6	66
24	BTNL2_20_32570542_32582104_32597196_32598340_RF	BTNL2	6	66
25	BTNL2_20_32570542_32582104_32598340_32606017_RR	BTNL2	6	66
26	BTNL2_20_32570542_32582104_32672903_32675921_RF	BTNL2	6	66
27	BTNL2_20_32585002_32592656_32716550_32722709_FF	BTNL2	6	66
28	BTNL2_20_32598340_32606017_32645786_32652591_RR	BTNL2	6	66
29	CACNA1G_11_26122948_26135515_26185131_26187822_RF	CACNA1G	2	33
30	CACNA1G_11_26122948_26135515_26187822_26192201_RF	CACNA1G	2	33
31	CACNA2D3_16_33352821_33354631_33641948_33654248_RF	CACNA2D3	14	766
32	CACNA2D3_16_33410233_33413906_33641948_33654248_RF	CACNA2D3	14	766
33	CACNA2D3_16_33479236_33480664_33641948_33654248_RF	CACNA2D3	14	766

34	CACNA2D3_16_33563090_33565331_33641948_33654248_RF	CACNA2D3	14	766
35	CACNA2D3_16_33622760_33627636_33641948_33654248_RF	CACNA2D3	14	766
36	CACNA2D3_16_33641948_33654248_33704852_33706847_FF	CACNA2D3	14	766
37	CACNA2D3_16_33641948_33654248_33729470_33733482_FF	CACNA2D3	14	766
38	CACNA2D3_16_33641948_33654248_33733482_33741095_FF	CACNA2D3	14	766
39	CACNA2D3_16_33641948_33654248_33733482_33741095_FR	CACNA2D3	14	766
40	CACNA2D3_16_33641948_33654248_33757281_33760491_FF	CACNA2D3	14	766
41	CACNA2D3_16_33641948_33654248_33760582_33768051_FR	CACNA2D3	14	766
42	CACNA2D3_16_33641948_33654248_33768286_33770169_FR	CACNA2D3	14	766
43	CACNA2D3_16_33641948_33654248_33815034_33817501_FR	CACNA2D3	14	766
44	CACNA2D3_16_33641948_33654248_33848517_33852225_FF	CACNA2D3	14	766
45	CACNB2_29_17033576_17046068_17154781_17155878_RF	CACNB2	6	225
46	CACNB2_29_17048693_17053442_17144042_17154089_RR	CACNB2	6	225
47	CACNB2_29_17144042_17154089_17262741_17269092_RR	CACNB2	6	225
48	CACNB2_29_17144042_17154089_17332733_17336468_RF	CACNB2	6	225
49	CACNB2_29_17144042_17154089_17332733_17336468_RR	CACNB2	6	225
50	CACNB2_29_17286082_17289972_17348926_17357613_RF	CACNB2	6	225
51	CAMK2G_1_61385709_61392305_61537867_61544849_FF	CAMK2G	4	87
52	CAMK2G_1_61385709_61392305_61570715_61577474_FF	CAMK2G	4	87
53	CAMK2G_1_61385709_61392305_61570715_61577474_FR	CAMK2G	4	87
54	CAMK2G_1_61385709_61392305_61578119_61589600_FR	CAMK2G	4	87
55	CARD11_13_4269642_4272623_4440946_4446573_RR	CARD11	1	31
56	CASP3_27_25376884_25380938_25471835_25478467_RR	CASP3	1	60
57	CCNDBP1_1_145659771_145664399_145699582_145711153_RR	CCNDBP1	4	96
58	CCNDBP1_1_145659771_145664399_145762480_145771097_RR	CCNDBP1	4	96
59	CCNDBP1_1_145659771_145664399_145793388_145800297_RF	CCNDBP1	4	96
60	CCNDBP1_1_145659771_145664399_145793388_145800297_RR	CCNDBP1	4	96
61	CD19_13_19942675_19947695_20028912_20034792_RF	CD19	3	29
62	CD19_13_20002320_20006400_20028912_20034792_RF	CD19	3	29
63	CD19_13_20007058_20010478_20028912_20034792_RF	CD19	3	29
64	CD2_5_52197323_52200100_52321910_52330791_FF	CD2	1	30

Table 33.a1

N	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr
1	0.283590396	0.318114445	1.89	0.320518457	9.948416738
2	0.071740684	0.151713905	1.83	-0.293607855	7.847234944
3	0.071740684	0.151713905	1.83	-0.210300022	8.374350236
4	0.071740684	0.151713905	1.83	0.231385222	8.833918508
5	0.071740684	0.151713905	1.83	-0.305200929	6.737863734
6	0.198752749	0.267074007	3.23	-0.96134378	7.26378007
7	0.149176662	0.267074007	1.46	-0.26093573	9.509514883
8	0.149176662	0.267074007	1.46	-0.258481627	9.295947643
9	0.149176662	0.267074007	1.46	-0.281768793	9.595365742
10	0.266652717	0.310300562	0.96	-0.295771266	9.712393304
11	0.266652717	0.310300562	0.96	-0.335883754	9.167228863
12	0.039967104	0.109696945	4.88	0.305246417	7.108599809
13	0.039967104	0.109696945	4.88	0.30390975	9.437958235
14	0.104263108	0.213491126	2.63	-0.21158792	10.04027255
15	0.104263108	0.213491126	2.63	-0.18597646	10.12135456
16	0.014396814	0.064041001	4.62	-0.285169774	10.6370881
17	0.014396814	0.064041001	4.62	-0.188307832	9.94119358
18	0.014396814	0.064041001	4.62	-0.35682778	10.37459386
19	0.001460812	0.014841655	10.71	-0.806200399	8.954094586
20	0.001460812	0.014841655	10.71	-0.172300256	11.08935116
21	0.001460812	0.014841655	10.71	-0.689404695	9.24381568
22	0.369972517	0.369972517	0.82	-0.188359359	10.5379586

23	0.0000162598909570469	0.000524381	9.09	-0.626172706	7.90082566
24	0.0000162598909570469	0.000524381	9.09	-0.914586684	9.145982862
25	0.0000162598909570469	0.000524381	9.09	-0.419132349	9.090576394
26	0.0000162598909570469	0.000524381	9.09	-0.87421888	9.197203863
27	0.0000162598909570469	0.000524381	9.09	-0.774602225	7.429403071
28	0.0000162598909570469	0.000524381	9.09	-0.630265492	10.1595488
29	0.027478161	0.080560972	6.06	-0.802327215	9.327353317
30	0.027478161	0.080560972	6.06	-0.583404038	9.095292225
31	0.002885548	0.019591352	1.83	0.209398931	11.18280673
32	0.002885548	0.019591352	1.83	0.194627322	11.7177864
33	0.002885548	0.019591352	1.83	0.198440578	11.24724562
34	0.002885548	0.019591352	1.83	0.200166764	10.76693749
35	0.002885548	0.019591352	1.83	0.242678129	10.92474812
36	0.002885548	0.019591352	1.83	0.19266085	11.39119603
37	0.002885548	0.019591352	1.83	0.199552427	11.12621619
38	0.002885548	0.019591352	1.83	0.221089342	11.19545935
39	0.002885548	0.019591352	1.83	0.276958928	10.73545888
40	0.002885548	0.019591352	1.83	0.203939961	11.05986864
41	0.002885548	0.019591352	1.83	0.210750359	11.34843609
42	0.002885548	0.019591352	1.83	0.20067327	11.31423277
43	0.002885548	0.019591352	1.83	0.245046459	10.85328784
44	0.002885548	0.019591352	1.83	0.219462879	10.72704267
45	0.008301566	0.042836079	2.67	-0.593545035	8.631773695
46	0.008301566	0.042836079	2.67	-0.195749334	7.90944735
47	0.008301566	0.042836079	2.67	-0.287774413	9.577708179
48	0.008301566	0.042836079	2.67	-0.274080009	7.326771399
49	0.008301566	0.042836079	2.67	-0.292274875	9.957522807
50	0.008301566	0.042836079	2.67	0.283385806	7.748329166
51	0.005032361	0.029507937	4.6	-0.236733028	11.38171809
52	0.005032361	0.029507937	4.6	-0.484010849	10.01269368
53	0.005032361	0.029507937	4.6	-0.303821538	10.44275862
54	0.005032361	0.029507937	4.6	-0.378665253	10.33209023
55	0.198752749	0.267074007	3.23	-0.205289586	10.29956667
56	0.303088108	0.331342084	1.67	-0.355934967	8.751256232
57	0.006979045	0.037512367	4.17	-0.63182397	10.94820024
58	0.006979045	0.037512367	4.17	-0.696810436	10.48066661
59	0.006979045	0.037512367	4.17	-0.322489712	9.760585457
60	0.006979045	0.037512367	4.17	-0.625156464	10.77930783
61	0.001616117	0.014841655	10.34	-0.390037974	8.434827236
62	0.001616117	0.014841655	10.34	-0.673915806	8.40536563
63	0.001616117	0.014841655	10.34	-0.395313235	7.939097247
64	0.193928419	0.267074007	3.33	-0.259547189	9.581323717

Table 33.a2

N	t	P.Value	adj.P.Val	B	FC
1	7.263712103	0.000000658532712373121	0.000395221	6.182644836	1.248779238
2	-5.291321916	0.0000408766051478055	0.006156743	2.287156198	0.815859225
3	-5.050567397	0.0000698310885505510	0.008902323	1.777241611	0.864357461
4	5.096854125	0.0000629720358323017	0.008441715	1.875717506	1.173961602
5	-5.402991698	0.0000319491285625712	0.005171517	2.521615893	0.809329491
6	-7.453856126	0.000000454451923050407	0.000311021	6.527700337	0.513578324
7	-5.529047183	0.0000242301608260188	0.004416684	2.784577889	0.834546458
8	-5.399685477	0.0000321824586248703	0.005178058	2.514694153	0.835967276
9	-6.654810658	0.00000223206986757685	0.000837241	5.040151004	0.822581886
10	-6.241524808	0.00000525766136243176	0.001576825	4.232788024	0.814636711
11	-6.320309917	0.00000445769617599177	0.001402377	4.388632115	0.792298649

12	5.609172308	0.0000203429879959953	0.0039679	2.950743157	1.235629669
13	7.008043044	0.00000109276077875550	0.000532857	5.709861189	1.23448538
14	-5.526775502	0.0000243508405008230	0.004416684	2.779855512	0.863586191
15	-5.184267596	0.0000518309913407067	0.007221168	2.06113207	0.879053904
16	-5.131092219	0.0000583432064738677	0.007902668	1.948429433	0.820645031
17	-5.090952536	0.0000638069334895659	0.008495251	1.863172915	0.877634514
18	-5.320752831	0.0000383014725598130	0.005929129	2.34908169	0.780879703
19	-10.73162962	0.00000000156642896568417	0.00000555512672284904	11.63110669	0.571886043
20	-5.071479915	0.0000666425700694542	0.008670693	1.821758099	0.887426625
21	-11.43551668	0.00000000054375531418 6107	0.00000265148685080001	12.53781121	0.620109675
22	-5.281294908	0.0000417937674137867	0.006270673	2.266037132	0.877603169
23	-6.43285853	0.00000352629587947274	0.001196181	4.609695945	0.647892918
24	-5.936360791	0.0000100392087096020	0.002463079	3.620834864	0.53049583
25	-6.27688641	0.00000488175309950516	0.001499505	4.302847451	0.747874268
26	-5.895655257	0.0000109534936492495	0.002605462	3.538234643	0.545549164
27	-5.294894055	0.0000405548509879891	0.006131956	2.294677302	0.584549772
28	-5.091526221	0.0000637252817777454	0.008495251	1.864392502	0.646057513
29	-10.17863513	0.00000000372947965181301	0.00000909293757607660	10.87544294	0.57342344
30	-6.90646185	0.00000133961123275428	0.000598065	5.519220905	0.667387219
31	5.662783116	0.0000181042793666228	0.003741337	3.061481776	1.156206374
32	5.631236286	0.0000193891442127443	0.003919018	2.996361868	1.144428493
33	5.666098866	0.0000179743992793013	0.003741337	3.068319007	1.147457388
34	5.427843178	0.0000302497258239690	0.005000177	2.573603928	1.148831143
35	5.312745619	0.0000389852287177481	0.005987456	2.332243017	1.183187018
36	5.053579322	0.0000693624553048217	0.008871572	1.783655581	1.142869637
37	5.139332812	0.0000572818435901524	0.007813163	1.965913201	1.148342045
38	5.771451184	0.0000143085584536262	0.003153542	3.284832702	1.165613379
39	7.603984521	0.00000034024783095 8195	0.000270685	6.796180224	1.211638166
40	5.197633668	0.0000503139299503325	0.007169673	2.08941646	1.151839706
41	5.184590564	0.0000517937896507643	0.007221168	2.061815727	1.157289945
42	5.508845037	0.0000253252202636046	0.00443021	2.742560003	1.149234549
43	6.888512233	0.00000138890201289527	0.000606823	5.485369802	1.185130935
44	5.190118523	0.0000511612462532849	0.007206844	2.073515633	1.164300032
45	-5.951345629	0.00000972270336819660	0.002446985	3.651185844	0.662712467
46	-5.006721458	0.0000770300340578710	0.009606804	1.683777572	0.873119281
47	-5.945124115	0.00000985284933645142	0.002463079	3.638588206	0.819164776
48	-5.085844945	0.0000645386031849005	0.00853441	1.852313415	0.826977505
49	-6.066098719	0.00000761463569393438	0.0020486	3.882591854	0.816613388
50	5.41620177	0.0000310339784093617	0.00506542	2.549259461	1.217047779
51	-6.036325672	0.00000811181608888997	0.002138121	3.822727459	0.848664933
52	-8.409111112	0.00000007584765795553 09	0.000084511023122425	8.176782156	0.714987116
53	-6.341938105	0.00000426082327745524	0.001351339	4.431257193	0.810103678
54	-7.527123857	0.00000039444018252622 3	0.000284947	6.659163938	0.76914886
55	-6.66299269	0.00000219503072654509	0.000837079	5.055878269	0.867364567
56	-5.372396859	0.0000341760619744322	0.005375839	2.457516974	0.781363101
57	-12.0166013	0.00000000023546298218 8889	0.00000183708218703771	13.24249697	0.645359984
58	-12.8061782	0.00000000007932128104 35301	0.00000960392461716811	14.14079379	0.616934642
59	-7.657502685	0.00000030711869460296 1	0.000254909	6.891044499	0.799688634
60	-12.70330829	0.00000000009112148463 80425	0.00000960392461716811	14.02745955	0.648349459
61	-5.835579933	0.0000124617597410427	0.002859607	3.415923184	0.763109518
62	-9.840705036	0.00000000644260267107065	0.000013962551677693	10.39393487	0.626803089
63	-5.795472953	0.0000135859288607979	0.00308132	3.334000537	0.760324279
64	-5.940740709	0.00000994561781482989	0.002463079	3.629709305	0.835350065

Table 33.a3

N				Probe sequence
	FC_1	LS	Loop Detected	60 mer
1	1.248779238	1	Sprinter	AAAAAGAAAGAGGGAAGAAGGAAAGAAGTCGATGAAACATGCAGTCAACTTGGGAGGCCC
2	-1.225701652	-1	Stayer	ATGAAGGTAATAGTACCTTACCTCGTAGTCGAAAAAAAAATTCCTCCCCATAAAGAGACC
3	-1.156928753	-1	Stayer	ATGAAGGTAATAGTACCTTACCTCGTAGTCGATTATCAGCCTTTTTCTTGAAGAACCTCC
4	1.173961602	1	Sprinter	AACACAGATGATCATCATAAGACGTAGGTCGACTACGAGGTAAGGTACTATTACCTTCAT
5	-1.23559071	-1	Stayer	GATGCAAGTACTTCCTAATTTCTCTAAGTCGAATCAAACTTTAATTTTTAGAAATTCAAA
6	-1.947122673	-1	Stayer	ATTTTCATAGCTATTGCATTTAACTCTTTCGAAATTGATTTTTTTTAAATAGATAAGCAA
7	-1.198255639	-1	Stayer	ACCAGCAATATTTGTGAGAGTACCAGTTTCGAACTTGATTCACACTGTACTGTGAGCCAG
8	-1.196219074	-1	Stayer	ACCAGCAATATTTGTGAGAGTACCAGTTTCGATTTTCTAGAGATGTCCAAGTGTACACTT
9	-1.215684441	-1	Stayer	ACCAGCAATATTTGTGAGAGTACCAGTTTCGAGAGAGCTATTGTTTGATGCTGTGTATTC
10	-1.227541046	-1	Stayer	TTGCAGTTTGAAGAGATCAGCATTGAAATCGACCCAGCTCAGAAGTACTTCCTGCTGCCC
11	-1.262150329	-1	Stayer	TGGTATACTAATTTTACAGATAAAGAAATCGACCCAGCTCAGAAGTACTTCCTGCTGCCC
12	1.235629669	1	Sprinter	CCCCAAAATCTTTTATTTCTGTAGAAAATCGACAAATGTAGGTAATAAAAAAACATATGA
13	1.23448538	1	Sprinter	TGCAAGTAGAGGATTAGTAGCAGTTAAATCGACAAATGTAGGTAATAAAAAAACATATGA
14	-1.157962008	-1	Stayer	ACAGCTCTAGGTTTCTTCAATACGTTTGTCGAAGGCATTCTTTGCAAAGACATTTTTATG
15	-1.137586666	-1	Stayer	ACAGCTCTAGGTTTCTTCAATACGTTTGTCGAACCCTAGAAATTAAGCAAATTATAGATA
16	-1.218553653	-1	Stayer	TGATGTTGGTATAGAGAGGGCCCAGCTCTCGACTTCAAGACCCACCGAAAGACTGGGACT
17	-1.139426474	-1	Stayer	AGTCCCAGTCTTTCGGTGGGTCTTGAAGTCGACTACCACTAAGCTCTCACTACTAAGCTG
18	-1.280606982	-1	Stayer	TGATGTTGGTATAGAGAGGGCCCAGCTCTCGAGGGGAATGAAAAATTAAAGGAACTGACC
19	-1.748600115	-1	Stayer	ATCTGGTCTATGTCCAGGTACTCTCGGATCGAGGTTAAGAGCATAGACTTTGGAGTTTCA
20	-1.126853727	-1	Stayer	TGAGATCAGAGAACAAATTGTCCGGGAGTCGAGGTTAAGAGCATAGACTTTGGAGTTTCA
21	-1.61261796	-1	Stayer	ATCTGGTCTATGTCCAGGTACTCTCGGATCGAGTGCAGGTATGTGGAAACATGTTTAGTG
22	-1.139467171	-1	Stayer	ACCTGAAGTCAGAGTATGTGTGACAGTTTCGACCACGGGAGGAAAAAAGCGGTCCAAGTA
23	-1.543464933	-1	Stayer	TAGAATATGTAGAGATGTCTCCTTTCTATCGATGTGAGTATCAAGCAGTAACCTGAAAAA
24	-1.885028954	-1	Stayer	TAGGCAGATAAGGACATATCTGTAATTCTCGAAACAACACCTGTTTATTTGTTTACAGTT
25	-1.337123154	-1	Stayer	AACTGTAAACAAATAAACAGGTGTTGTTTCGACAGAAGCAGCACTATGATCTCTCACTGA
26	-1.833015367	-1	Stayer	GGTATCAATTATAGCCGTCTACCTTGTGTCGAAACAACACCTGTTTATTTGTTTACAGTT
27	-1.710718313	-1	Stayer	TAGAATATGTAGAGATGTCTCCTTTCTATCGACAACACTAGGTTATGGTGTGATAAGGAC
28	-1.547849811	-1	Stayer	TCAGTGAGAGATCATAGTGCTGCTTCTGTCGAGTCAGACTATAGCGCTACAGGCAACATG
29	-1.743911968	-1	Stayer	ATCCAGACACTCAAGGACTTCCAGTACATCGAATGGCCAAATAATATCCCATTGTATGAA
30	-1.498380509	-1	Stayer	TCCTCCTTCACTAGCTCTTGGTGGTACCTCGAATGGCCAAATAATATCCCATTGTATGAA
31	1.156206374	1	Sprinter	TCCCTCACACACAAGTCATGCAGTTTTTTCGATTCAGCCAGGCTTAGCTTTTCCAGGGAA
32	1.144428493	1	Sprinter	TCCCTCACACACAAGTCATGCAGTTTTTTCGAAGTCAGGGCTCAATGGGCCTTGGGGGGG
33	1.147457388	1	Sprinter	TCCCTCACACACAAGTCATGCAGTTTTTTCGAAATTGTCGTTTAATTGCCTAACCTGCAC
34	1.148831143	1	Sprinter	TCCCTCACACACAAGTCATGCAGTTTTTTCGACTTGGGTCTTAATTAGGATCTTTTATGC
35	1.183187018	1	Sprinter	TCCCTCACACACAAGTCATGCAGTTTTTTCGAATCTCTAAGACTAAAATGAAATCCTGGA
36	1.142869637	1	Sprinter	TCCCTCACACACAAGTCATGCAGTTTTTTCGATTTATTTACGTTGGTGGCCACTTGGACT
37	1.148342045	1	Sprinter	TCCCTCACACACAAGTCATGCAGTTTTTTCGACCCCAACAAAAATGGAATAAAACCCACC
38	1.165613379	1	Sprinter	TCCCTCACACACAAGTCATGCAGTTTTTTCGAAGCTTGTTAAGATCCAGTTTCTGGCCTC
39	1.211638166	1	Sprinter	TCCCTCACACACAAGTCATGCAGTTTTTTCGAGTAAACTACATTTTACAGTGTGAAAAAT
40	1.151839706	1	Sprinter	TCCCTCACACACAAGTCATGCAGTTTTTTCGAATGTCCCTTACTATTTATTCCCCCAAAT
41	1.157289945	1	Sprinter	TCCCTCACACACAAGTCATGCAGTTTTTTCGAATCTGACTCCATCACTTGATCTTGGGCA
42	1.149234549	1	Sprinter	TCCCTCACACACAAGTCATGCAGTTTTTTCGACAAACGTCACCTCTGATGGAGAATGCTG
43	1.185130935	1	Sprinter	TCCCTCACACACAAGTCATGCAGTTTTTTCGATTGAAGAGTTAATGAAATAACCATAATT
44	1.164300032	1	Sprinter	TCCCTCACACACAAGTCATGCAGTTTTTTCGAAAAGGCTGCATACTATATGATTCCGATT
45	-1.508950035	-1	Stayer	TGCTATAGAGGCAGCTGTAAATATAAATTCGAAAGTGTAGATTCAGAGATATCACATGGT
46	-1.145318884	-1	Stayer	GAAGGCAACCAGCTTGCCTTCTGAAGGATCGAGGGTACATAAGAGGAGTCTACACTATGA
47	-1.220755615	-1	Stayer	TCATAGTGTAGACTCCTCTTATGTACCCTCGATGAGGTGGGTAGAATCTTCATTTTAATC
48	-1.209222735	-1	Stayer	TTTTTTAAAATTAAAATCATTTTTTGACTCGAGGGTACATAAGAGGAGTCTACACTATGA
49	-1.224569686	-1	Stayer	TCATAGTGTAGACTCCTCTTATGTACCCTCGACCTAGAGCTGTTCTCTGGATTCTCAGAA
50	1.217047779	1	Sprinter	TAAGGAAATGTAAATGTAAAAAGATGATTCGATTCCCTGATGTTGACACTTCAATTTCCA
51	-1.178321338	-1	Stayer	CTGTACCCCATTTCTTCCCACGTATTCCTCGAGGAAGGTTAGCCCTGAGCTAACATCTGC
52	-1.3986266	-1	Stayer	CTGTACCCCATTTCTTCCCACGTATTCCTCGAAACTAGGAAATTAACATTAGTATAGTAC
53	-1.2344099	-1	Stayer	CTGTACCCCATTTCTTCCCACGTATTCCTCGAGCCCAACGTTTTTTATTGACAAGTAATT
54	-1.300138442	-1	Stayer	CTGTACCCCATTTCTTCCCACGTATTCCTCGATGGTCAGAGAGTTCTGAGCATGTTTGCA

55	-1.152917744	-1	Stayer	GATGGCCAATAAACACTTGAAAAGGTACTCGATTTGCCAATATTTTGCTGAGGATTTTTC
56	-1.279814722	-1	Stayer	TCTTTATATTGAGGTTCTAGCTTGTGATTCGAGAAGGAGACCTTGGTTATTTATTCTTAC
57	-1.549522786	-1	Stayer	TGGTACTTACTCATTTGATATCTGCCCGTCGAATGCAAACTATGCCATTCTCCACTACAA
58	-1.620917244	-1	Stayer	TGGTACTTACTCATTTGATATCTGCCCGTCGAAGACATGGATATATAAATATATGTTTTC
59	-1.250486699	-1	Stayer	ATGCAAAAATTCTCAAAATTTTGGCAACTCGACGGGCAGATATCAAATGAGTAAGTACCA
60	-1.542378091	-1	Stayer	TGGTACTTACTCATTTGATATCTGCCCGTCGATCTAAGCAGAAAACACGAAGAAACATAA
61	-1.310427896	-1	Stayer	ATATTAACAGCAAACCCTTAGTGGGTACTCGAAGCTCCCTAAGATTAGGAACCTTGTCTT
62	-1.595397371	-1	Stayer	ATATTAACAGCAAACCCTTAGTGGGTACTCGAGGGTACTGAGTTGCAGACAGGTTAATGG
63	-1.315228289	-1	Stayer	ATATTAACAGCAAACCCTTAGTGGGTACTCGAAGAAAGTAAAACAAATGGAGAGAAGTGT
64	-1.197102917	-1	Stayer	TCAAAGTCCCGTTCAACTGTACATTTCTTCGAGTTATATCAGCCACTAACTAACAAAAAT

Table 33.a4

N	Probe Location					4 kb Sequence Location			
	Chr	Start1	End1	Start2	End2	Chr	Start1	End1	Start2
1	6	47915416	47915447	48137538	48137569	6	47915416	47919417	48133568
2	11	36333514	36333545	36350786	36350817	11	36333514	36337515	36350786
3	11	36333514	36333545	36436048	36436079	11	36333514	36337515	36436048
4	11	36333514	36333545	36552325	36552356	11	36333514	36337515	36548355
5	11	36448245	36448276	36631315	36631346	11	36444275	36448276	36627345
6	8	11863063	11863094	11908667	11908698	8	11863063	11867064	11908667
7	5	17680263	17680294	17812085	17812116	5	17676293	17680294	17812085
8	5	17680263	17680294	17962676	17962707	5	17676293	17680294	17958706
9	5	17680263	17680294	17952666	17952697	5	17676293	17680294	17952666
10	4	84046655	84046686	84262207	84262238	4	84042685	84046686	84262207
11	4	84093825	84093856	84262207	84262238	4	84089855	84093856	84262207
12	5	13718587	13718618	13770118	13770149	5	13714617	13718618	13770118
13	5	13716369	13716400	13770118	13770149	5	13716369	13720370	13770118
14	14	59182856	59182887	59248524	59248555	14	59178886	59182887	59244554
15	14	59182856	59182887	59237657	59237688	14	59178886	59182887	59237657
16	5	35820030	35820061	35852447	35852478	5	35820030	35824031	35848477
17	5	35820030	35820061	35866091	35866122	5	35820030	35824031	35866091
18	5	35852447	35852478	35900637	35900668	5	35848477	35852478	35900637
19	11	20175502	20175533	20248248	20248279	11	20175502	20179503	20244278
20	11	20175502	20175533	20322464	20322495	11	20175502	20179503	20318494
21	11	20248248	20248279	20281555	20281586	11	20244278	20248279	20281555
22	20	24605232	24605263	24706408	24706439	20	24601262	24605263	24706408
23	20	32536895	32536926	32592625	32592656	20	32536895	32540896	32588655
24	20	32570542	32570573	32598309	32598340	20	32570542	32574543	32594339
25	20	32570542	32570573	32598340	32598371	20	32570542	32574543	32598340
26	20	32570542	32570573	32675890	32675921	20	32570542	32574543	32671920
27	20	32592625	32592656	32722678	32722709	20	32588655	32592656	32718708
28	20	32598340	32598371	32645786	32645817	20	32598340	32602341	32645786
29	11	26122948	26122979	26187791	26187822	11	26122948	26126949	26183821
30	11	26122948	26122979	26192170	26192201	11	26122948	26126949	26188200
31	16	33352821	33352852	33654217	33654248	16	33352821	33356822	33650247
32	16	33410233	33410264	33654217	33654248	16	33410233	33414234	33650247
33	16	33479236	33479267	33654217	33654248	16	33479236	33483237	33650247
34	16	33563090	33563121	33654217	33654248	16	33563090	33567091	33650247
35	16	33622760	33622791	33654217	33654248	16	33622760	33626761	33650247
36	16	33654217	33654248	33706816	33706847	16	33650247	33654248	33702846
37	16	33654217	33654248	33733451	33733482	16	33650247	33654248	33729481
38	16	33654217	33654248	33741064	33741095	16	33650247	33654248	33737094
39	16	33654217	33654248	33733482	33733513	16	33650247	33654248	33733482
40	16	33654217	33654248	33760460	33760491	16	33650247	33654248	33756490
41	16	33654217	33654248	33760582	33760613	16	33650247	33654248	33760582
42	16	33654217	33654248	33768286	33768317	16	33650247	33654248	33768286

43	16	33654217	33654248	33815034	33815065	16	33650247	33654248	33815034
44	16	33654217	33654248	33852194	33852225	16	33650247	33654248	33848224
45	29	17033576	17033607	17155847	17155878	29	17033576	17037577	17151877
46	29	17048693	17048724	17144042	17144073	29	17048693	17052694	17144042
47	29	17144042	17144073	17262741	17262772	29	17144042	17148043	17262741
48	29	17144042	17144073	17336437	17336468	29	17144042	17148043	17332467
49	29	17144042	17144073	17332733	17332764	29	17144042	17148043	17332733
50	29	17286082	17286113	17357582	17357613	29	17286082	17290083	17353612
51	1	61392274	61392305	61544818	61544849	1	61388304	61392305	61540848
52	1	61392274	61392305	61577443	61577474	1	61388304	61392305	61573473
53	1	61392274	61392305	61570715	61570746	1	61388304	61392305	61570715
54	1	61392274	61392305	61578119	61578150	1	61388304	61392305	61578119
55	13	4269642	4269673	4440946	4440977	13	4269642	4273643	4440946
56	27	25376884	25376915	25471835	25471866	27	25376884	25380885	25471835
57	1	145659771	145659802	145699582	145699613	1	145659771	145663772	145699582
58	1	145659771	145659802	145762480	145762511	1	145659771	145663772	145762480
59	1	145659771	145659802	145800266	145800297	1	145659771	145663772	145796296
60	1	145659771	145659802	145793388	145793419	1	145659771	145663772	145793388
61	13	19942675	19942706	20034761	20034792	13	19942675	19946676	20030791
62	13	20002320	20002351	20034761	20034792	13	20002320	20006321	20030791
63	13	20007058	20007089	20034761	20034792	13	20007058	20011059	20030791
64	5	52200069	52200100	52330760	52330791	5	52196099	52200100	52326790

Table 33.a5

N	**4 kb Sequence Location**		
	End2	Probe	Primer ID-1
1	48137569	ABCC9_6_47915416_47925286_48134697_48137569_RF	OBD RD043.001
2	36354787	ACACA_11_36333514_36339214_36350786_36357493_RR	OBD RD043.005
3	36440049	ACACA_11_36333514_36339214_36436048_36448276_RR	OBD RD043.009
4	36552356	ACACA_11_36333514_36339214_36541652_36552356_RF	OBD RD043.013
5	36631346	ACACA_11_36436048_36448276_36626441_36631346_FF	OBD RD043.017
6	11912668	ACACB_8_11863063_11867350_11908667_11911946_RR	OBD RD043.021
7	17816086	ACBD6_5_17677182_17680294_17812085_17822701_FR	OBD RD043.025
8	17962707	ACBD6_5_17677182_17680294_17952666_17962707_FF	OBD RD043.029
9	17956667	ACBD6_5_17677182_17680294_17952666_17962707_FR	OBD RD043.033
10	84266208	AHCYL2_4_84035626_84046686_84262207_84266431_FR	OBD RD043.037
11	84266208	AHCYL2_4_84081753_84093856_84262207_84266431_FR	OBD RD043.041
12	13774119	ANGPTL1_5_13716369_13718618_13770118_13781369_FR	OBD RD043.045
13	13774119	ANGPTL1_5_13716369_13718618_13770118_13781369_RR	OBD RD043.049
14	59248555	APC_14_59179179_59182887_59237657_59248555_FF	OBD RD043.053
15	59241658	APC_14_59179179_59182887_59237657_59248555_FR	OBD RD043.057
16	35852478	APOA2_5_35820030_35830912_35848600_35852478_RF	OBD RD043.061
17	35870092	APOA2_5_35820030_35830912_35866091_35873759_RR	OBD RD043.065
18	35904638	APOA2_5_35848600_35852478_35900637_35912475_FR	OBD RD043.069
19	20248279	BECN1_11_20175502_20184049_20243179_20248279_RF	OBD RD043.073
20	20322495	BECN1_11_20175502_20184049_20320840_20322495_RF	OBD RD043.077
21	20285556	BECN1_11_20243179_20248279_20281555_20289129_FR	OBD RD043.081
22	24710409	BTN1A1_20_24591764_24605263_24706408_24710466_FR	OBD RD043.085
23	32592656	BTNL2_20_32536895_32543196_32585002_32592656_RF	OBD RD043.089
24	32598340	BTNL2_20_32570542_32582104_32597196_32598340_RF	OBD RD043.093
25	32602341	BTNL2_20_32570542_32582104_32598340_32606017_RR	OBD RD043.097
26	32675921	BTNL2_20_32570542_32582104_32672903_32675921_RF	OBD RD043.101
27	32722709	BTNL2_20_32585002_32592656_32716550_32722709_FF	OBD RD043.105
28	32649787	BTNL2_20_32598340_32606017_32645786_32652591_RR	OBD RD043.109

29	26187822	CACNA1G_11_26122948_26135515_26185131_26187822_RF	OBD RD043.113
30	26192201	CACNA1G_11_26122948_26135515_26187822_26192201_RF	OBD RD043.117
31	33654248	CACNA2D3_16_33352821_33354631_33641948_33654248_RF	OBD RD043.121
32	33654248	CACNA2D3_16_33410233_33413906_33641948_33654248_RF	OBD RD043.125
33	33654248	CACNA2D3_16_33479236_33480664_33641948_33654248_RF	OBD RD043.129
34	33654248	CACNA2D3_16_33563090_33565331_33641948_33654248_RF	OBD RD043.133
35	33654248	CACNA2D3_16_33622760_33627636_33641948_33654248_RF	OBD RD043.137
36	33706847	CACNA2D3_16_33641948_33654248_33704852_33706847_FF	OBD RD043.141
37	33733482	CACNA2D3_16_33641948_33654248_33729470_33733482_FF	OBD RD043.145
38	33741095	CACNA2D3_16_33641948_33654248_33733482_33741095_FF	OBD RD043.149
39	33737483	CACNA2D3_16_33641948_33654248_33733482_33741095_FR	OBD RD043.153
40	33760491	CACNA2D3_16_33641948_33654248_33757281_33760491_FF	OBD RD043.157
41	33764583	CACNA2D3_16_33641948_33654248_33760582_33768051_FR	OBD RD043.161
42	33772287	CACNA2D3_16_33641948_33654248_33768286_33770169_FR	OBD RD043.165
43	33819035	CACNA2D3_16_33641948_33654248_33815034_33817501_FR	OBD RD043.169
44	33852225	CACNA2D3_16_33641948_33654248_33848517_33852225_FF	OBD RD043.173
45	17155878	CACNB2_29_17033576_17046068_17154781_17155878_RF	OBD RD043.177
46	17148043	CACNB2_29_17048693_17053442_17144042_17154089_RR	OBD RD043.181
47	17266742	CACNB2_29_17144042_17154089_17262741_17269092_RR	OBD RD043.185
48	17336468	CACNB2_29_17144042_17154089_17332733_17336468_RF	OBD RD043.189
49	17336734	CACNB2_29_17144042_17154089_17332733_17336468_RR	OBD RD043.193
50	17357613	CACNB2_29_17286082_17289972_17348926_17357613_RF	OBD RD043.197
51	61544849	CAMK2G_1_61385709_61392305_61537867_61544849_FF	OBD RD043.201
52	61577474	CAMK2G_1_61385709_61392305_61570715_61577474_FF	OBD RD043.205
53	61574716	CAMK2G_1_61385709_61392305_61570715_61577474_FR	OBD RD043.209
54	61582120	CAMK2G_1_61385709_61392305_61578119_61589600_FR	OBD RD043.213
55	4444947	CARD11_13_4269642_4272623_4440946_4446573_RR	OBD RD043.217
56	25475836	CASP3_27_25376884_25380938_25471835_25478467_RR	OBD RD043.221
57	145703583	CCNDBP1_1_145659771_145664399_145699582_145711153_RR	OBD RD043.225
58	145766481	CCNDBP1_1_145659771_145664399_145762480_145771097_RR	OBD RD043.229
59	145800297	CCNDBP1_1_145659771_145664399_145793388_145800297_RF	OBD RD043.233
60	145797389	CCNDBP1_1_145659771_145664399_145793388_145800297_RR	OBD RD043.237
61	20034792	CD19_13_19942675_19947695_20028912_20034792_RF	OBD RD043.241
62	20034792	CD19_13_20002320_20006400_20028912_20034792_RF	OBD RD043.245
63	20034792	CD19_13_20007058_20010478_20028912_20034792_RF	OBD RD043.249
64	52330791	CD2_5_52197323_52200100_52321910_52330791_FF	OBD RD043.253

Table 33.a6

N	Primer Sequence	Primer ID-2	Primer Sequence
1	CTGGGAATACTTATGATTTGGCGACC	OBD RD043.003	TCCTTGTGACCTATTGGACTGAGGGC
2	GCAGATTAGAAAGGAGTCATCAGAAA	OBD RD043.007	CCTGATTCTAAACAGCATTCTGGGAG
3	CCAACTCTGTCGCTTGTTACACTTAG	OBD RD043.011	ACTCTTTACCCTGTGGTGTGGACGGT
4	CAGTTCACGGAAATGTCCCCAGAGCA	OBD RD043.015	CCAACTCTGTCGCTTGTTACACTTAG
5	CCAACTCTGTCGCTTGTTACACTTAG	OBD RD043.019	GCACAACAATGGAGTGACCCACAGCA
6	GGAGAGCCACCCTGGATACACAG	OBD RD043.023	CCGACAAAGGGCAGAGGTGAGAT
7	CGGATTTTAGAGTTGATAAGCACACC	OBD RD043.027	CACCAGGTTTTCCCCTTCAGTGTGAC
8	CGGATTTTAGAGTTGATAAGCACACC	OBD RD043.031	GACCGATTTGAGGTGCTTACGGATGG
9	CGGATTTTAGAGTTGATAAGCACACC	OBD RD043.035	GCTGGGTCACCACGCATAGGATGA
10	GCAGCAGAGTATCATTCTTGCCCTC	OBD RD043.039	AGGGCAGAGGGCTATGGGTGCTT
11	CGTCTGAGGAAAGTGCCAGGAAAG	OBD RD043.043	AGGGCAGAGGGCTATGGGTGCTT
12	TGCTAAACAACCACTGGACCACTGGG	OBD RD043.047	ATGGATGGCTCTGTCAACTTCTTCAG
13	CGGGCAAAGGTCTAACAGAAGCAGGA	OBD RD043.051	ATGGATGGCTCTGTCAACTTCTTCAG
14	CTCCTCTGGACTCCTATTTCTGGGCA	OBD RD043.055	CACTTGGAGCGGTTTTGTTCACACTT
15	CTCCTCTGGACTCCTATTTCTGGGCA	OBD RD043.059	GATGGCAGCATAGTAACAGTTCTACA
16	CACTTCCTTCAGAAAGCGGGTGCTCA	OBD RD043.063	GAACAACTGCTCCAACACAAACAAGC

17	TGGGAGGAACCAGGTGGGTAACG	OBD RD043.067	TTCCCCTCCTCTCCATTGGGTCA
18	TGGGAGGAACCAGGTGGGTAACG	OBD RD043.071	CTTCCTTCAGAAAGCGGGTGCTC
19	GTCGCCAGGTTCCGTTCTTGGTG	OBD RD043.075	GACTGAGCATTATGGAGGCAGCC
20	TGTGGGCTTGTTCTTACTTCCTGAAT	OBD RD043.079	TCCATCTTGGGTCCCTTCTCCATCCT
21	AAGCAACAGTGGTGGAGGAGACC	OBD RD043.083	TTGGGTCCCTTCTCCATCCTGCC
22	GGTTAGGGAGTGCTATGAGGGAG	OBD RD043.087	GCCCTCGGTGTAGTCCTTGCTGT
23	TACACTTTGGGAGTTTGTCTTTGAAG	OBD RD043.091	ACTTGAAGACAGAACTGCTTTGACAA
24	CACTATGGAAAACAGTATGGAGAT	OBD RD043.095	TCTGAGATGTCCTTCTTGATTCATA
25	TACACTTTGGGAGTTTGTCTTTGAAG	OBD RD043.099	CACCTGCGTAGATTTGTGTAACCACG
26	TCTGATAGGGCTTGTGATTTTATTT	OBD RD043.103	ACTATGGAAAACAGTATGGAGATTT
27	GTCTTTCCCTATGTCAACCTTGTGT	OBD RD043.107	GCCACTATGGAAAACAGTATGGAGAT
28	TCTTCACCTTAGTCTCCTTATCTCTA	OBD RD043.111	GGACTCAGGGCTCATCTCTCATTTGT
29	CCACCAGTGCCACGAGAACCTCT	OBD RD043.115	CCCAAAGGTCCAGAGCGGAGAAA
30	CAGGGCTGCTTGAATGGAAAGGG	OBD RD043.119	CAACCCAAAGGTCCAGAGCGGAG
31	GGGCAGCCAGAAAGCACACAGTT	OBD RD043.123	CCCTTGTGACCTCCTACTCTGCC
32	AACCCAATCCAGGCAAGCCACCC	OBD RD043.127	GCTGAAGTTGACCTTGTCTCCGC
33	GGGCAGCCAGAAAGCACACAGTT	OBD RD043.131	ATTCGGTGGGTCTGGAGAGAGGC
34	GGGCAGCCAGAAAGCACACAGTT	OBD RD043.135	GGGAGGAGAAGCAGAGCACACAG
35	GGGCAGCCAGAAAGCACACAGTT	OBD RD043.139	GGAGGCTGATGTCTGTCCTTGGG
36	GGGCAGCCAGAAAGCACACAGTT	OBD RD043.143	CCCGCTGCTCTCAACAGACACTG
37	TCCATTTTCCCCATCTCTCACCCTCC	OBD RD043.147	ATGAGAACCAAGGTCAGGGAGGTAAA
38	TCCATTTTCCCCATCTCTCACCCTCC	OBD RD043.151	CCCACTCTCTTTGAAGGAAATCACAT
39	GGGCAGCCAGAAAGCACACAGTT	OBD RD043.155	CCTCCACCATTCTCCTCCAGTCC
40	GGGCAGCCAGAAAGCACACAGTT	OBD RD043.159	GGCAGGGTCATTGTGATGGTCCG
41	AACCCAATCCAGGCAAGCCACCC	OBD RD043.163	CCTCCTATCATCTCTCTCCCCAC
42	GGGCAGCCAGAAAGCACACAGTT	OBD RD043.167	AGTCTCCCCTCCCACTGTTGGCA
43	ATCCATTTTCCCCATCTCTCACCCTC	OBD RD043.171	CTTAGACTCCAGTGGCTGAATGTCCA
44	GTTGGGCAGCCAGAAAGCACACAG	OBD RD043.175	GAACTTCTCGTGGGACACCCTCA
45	GAGCAAAGTAGTCAGCCAGCCAGAAT	OBD RD043.179	GTTCTTTTCCTGGTAGGTCATCCTGT
46	AAACCTGTGCGGGCTGTCTGACCA	OBD RD043.183	GCCTGAACCCACTTAGATAATGTGTG
47	TCCCGCTCCCTGTTTTCCACCAT	OBD RD043.187	CACTGTGGCACTGGGAGGAAACG
48	GCCTGAACCCACTTAGATAATGTGTG	OBD RD043.191	GTTCCTGTGGTTGGTTGGTTGGGATG
49	CCTGGGTAGATGAGCCTGTAGCC	OBD RD043.195	TCCCGCTCCCTGTTTTCCACCAT
50	CCCTCGCCTCCTATTCCTATGGC	OBD RD043.199	CCCATCCCTTTCAGCCTCACTCA
51	CCACGCCATTTAGGACTCGGGTC	OBD RD043.203	GGGTCAGTCTTCCGCAGCACAAA
52	TATGGGATTTCTTTGGTAGGGACG	OBD RD043.207	TCAGTCAATACATACAGTTCATACT
53	GCCCAACCTCTGTGTTCCCATTC	OBD RD043.211	TCCACGGTTCAGGCATCCACTGG
54	GCCCAACCTCTGTGTTCCCATTC	OBD RD043.215	CCCCGAAGGCAGGCTATGGAGAA
55	GAACAGGTGGCTCACAAAGGAGGATA	OBD RD043.219	GACAAGGACAACACAAAGAAGGAAAA
56	GCTCCAGTTTGCTGAACCAACCC	OBD RD043.223	AGAGCGTCCCTGGAAAGTGGCAG
57	GGCACCCCTTATCAGAGACCAGC	OBD RD043.227	TTGGGCAGAGGAGAAGAGTGTGC
58	GGCACCCCTTATCAGAGACCAGC	OBD RD043.231	GGCATCTCCTCTTCTGCTCACAC
59	CCAAAACCTGACAAGCACAGCAT	OBD RD043.235	GAGACAGGTGGATGGCGATGGTA
60	GGCACCCCTTATCAGAGACCAGC	OBD RD043.239	CCTCCATCTCTGCCACTCAGGAA
61	GACCTTCATCCGAGCCTCCGTTT	OBD RD043.243	TGCCTCTCCTGCCTCTGTCTCAC
62	GAGACCTTCATCCGAGCCTCCGT	OBD RD043.247	GGGCGAACAGCAAGAGACAAGCA
63	GACCTTCATCCGAGCCTCCGTTT	OBD RD043.251	CCCTGGATGTGTGACCTTCGGCA
64	ATCCAAACCATTGAAACCCTGGGC	OBD RD043.255	GATTGAGACTTGCGTTTTGAGGGC

Table 33.a7

N	Probe	Marker
1	ABCC9	OBD RD043.001.003
2	ACACA	OBD RD043.005.007
3	ACACA	OBD RD043.009.011
4	ACACA	OBD RD043.013.015

5	ACACA	OBD RD043.017.019
6	ACACB	OBD RD043.021.023
7	ACBD6	OBD RD043.025.027
8	ACBD6	OBD RD043.029.031
9	ACBD6	OBD RD043.033.035
10	AHCYL2	OBD RD043.037.039
11	AHCYL2	OBD RD043.041.043
12	ANGPTL1	OBD RD043.045.047
13	ANGPTL1	OBD RD043.049.051
14	APC	OBD RD043.053.055
15	APC	OBD RD043.057.059
16	APOA2	OBD RD043.061.063
17	APOA2	OBD RD043.065.067
18	APOA2	OBD RD043.069.071
19	BECN1	OBD RD043.073.075
20	BECN1	OBD RD043.077.079
21	BECN1	OBD RD043.081.083
22	BTN1A1	OBD RD043.085.087
23	BTNL2	OBD RD043.089.091
24	BTNL2	OBD RD043.093.095
25	BTNL2	OBD RD043.097.099
26	BTNL2	OBD RD043.101.103
27	BTNL2	OBD RD043.105.107
28	BTNL2	OBD RD043.109.111
29	CACNA1G	OBD RD043.113.115
30	CACNA1G	OBD RD043.117.119
31	CACNA2D3	OBD RD043.121.123
32	CACNA2D3	OBD RD043.125.127
33	CACNA2D3	OBD RD043.129.131
34	CACNA2D3	OBD RD043.133.135
35	CACNA2D3	OBD RD043.137.139
36	CACNA2D3	OBD RD043.141.143
37	CACNA2D3	OBD RD043.145.147
38	CACNA2D3	OBD RD043.149.151
39	CACNA2D3	OBD RD043.153.155
40	CACNA2D3	OBD RD043.157.159
41	CACNA2D3	OBD RD043.161.163
42	CACNA2D3	OBD RD043.165.167
43	CACNA2D3	OBD RD043.169.171
44	CACNA2D3	OBD RD043.173.175
45	CACNB2	OBD RD043.177.179
46	CACNB2	OBD RD043.181.183
47	CACNB2	OBD RD043.185.187
48	CACNB2	OBD RD043.189.191
49	CACNB2	OBD RD043.193.195
50	CACNB2	OBD RD043.197.199
51	CAMK2G	OBD RD043.201.203
52	CAMK2G	OBD RD043.205.207
53	CAMK2G	OBD RD043.209.211
54	CAMK2G	OBD RD043.213.215
55	CARD11	OBD RD043.217.219
56	CASP3	OBD RD043.221.223
57	CCNDBP1	OBD RD043.225.227
58	CCNDBP1	OBD RD043.229.231
59	CCNDBP1	OBD RD043.233.235
60	CCNDBP1	OBD RD043.237.239
61	CD19	OBD RD043.241.243

62	CD19	OBD RD043.245.247
63	CD19	OBD RD043.249.251
64	CD2	OBD RD043.253.255

Table 33.a8

N	Probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig
65	CD226_8_85390137_85395670_85431393_85435046_RR	CD226	1	31
66	CD40_22_34955976_34961456_35003447_35009473_FF	CD40	1	30
67	CD5_12_20785118_20787274_20916990_20922807_RF	CD5	2	31
68	CD5_12_20843696_20847942_20916990_20922807_RF	CD5	2	31
69	CDH1_3_18955128_18959809_19065895_19074313_FF	CDH1	1	28
70	CERK_28_42579274_42585201_42607249_42612447_RR	CERK	1	31
71	CHL1_16_15145284_15151298_15196227_15203340_FF	CHL1	6	73
72	CHL1_16_15145284_15151298_15255076_15264032_FF	CHL1	6	73
73	CHL1_16_15145284_15151298_15255076_15264032_FR	CHL1	6	73
74	CHL1_16_15145284_15151298_15301390_15310795_FR	CHL1	6	73
75	CHL1_16_15145284_15151298_15326701_15332680_FF	CHL1	6	73
76	CHL1_16_15165960_15173124_15233430_15239181_RF	CHL1	6	73
77	CHRDL2_7_69179023_69184961_69220436_69225536_RF	CHRDL2	2	61
78	CHRDL2_7_69220436_69225536_69328532_69336827_FR	CHRDL2	2	61
79	CHST10_15_8874159_8888709_8973363_8982576_FR	CHST10	3	64
80	CHST10_15_8874159_8888709_9029805_9032751_FF	CHST10	3	64
81	CHST10_15_8936185_8939355_8973363_8982576_RR	CHST10	3	64
82	COL15A1_25_5777848_5781338_5838527_5844153_RR	COL15A1	1	31
83	COL18A1_26_40666594_40668538_40680588_40685271_RR	COL18A1	1	30
84	COL4A4_6_15299757_15310450_15375645_15378009_RF	COL4A4	2	48
85	COL4A4_6_15436171_15443495_15487479_15493934_FR	COL4A4	2	48
86	CREBBP_13_38904201_38905631_39179236_39195594_RF	CREBBP	7	139
87	CREBBP_13_38931046_38933583_39179236_39195594_RF	CREBBP	7	139
88	CREBBP_13_38974958_38977634_39179236_39195594_RF	CREBBP	7	139
89	CREBBP_13_38981963_38985123_39179236_39195594_RF	CREBBP	7	139
90	CREBBP_13_38999154_39003472_39179236_39195594_RF	CREBBP	7	139
91	CREBBP_13_39073684_39080240_39179236_39195594_RF	CREBBP	7	139
92	CREBBP_13_39112330_39113797_39179236_39195594_RF	CREBBP	7	139
93	CRP_5_37768331_37775673_37803790_37809028_RF	CRP	3	33
94	CRP_5_37768331_37775673_37803790_37809028_RR	CRP	3	33
95	CRP_5_37768331_37775673_37834953_37842330_RR	CRP	3	33
96	CTLA4_18_78522827_78530189_78600391_78604267_FR	CTLA4	1	29
97	DDIT3_6_75012399_75018811_75092742_75096887_RR	DDIT3	2	23
98	DDIT3_6_75012399_75018811_75098342_75106967_RR	DDIT3	2	23
99	DGKH_17_27888277_27893919_27983597_27991700_RR	DGKH	4	168
100	DGKH_17_27888277_27893919_28023161_28030553_RR	DGKH	4	168
101	DGKH_17_27888277_27893919_28087062_28095320_RR	DGKH	4	168
102	DGKH_17_27983597_27991700_28038960_28044643_FF	DGKH	4	168
103	DIAPH3_17_35244506_35247777_35523297_35543766_RR	DIAPH3	2	250
104	DIAPH3_17_35550338_35555886_35584820_35594304_FR	DIAPH3	2	250
105	DLK1_24_42596087_42597712_42651466_42656554_FF	DLK1	1	31
106	DOK5_22_41633839_41639527_41876029_41882809_RF	DOK5	2	31
107	DOK5_22_41845220_41849884_41876029_41882809_RF	DOK5	2	31
108	ETS1_7_37223720_37228234_37244778_37252642_RR	ETS1	1	56
109	GABPA_26_23335158_23338855_23360793_23370765_RR	GABPA	1	91
110	GJA5_5_48248931_48256193_48407852_48413621_FR	GJA5	5	88
111	GJA5_5_48248931_48256193_48407852_48413621_RR	GJA5	5	88
112	GJA5_5_48256193_48265184_48407852_48413621_FR	GJA5	5	88

113	GJA5_5_48297725_48306379_48407852_48413621_FR	GJA5	5	88
114	GJA5_5_48370294_48376643_48407852_48413621_RR	GJA5	5	88
115	GPC5_17_62030628_62037968_62292109_62298602_FR	GPC5	2	249
116	GPC5_17_62161244_62167825_62292109_62298602_FR	GPC5	2	249
117	GRK5_1_13009800_13016170_13161461_13167914_FR	GRK5	3	31
118	GRK5_1_13009800_13016170_13204085_13213606_FF	GRK5	3	31
119	GRK5_1_13135627_13139975_13204085_13213606_FF	GRK5	3	31
120	GSK3B_19_38827199_38835574_39055705_39060019_RR	GSK3B	1	132
121	HDAC3_14_35404443_35406152_35458546_35471150_RR	HDAC3	1	104
122	HDAC5_11_19330735_19336727_19434549_19441692_RR	HDAC5	2	30
123	HDAC5_11_19372111_19379011_19491838_19494990_FF	HDAC5	2	30
124	HDAC9_4_51008167_51021720_51107519_51111219_RF	HDAC9	1	280
125	HOXC6_6_70794688_70801196_70818032_70820676_RF	HOXC6	1	31
126	HSDL2_25_17089584_17093930_17167460_17175476_FF	HSDL2	3	102
127	HSDL2_25_17089584_17093930_17167460_17175476_FR	HSDL2	3	102
128	HSDL2_25_17089584_17093930_17197980_17209878_FF	HSDL2	3	102

Table 33.b1

N	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr
65	0.198752749	0.267074007	3.23	0.341840161	7.247636443
66	0.193928419	0.267074007	3.33	-0.178317344	10.69384186
67	0.024599258	0.075554863	6.45	-0.242153231	10.73889105
68	0.024599258	0.075554863	6.45	-0.260248811	11.120971
69	0.183998999	0.267074007	3.57	-0.282497053	11.11483854
70	0.198752749	0.267074007	3.23	-0.448599336	8.889809603
71	0.0000287855939384343	0.000742668	8.22	0.462470187	8.5481053
72	0.0000287855939384343	0.000742668	8.22	0.410028111	8.628990709
73	0.0000287855939384343	0.000742668	8.22	0.445873686	8.369941593
74	0.0000287855939384343	0.000742668	8.22	0.413519891	8.631292888
75	0.0000287855939384343	0.000742668	8.22	0.451423499	8.55317371
76	0.0000287855939384343	0.000742668	8.22	-0.251896305	6.606225387
77	0.075709775	0.157525178	3.28	0.284071373	7.894826629
78	0.075709775	0.157525178	3.28	0.298147218	7.7720811
79	0.013845037	0.064041001	4.69	-0.409059439	7.708930887
80	0.013845037	0.064041001	4.69	-0.25346967	8.649906865
81	0.013845037	0.064041001	4.69	0.252289513	8.203650527
82	0.198752749	0.267074007	3.23	-0.638663316	8.462246587
83	0.193928419	0.267074007	3.33	-0.691447546	9.504132323
84	0.051914218	0.131312433	4.17	0.26396571	9.117422855
85	0.051914218	0.131312433	4.17	0.357277506	7.749299691
86	0.000137621	0.002219133	5.04	-0.489675835	8.316954487
87	0.000137621	0.002219133	5.04	-0.59449685	8.143398203
88	0.000137621	0.002219133	5.04	-0.258158385	9.427438624
89	0.000137621	0.002219133	5.04	-0.542091889	7.809236934
90	0.000137621	0.002219133	5.04	-0.570549519	8.272773989
91	0.000137621	0.002219133	5.04	-0.519347042	8.352346785
92	0.000137621	0.002219133	5.04	-0.474046419	8.086674809
93	0.002335573	0.01673827	9.09	0.225177272	9.290490657
94	0.002335573	0.01673827	9.09	0.257141717	10.68770958
95	0.002335573	0.01673827	9.09	0.225607706	10.55701332
96	0.189010904	0.267074007	3.45	0.244602905	8.422577617
97	0.014290491	0.064041001	8.7	0.215926084	10.1135098
98	0.014290491	0.064041001	8.7	0.413805259	9.019249379
99	0.037378088	0.104821159	2.38	0.406030868	7.865506845
100	0.037378088	0.104821159	2.38	0.335540786	8.434376341

101	0.037378088	0.104821159	2.38	0.268362014	8.83590478
102	0.037378088	0.104821159	2.38	-0.1949879	9.068498407
103	0.272436907	0.310300562	0.8	1.177347719	8.350585003
104	0.272436907	0.310300562	0.8	0.198636698	10.37949827
105	0.198752749	0.267074007	3.23	-0.400257671	9.279193522
106	0.024599258	0.075554863	6.45	-0.255902452	11.31369569
107	0.024599258	0.075554863	6.45	-0.197532334	11.33660679
108	0.292341721	0.325104155	1.79	-0.325806823	7.500438844
109	0.356204452	0.369972517	1.1	-1.140777936	8.452195491
110	0.00071906	0.009275877	5.68	-0.415749473	11.59733518
111	0.00071906	0.009275877	5.68	-0.307210255	11.22897697
112	0.00071906	0.009275877	5.68	-0.383777265	9.880520247
113	0.00071906	0.009275877	5.68	-0.367375654	10.47600421
114	0.00071906	0.009275877	5.68	-0.418188826	11.1638961
115	0.272492977	0.310300562	0.8	0.312761226	8.158780766
116	0.272492977	0.310300562	0.8	0.218475376	9.612836388
117	0.001955877	0.014841655	9.68	-0.376092453	10.23852086
118	0.001955877	0.014841655	9.68	-0.346076177	10.08178634
119	0.001955877	0.014841655	9.68	-0.19700025	11.98270597
120	0.368643954	0.369972517	0.76	0.236007177	7.969612712
121	0.365777771	0.369972517	0.96	-0.318530813	7.005872794
122	0.023201487	0.075554863	6.67	-0.567555056	9.695872092
123	0.023201487	0.075554863	6.67	-0.311003579	8.846166998
124	0.230471214	0.297307866	0.36	0.267534336	7.807343578
125	0.198752749	0.267074007	3.23	-0.284488126	10.50098524
126	0.04181789	0.112385579	2.94	0.409504025	8.955642386
127	0.04181789	0.112385579	2.94	0.275378575	9.43472352
128	0.04181789	0.112385579	2.94	0.37672213	9.562492703

Table 33.b2

N	t	P.Value	adj.P.Val	B	FC
65	5.618655797	0.0000199272532249328	0.003966133	2.970358272	1.2673721
66	-5.10596284	0.0000617052113463042	0.008329136	1.895072775	0.883733119
67	-5.936420225	0.0000100379326708335	0.002463079	3.620955306	0.845482482
68	-6.14157352	0.00000648983188875642	0.001782876	4.03379312	0.834943911
69	-7.909652841	0.00000019051735250956 5	0.000176954	7.332040725	0.822166758
70	-7.419021619	0.00000048622919039906 8	0.000327031	6.464905236	0.732753909
71	6.686410206	0.00000209248781498571	0.000822758	5.100834912	1.377899042
72	5.428175718	0.0000302276235200180	0.005000177	2.574299106	1.328711704
73	6.52733514	0.00000290021776169651	0.001037747	4.793822411	1.362138768
74	5.554618228	0.0000229132183097780	0.004269944	2.83769231	1.331931503
75	5.455049104	0.0000284949740889623	0.004832995	2.630436111	1.367388786
76	-5.621056707	0.0000198233899082524	0.003965695	2.975322416	0.839791852
77	4.983263565	0.0000811872515612103	0.009898247	1.633703508	1.217626256
78	5.44278257	0.0000292728922433219	0.004943444	2.604822343	1.22956433
79	-5.983309313	0.00000908136757827868	0.002361761	3.715824347	0.753114204
80	-5.190006848	0.0000511739465631575	0.007206844	2.073279303	0.838876496
81	5.71974371	0.0000160008558050293	0.003467741	3.178744012	1.191095848
82	-6.403087538	0.00000375123437915977	0.001240133	4.551401529	0.642307783
83	-10.26896099	0.00000000322944539582748	0.00000854970466866222	11.00157549	0.619232224
84	6.538599393	0.00000283363426460291	0.001033085	4.815686956	1.200774887
85	8.497455807	0.00000006466330505895 55	0.000078597025797400	8.322263656	1.281006243
86	-6.177261672	0.00000601894082752241	0.001701441	4.105008693	0.712185103
87	-5.47299969	0.0000273945059932764	0.004693558	2.66788725	0.662275388
88	-5.496015116	0.0000260468384551831	0.004515943	2.715850222	0.836154599

89	-6.291593561	0.0000047336629556504 9	0.001465557	4.331932541	0.686774373
90	-5.958739229	0.0000095703321247116 7	0.002438159	3.666149932	0.673360258
91	-7.020935167	0.0000010649821476068 9	0.000532857	5.733942795	0.697687533
92	-5.913971946	0.000010531943308529 6	0.00255187	3.57543078	0.719942494
93	5.231815445	0.0000046636927424953 1	0.006813882	2.161666862	1.168920872
94	5.007912479	0.0000076824832680341 0	0.009606804	1.68631868	1.195108595
95	7.210365056	0.0000007313983003229 28	0.000419586	6.084829449	1.169269676
96	6.094643967	0.0000071673494952780 7	0.001955233	3.939871515	1.184766624
97	5.419098482	0.0000030836911996344 4	0.005054403	2.555318501	1.161449224
98	6.915832549	0.0000013146003641666 7	0.000596309	5.536873458	1.332194988
99	5.856598637	0.0000119111980213138	0.002765809	3.458771257	1.325035367
100	6.902941252	0.0000013491345028101 8	0.000598065	5.512585315	1.261850317
101	5.17067204	0.0000053421990848131 0	0.007416341	2.032343624	1.204439572
102	-5.2490489	0.0000044888230755304 5	0.006607886	2.198047673	0.873580223
103	5.956066197	0.0000096251342821813 0	0.002438159	3.660740777	2.261606163
104	5.540348785	0.0000023638814288163 7	0.004367942	2.808062497	1.147613384
105	-5.662792363	0.0000018103915841854 1	0.003741337	3.061500844	0.757722939
106	-5.516430295	0.0000249082421012251	0.004416684	2.758342073	0.83746311
107	-4.983217873	0.0000081195568086276 7	0.009898247	1.633605924	0.872040876
108	-8.393742068	0.0000000779901777084671	0.000084511023122425	8.151353285	0.797852065
109	-7.690570015	0.0000002883374686520 26	0.000248829	6.94943685	0.453514966
110	-8.767490453	0.0000000399545356666192	0.000064942768181451	8.759712775	0.749629965
111	-6.227343692	0.0000054166688908059 5	0.001588754	4.204641449	0.808203075
112	-6.509359957	0.0000030009830197002 69	0.001051643	4.75889243	0.766428298
113	-5.587701438	0.0000213173634345125	0.004137265	2.906293096	0.775191333
114	-6.963670287	0.0000011942329960634 7	0.00057037	5.626780498	0.748363538
115	5.331375489	0.0000374132338335943	0.005860047	2.371409711	1.242082693
116	5.387261614	0.0000330749297047718	0.005266339	2.488673122	1.163503359
117	-5.679474637	0.0000174600811226560	0.003701727	3.095886422	0.770521729
118	-7.010703269	0.0000010869680812098 2	0.000532857	5.714832403	0.786720904
119	-6.14332049	0.0000064659218293122 9	0.001782876	4.037283391	0.872362554
120	4.997714723	0.0000078599973775624 3	0.009703117	1.664557166	1.177728649
121	-5.976961259	0.0000092051864981726 4	0.002378108	3.702998116	0.801886073
122	-7.630840053	0.0000003232183938391 8	0.000262654	6.843838746	0.674759339
123	-5.872236016	0.0000011517835904795 6	0.002706691	3.490611042	0.806080832
124	5.079901556	0.0000065400769439631 2	0.008590182	1.839673798	1.20374878
125	-5.695385681	0.0000016867867800567 4	0.00361547	3.128649589	0.821032863
126	6.025225618	0.0000083056099380354 1	0.002174509	3.800377209	1.328229112
127	5.861408292	0.0000011788762875250 7	0.00275377	3.468567823	1.210311644
128	7.68141304	0.0000002934159560968 93	0.000248829	6.933283828	1.298388503

Table 33.b3

N				**Probe sequence**
	FC_1	LS	Loop Detected	**60 mer**
65	1.2673721	1	Sprinter	ATTGAAATAAAAAAGTCAGTAGAAAAGATCGACAATAAAGACTATCAAGTATTGTACTAA
66	-1.131563341	-1	Stayer	GCTGGGGCCATGTACATCCTGGGCACCATCGATAAGAAAACAAAATGCCTCAAAAGAAGT
67	-1.182756616	-1	Stayer	GCCTTTCTCAAAACCCACTGTACACAGCTCGATTTTAATGGCTGCTTAATCTGAGTGGCT
68	-1.197685243	-1	Stayer	GCCTTTCTCAAAACCCACTGTACACAGCTCGAGCCACCAGCTCATAAAGCCCCTGTGATC
69	-1.216298263	-1	Stayer	TGAACAGTCAAGACTGGTGAGGAAGAATTCGAAGCCTATGCTGCCTTCCTGAAGCCTCCT
70	-1.364714658	-1	Stayer	CGTGTACCTCACAGGGTTCTTCTAAAGATCGATGAGAACTTTTAAGATCTACTCTCTTAG
71	1.377899042	1	Sprinter	ATTTCTTGACAGCGTGAATTCTTTACCCTCGAGCTAAAAATTTCACAAATAAACTCATAA
72	1.328711704	1	Sprinter	ATTTCTTGACAGCGTGAATTCTTTACCCTCGATTATCTACTTGCAGATAACCTTTTTTCC
73	1.362138768	1	Sprinter	ATTTCTTGACAGCGTGAATTCTTTACCCTCGAGGTACATAGAAGTACTAAAATACACAAA
74	1.331931503	1	Sprinter	ATTTCTTGACAGCGTGAATTCTTTACCCTCGAGAGAAGTCAGAAGAATCTCTGGTTACTT

75	1.367388786	1	Sprinter	ATTTCTTGACAGCGTGAATTCTTTACCCTCGATGATATTTATCTGTGTCATTTTTAATAG
76	-1.190771258	-1	Stayer	ATTCAAAAACACACAAGTACTATTAAATTCGAATCCTTGCAAAAATTTCTCTTTTGTTTA
77	1.217626256	1	Sprinter	AAAAAAATCTGTTCAGCTAATTTCTAACTCGACAAAGCTCTGTATTCTTTTTTTTAATTG
78	1.22956433	1	Sprinter	AAAAAAATCTGTTCAGCTAATTTCTAACTCGAATAAAGGATGGTTGGAAAAAAAATAAAT
79	-1.327819863	-1	Stayer	TACAGCTCAGATCAAATTGTTCTCAGAATCGATTGTATCCTGTTGGTCTATACTTCTGTC
80	-1.19207059	-1	Stayer	TACAGCTCAGATCAAATTGTTCTCAGAATCGAAATGCACCAAGAAAAAGACTGCTATGTA
81	1.191095848	1	Sprinter	TTAAGCACTTAATTTTTTTTTCTTGTGTTCGATTGTATCCTGTTGGTCTATACTTCTGTC
82	-1.556886007	-1	Stayer	TCTCTCTAGAGCTCCACGGAGTTCGCAGTCGACTAATAAAGTAGCATCAAAATATATAAG
83	-1.614903039	-1	Stayer	CTGTGCGTATGTACAATTGTTTTAATCCTCGACAGACGCGGTACCCGACCAGGTTGTCAC
84	1.200774887	1	Sprinter	AGTTATTGACTCAACAAACATTATTGACTCGATGTACACTCTGGCTAGACCAGGGCAGGA
85	1.281006243	1	Sprinter	GAGATATATACAGCATTTTTTCAGAAAATCGAGAGCAAAGAGACACTGGTTGAAATGAGA
86	-1.404129341	-1	Stayer	TAAAGAAACGTCTATGAAAATTCAAAACTCGAAACACAATAATATTTGTATTTGGCTGTT
87	-1.509945889	-1	Stayer	TAAAGAAACGTCTATGAAAATTCAAAACTCGAAGATATAATTCCACTACTTTTGGCTTCT
88	-1.195951086	-1	Stayer	TAAAGAAACGTCTATGAAAATTCAAAACTCGACAGCGCTAACAGCAACAAAAACAGTCAA
89	-1.456082288	-1	Stayer	TAAAGAAACGTCTATGAAAATTCAAAACTCGAGTTGAGTTTGATGTTAATTTCGTAAAAT
90	-1.48508913	-1	Stayer	TAAAGAAACGTCTATGAAAATTCAAAACTCGATTCTGTAAAATGAAAAGCTTTTTCAGAG
91	-1.433306392	-1	Stayer	TAAAGAAACGTCTATGAAAATTCAAAACTCGACAGTTATGTAAATCAAAGTATGAAGACA
92	-1.388999827	-1	Stayer	TAAAGAAACGTCTATGAAAATTCAAAACTCGAGTCTTGAGTTTTAATGTAGATTAAGCCA
93	1.168920872	1	Sprinter	CGGGCAAAAACTAGCTATTTAATATCTCTCGAGAGGGGCAGAATAAATGATCGCTAATGC
94	1.195108595	1	Sprinter	GCATTAGCGATCATTTATTCTGCCCCTCTCGAAGACTCTGATGGTTTCTGGTTTGTTGAA
95	1.169269676	1	Sprinter	GCATTAGCGATCATTTATTCTGCCCCTCTCGAGGTGGGGTTTTTCTTGCGCTTGCACTGT
96	1.184766624	1	Sprinter	CTCCACTCATATGTGGAAATTAAACATGTCGATTCAGTTTTGATGGACGAGGTTCAGAGA
97	1.161449224	1	Sprinter	TGTCTTCAATAAATTGTGTTGGGAAAATTCGAGTCCCTCCTACAACTCCACTTAATGGGG
98	1.332194988	1	Sprinter	TGTCTTCAATAAATTGTGTTGGGAAAATTCGAAATGAGGGTTTCAATAGTTCAAAATTTT
99	1.325035367	1	Sprinter	GAACGTGATGATGTAGTCTATACAGAAGTCGAAGTGAGACTTCTTCAAAAAAAGTTCACG
100	1.261850317	1	Sprinter	GAACGTGATGATGTAGTCTATACAGAAGTCGAAGTTTCACACAATATTCTATTAACTCAC
101	1.204439572	1	Sprinter	GAACGTGATGATGTAGTCTATACAGAAGTCGACTGAACACCACAATCCAACGGAAGTTCC
102	-1.14471456	-1	Stayer	CAACGGCATGTTGGATGTACAAATGGGTTCGAATAGTTACCATCTGTAGTCTTGATCTCT
103	2.261606163	1	Sprinter	AGAATTGGTAGGTATTGTAGTGATGTATTCGAAGATTGTTCATTATATCAAACCATGACA
104	1.147613384	1	Sprinter	ACTGGAGACTAGGCAGAGGAAAAACCTTTCGAGACAATTTATGATCAGGAAAAATGGACC
105	-1.319743601	-1	Stayer	AATATAGTACAGGAACATCTTAGATTCCTCGAGTTCACACAGCCAAGAATGATCCGATTT
106	-1.194082447	-1	Stayer	GCTGCAGGAAGTGATGTCAAAAGGAGGGTCGAAAACTACCACATTTCCATTTCAGTTTAA
107	-1.146735237	-1	Stayer	GCTGCAGGAAGTGATGTCAAAAGGAGGGTCGATCAGTGGTCAACCCTTGTAAGTTCATCA
108	-1.253365184	-1	Stayer	TTCCTTCTCTGTACACAAAGAAGTGAACTCGACTGCATTAATTTTTCCTTTTGAAACAGT
109	-2.204998899	-1	Stayer	GGGGCCAAGAGTAATGCTTCGTATATAGTCGAATTTCCACAAGTAATTTTGAATTTCAGG
110	-1.333991499	-1	Stayer	GGTTAAGAGCAGAGCCTTTAAAATCAGATCGAGAGCCGCGAGTTATGAGCTCTCCGCCTT
111	-1.237312788	-1	Stayer	AGAGTTTGGAGAAGGAAGTTGGTCTCCTTCGAGAGCCGCGAGTTATGAGCTCTCCGCCTT
112	-1.304753494	-1	Stayer	ATGTATTTAAAAACATTTCTTGAAGGCCTCGAGAGCCGCGAGTTATGAGCTCTCCGCCTT
113	-1.290004103	-1	Stayer	ACTTTTCATAGTTTCTCCTTCTAAACTCTCGAGAGCCGCGAGTTATGAGCTCTCCGCCTT
114	-1.336248961	-1	Stayer	TTTAAGCTCTGAGTTAGTCTATTTTCTATCGAGAGCCGCGAGTTATGAGCTCTCCGCCTT
115	1.242082693	1	Sprinter	AAAAGAAATTATAGAGTTAATTACCTCATCGATTTCTGTTTGGGATGTGACGTACAATTC
116	1.163503359	1	Sprinter	TTGTATCATTAATTAGGGCTTTGAATGGTCGATTTCTGTTTGGGATGTGACGTACAATTC
117	-1.297821933	-1	Stayer	TCATTCATGGGTGAGTTGGTACTTTTTCTCGATGCTCAAACAGTGTTTGCCAAGTGGATG
118	-1.271098804	-1	Stayer	TCATTCATGGGTGAGTTGGTACTTTTTCTCGACCACCTGTATAGCTGTGAGGCCACTGGT
119	-1.146312385	-1	Stayer	ATACCCACATTCTGACCCCCGAGTCAGCTCGACCACCTGTATAGCTGTGAGGCCACTGGT
120	1.177728649	1	Sprinter	ACATCATTAGTCATTGTGGAAATACAAATCGAAGTGTTTTATTTTCAAGAGCAAAGGTTA
121	-1.247059943	-1	Stayer	TGGGAGTACAGAGAAAATTCTATAAGATTCGAACATCCAGGGAATCCATATTTTCTTTTA
122	-1.482009871	-1	Stayer	TTCCGTGACTCAGAGCTGTTGGTACCTTTCGAGTGCATTGAATGAGATGTAAGTCATCAC
123	-1.240570375	-1	Stayer	TGGCCTCATAATTTTTCAATATGCTCAATCGATAATTTGCTGGAACAGCTCAGAGAACTC
124	1.20374878	1	Sprinter	CACAATGAAAATTTGAAAATATTTTGAGTCGAAAACAAAATATTGGTTTCACCTAAGATA
125	-1.217978043	-1	Stayer	CCGTTCACGGAAGAAGCGCAAGCCCTATTCGATCAGCTCTGGCGCCGTGGGGAGTGGAGC
126	1.328229112	1	Sprinter	ATGAGAGACTCCCATTAAAAATCGTGTCTCGATGATTTACAGGAAGGCATCAACTAAAAA
127	1.210311644	1	Sprinter	ATGAGAGACTCCCATTAAAAATCGTGTCTCGATGCAGAGCAGTGAATAATATGTGTGCAG
128	1.298388503	1	Sprinter	ATGAGAGACTCCCATTAAAAATCGTGTCTCGACACCAAGAACTGAACATCTATACTCTTC

Table 33.b4

N	Probe Location					4 kb Sequence Location			
	Chr	Start1	End1	Start2	End2	Chr	Start1	End1	Start2
65	8	85390137	85390168	85431393	85431424	8	85390137	85394138	85431393
66	22	34961425	34961456	35009442	35009473	22	34957455	34961456	35005472
67	12	20785118	20785149	20922776	20922807	12	20785118	20789119	20918806
68	12	20843696	20843727	20922776	20922807	12	20843696	20847697	20918806
69	3	18959778	18959809	19074282	19074313	3	18955808	18959809	19070312
70	28	42579274	42579305	42607249	42607280	28	42579274	42583275	42607249
71	16	15151267	15151298	15203309	15203340	16	15147297	15151298	15199339
72	16	15151267	15151298	15264001	15264032	16	15147297	15151298	15260031
73	16	15151267	15151298	15255076	15255107	16	15147297	15151298	15255076
74	16	15151267	15151298	15301390	15301421	16	15147297	15151298	15301390
75	16	15151267	15151298	15332649	15332680	16	15147297	15151298	15328679
76	16	15165960	15165991	15239150	15239181	16	15165960	15169961	15235180
77	7	69179023	69179054	69225505	69225536	7	69179023	69183024	69221535
78	7	69225505	69225536	69328532	69328563	7	69221535	69225536	69328532
79	15	8888678	8888709	8973363	8973394	15	8884708	8888709	8973363
80	15	8888678	8888709	9032720	9032751	15	8884708	8888709	9028750
81	15	8936185	8936216	8973363	8973394	15	8936185	8940186	8973363
82	25	5777848	5777879	5838527	5838558	25	5777848	5781849	5838527
83	26	40666594	40666625	40680588	40680619	26	40666594	40670595	40680588
84	6	15299757	15299788	15377978	15378009	6	15299757	15303758	15374008
85	6	15443464	15443495	15487479	15487510	6	15439494	15443495	15487479
86	13	38904201	38904232	39195563	39195594	13	38904201	38908202	39191593
87	13	38931046	38931077	39195563	39195594	13	38931046	38935047	39191593
88	13	38974958	38974989	39195563	39195594	13	38974958	38978959	39191593
89	13	38981963	38981994	39195563	39195594	13	38981963	38985964	39191593
90	13	38999154	38999185	39195563	39195594	13	38999154	39003155	39191593
91	13	39073684	39073715	39195563	39195594	13	39073684	39077685	39191593
92	13	39112330	39112361	39195563	39195594	13	39112330	39116331	39191593
93	5	37768331	37768362	37808997	37809028	5	37768331	37772332	37805027
94	5	37768331	37768362	37803790	37803821	5	37768331	37772332	37803790
95	5	37768331	37768362	37834953	37834984	5	37768331	37772332	37834953
96	18	78530158	78530189	78600391	78600422	18	78526188	78530189	78600391
97	6	75012399	75012430	75092742	75092773	6	75012399	75016400	75092742
98	6	75012399	75012430	75098342	75098373	6	75012399	75016400	75098342
99	17	27888277	27888308	27983597	27983628	17	27888277	27892278	27983597
100	17	27888277	27888308	28023161	28023192	17	27888277	27892278	28023161
101	17	27888277	27888308	28087062	28087093	17	27888277	27892278	28087062
102	17	27991669	27991700	28044612	28044643	17	27987699	27991700	28040642
103	17	35244506	35244537	35523297	35523328	17	35244506	35248507	35523297
104	17	35555855	35555886	35584820	35584851	17	35551885	35555886	35584820
105	24	42597681	42597712	42656523	42656554	24	42593711	42597712	42652553
106	22	41633839	41633870	41882778	41882809	22	41633839	41637840	41878808
107	22	41845220	41845251	41882778	41882809	22	41845220	41849221	41878808
108	7	37223720	37223751	37244778	37244809	7	37223720	37227721	37244778
109	26	23335158	23335189	23360793	23360824	26	23335158	23339159	23360793
110	5	48256162	48256193	48407852	48407883	5	48252192	48256193	48407852
111	5	48248931	48248962	48407852	48407883	5	48248931	48252932	48407852
112	5	48265153	48265184	48407852	48407883	5	48261183	48265184	48407852
113	5	48306348	48306379	48407852	48407883	5	48302378	48306379	48407852
114	5	48370294	48370325	48407852	48407883	5	48370294	48374295	48407852
115	17	62037937	62037968	62292109	62292140	17	62033967	62037968	62292109
116	17	62167794	62167825	62292109	62292140	17	62163824	62167825	62292109
117	1	13016139	13016170	13161461	13161492	1	13012169	13016170	13161461
118	1	13016139	13016170	13213575	13213606	1	13012169	13016170	13209605
119	1	13139944	13139975	13213575	13213606	1	13135974	13139975	13209605

120	19	38827199	38827230	39055705	39055736	19	38827199	38831200	39055705
121	14	35404443	35404474	35458546	35458577	14	35404443	35408444	35458546
122	11	19330735	19330766	19434549	19434580	11	19330735	19334736	19434549
123	11	19378980	19379011	19494959	19494990	11	19375010	19379011	19490989
124	4	51008167	51008198	51111188	51111219	4	51008167	51012168	51107218
125	6	70794688	70794719	70820645	70820676	6	70794688	70798689	70816675
126	25	17093899	17093930	17175445	17175476	25	17089929	17093930	17171475
127	25	17093899	17093930	17167460	17167491	25	17089929	17093930	17167460
128	25	17093899	17093930	17209847	17209878	25	17089929	17093930	17205877

Table 33.b5

N	**4 kb Sequence Location**		
	End2	Probe	Primer ID-1
65	85435394	CD226_8_85390137_85395670_85431393_85435046_RR	OBD RD043.257
66	35009473	CD40_22_34955976_34961456_35003447_35009473_FF	OBD RD043.261
67	20922807	CD5_12_20785118_20787274_20916990_20922807_RF	OBD RD043.265
68	20922807	CD5_12_20843696_20847942_20916990_20922807_RF	OBD RD043.269
69	19074313	CDH1_3_18955128_18959809_19065895_19074313_FF	OBD RD043.273
70	42611250	CERK_28_42579274_42585201_42607249_42612447_RR	OBD RD043.277
71	15203340	CHL1_16_15145284_15151298_15196227_15203340_FF	OBD RD043.281
72	15264032	CHL1_16_15145284_15151298_15255076_15264032_FF	OBD RD043.285
73	15259077	CHL1_16_15145284_15151298_15255076_15264032_FR	OBD RD043.289
74	15305391	CHL1_16_15145284_15151298_15301390_15310795_FR	OBD RD043.293
75	15332680	CHL1_16_15145284_15151298_15326701_15332680_FF	OBD RD043.297
76	15239181	CHL1_16_15165960_15173124_15233430_15239181_RF	OBD RD043.301
77	69225536	CHRDL2_7_69179023_69184961_69220436_69225536_RF	OBD RD043.305
78	69332533	CHRDL2_7_69220436_69225536_69328532_69336827_FR	OBD RD043.309
79	8977364	CHST10_15_8874159_8888709_8973363_8982576_FR	OBD RD043.313
80	9032751	CHST10_15_8874159_8888709_9029805_9032751_FF	OBD RD043.317
81	8977364	CHST10_15_8936185_8939355_8973363_8982576_RR	OBD RD043.321
82	5842528	COL15A1_25_5777848_5781338_5838527_5844153_RR	OBD RD043.325
83	40684589	COL18A1_26_40666594_40668538_40680588_40685271_RR	OBD RD043.329
84	15378009	COL4A4_6_15299757_15310450_15375645_15378009_RF	OBD RD043.333
85	15491480	COL4A4_6_15436171_15443495_15487479_15493934_FR	OBD RD043.337
86	39195594	CREBBP_13_38904201_38905631_39179236_39195594_RF	OBD RD043.341
87	39195594	CREBBP_13_38931046_38933583_39179236_39195594_RF	OBD RD043.345
88	39195594	CREBBP_13_38974958_38977634_39179236_39195594_RF	OBD RD043.349
89	39195594	CREBBP_13_38981963_38985123_39179236_39195594_RF	OBD RD043.353
90	39195594	CREBBP_13_38999154_39003472_39179236_39195594_RF	OBD RD043.357
91	39195594	CREBBP_13_39073684_39080240_39179236_39195594_RF	OBD RD043.361
92	39195594	CREBBP_13_39112330_39113797_39179236_39195594_RF	OBD RD043.365
93	37809028	CRP_5_37768331_37775673_37803790_37809028_RF	OBD RD043.369
94	37807791	CRP_5_37768331_37775673_37803790_37809028_RR	OBD RD043.373
95	37838954	CRP_5_37768331_37775673_37834953_37842330_RR	OBD RD043.377
96	78604392	CTLA4_18_78522827_78530189_78600391_78604267_FR	OBD RD043.381
97	75096743	DDIT3_6_75012399_75018811_75092742_75096887_RR	OBD RD043.385
98	75102343	DDIT3_6_75012399_75018811_75098342_75106967_RR	OBD RD043.389
99	27987598	DGKH_17_27888277_27893919_27983597_27991700_RR	OBD RD043.393
100	28027162	DGKH_17_27888277_27893919_28023161_28030553_RR	OBD RD043.397
101	28091063	DGKH_17_27888277_27893919_28087062_28095320_RR	OBD RD043.401
102	28044643	DGKH_17_27983597_27991700_28038960_28044643_FF	OBD RD043.405
103	35527298	DIAPH3_17_35244506_35247777_35523297_35543766_RR	OBD RD043.409
104	35588821	DIAPH3_17_35550338_35555886_35584820_35594304_FR	OBD RD043.413
105	42656554	DLK1_24_42596087_42597712_42651466_42656554_FF	OBD RD043.417

106	41882809	DOK5_22_41633839_41639527_41876029_41882809_RF	OBD RD043.421
107	41882809	DOK5_22_41845220_41849884_41876029_41882809_RF	OBD RD043.425
108	37248779	ETS1_7_37223720_37228234_37244778_37252642_RR	OBD RD043.429
109	23364794	GABPA_26_23335158_23338855_23360793_23370765_RR	OBD RD043.433
110	48411853	GJA5_5_48248931_48256193_48407852_48413621_FR	OBD RD043.437
111	48411853	GJA5_5_48248931_48256193_48407852_48413621_RR	OBD RD043.441
112	48411853	GJA5_5_48256193_48265184_48407852_48413621_FR	OBD RD043.445
113	48411853	GJA5_5_48297725_48306379_48407852_48413621_FR	OBD RD043.449
114	48411853	GJA5_5_48370294_48376643_48407852_48413621_RR	OBD RD043.453
115	62296110	GPC5_17_62030628_62037968_62292109_62298602_FR	OBD RD043.457
116	62296110	GPC5_17_62161244_62167825_62292109_62298602_FR	OBD RD043.461
117	13165462	GRK5_1_13009800_13016170_13161461_13167914_FR	OBD RD043.465
118	13213606	GRK5_1_13009800_13016170_13204085_13213606_FF	OBD RD043.469
119	13213606	GRK5_1_13135627_13139975_13204085_13213606_FF	OBD RD043.473
120	39059706	GSK3B_19_38827199_38835574_39055705_39060019_RR	OBD RD043.477
121	35462547	HDAC3_14_35404443_35406152_35458546_35471150_RR	OBD RD043.481
122	19438550	HDAC5_11_19330735_19336727_19434549_19441692_RR	OBD RD043.485
123	19494990	HDAC5_11_19372111_19379011_19491838_19494990_FF	OBD RD043.489
124	51111219	HDAC9_4_51008167_51021720_51107519_51111219_RF	OBD RD043.493
125	70820676	HOXC6_6_70794688_70801196_70818032_70820676_RF	OBD RD043.497
126	17175476	HSDL2_25_17089584_17093930_17167460_17175476_FF	OBD RD043.501
127	17171461	HSDL2_25_17089584_17093930_17167460_17175476_FR	OBD RD043.505
128	17209878	HSDL2_25_17089584_17093930_17197980_17209878_FF	OBD RD043.509

Table 33.b6

N	Primer Sequence	Primer ID-2	Primer Sequence
65	GTCAATGGAAGGAGGGAAATAATA	OBD RD043.259	TCTCAACAGAGGAGTAAGATGTAT
66	CCTCGGACCTCTCTCGCTGATAC	OBD RD043.263	GCCGTCAGTATTGTTTGGCTGGC
67	AGAACTGCTGGCAAGGGAGACAG	OBD RD043.267	ACACAGAGAGAGCCCCTCAGAGC
68	AACTGCTGGCAAGGGAGACAGGG	OBD RD043.271	GACAAGGGAAGGACCGAAAAGCC
69	AGCCTGAAGTGGGAACCAACCCC	OBD RD043.275	GACAAGGTGGAAAGGTAGGCACG
70	ACTGTAAACCTGGGAACAACACCA	OBD RD043.279	AATAAGTCCTCGGGATGTAATGTA
71	GGATGACCCTAACATTTCAGCAAACA	OBD RD043.283	CCTACAATCACCACAGGACCTCTCCA
72	CTTTGCTCTTAGACCCTCCTTCCACA	OBD RD043.287	GGATAGGAACAAAGCAAGAATGATGT
73	CTTTGCTCTTAGACCCTCCTTCCACA	OBD RD043.291	GAAGATAGTGGAATGCTTTTGGTGAC
74	TGACCCTAACATTTCAGCAAACATTG	OBD RD043.295	CACTAACAGAGCATTTTCTTCAAGGA
75	TGAAGGCAGGCTTTGTTCTATTTT	OBD RD043.299	TGAAGAATAAAACCCAGACCAAAA
76	TTTGCTCTTAGACCCTCCTTCCACAT	OBD RD043.303	GCCGACCTTCTGAGATACTAACGGTG
77	CTGTAGGTTCAACTTCTTATCAGTGC	OBD RD043.307	CAGTTGTTAGCCCAGGTGCCAAT
78	CCCCTGTAGGTTCAACTTCTTATCAG	OBD RD043.311	CCGTTTCCTACCAGTGTGACTACCAG
79	GTGAGCACAGAGTGAGAGAATCATCT	OBD RD043.315	GCAGTCCCTATGAGAAACCCAGC
80	GTGAGCACAGAGTGAGAGAATCATCT	OBD RD043.319	CAAATCTGGTGATAAATCCGCATCCA
81	AGGGAGGCTCACGCTGGCAGTAA	OBD RD043.323	GCAGTCCCTATGAGAAACCCAGC
82	GTCAGCAACCATCATTATTTCCTA	OBD RD043.327	TGTTACTCCGATACTGCTTTCTTA
83	GACTCCGCTGGCTCATCTCCTTC	OBD RD043.331	GGACTTGCCCTCGGTGTTTTGTG
84	GGCATACTGTCGTGTCTCAGGAG	OBD RD043.335	CCTCCTCTCCCTTCTGCCATCAG
85	CACTCGTGGCATTGAAACCAAAGTCT	OBD RD043.339	AGTCTGTCTTCACTAACGATGGC
86	CTGACCTGCTCCCCAGTGAAACT	OBD RD043.343	TCCCTTTTCCTGCCTCCCTCCCC
87	CTGACCTGCTCCCCAGTGAAACT	OBD RD043.347	GACAGTGGTCTCCTTCTTACCTG
88	CTGACCTGCTCCCCAGTGAAACT	OBD RD043.351	CAGGGACAATCACTTCTAAACACTAA
89	CTGACCTGCTCCCCAGTGAAACT	OBD RD043.355	GTTTTGTTGACTTCTCACCAGCAAGA
90	CTGACCTGCTCCCCAGTGAAACT	OBD RD043.359	ATCCACACAGAAGTTAGGGCTGC
91	ATGCTGACCTGCTCCCCAGTGAA	OBD RD043.363	AGGAAGAGCAGCACCAGGCACCT
92	CTGACCTGCTCCCCAGTGAAACT	OBD RD043.367	CCACATTTCTCACTTCAGGTAAGC
93	GGAGAAAGCAACCAATGAACGGAAGA	OBD RD043.371	GATTTCCCTCTGTCCTGCCTCAATGC

94	TTCCCTCTGTCCTGCCTCAATGC	OBD RD043.375	CAAGCGGAGAGAGACGACACTGC
95	GTGCGGTCACAAGAATCTCTAATACG	OBD RD043.379	CTTTCCGCACCCTCTGAACTTTTGGG
96	GTGAAATAAGCCAGATAGAGAAAGAC	OBD RD043.383	GAGCGAAAGAACGGATGAAGCATTTT
97	TAGAGAGCCCAGAAATAAATCCAT	OBD RD043.387	CAGGACCATCAAGATAAATGAATA
98	GAATAGAGAGCCCAGAAATAAATCCA	OBD RD043.391	TGGAGGAAGGGAGCCAGGACCCC
99	GCGACACCTCCTCTGTTGCCAAG	OBD RD043.395	GCACCACTGGCAGAGTTTACGGT
100	TACAGAGAACAGATTGGTGGTCAC	OBD RD043.399	CTGGAGAAAAGGAGTATGGAGAAT
101	TACAGAGAACAGATTGGTGGTCAC	OBD RD043.403	AAGGCTTTTATGTGAACAGAGATA
102	TACAGAGAACAGATTGGTGGTCAC	OBD RD043.407	GAAATAAAGTCAATCTTCCTGAAAA
103	CACTGCCACAAAAGCCGCTCTGG	OBD RD043.411	CACTGACTACACGGAAGATGGCG
104	GAAAGATGCCCAGTCTGTGTCGGAGA	OBD RD043.415	TTTTGACCAGCAGATAGTGTCGTGTC
105	TGGAGTAAGACGCCGAAAACACT	OBD RD043.419	GGGCACTCTGGATTGAGACAGTA
106	AGGAGTCCCTGCCCTCGGAATCT	OBD RD043.423	GCTTCCCAGAACCCAAATCTCCC
107	AGGAGTCCCTGCCCTCGGAATCT	OBD RD043.427	CTTCCGATGGACGAATCTCAGGC
108	GCAGGGAGTCAGTCATTTTGTTTCTC	OBD RD043.431	CCCTCCAATGAAAGTAGTCTGCCTGC
109	TTATCTTCTTTACCTACATTCCAGGG	OBD RD043.435	TGGGCACAAAGGGTGAAGTGGTG
110	ACTTACAAACCCAATCACTACATA	OBD RD043.439	GGAAGACCAGAGAACAGAACTGAT
111	AATCTATTCCCACTCACCTCTGG	OBD RD043.443	GGAAGACCAGAGAACAGAACTGAT
112	GAATAGGTCCTTTTGTTTTGTTTT	OBD RD043.447	GGAAGACCAGAGAACAGAACTGAT
113	ACGGAAGCAGAATGGAGAGTGGG	OBD RD043.451	GGAAGACCAGAGAACAGAACTGAT
114	CCCAAGTGCTGCTTCTATTTCCT	OBD RD043.455	GGAAGACCAGAGAACAGAACTGAT
115	TCCCAGATTCTACCCTTGACCCTCAT	OBD RD043.459	GACCTCAACAGAAAGTCCTCAACAGG
116	GGATGAGTTCTAAATGAATAATGA	OBD RD043.463	CCTCAACAGAAAGTCCTCAACAGG
117	ATTGAGTGGCTGGCGGTCACGGT	OBD RD043.467	GGTCCTGCTCTATCTTTCCCCTC
118	TTATTGAGTGGCTGGCGGTCACG	OBD RD043.471	AGGGCTTCAGCAGGCAGAGGGAT
119	GGTGGCAAAAGCCCCAAGAGAATGAG	OBD RD043.475	GGTAACTTGAAATAAGCCACAGAGGG
120	GGCAAAGGACTTGAAAAGACATTT	OBD RD043.479	TTGAAGTTTACCAGGAGAGGAAAA
121	GAGGATTGGCAGCAGATGTTAGC	OBD RD043.483	GGAGATGAAAGACAATGGATGAGATA
122	CCCTACCAGGCTCAGATGGGATT	OBD RD043.487	CCTGCCTCCCCTCACAACACACA
123	CCCAGGACCCAGGTTTTCTTACC	OBD RD043.491	CTCGCCCTGTGTAGCACCTCTCT
124	TGTGCCCATCTTCCTCTACTTTAT	OBD RD043.495	TCCAACATTGCTTTACTCTTATGA
125	CCCTACTGGTTCATCTCCACCCA	OBD RD043.499	GCCGCTTCCACCCAGGACAGTAA
126	CCCCTCTCCAGCAGTTTTGAGTAATA	OBD RD043.503	CTGACACTGAGCACAGGGTTTGGAAG
127	GCCCCTCTCCAGCAGTTTTGAGTAAT	OBD RD043.507	GAGAGAAGCCACCAAGATAAGTCCAC
128	CCCTCTCCAGCAGTTTTGAGTAA	OBD RD043.511	CTTTGTTTACCTGGCATCTTGAGTCA

Table 33.b7

N	Probe	Marker
65	CD226	OBD RD043.257.259
66	CD40	OBD RD043.261.263
67	CD5	OBD RD043.265.267
68	CD5	OBD RD043.269.271
69	CDH1	OBD RD043.273.275
70	CERK	OBD RD043.277.279
71	CHL1	OBD RD043.281.283
72	CHL1	OBD RD043.285.287
73	CHL1	OBD RD043.289.291
74	CHL1	OBD RD043.293.295
75	CHL1	OBD RD043.297.299
76	CHL1	OBD RD043.301.303
77	CHRDL2	OBD RD043.305.307
78	CHRDL2	OBD RD043.309.311
79	CHST10	OBD RD043.313.315
80	CHST10	OBD RD043.317.319
81	CHST10	OBD RD043.321.323

82	COL15A1	OBD RD043.325.327
83	COL18A1	OBD RD043.329.331
84	COL4A4	OBD RD043.333.335
85	COL4A4	OBD RD043.337.339
86	CREBBP	OBD RD043.341.343
87	CREBBP	OBD RD043.345.347
88	CREBBP	OBD RD043.349.351
89	CREBBP	OBD RD043.353.355
90	CREBBP	OBD RD043.357.359
91	CREBBP	OBD RD043.361.363
92	CREBBP	OBD RD043.365.367
93	CRP	OBD RD043.369.371
94	CRP	OBD RD043.373.375
95	CRP	OBD RD043.377.379
96	CTLA4	OBD RD043.381.383
97	DDIT3	OBD RD043.385.387
98	DDIT3	OBD RD043.389.391
99	DGKH	OBD RD043.393.395
100	DGKH	OBD RD043.397.399
101	DGKH	OBD RD043.401.403
102	DGKH	OBD RD043.405.407
103	DIAPH3	OBD RD043.409.411
104	DIAPH3	OBD RD043.413.415
105	DLK1	OBD RD043.417.419
106	DOK5	OBD RD043.421.423
107	DOK5	OBD RD043.425.427
108	ETS1	OBD RD043.429.431
109	GABPA	OBD RD043.433.435
110	GJA5	OBD RD043.437.439
111	GJA5	OBD RD043.441.443
112	GJA5	OBD RD043.445.447
113	GJA5	OBD RD043.449.451
114	GJA5	OBD RD043.453.455
115	GPC5	OBD RD043.457.459
116	GPC5	OBD RD043.461.463
117	GRK5	OBD RD043.465.467
118	GRK5	OBD RD043.469.471
119	GRK5	OBD RD043.473.475
120	GSK3B	OBD RD043.477.479
121	HDAC3	OBD RD043.481.483
122	HDAC5	OBD RD043.485.487
123	HDAC5	OBD RD043.489.491
124	HDAC9	OBD RD043.493.495
125	HOXC6	OBD RD043.497.499
126	HSDL2	OBD RD043.501.503
127	HSDL2	OBD RD043.505.507
128	HSDL2	OBD RD043.509.511

Table 33.b8

N	Probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig
129	IGF1_28_26127450_26135782_26165074_26175137_FF	IGF1	1	83
130	IL17F_20_49908438_49915179_49992351_49998114_RR	IL17F	1	23
131	IL1R1_15_7480700_7491275_7547275_7554471_FR	IL1R1	1	34
132	IL1RAP_19_27981648_27987302_28153765_28161424_FR	IL1RAP	3	212

133	IL1RAP_19_28069654_28081538_28153765_28161424_FR	IL1RAP	3	212
134	IL1RAP_19_28153765_28161424_28173183_28182762_RR	IL1RAP	3	212
135	IL21R_13_20649899_20654880_20738447_20749797_FF	IL21R	1	43
136	IL6ST_21_16316515_16320787_16507936_16519953_RF	IL6ST	5	74
137	IL6ST_21_16361905_16367133_16507936_16519953_RF	IL6ST	5	74
138	IL6ST_21_16380568_16382969_16507936_16519953_FF	IL6ST	5	74
139	IL6ST_21_16389402_16396020_16507936_16519953_RF	IL6ST	5	74
140	IL6ST_21_16427757_16430421_16507936_16519953_FF	IL6ST	5	74
141	IPMK_1_47907514_47915619_47934069_47940539_RF	IPMK	1	49
142	KCND3_5_56337143_56347199_56370847_56374140_RF	KCND3	2	315
143	KCND3_5_56337143_56347199_56514669_56519275_RF	KCND3	2	315
144	KCNE2_26_30910971_30912196_30981829_30991799_FF	KCNE2	2	53
145	KCNE2_26_30910971_30912196_30981829_30991799_FR	KCNE2	2	53
146	KCNH2_4_102471847_102478321_102526070_102533652_RF	KCNH2	1	31
147	KCNJ2_11_10875120_10880378_10941535_10945829_RF	KCNJ2	2	24
148	KCNJ2_11_10907501_10914338_10941535_10945829_RF	KCNJ2	2	24
149	KDM1A_2_31709535_31721093_31731426_31738065_RR	KDM1A	8	105
150	KDM1A_2_31709535_31721093_31749361_31751529_RR	KDM1A	8	105
151	KDM1A_2_31709535_31721093_31757482_31759922_RR	KDM1A	8	105
152	KDM1A_2_31709535_31721093_31759922_31772142_RR	KDM1A	8	105
153	KDM1A_2_31709535_31721093_31779719_31783168_RR	KDM1A	8	105
154	KDM1A_2_31709535_31721093_31795486_31798526_RR	KDM1A	8	105
155	KDM1A_2_31709535_31721093_31816722_31820715_RR	KDM1A	8	105
156	KDM1A_2_31709535_31721093_31841824_31843977_RR	KDM1A	8	105
157	LAMA2_10_75419882_75421720_75481925_75491582_FF	LAMA2	33	325
158	LAMA2_10_75419882_75421720_75481925_75491582_FR	LAMA2	33	325
159	LAMA2_10_75419882_75421720_75481925_75491582_RR	LAMA2	33	325
160	LAMA2_10_75433825_75441819_75481925_75491582_RR	LAMA2	33	325
161	LAMA2_10_75481925_75491582_75503397_75505438_RF	LAMA2	33	325
162	LAMA2_10_75481925_75491582_75503397_75505438_RR	LAMA2	33	325
163	LAMA2_10_75481925_75491582_75510267_75513025_RR	LAMA2	33	325
164	LAMA2_10_75481925_75491582_75515462_75518504_RF	LAMA2	33	325
165	LAMA2_10_75481925_75491582_75515462_75518504_RR	LAMA2	33	325
166	LAMA2_10_75481925_75491582_75537867_75543336_RR	LAMA2	33	325
167	LAMA2_10_75481925_75491582_75558780_75560310_RR	LAMA2	33	325
168	LAMA2_10_75481925_75491582_75583879_75585705_RF	LAMA2	33	325
169	LAMA2_10_75481925_75491582_75583879_75585705_RR	LAMA2	33	325
170	LAMA2_10_75481925_75491582_75598703_75603065_RR	LAMA2	33	325
171	LAMA2_10_75481925_75491582_75630159_75632019_RR	LAMA2	33	325
172	LAMA2_10_75481925_75491582_75657275_75659989_RF	LAMA2	33	325
173	LAMA2_10_75481925_75491582_75657275_75659989_RR	LAMA2	33	325
174	LAMA2_10_75481925_75491582_75673465_75680786_RF	LAMA2	33	325
175	LAMA2_10_75481925_75491582_75673465_75680786_RR	LAMA2	33	325
176	LAMA2_10_75481925_75491582_75689296_75698651_RF	LAMA2	33	325
177	LAMA2_10_75481925_75491582_75689296_75698651_RR	LAMA2	33	325
178	LAMA2_10_75481925_75491582_75699217_75700676_RR	LAMA2	33	325
179	LAMA2_10_75481925_75491582_75710114_75711790_RF	LAMA2	33	325
180	LAMA2_10_75481925_75491582_75710114_75711790_RR	LAMA2	33	325
181	LAMA2_10_75481925_75491582_75727142_75730779_RR	LAMA2	33	325
182	LAMA2_10_75481925_75491582_75731193_75737098_RF	LAMA2	33	325
183	LAMA2_10_75481925_75491582_75731193_75737098_RR	LAMA2	33	325
184	LAMA2_10_75481925_75491582_75761081_75765848_RR	LAMA2	33	325
185	LAMA2_10_75481925_75491582_75767487_75769615_RF	LAMA2	33	325
186	LAMA2_10_75481925_75491582_75772669_75776905_RR	LAMA2	33	325
187	LAMA2_10_75481925_75491582_75789669_75791964_RF	LAMA2	33	325
188	LAMA2_10_75985731_76002512_76077151_76079817_FF	LAMA2	33	325
189	LAMA2_10_75985731_76002512_76077151_76079817_RF	LAMA2	33	325

190	LDB2_3_106480842_106484500_106716847_106728445_RR	LDB2	2	196
191	LDB2_3_106716847_106728445_106944178_106947885_RF	LDB2	2	196
192	LEPR_5_95193431_95200537_95211956_95218723_RR	LEPR	1	31

Table 33.c1

N	HyperG_Stats	FDR_HyperG
129	0.346998557	0.36994061
130	0.157480479	0.267074007
131	0.212678487	0.282840462
132	0.154850013	0.267074007
133	0.154850013	0.267074007
134	0.154850013	0.267074007
135	0.249797286	0.310300562
136	0.00033129	0.004748485
137	0.00033129	0.004748485
138	0.00033129	0.004748485
139	0.00033129	0.004748485
140	0.00033129	0.004748485
141	0.270953196	0.310300562
142	0.253289491	0.310300562
143	0.253289491	0.310300562
144	0.060873696	0.137915817
145	0.060873696	0.137915817
146	0.198752749	0.267074007
147	0.015462469	0.066488616
148	0.015462469	0.066488616
149	0.00000240079898941557	0.000103234
150	0.00000240079898941557	0.000103234
151	0.00000240079898941557	0.000103234
152	0.00000240079898941557	0.000103234
153	0.00000240079898941557	0.000103234
154	0.00000240079898941557	0.000103234
155	0.00000240079898941557	0.000103234
156	0.00000240079898941557	0.000103234
157	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
158	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
159	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
160	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
161	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
162	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
163	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
164	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
165	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
166	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
167	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
168	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
169	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
170	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
171	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
172	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
173	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
174	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
175	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
176	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
177	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766

178	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
179	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
180	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
181	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
182	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
183	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
184	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
185	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
186	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
187	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
188	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
189	0.00000000000000000000000000509616413350981	0.00000000000000000000000657405173222766
190	0.260903936	0.310300562
191	0.260903936	0.310300562
192	0.198752749	0.267074007

Table 33.c2

N	Percent_Sig	logFC	AveExpr	t	P.Value
129	1.2	-0.25974584	9.184771261	-5.05789465	0.0000686965968072954
130	4.35	-0.42286988	9.795885578	-8.986284737	0.0000002723162782424 42
131	2.94	-0.285238748	8.475210157	-5.003309015	0.0000776210585910804
132	1.42	-0.233297428	7.917147257	-5.063868868	0.0000677854972204880
133	1.42	-0.261678217	7.906642716	-7.35841864	0.00000054711323892 9680
134	1.42	-0.247346127	10.12235567	-6.078434637	0.0000074179191342 3433
135	2.33	-0.504771054	9.843131031	-10.25775021	0.00000000328750499948560
136	6.76	-0.416415403	12.34496702	-5.613648976	0.0000201456451707163
137	6.76	-0.426151333	12.51889676	-5.249917488	0.0000448018862245979
138	6.76	-0.23353917	12.44377995	-5.538440914	0.0000237375958014509
139	6.76	-0.411700512	12.62002559	-5.185430873	0.0000516971247274845
140	6.76	-0.223557802	11.04467508	-5.194995118	0.0000506097781533960
141	2.04	0.248972748	9.763034476	5.472372277	0.0000274322269039290
142	0.63	-0.826874049	9.755934263	-11.64073761	0.000000000403131843228993
143	0.63	-0.188752779	9.124965652	-5.134174071	0.0000579439468653047
144	3.77	-0.263863415	9.389840285	-5.665269959	0.0000180067783076360
145	3.77	-0.277105906	9.211949107	-5.081146529	0.0000652192037780800
146	3.23	-0.350022028	11.18568763	-6.168156484	0.0000061356358258 4375
147	8.33	0.694351653	8.391007916	7.96791572	0.00000017082088732 2144
148	8.33	0.461719332	8.783986871	6.236727656	0.0000053109052063 2885
149	7.62	-0.734667206	8.882775953	-7.565318365	0.00000036647308028 7362
150	7.62	-0.260872283	10.51288503	-6.881875363	0.0000014075985374 2685
151	7.62	-0.302726916	10.11606951	-5.433872607	0.0000298515328569823
152	7.62	-0.53472543	9.308125792	-11.46362698	0.000000000521792977583466
153	7.62	-0.364206415	9.729541969	-6.308264284	0.0000045713811591 6845
154	7.62	-0.460314357	9.475119298	-7.40716807	0.00000049756011421 3970
155	7.62	-0.621721431	8.876491488	-7.539008509	0.00000038550837245 9963
156	7.62	-0.47363865	9.446359898	-7.234458458	0.00000069750810471 2342
157	10.15	-0.501711845	10.09895493	-8.589317091	0.000000054837363418 2702
158	10.15	-0.428220161	13.02189528	-7.167747421	0.00000079558037915 8680
159	10.15	-0.339941253	12.88803216	-5.561186413	0.0000225869301073419
160	10.15	-0.228417033	13.56928534	-5.920840322	0.0000103781975494252
161	10.15	-0.30207162	13.37620496	-5.439499489	0.0000294847593610427
162	10.15	-0.39204058	13.89495223	-5.801140554	0.0000134209610425670
163	10.15	-0.343069197	13.96715152	-6.417777669	0.0000036384497513 0824
164	10.15	-0.354475767	13.22017743	-5.259160113	0.0000438935269293937
165	10.15	-0.446958091	13.8037429	-5.840868856	0.0000123208089585518

166	10.15	-0.379960986	13.89492979	-6.236715524	0.00000531104056573792
167	10.15	-0.449915255	13.94340659	-9.137780656	0.0000000209555895296964
168	10.15	-0.356701022	12.87002792	-5.553163982	0.0000229861111463834
169	10.15	-0.428629599	13.82169896	-6.617643858	0.00000240861706096913
170	10.15	-0.419629634	13.93664391	-8.158999079	0.000000119804038144258
171	10.15	-0.430573855	13.96364886	-8.446068963	0.0000000709422502038841
172	10.15	-0.256004051	13.24896441	-5.56584902	0.0000223581954829190
173	10.15	-0.41467922	14.1640228	-7.07939174	0.000000947891998878803
174	10.15	-0.331716046	12.41203838	-4.98917938	0.0000801177911327344
175	10.15	-0.393636052	13.86311599	-5.696573254	0.0000168245001760445
176	10.15	-0.33697792	12.45047432	-5.039670375	0.0000715536819400699
177	10.15	-0.43042349	13.94505376	-5.895952776	0.0000109465097531085
178	10.15	-0.417317056	13.83868121	-7.743329932	0.000000260799615293896
179	10.15	-0.349687395	12.88984807	-6.592764316	0.0000025347952808473 8
180	10.15	-0.401014761	13.96210217	-5.511317857	0.0000251885049881526
181	10.15	-0.376700577	13.82296798	-7.462445086	0.000000446952562820082
182	10.15	-0.361735429	12.82385418	-5.647753484	0.0000187051686375902
183	10.15	-0.384425532	13.87283328	-5.612599396	0.0000201917366403219
184	10.15	-0.481052786	13.9255892	-9.4062159	0.0000000132641985345548
185	10.15	-0.302151184	13.18318606	-5.156392006	0.0000551467689003870
186	10.15	-0.362843331	14.28924283	-6.234521481	0.0000053355776639 2404
187	10.15	-0.346934118	12.83387771	-5.572053104	0.0000220575120754949
188	10.15	-0.387765562	8.971457443	-8.562458613	0.0000000575383157451633
189	10.15	-0.346223991	10.11461327	-6.659629102	0.0000022101799336599 2
190	1.02	-0.479413897	9.999705501	-7.255881323	0.0000006687396099394 00
191	1.02	-0.24620165	9.243513309	-5.088361737	0.0000641770071013719
192	3.23	0.414997972	6.542688969	7.586596983	0.0000035179153901882 6

Table 33.c3

N	adj.P.Val	B	FC	FC_1	LS	Loop Detected
129	0.00881531	1.792843727	0.83523505	-1.197267763	-1	Stayer
130	0.000048275438684640	9.106256241	0.745939288	-1.340591675	-1	Stayer
131	0.00961269	1.676496246	0.820605797	-1.218611912	-1	Stayer
132	0.008756001	1.805561135	0.850688333	-1.17551865	-1	Stayer
133	0.00033823	6.355209789	0.834117067	-1.198872484	-1	Stayer
134	0.002009535	3.907359412	0.842444688	-1.18702155	-1	Stayer
135	0.00000854970466866222	10.98597877	0.704772211	-1.418898169	-1	Stayer
136	0.0039679	2.96000383	0.749284025	-1.334607395	-1	Stayer
137	0.006607886	2.199880493	0.744244555	-1.343644361	-1	Stayer
138	0.004367942	2.804099038	0.8505458	-1.17571564	-1	Stayer
139	0.007221168	2.063594435	0.751736775	-1.330252866	-1	Stayer
140	0.007179227	2.083834368	0.856450753	-1.167609458	-1	Stayer
141	0.004693558	2.666578884	1.188360657	1.188360657	1	Sprinter
142	0.00000262102886739384	12.79107546	0.563749421	-1.773837743	-1	Stayer
143	0.007875935	1.954968861	0.877363882	-1.139777943	-1	Stayer
144	0.003741337	3.066609893	0.832854617	-1.200689748	-1	Stayer
145	0.008590182	1.842321715	0.825244826	-1.211761611	-1	Stayer
146	0.001721951	4.086856496	0.784572118	-1.274580088	-1	Stayer
147	0.00016253	7.432545616	1.61815707	1.61815707	1	Sprinter
148	0.001576825	4.223269904	1.377182098	1.377182098	1	Sprinter
149	0.000274925	6.727366085	0.600956635	-1.664013578	-1	Stayer
150	0.000606823	5.472840867	0.834583161	-1.198202944	-1	Stayer
151	0.004995541	2.58620654	0.810718564	-1.233473667	-1	Stayer
152	0.00000265148685080001	12.57279103	0.690290038	-1.448666422	-1	Stayer
153	0.001426637	4.364862947	0.776896105	-1.287173398	-1	Stayer

154	0.00032898	6.443494308	0.726827869	-1.375841575	-1	Stayer
155	0.000283749	6.680410031	0.649895007	-1.538710083	-1	Stayer
156	0.000406116	6.129060869	0.720146011	-1.388607289	-1	Stayer
157	0.000076400198105240	8.472295113	0.706268254	-1.415892608	-1	Stayer
158	0.000449791	6.006370737	0.743178071	-1.345572533	-1	Stayer
159	0.004245102	2.851322566	0.790073483	-1.265705053	-1	Stayer
160	0.002530334	3.5893669	0.853570941	-1.171548787	-1	Stayer
161	0.004957761	2.597963987	0.81108689	-1.23291353	-1	Stayer
162	0.003061706	3.345590015	0.76205098	-1.312248165	-1	Stayer
163	0.001213128	4.580182501	0.788362361	-1.268452237	-1	Stayer
164	0.006535445	2.219378577	0.782153803	-1.27852092	-1	Stayer
165	0.002843993	3.426710531	0.733587982	-1.363163008	-1	Stayer
166	0.001576825	4.223245828	0.768458371	-1.301306665	-1	Stayer
167	0.000038927502264450	9.342123058	0.73208585	-1.365960017	-1	Stayer
168	0.004269944	2.834673761	0.780948316	-1.28049447	-1	Stayer
169	0.000894859	4.968583134	0.742967187	-1.345954461	-1	Stayer
170	0.000119835	7.758516636	0.747616527	-1.337584128	-1	Stayer
171	0.000081395799425103	8.23778519	0.741966597	-1.347769567	-1	Stayer
172	0.004245102	2.860995205	0.837404136	-1.19416654	-1	Stayer
173	0.000513573	5.842814484	0.750186279	-1.333002254	-1	Stayer
174	0.009828286	1.64633615	0.794590778	-1.258509447	-1	Stayer
175	0.00361547	3.131093689	0.761208696	-1.313700179	-1	Stayer
176	0.009092212	1.754029209	0.791697982	-1.26310793	-1	Stayer
177	0.002605462	3.538839183	0.742043933	-1.347629103	-1	Stayer
178	0.0002366	7.042253477	0.748815885	-1.335441756	-1	Stayer
179	0.000932852	4.920559418	0.784754121	-1.274284484	-1	Stayer
180	0.00443021	2.747705761	0.757325409	-1.320436351	-1	Stayer
181	0.000311021	6.543154484	0.770197007	-1.298369106	-1	Stayer
182	0.003840466	3.030472673	0.77822788	-1.284970669	-1	Stayer
183	0.0039679	2.957832836	0.766083985	-1.305339909	-1	Stayer
184	0.000025871819241649	9.751972552	0.716454611	-1.395761832	-1	Stayer
185	0.007628636	2.002085961	0.81104216	-1.232981526	-1	Stayer
186	0.001576825	4.21889148	0.777630478	-1.285957827	-1	Stayer
187	0.004238737	2.873861568	0.786253196	-1.271854925	-1	Stayer
188	0.000077398955076511	8.4285593	0.764312451	-1.308365444	-1	Stayer
189	0.000837079	5.049414099	0.786640303	-1.271229043	-1	Stayer
190	0.000395266	6.168314166	0.717268959	-1.394177159	-1	Stayer
191	0.008515459	1.857664798	0.843113258	-1.18608027	-1	Stayer
192	0.000270685	6.765264284	1.333296803	1.333296803	1	Sprinter

Table 33.c4

N	Probe sequence	Probe Location	
	60 mer	Chr	Start1
129	TTCCTTCATCATTTGTTATTTCCTCTGTTCGAATAGGGCTGAACCAATGGCCATACACAC	28	26135751
130	GAGGCCCATTGCAGGTACTTGGGCTGCATCGATTATCCCACTACACAGGATTTATATAAG	20	49908438
131	CCAGACTGAATTTTGTACAGAGTACACCTCGAAGTAATCTGACTTTAAAATGGTTCTTTT	15	7491244
132	TGGTAAGTGTATTATATAAGAAAAAAACTCGATCCTCTAATCCTGAATACCAGGTTGGGC	19	27987271
133	TTGCATTCATTCTTTTGCAGAAACATACTCGATCCTCTAATCCTGAATACCAGGTTGGGC	19	28081507
134	GCCCAACCTGGTATTCAGGATTAGAGGATCGAGAAGCCAGGCATGAATTCTGGTGTTTGC	19	28153765
135	CTCGTCAGTACTCTCAGTGTTTCCTCATTCGATCACTTTGGACATTTTAACAGCACTAAG	13	20654849
136	TCTTGCCCGAAGGCAGAGAGCTCAGAACTCGAAGTGAGCAGGATTTATTGAATAACAGAA	21	16316515
137	TCTTGCCCGAAGGCAGAGAGCTCAGAACTCGAACACTCTTGTTCTGCTTCCTCATCACTT	21	16361905
138	TTGCTTGGGTTTATGATTTTGTGCGGGGTCGAGTTCTGAGCTCTCTGCCTTCGGGCAAGA	21	16382938
139	TCTTGCCCGAAGGCAGAGAGCTCAGAACTCGAGCTGCTGCAGTCATTTTGTCACCATACA	21	16389402
140	CTGTCTAGTATCTTAAAATTGACATGGATCGAGTTCTGAGCTCTCTGCCTTCGGGCAAGA	21	16430390

141	AGTCTATCCAATTACAGTAATTTAAGCTTCGAGAGCCTGTGGTCTAAGAAAGAGTGAGAG	1	47907514
142	CCTTAGTACCTGCTTAGTACCCGCTTTGTCGAAGCAAAAGCAATTACCACCCCCAGCTTT	5	56337143
143	TAAAAACACATTTACAGTGCCACTGTACTCGAAGCAAAAGCAATTACCACCCCCAGCTTT	5	56337143
144	GACCTCCCTTACAGTACCTGCAGACTTGTCGATGAACTCCCACTCCAGTGGTGAGAAACC	26	30912165
145	GACCTCCCTTACAGTACCTGCAGACTTGTCGAGTTCCCATATGGGCAGTATGTAGGGCAC	26	30912165
146	TAATTCTCTGTAGTGAATCCCTTCCTGATCGAGGGGGCATCACAGAGTCAAAGGCAGCGA	4	102471847
147	GGAATATAATCTAACACCGTGTAACCATTCGACTCCAAATAAACTGAATACAGAAAGTTT	11	10875120
148	GGAATATAATCTAACACCGTGTAACCATTCGAAAATTTTGAAACAATTCCTCTGCCATTT	11	10907501
149	GGTACTAGATGACGTAGTCCGATAAGATTCGATTTCCCCATCTGTAAAATGTTTTCTTTG	2	31709535
150	GGTACTAGATGACGTAGTCCGATAAGATTCGACACAAATCCCCCTGCTACTGTTTAATTC	2	31709535
151	GGTACTAGATGACGTAGTCCGATAAGATTCGAAAAGTTCTGCCAGTCCTCCACTTACAGC	2	31709535
152	GGTACTAGATGACGTAGTCCGATAAGATTCGAAACCCGAAATAAAATTCTTACCCTGGCT	2	31709535
153	GGTACTAGATGACGTAGTCCGATAAGATTCGAGTTCCAATTCCTTAGCCTGGTAACCAAG	2	31709535
154	GGTACTAGATGACGTAGTCCGATAAGATTCGACAACATTCTGGTGTGACTGTGAATGAGC	2	31709535
155	GGTACTAGATGACGTAGTCCGATAAGATTCGACTCTGCAGAGTTCTCACTACTCCGCTTG	2	31709535
156	GGTACTAGATGACGTAGTCCGATAAGATTCGATTGGTTTGGCTGTTCTTGATCCGTTTAC	2	31709535
157	AAACTGCCTCATAGGTTTCTTGTGAGGATCGAAAAAGATGCTTGATATGATTTCACTCTT	10	75421689
158	AAACTGCCTCATAGGTTTCTTGTGAGGATCGATGATGTTAGTGGTTGTAGTGGCTCTTTG	10	75421689
159	GCAATGTGCTATACTGCAGATTCTAAACTCGATGATGTTAGTGGTTGTAGTGGCTCTTTG	10	75419882
160	CTAGAGCTCTGGAGGCCCTGCTGACGGCTCGATGATGTTAGTGGTTGTAGTGGCTCTTTG	10	75433825
161	AAGACTAATTCTGGGCTGTGCCAATTGGTCGATGATGTTAGTGGTTGTAGTGGCTCTTTG	10	75481925
162	CAAAGAGCCACTACAACCACTAACATCATCGAATTTTTGGAAGGCTTGTTATTTGGAAGA	10	75481925
163	CAAAGAGCCACTACAACCACTAACATCATCGAAAAGTTGCAATCATGCTTAATACATAAT	10	75481925
164	CAAGAGAAGACAACATTTATCTGTTATGTCGATGATGTTAGTGGTTGTAGTGGCTCTTTG	10	75481925
165	CAAAGAGCCACTACAACCACTAACATCATCGAGAGAAGCATTTTCCTTTGTTTCTATCTC	10	75481925
166	CAAAGAGCCACTACAACCACTAACATCATCGATGCTTCTGTGGGATAAAAAGTGTAGTTC	10	75481925
167	CAAAGAGCCACTACAACCACTAACATCATCGATAGGAGGCAACTATTAAGAAAGGGCTTT	10	75481925
168	TGATACTTTAAAAAATTTTTTTAAATGATCGATGATGTTAGTGGTTGTAGTGGCTCTTTG	10	75481925
169	CAAAGAGCCACTACAACCACTAACATCATCGAAGTGTTTAGTGAGAGAATCTTTTTTCTT	10	75481925
170	CAAAGAGCCACTACAACCACTAACATCATCGATGTGGAGAATAGCCCATCTTGCTCATTT	10	75481925
171	CAAAGAGCCACTACAACCACTAACATCATCGAAGGTAGAGAGAGAATGCTCTGGGGATGA	10	75481925
172	TTTTAGAGCCTGCCCTCTGTACTCCAAATCGATGATGTTAGTGGTTGTAGTGGCTCTTTG	10	75481925
173	CAAAGAGCCACTACAACCACTAACATCATCGACAAAAAGAAAAATCAGCCTCATAATGCA	10	75481925
174	TGCATTTGTCAAAATTAAGAAATTAACATCGATGATGTTAGTGGTTGTAGTGGCTCTTTG	10	75481925
175	CAAAGAGCCACTACAACCACTAACATCATCGAATGCCCCCATTTGAAAAGAGTTATAATA	10	75481925
176	TTAACTATCCCAAATTCCATTCTCTTTCTCGATGATGTTAGTGGTTGTAGTGGCTCTTTG	10	75481925
177	CAAAGAGCCACTACAACCACTAACATCATCGATTTCAAAGCACTTGTCATACACTCTTTC	10	75481925
178	CAAAGAGCCACTACAACCACTAACATCATCGAGGAAATGAGTATCCTCAAGAGTCTACAC	10	75481925
179	GCTCCAAGACAGGACATGGAGGTGTTCATCGATGATGTTAGTGGTTGTAGTGGCTCTTTG	10	75481925
180	CAAAGAGCCACTACAACCACTAACATCATCGAAAATTTCCGAGACTTCGTTGGCTTTGTT	10	75481925
181	CAAAGAGCCACTACAACCACTAACATCATCGATAAATCTGTTAAAAATGAGCAAAGATCA	10	75481925
182	CTTGACAAGTTCAATCTAAACAAATATATCGATGATGTTAGTGGTTGTAGTGGCTCTTTG	10	75481925
183	CAAAGAGCCACTACAACCACTAACATCATCGATTTTAAAGAGAAACATGGTATTTCACCC	10	75481925
184	CAAAGAGCCACTACAACCACTAACATCATCGAATCAGAGCCTTTGCCAGAATCTGACAGA	10	75481925
185	GTCTTCACATTGCTTCCAACAGTAGTCGTCGATGATGTTAGTGGTTGTAGTGGCTCTTTG	10	75481925
186	CAAAGAGCCACTACAACCACTAACATCATCGACCCCACAAGGCTTAGCAGGGACAAGGTT	10	75481925
187	CCCCTCTTTGAACTCTTCGTTGGAAGTTTCGATGATGTTAGTGGTTGTAGTGGCTCTTTG	10	75481925
188	AGAGAATAGTGTGAGAAATGGTCATCTTTCGAGGAATGAGATGGTCGGTACATGAGAACA	10	76002481
189	TGTTCTCATGTACCGACCATCTCATTCCTCGAGTGAGGCTGTTTTATTTGCTTGGTGCAC	10	75985731
190	GCGCCATGTTAACCGTCAAACGGGTACCTCGATGCTGGTAGATAGGGGAATGGTTCCTGG	3	106480842
191	CTATGTAATCACAGCTTGATGTTCCAATTCGATGCTGGTAGATAGGGGAATGGTTCCTGG	3	106716847
192	AACTACATTAATTAAGAACTTCTGTTCATCGATTTCAGTTTTGAAACTGTAAGAGTAATT	5	95193431

Table 33.c5

N	Probe Location			4 kb Sequence Location				
	End1	Start2	End2	Chr	Start1	End1	Start2	End2
129	26135782	26175106	26175137	28	26131781	26135782	26171136	26175137
130	49908469	49992351	49992382	20	49908438	49912439	49992351	49996352
131	7491275	7547275	7547306	15	7487274	7491275	7547275	7551276
132	27987302	28153765	28153796	19	27983301	27987302	28153765	28157766
133	28081538	28153765	28153796	19	28077537	28081538	28153765	28157766
134	28153796	28173183	28173214	19	28153765	28157766	28173183	28177184
135	20654880	20749766	20749797	13	20650879	20654880	20745796	20749797
136	16316546	16519922	16519953	21	16316515	16320516	16515952	16519953
137	16361936	16519922	16519953	21	16361905	16365906	16515952	16519953
138	16382969	16519922	16519953	21	16378968	16382969	16515952	16519953
139	16389433	16519922	16519953	21	16389402	16393403	16515952	16519953
140	16430421	16519922	16519953	21	16426420	16430421	16515952	16519953
141	47907545	47940508	47940539	1	47907514	47911515	47936538	47940539
142	56337174	56374109	56374140	5	56337143	56341144	56370139	56374140
143	56337174	56519244	56519275	5	56337143	56341144	56515274	56519275
144	30912196	30991768	30991799	26	30908195	30912196	30987798	30991799
145	30912196	30981829	30981860	26	30908195	30912196	30981829	30985830
146	102471878	102533621	102533652	4	102471847	102475848	102529651	102533652
147	10875151	10945798	10945829	11	10875120	10879121	10941828	10945829
148	10907532	10945798	10945829	11	10907501	10911502	10941828	10945829
149	31709566	31731426	31731457	2	31709535	31713536	31731426	31735427
150	31709566	31749361	31749392	2	31709535	31713536	31749361	31753362
151	31709566	31757482	31757513	2	31709535	31713536	31757482	31761483
152	31709566	31759922	31759953	2	31709535	31713536	31759922	31763923
153	31709566	31779719	31779750	2	31709535	31713536	31779719	31783720
154	31709566	31795486	31795517	2	31709535	31713536	31795486	31799487
155	31709566	31816722	31816753	2	31709535	31713536	31816722	31820723
156	31709566	31841824	31841855	2	31709535	31713536	31841824	31845825
157	75421720	75491551	75491582	10	75417719	75421720	75487581	75491582
158	75421720	75481925	75481956	10	75417719	75421720	75481925	75485926
159	75419913	75481925	75481956	10	75419882	75423883	75481925	75485926
160	75433856	75481925	75481956	10	75433825	75437826	75481925	75485926
161	75481956	75505407	75505438	10	75481925	75485926	75501437	75505438
162	75481956	75503397	75503428	10	75481925	75485926	75503397	75507398
163	75481956	75510267	75510298	10	75481925	75485926	75510267	75514268
164	75481956	75518473	75518504	10	75481925	75485926	75514503	75518504
165	75481956	75515462	75515493	10	75481925	75485926	75515462	75519463
166	75481956	75537867	75537898	10	75481925	75485926	75537867	75541868
167	75481956	75558780	75558811	10	75481925	75485926	75558780	75562781
168	75481956	75585674	75585705	10	75481925	75485926	75581704	75585705
169	75481956	75583879	75583910	10	75481925	75485926	75583879	75587880
170	75481956	75598703	75598734	10	75481925	75485926	75598703	75602704
171	75481956	75630159	75630190	10	75481925	75485926	75630159	75634160
172	75481956	75659958	75659989	10	75481925	75485926	75655988	75659989
173	75481956	75657275	75657306	10	75481925	75485926	75657275	75661276
174	75481956	75680755	75680786	10	75481925	75485926	75676785	75680786
175	75481956	75673465	75673496	10	75481925	75485926	75673465	75677466
176	75481956	75698620	75698651	10	75481925	75485926	75694650	75698651
177	75481956	75689296	75689327	10	75481925	75485926	75689296	75693297
178	75481956	75699217	75699248	10	75481925	75485926	75699217	75703218
179	75481956	75711759	75711790	10	75481925	75485926	75707789	75711790
180	75481956	75710114	75710145	10	75481925	75485926	75710114	75714115
181	75481956	75727142	75727173	10	75481925	75485926	75727142	75731143
182	75481956	75737067	75737098	10	75481925	75485926	75733097	75737098
183	75481956	75731193	75731224	10	75481925	75485926	75731193	75735194

184	75481956	75761081	75761112	10	75481925	75485926	75761081	75765082
185	75481956	75769584	75769615	10	75481925	75485926	75765614	75769615
186	75481956	75772669	75772700	10	75481925	75485926	75772669	75776670
187	75481956	75791933	75791964	10	75481925	75485926	75787963	75791964
188	76002512	76079786	76079817	10	75998511	76002512	76075816	76079817
189	75985762	76079786	76079817	10	75985731	75989732	76075816	76079817
190	106480873	106716847	106716878	3	106480842	106484843	106716847	106720848
191	106716878	106947854	106947885	3	106716847	106720848	106943884	106947885
192	95193462	95211956	95211987	5	95193431	95197432	95211956	95215957

Table 33.c6

N	Probe	Primer ID-1	Primer Sequence
129	IGF1_28_26127450_26135782_26165074_26175137_FF	OBD RD043.513	ACTTGTAGGTGAGAAAGAAATAGC
130	IL17F_20_49908438_49915179_49992351_49998114_RR	OBD RD043.517	CCTGTCTCACCATCTTCTTTTGCCTG
131	IL1R1_15_7480700_7491275_7547275_7554471_FR	OBD RD043.521	CCAACTGAACAAGTGAACGCTGCCAG
132	IL1RAP_19_27981648_27987302_28153765_28161424_FR	OBD RD043.525	AAATCGGTGAAGAAATGTAGAAAA
133	IL1RAP_19_28069654_28081538_28153765_28161424_FR	OBD RD043.529	ATTTCCCCTTGTAGGCTGGTGGC
134	IL1RAP_19_28153765_28161424_28173183_28182762_RR	OBD RD043.533	TATGCCAGGGAGGTAGAGCAGCC
135	IL21R_13_20649899_20654880_20738447_20749797_FF	OBD RD043.537	GACCTTGTTTTGTTCCCGTGACAGCA
136	IL6ST_21_16316515_16320787_16507936_16519953_RF	OBD RD043.541	GCAAAGAGCAATGAGATGTCTATGAT
137	IL6ST_21_16361905_16367133_16507936_16519953_RF	OBD RD043.545	AGCCTCTCCCTCCCAGCAAAGCG
138	IL6ST_21_16380568_16382969_16507936_16519953_FF	OBD RD043.549	AGCCTCTCCCTCCCAGCAAAGCG
139	IL6ST_21_16389402_16396020_16507936_16519953_RF	OBD RD043.553	AGCCTCTCCCTCCCAGCAAAGCG
140	IL6ST_21_16427757_16430421_16507936_16519953_FF	OBD RD043.557	TATCAGTCAGCAACTCAGAGGAAC
141	IPMK_1_47907514_47915619_47934069_47940539_RF	OBD RD043.561	AGCCAGAGCCTTGCTGTAGTCAG
142	KCND3_5_56337143_56347199_56370847_56374140_RF	OBD RD043.565	TGTCCTCCTTTTGCCCCTCCCCT
143	KCND3_5_56337143_56347199_56514669_56519275_RF	OBD RD043.569	GCCCTCTGCTTAGTAACCCCTCC
144	KCNE2_26_30910971_30912196_30981829_30991799_FF	OBD RD043.573	CCAAAACCCCACCCACGCTGAGC
145	KCNE2_26_30910971_30912196_30981829_30991799_FR	OBD RD043.577	TCCAAAACCCCACCCACGCTGAG
146	KCNH2_4_102471847_102478321_102526070_102533652_RF	OBD RD043.581	GAGGTCACAGTTCCCTTGTTGGC
147	KCNJ2_11_10875120_10880378_10941535_10945829_RF	OBD RD043.585	GGAGGAGTAAATGAATGTTTGTTT
148	KCNJ2_11_10907501_10914338_10941535_10945829_RF	OBD RD043.589	CGTAATGAAGCAGACTTTTGGTCAGG
149	KDM1A_2_31709535_31721093_31731426_31738065_RR	OBD RD043.593	CCAGCAGATGACAGCAGCAATAAGGG
150	KDM1A_2_31709535_31721093_31749361_31751529_RR	OBD RD043.597	CGCCAGCAGATGACAGCAGCAAT
151	KDM1A_2_31709535_31721093_31757482_31759922_RR	OBD RD043.601	CGCCAGCAGATGACAGCAGCAAT
152	KDM1A_2_31709535_31721093_31759922_31772142_RR	OBD RD043.605	CGCCAGCAGATGACAGCAGCAAT
153	KDM1A_2_31709535_31721093_31779719_31783168_RR	OBD RD043.609	CGCCAGCAGATGACAGCAGCAAT
154	KDM1A_2_31709535_31721093_31795486_31798526_RR	OBD RD043.613	GCACCTGACAGCAGCACAGACTG
155	KDM1A_2_31709535_31721093_31816722_31820715_RR	OBD RD043.617	CGCCAGCAGATGACAGCAGCAAT
156	KDM1A_2_31709535_31721093_31841824_31843977_RR	OBD RD043.621	GCACCTGACAGCAGCACAGACTG
157	LAMA2_10_75419882_75421720_75481925_75491582_FF	OBD RD043.625	GGATGTTCCAGCCTGAGTTCCTC
158	LAMA2_10_75419882_75421720_75481925_75491582_FR	OBD RD043.629	GCTCGCCGTAGCATTCCTCACAC
159	LAMA2_10_75419882_75421720_75481925_75491582_RR	OBD RD043.633	CAACCTATTGCCGATGCCCTCAAACT
160	LAMA2_10_75433825_75441819_75481925_75491582_RR	OBD RD043.637	CCTACTACAACCTATTGCCGATGCCC
161	LAMA2_10_75481925_75491582_75503397_75505438_RF	OBD RD043.641	GCCGATGCCCTCAAACTATTTATCAA
162	LAMA2_10_75481925_75491582_75503397_75505438_RR	OBD RD043.645	GCAAAGGACCCAACATCGTAGGC
163	LAMA2_10_75481925_75491582_75510267_75513025_RR	OBD RD043.649	GCAAAGGACCCAACATCGTAGGC
164	LAMA2_10_75481925_75491582_75515462_75518504_RF	OBD RD043.653	GCTCGCCGTAGCATTCCTCACAC
165	LAMA2_10_75481925_75491582_75515462_75518504_RR	OBD RD043.657	TGTGATTGATAGGACTGCTTTGAGGC
166	LAMA2_10_75481925_75491582_75537867_75543336_RR	OBD RD043.661	TTGTGTTTGAGTCTGGCTTGTCTAAT
167	LAMA2_10_75481925_75491582_75558780_75560310_RR	OBD RD043.665	GCAAAGGACCCAACATCGTAGGC
168	LAMA2_10_75481925_75491582_75583879_75585705_RF	OBD RD043.669	CAACCTATTGCCGATGCCCTCAAACT
169	LAMA2_10_75481925_75491582_75583879_75585705_RR	OBD RD043.673	CTACAACCTATTGCCGATGCCCTC
170	LAMA2_10_75481925_75491582_75598703_75603065_RR	OBD RD043.677	GGCTTAGGGCATTGGTTAGGAGC

171	LAMA2_10_75481925_75491582_75630159_75632019_RR	OBD RD043.681	TCTCTCTGTTTCTCAGTTCTATCGC
172	LAMA2_10_75481925_75491582_75657275_75659989_RF	OBD RD043.685	ATCATTGAAGTTAGAAAAGGTCTT
173	LAMA2_10_75481925_75491582_75657275_75659989_RR	OBD RD043.689	GCAAAGGAATGCCAACTGCCAGC
174	LAMA2_10_75481925_75491582_75673465_75680786_RF	OBD RD043.693	CCTTTACCCAACTCCCACTGAGG
175	LAMA2_10_75481925_75491582_75673465_75680786_RR	OBD RD043.697	CCTACTACAACCTATTGCCGATGCCC
176	LAMA2_10_75481925_75491582_75689296_75698651_RF	OBD RD043.701	GCAAAGGACCCAACATCGTAGGC
177	LAMA2_10_75481925_75491582_75689296_75698651_RR	OBD RD043.705	CTGATTTGTGGGCATCGTCTACAGTT
178	LAMA2_10_75481925_75491582_75699217_75700676_RR	OBD RD043.709	GCAAAGGACCCAACATCGTAGGC
179	LAMA2_10_75481925_75491582_75710114_75711790_RF	OBD RD043.713	CGAGGGAGAGAGTAAAGCCAACC
180	LAMA2_10_75481925_75491582_75710114_75711790_RR	OBD RD043.717	CCTACTACAACCTATTGCCGATGCCC
181	LAMA2_10_75481925_75491582_75727142_75730779_RR	OBD RD043.721	TCAGGTAGCACTCTTATCTTTCCAGA
182	LAMA2_10_75481925_75491582_75731193_75737098_RF	OBD RD043.725	TAGGGAGTTGGCACTGGCACTTTT
183	LAMA2_10_75481925_75491582_75731193_75737098_RR	OBD RD043.729	GCTCGCCGTAGCATTCCTCACAC
184	LAMA2_10_75481925_75491582_75761081_75765848_RR	OBD RD043.733	CAGGAAGACTTTATTATGGAATGCGT
185	LAMA2_10_75481925_75491582_75767487_75769615_RF	OBD RD043.737	CCTACTACAACCTATTGCCGATGCCC
186	LAMA2_10_75481925_75491582_75772669_75776905_RR	OBD RD043.741	CTTGAAACCTGACAAAGATACCAGC
187	LAMA2_10_75481925_75491582_75789669_75791964_RF	OBD RD043.745	TTCCATTCCAAGATTGATGAAAAT
188	LAMA2_10_75985731_76002512_76077151_76079817_FF	OBD RD043.749	GCAGACACAAGCAAGTAAATAGACAA
189	LAMA2_10_75985731_76002512_76077151_76079817_RF	OBD RD043.753	CCTACTACAACCTATTGCCGATGCCC
190	LDB2_3_106480842_106484500_106716847_106728445_RR	OBD RD043.757	CACAGAATAGTCTCCCAAATAGTTTATG
191	LDB2_3_106716847_106728445_106944178_106947885_RF	OBD RD043.761	AGTGAAGGAGGAGAGTCATCTGCT
192	LEPR_5_95193431_95200537_95211956_95218723_RR	OBD RD043.765	GAGCCAAACCATAAAGAGAAAGACTG

Table 33.c7

N	Primer ID-2	Primer Sequence	Probe	Marker
129	OBD RD043.515	TCCATAAACAGGTGAGGAAGACAC	IGF1	OBD RD043.513.515
130	OBD RD043.519	TTAGTCTCTTTCTTCAGATGGCTATC	IL17F	OBD RD043.517.519
131	OBD RD043.523	ACAACGAGGACTCAGATTTCTCAGAG	IL1R1	OBD RD043.521.523
132	OBD RD043.527	GCAAGTTAGTGGTTGAGATTGGAT	IL1RAP	OBD RD043.525.527
133	OBD RD043.531	TATGCCAGGGAGGTAGAGCAGCC	IL1RAP	OBD RD043.529.531
134	OBD RD043.535	GCTTGACTTGCTCTGGGAGGAGA	IL1RAP	OBD RD043.533.535
135	OBD RD043.539	CTAATAAACTCAGCGAGGCAGCAGGA	IL21R	OBD RD043.537.539
136	OBD RD043.543	AGCCTCTCCCTCCCAGCAAAGCG	IL6ST	OBD RD043.541.543
137	OBD RD043.547	GCCTCAGAAAGAGTTGTAGTTATTGT	IL6ST	OBD RD043.545.547
138	OBD RD043.551	CAGTTTTGTAGAGCACCTGATTAGAA	IL6ST	OBD RD043.549.551
139	OBD RD043.555	GGGCTCTACTCAGTGATTGCCTG	IL6ST	OBD RD043.553.555
140	OBD RD043.559	AGCCTCTCCCTCCCAGCAAAGCG	IL6ST	OBD RD043.557.559
141	OBD RD043.563	GCCATCAGTGACCAAGGCACCTC	IPMK	OBD RD043.561.563
142	OBD RD043.567	ATCAGAGGGTGGTTATGTCGGGC	KCND3	OBD RD043.565.567
143	OBD RD043.571	ATCAGAGGGTGGTTATGTCGGGC	KCND3	OBD RD043.569.571
144	OBD RD043.575	GGGTCAGGTTGGTGAGAGAAGGG	KCNE2	OBD RD043.573.575
145	OBD RD043.579	ATGGATGGTGGATGGTGGGAACC	KCNE2	OBD RD043.577.579
146	OBD RD043.583	TTCCACCCCGTCCCCATCTTCAC	KCNH2	OBD RD043.581.583
147	OBD RD043.587	AAGAGTAATCTGCTTGGTAAATAG	KCNJ2	OBD RD043.585.587
148	OBD RD043.591	CTACTTGAAGAAATAAGCCTTGCTGC	KCNJ2	OBD RD043.589.591
149	OBD RD043.595	CCACTTTATGAAGCAAATGGACAAGC	KDM1A	OBD RD043.593.595
150	OBD RD043.599	CCCTTCTCTCTGTTGCTGCCGTG	KDM1A	OBD RD043.597.599
151	OBD RD043.603	GCTCGCAGGTGCTGGGAATACAG	KDM1A	OBD RD043.601.603
152	OBD RD043.607	TGGTGTCTCAGGCTTGGCAGCAG	KDM1A	OBD RD043.605.607
153	OBD RD043.611	GAGAGAGCCCAGGTTAGACAGCG	KDM1A	OBD RD043.609.611
154	OBD RD043.615	AAACAAAGCCAGGGAGGAGGACG	KDM1A	OBD RD043.613.615
155	OBD RD043.619	GCCAGAAAGGAAGGTGGGAGCCT	KDM1A	OBD RD043.617.619
156	OBD RD043.623	CCACTACTCTCATAGGGAGGGAG	KDM1A	OBD RD043.621.623

157	OBD RD043.627	GCTCGCCGTAGCATTCCTCACAC	LAMA2	OBD RD043.625.627
158	OBD RD043.631	GGCTTCAACCGTCTCCAAGGCTT	LAMA2	OBD RD043.629.631
159	OBD RD043.635	TTCTGTAGAGCCTCACCAACACTGTG	LAMA2	OBD RD043.633.635
160	OBD RD043.639	CGACTTCTCGGTTGTTTAGCATCACA	LAMA2	OBD RD043.637.639
161	OBD RD043.643	CGTGACAGCAGTTTTATTGTTTGGG	LAMA2	OBD RD043.641.643
162	OBD RD043.647	GGACCCGAGCACCACTCTTGAGA	LAMA2	OBD RD043.645.647
163	OBD RD043.651	TCCCAGAACAGCCAGCACAGCAG	LAMA2	OBD RD043.649.651
164	OBD RD043.655	GTGACTGCCAGGTTTGCCACCAA	LAMA2	OBD RD043.653.655
165	OBD RD043.659	CCTACTACAACCTATTGCCGATGCCC	LAMA2	OBD RD043.657.659
166	OBD RD043.663	CGATGCCCTCAAACTATTTATCAAAG	LAMA2	OBD RD043.661.663
167	OBD RD043.667	GACCACACACCAGGAGGCTGATG	LAMA2	OBD RD043.665.667
168	OBD RD043.671	CCACTATTTCCACACCACACAGTCTG	LAMA2	OBD RD043.669.671
169	OBD RD043.675	TGGCACTCCTCCTCGTCATCAGG	LAMA2	OBD RD043.673.675
170	OBD RD043.679	GCTCGCCGTAGCATTCCTCACAC	LAMA2	OBD RD043.677.679
171	OBD RD043.683	ACATAAAGAACACTCTATCCAAAA	LAMA2	OBD RD043.681.683
172	OBD RD043.687	TTCGCAAAGGACCCAACATCGTAG	LAMA2	OBD RD043.685.687
173	OBD RD043.691	GCTCGCCGTAGCATTCCTCACAC	LAMA2	OBD RD043.689.691
174	OBD RD043.695	GCTCGCCGTAGCATTCCTCACAC	LAMA2	OBD RD043.693.695
175	OBD RD043.699	TCGCTGAGGAGCATCCAACTTGATTA	LAMA2	OBD RD043.697.699
176	OBD RD043.703	CTGTCAACGGGATGTGAGGTCAGC	LAMA2	OBD RD043.701.703
177	OBD RD043.707	CCTACTACAACCTATTGCCGATGCCC	LAMA2	OBD RD043.705.707
178	OBD RD043.711	CTCAGCAGGAAATCGCCCTCCAG	LAMA2	OBD RD043.709.711
179	OBD RD043.715	GCTCGCCGTAGCATTCCTCACAC	LAMA2	OBD RD043.713.715
180	OBD RD043.719	GCTCCAACACAACCCAGTTATTTCTG	LAMA2	OBD RD043.717.719
181	OBD RD043.723	CCTACTACAACCTATTGCCGATGCCC	LAMA2	OBD RD043.721.723
182	OBD RD043.727	CCTACTACAACCTATTGCCGATGCCC	LAMA2	OBD RD043.725.727
183	OBD RD043.731	GACCCAAAGCAGAGAGGCAACTG	LAMA2	OBD RD043.729.731
184	OBD RD043.735	CAACCTATTGCCGATGCCCTCAAACT	LAMA2	OBD RD043.733.735
185	OBD RD043.739	TAGGGAACCGACTGAATCTGATACAG	LAMA2	OBD RD043.737.739
186	OBD RD043.743	CAATACTTTAGAGTCACATCTCGTGC	LAMA2	OBD RD043.741.743
187	OBD RD043.747	GTGTGTAAGTTCTAAGTGTTTATTA	LAMA2	OBD RD043.745.747
188	OBD RD043.751	CAACCTATTGCCGATGCCCTCAAACT	LAMA2	OBD RD043.749.751
189	OBD RD043.755	CAACCCAAAGCAATCCAGCAAAGCAT	LAMA2	OBD RD043.753.755
190	OBD RD043.759	GATGTTTCTTATTTTGAGTTTTCCCAGG	LDB2	OBD RD043.757.759
191	OBD RD043.763	GTCATCATTTATGTGGAAGGAATA	LDB2	OBD RD043.761.763
192	OBD RD043.767	AACCCTGTCATAAGTTGAAGAAGAGC	LEPR	OBD RD043.765.767

Table 33.c8

N	Probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig
193	LMO7_17_48756745_48760926_48985578_48994371_FR	LMO7	1	47
194	LY6D_9_81540380_81548206_81579682_81590550_FR	LY6D	2	31
195	LY6D_9_81540380_81548206_81579682_81590550_RR	LY6D	2	31
196	MAP3K4_31_2786762_2795002_2851292_2856203_FR	MAP3K4	1	31
197	MAP3K9_24_16803396_16807626_16910389_16918093_RF	MAP3K9	1	29
198	MAPK1_8_3352241_3355955_3404723_3412822_RR	MAPK1	3	31
199	MAPK1_8_3435741_3439526_3469888_3479148_FF	MAPK1	3	31
200	MAPK1_8_3435741_3439526_3469888_3479148_FR	MAPK1	3	31
201	MAPK3_13_19583177_19588616_19608792_19619090_FF	MAPK3	1	31
202	MAPK9_14_2229196_2237168_2274036_2279957_RR	MAPK9	2	38
203	MAPK9_14_2229196_2237168_2401910_2410518_RR	MAPK9	2	38
204	MDH1_15_37903511_37909683_38029907_38037711_RR	MDH1	2	125
205	MDH1_15_37903511_37909683_38069969_38081007_RR	MDH1	2	125
206	MDM4_5_1002213_1010298_1034976_1038480_FF	MDM4	1	31
207	MED25_10_19508221_19515457_19591613_19593754_RF	MED25	1	30

208	MEF2A_1_104992073_105002150_105161756_105164976_RF	MEF2A	1	181
209	MIPEP_17_4332285_4337643_4521242_4528379_FF	MIPEP	3	131
210	MIPEP_17_4413535_4418797_4506914_4517925_FF	MIPEP	3	131
211	MIPEP_17_4413535_4418797_4521242_4528379_FF	MIPEP	3	131
212	MMP1_7_12601995_12610418_12711728_12717668_RF	MMP1	2	33
213	MMP1_7_12711728_12717668_12737470_12745025_FR	MMP1	2	33
214	MS4A2_12_19894956_19896244_19962410_19974828_RF	MS4A2	2	112
215	MS4A2_12_19992086_20002065_20049543_20053548_RF	MS4A2	2	112
216	MSI2_11_31942510_31947907_32032038_32042221_RR	MSI2	3	204
217	MSI2_11_31953015_31955643_32032038_32042221_RF	MSI2	3	204
218	MSI2_11_31953015_31955643_32032038_32042221_RR	MSI2	3	204
219	MSTN_18_66448734_66450075_66490497_66500489_FF	MSTN	1	50
220	MTHFR_2_39760745_39767847_39804925_39808549_FR	MTHFR	3	29
221	MTHFR_2_39760745_39767847_39835824_39839260_FF	MTHFR	3	29
222	MTHFR_2_39760745_39767847_39835824_39839260_FR	MTHFR	3	29
223	MTMR3_8_6868138_6874813_6923181_6926871_RR	MTMR3	1	31
224	MYBPC2_10_20037236_20038811_20080873_20084086_RF	MYBPC2	1	31
225	MYH1_11_52882980_52886797_52907287_52915321_RF	MYH1	1	50
226	MYL1_6_1098854_1104299_989242_996235_RR	MYL1	1	44
227	MYL4_11_17193641_17194702_17358881_17368963_RF	MYL4	6	34
228	MYL4_11_17206623_17211708_17358881_17368963_RF	MYL4	6	34
229	MYL4_11_17246461_17251113_17358881_17368963_RF	MYL4	6	34
230	MYL4_11_17257199_17259878_17358881_17368963_RF	MYL4	6	34
231	MYL4_11_17267739_17271299_17358881_17368963_RF	MYL4	6	34
232	MYL4_11_17290815_17294484_17358881_17368963_RF	MYL4	6	34
233	MYOZ1_1_61314759_61323626_61385709_61392305_FF	MYOZ1	3	109
234	MYOZ1_1_61323626_61338801_61385709_61392305_FF	MYOZ1	3	109
235	MYOZ1_1_61350438_61357018_61385709_61392305_RF	MYOZ1	3	109
236	NDN_1_109635329_109640204_109733366_109741347_RF	NDN	3	31
237	NDN_1_109711483_109720818_109733366_109741347_RF	NDN	3	31
238	NDN_1_109733366_109741347_109779877_109789352_FR	NDN	3	31
239	NDUFA8_25_25717207_25721463_25884535_25891335_FR	NDUFA8	1	31
240	NEUROD2_11_22762666_22765277_22824653_22836914_FR	NEUROD2	1	35
241	NFIB_23_34300375_34312881_34537544_34541097_RF	NFIB	2	195
242	NFIB_23_34364872_34370510_34413070_34423547_FR	NFIB	2	195
243	NPPA_2_39707018_39708108_39760745_39767847_RF	NPPA	4	31
244	NPPA_2_39714609_39718671_39760745_39767847_FF	NPPA	4	31
245	NPPA_2_39714609_39718671_39760745_39767847_RF	NPPA	4	31
246	NPPA_2_39741527_39742701_39760745_39767847_RF	NPPA	4	31
247	PALLD_2_66194319_66195345_66291709_66310979_FF	PALLD	5	288
248	PALLD_2_66194319_66195345_66291709_66310979_FR	PALLD	5	288
249	PALLD_2_66212034_66222303_66449615_66454401_FF	PALLD	5	288
250	PALLD_2_66291709_66310979_66324859_66327343_FR	PALLD	5	288
251	PALLD_2_66291709_66310979_66449615_66454401_RF	PALLD	5	288
252	PCBP4_16_35681721_35687901_35707118_35711409_FF	PCBP4	2	31
253	PCBP4_16_35681721_35687901_35729420_35734814_FF	PCBP4	2	31
254	PHOSPHO1_11_25089999_25092180_25214955_25221072_RR	PHOSPHO1	2	30
255	PHOSPHO1_11_25177016_25183355_25214955_25221072_RR	PHOSPHO1	2	30
256	PIK3R1_21_5606382_5618174_5697527_5698879_RF	PIK3R1	1	44

Table 33.d1

N	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr
193	0.264202412	0.310300562	2.13	0.308955	8.756434343
194	0.024599258	0.075554863	6.45	-0.510502405	10.21074765
195	0.024599258	0.075554863	6.45	-0.475839307	10.73785324

196	0.198752749	0.267074007	3.23	-0.262976484	8.919564336
197	0.189010904	0.267074007	3.45	-0.180023399	10.17483943
198	0.001955877	0.014841655	9.68	-0.189403578	11.32640428
199	0.001955877	0.014841655	9.68	-0.357643779	9.43283737
200	0.001955877	0.014841655	9.68	-0.455473419	9.347542263
201	0.198752749	0.267074007	3.23	-0.414926364	10.40126841
202	0.035117143	0.100669145	5.26	-0.304638764	10.45869573
203	0.035117143	0.100669145	5.26	-0.350361266	10.09820875
204	0.189650589	0.267074007	1.6	-0.39554798	7.948266107
205	0.189650589	0.267074007	1.6	-0.352490885	8.366984869
206	0.198752749	0.267074007	3.23	-0.184406239	9.603449014
207	0.193928419	0.267074007	3.33	-1.002322155	9.303488712
208	0.337499771	0.365861096	0.55	-0.268195094	9.66649256
209	0.070335458	0.151221234	2.29	0.181091948	9.982716815
210	0.070335458	0.151221234	2.29	-0.243481105	10.43396472
211	0.070335458	0.151221234	2.29	-0.262461763	10.1207347
212	0.027478161	0.080560972	6.06	-0.363422404	9.195426411
213	0.027478161	0.080560972	6.06	-0.344950706	9.351822484
214	0.169245181	0.267074007	1.79	-0.432136877	12.0727133
215	0.169245181	0.267074007	1.79	-0.227521522	9.522194245
216	0.147248814	0.267074007	1.47	0.571287251	9.737071247
217	0.147248814	0.267074007	1.47	-0.250081475	9.240013839
218	0.147248814	0.267074007	1.47	-0.454717411	10.26002015
219	0.274219102	0.310300562	2	0.301875352	8.089384778
220	0.001616117	0.014841655	10.34	-0.275284765	10.54722144
221	0.001616117	0.014841655	10.34	-0.290761819	10.35745977
222	0.001616117	0.014841655	10.34	-0.323026508	10.39283037
223	0.198752749	0.267074007	3.23	-0.306058656	10.27824044
224	0.198752749	0.267074007	3.23	0.218360553	10.39432728
225	0.274219102	0.310300562	2	-0.340884422	11.66695629
226	0.253514025	0.310300562	2.27	-0.590441109	8.581505532
227	0.000000311818145952167	0.0000201122704139147	17.65	0.269287734	9.380557343
228	0.000000311818145952167	0.0000201122704139147	17.65	0.204015501	9.601273444
229	0.000000311818145952167	0.0000201122704139147	17.65	0.256704897	9.061911736
230	0.000000311818145952167	0.0000201122704139147	17.65	0.183545822	10.10564073
231	0.000000311818145952167	0.0000201122704139147	17.65	0.205055848	10.06240784
232	0.000000311818145952167	0.0000201122704139147	17.65	0.220380659	9.12627111
233	0.048283923	0.124572522	2.75	-0.212727454	10.43860627
234	0.048283923	0.124572522	2.75	-0.281776187	9.409288269
235	0.048283923	0.124572522	2.75	-0.492368455	10.04957678
236	0.001955877	0.014841655	9.68	-0.340662221	9.476696148
237	0.001955877	0.014841655	9.68	-0.43400853	9.302335644
238	0.001955877	0.014841655	9.68	-0.3910292	9.299496898
239	0.198752749	0.267074007	3.23	0.253713189	8.751509754
240	0.217141868	0.285829602	2.86	-0.204232609	12.1874556
241	0.260374827	0.310300562	1.03	0.324297214	8.32941724
242	0.260374827	0.310300562	1.03	-0.228545891	7.918191482
243	0.000112254	0.002068688	12.9	-0.235040273	10.43931511
244	0.000112254	0.002068688	12.9	-0.298128772	9.961402566
245	0.000112254	0.002068688	12.9	-0.196073384	11.28835418
246	0.000112254	0.002068688	12.9	-0.358964974	10.23538918
247	0.057376468	0.137915817	1.74	-0.331113386	8.504927574
248	0.057376468	0.137915817	1.74	-0.333004015	8.42257663
249	0.057376468	0.137915817	1.74	0.337185069	9.542961911
250	0.057376468	0.137915817	1.74	-0.19420402	10.03309215
251	0.057376468	0.137915817	1.74	0.285252571	10.1390655
252	0.024599258	0.075554863	6.45	-0.606928989	7.90009089

253	0.024599258	0.075554863	6.45	-0.5741059	7.791564161
254	0.023201487	0.075554863	6.67	-0.435541833	8.652187929
255	0.023201487	0.075554863	6.67	-0.452293144	9.746122909
256	0.253514025	0.310300562	2.27	-0.222099166	10.2584473

Table 33.d2

N	t	P.Value	adj.P.Val	B	FC
193	5.578062929	0.0000217701905479979	0.004204233	2.8863206	1.238810056
194	-8.542517182	0.00000005963291889729 69	0.000077542672206118	8.396017365	0.701977938
195	-5.419897283	0.0000307827940531150	0.005054403	2.556989182	0.719048353
196	-5.295421974	0.0000405075194431574	0.006131956	2.295788713	0.833366791
197	-5.303171478	0.0000398191777050705	0.006067758	2.312100067	0.88268868
198	-5.26401715	0.0000434237366404068	0.006490268	2.229621301	0.876968192
199	-7.362483567	0.000000542792493499413	0.00033823	6.362585392	0.780438157
200	-6.920589559	0.0000130208881243147	0.000596309	5.545829579	0.729270823
201	-6.507834204	0.0000301932875673387	0.001051643	4.755925321	0.750057777
202	-5.2522991	0.0000445660037600909	0.006607886	2.204905558	0.809644918
203	-6.955664773	0.0000121355337901372	0.00057037	5.611759271	0.784387655
204	-5.962344466	0.0000094969252486 1803	0.002437336	3.673443959	0.760200574
205	-6.959876235	0.0000120334955772376	0.00057037	5.619662717	0.783230643
206	-5.197233953	0.0000503586344752859	0.007169673	2.088570872	0.880011182
207	-11.12974035	0.000000000855760191439498	0.00000370924500756165	12.15128673	0.49919585
208	-6.217777769	0.0000052671615692750	0.001607736	4.185638781	0.830357728
209	5.017111985	0.0000752584737618864	0.009531926	1.705942088	1.133741668
210	-6.41916147	0.0000362800718522512	0.001213128	4.582892014	0.844704648
211	-6.682538446	0.0000210909449126610	0.000822758	5.093407671	0.833664171
212	-5.560509533	0.0000226203345689378	0.004245102	2.849918149	0.777318413
213	-5.730820553	0.0000156218240048023	0.003423637	3.201499442	0.787334878
214	-5.520053358	0.0000247115601581872	0.004416684	2.76587789	0.741163183
215	-6.250406563	0.0000051605278280 0820	0.001572751	4.250401752	0.854100935
216	10.84451596	0.000000001317470896 17564	0.00000513945396598118	11.78059039	1.485848734
217	-5.219666256	0.0000479113597540456	0.006948038	2.136000723	0.840848928
218	-7.685287888	0.0000002912557275079 92	0.000248829	6.940120692	0.72965308
219	6.038727238	0.0000080705026714969 6	0.002138121	3.82756083	1.232745812
220	-5.887655696	0.0000111429983778881	0.002634475	3.521975599	0.826287206
221	-5.456068621	0.0000284312776732711	0.004832995	2.632564179	0.817470277
222	-6.439861138	0.0000034754358776 4876	0.00118927	4.623388743	0.799391142
223	-7.58351219	0.0000003538815863786 11	0.000270685	6.759774473	0.808848462
224	5.073968482	0.0000662731427137706	0.008670693	1.827052816	1.16341076
225	-8.114538033	0.0000001300570603809 18	0.000126838	7.683168577	0.789557138
226	-8.247664393	0.0000001017859707675 85	0.000104491	7.907878402	0.664139813
227	5.610514627	0.0000202836082244147	0.0039679	2.953520209	1.205212661
228	5.212827288	0.0000486443312060846	0.007002271	2.121546166	1.151900019
229	5.148455682	0.0000561297752836139	0.007709938	1.985261129	1.194746794
230	5.217277153	0.0000481661245096288	0.006959113	2.130951759	1.135671685
231	5.625048666	0.0000196519236843458	0.003951657	2.983574644	1.152730969
232	5.403530817	0.0000319112455916194	0.005171517	2.522744449	1.165040945
233	-5.566335209	0.0000223344813272804	0.004245102	2.862003659	0.862904344
234	-5.636876017	0.0000191527686471659	0.003891404	3.008012687	0.82257767
235	-7.033201866	0.0000010392286523 6368	0.000532857	5.756832398	0.710857134
236	-6.838387929	0.0000015367162436 7046	0.000651601	5.390579615	0.789678753
237	-8.482004556	0.0000000664881274369185	0.000078597025797400	8.296903933	0.740202273
238	-8.714888103	0.0000000438512643767021	0.000068425512933406	8.675347723	0.762585392
239	5.20108882	0.0000499291851743305	0.0071608	2.09672508	1.192271822
240	-5.785373903	0.0000138850583130889	0.00313096	3.313338935	0.868000266

241	5.491634267	0.000026298029094812 5	0.004539319	2.706725558	1.252054372
242	-5.2300823	0.000046816595276080 7	0.00681461	2.158006387	0.853494705
243	-5.382789941	0.000033402309875275 9	0.005277635	2.479303216	0.84966128
244	-5.150382787	0.000055889450704117 3	0.007704055	1.98934712	0.813306601
245	-5.523154669	0.000024544464839495 8	0.004416684	2.772327241	0.872923188
246	-6.676552256	0.000002135038552876 26	0.000824632	5.081919838	0.779723773
247	-5.77339837	0.000014248541181026 7	0.003153542	3.288821006	0.794922773
248	-6.210571382	0.000005611136917589 04	0.001609489	4.171314668	0.793881722
249	6.879077809	0.000001415557165272 36	0.000606823	5.467557689	1.263289306
250	-5.639859813	0.000019028906270125 0	0.00388648	3.01417515	0.874055006
251	5.102219822	0.000062222611350496 9	0.008370014	1.887120126	1.218623588
252	-4.99093597	0.000079803002829784 3	0.009820552	1.65008659	0.65659288
253	-5.313651741	0.000038907231217875 2	0.005987456	2.334148884	0.671702405
254	-10.36202183	0.000000002786900581 03200	0.000008362845512773 71	11.13041085	0.739416
255	-9.587137852	0.000000009793184673 45839	0.000020106954426927	10.02246539	0.7308802
256	-5.143048179	0.000056809772422044 9	0.007775962	1.973793794	0.857317105

Table 33.d3

N				**Probe sequence**
	FC_1	LS	Loop Detected	**60 mer**
193	1.238810056	1	Sprinter	AATATTTCTTTAAGACTAATTGTTCTACTCGAGGCATTAAATACTTTCCCTCTAGCCAGC
194	-1.424546194	-1	Stayer	CAGAATCTCTCTGCTTAATGGGCCCATATCGACAGCTTAACGGATTTTCACAGAGTACAC
195	-1.390727058	-1	Stayer	CATTGGAGTGGAATAGAGAGCTTATAAATCGACAGCTTAACGGATTTTCACAGAGTACAC
196	-1.199951823	-1	Stayer	GACCCTATGCTCCTTTCCTGGAACATCATCGAGATGTATGACAACAAATGCCAGTATTTA
197	-1.132902259	-1	Stayer	TAACCAAACCATAGTGTGAAAACAGCTTTCGATATGTAATTTTATTAAGAATATTATTTT
198	-1.140292212	-1	Stayer	GAATGGGTACTCTGCTGGAAAGTTGATTTCGAGGTGAAAGCCGAGGGAAGTGAGTAGCCA
199	-1.281331507	-1	Stayer	TTGGGTACTAGAACCCTTACAGCTCCTTTCGATAAGAATGCCAGGATCTTTTGCTGGGGA
200	-1.3712327	-1	Stayer	TTGGGTACTAGAACCCTTACAGCTCCTTTCGACAAATCTATGATATCAAGAATAACTAAC
201	-1.333230627	-1	Stayer	TAACATGCTCAGTAAATGCTACCTGTGGTCGAGCTTTTCTTATCCATGCTTCAGGGGTGA
202	-1.23510934	-1	Stayer	ATCCCTGTACTCCTGTGACCAGGGCACGTCGAGCTTTCAACTGAAACTTAGGATTTTGGA
203	-1.27487983	-1	Stayer	ATCCCTGTACTCCTGTGACCAGGGCACGTCGATTAATATAATACATCACATTAACAGAAT
204	-1.315442311	-1	Stayer	CAAAAAATGCACTCTTTCAAAGAATCTCTCGAAAAGCAAGATCCTTCTTTTAATGGAATT
205	-1.276763121	-1	Stayer	CAAAAAATGCACTCTTTCAAAGAATCTCTCGATTCAGTGTGATTGGAATCATGGAAGGAG
206	-1.136349196	-1	Stayer	TTAAACAACAAAACCCAACAGAGGAAATTCGACACTTACCACAATGAGGTGGATGCCTTC
207	-2.003221783	-1	Stayer	GTCACTGCCTTCAAACCTTATGGTACGATCGAGAAGCTAAAACAAGTATAAATATATATG
208	-1.204300227	-1	Stayer	CTGCTGTTTACTCAATATCATGACAATTTCGACTGGTAAATATGGTAACCCCAAAGCAAT
209	1.133741668	1	Sprinter	TTGTCACAGTGTAGTGAGGAGATAAATATCGAAGAGGATAAACTGGTCCCTGCACAGTCT
210	-1.183845741	-1	Stayer	GTTACAACCCCTGACATGAAAAAGGTACTCGATGCTGGGTTTGAGTAACGCTGGAGCTGC
211	-1.199523783	-1	Stayer	GTTACAACCCCTGACATGAAAAAGGTACTCGAAGAGGATAAACTGGTCCCTGCACAGTCT
212	-1.286474093	-1	Stayer	ACAGTAAAGGTGTTTTGGACTTATTGGCTCGATGTTAAAGAATAGTTCTATTCTACTTTG
213	-1.270107585	-1	Stayer	ACAGTAAAGGTGTTTTGGACTTATTGGCTCGAAATATATTATGATGTACCTCTGAAAAAA
214	-1.349230538	-1	Stayer	TGTGTTTTACTTTTAATGGAGTTGCTGTTCGAGAGTGGTGTGTTAGCTCTCCGCCTTGGG
215	-1.170821807	-1	Stayer	TAAGTCTCTTCTGAAAAAAAATAGCAGGTCGAATCCAATCACATTTGCGAATGCCCTTCA
216	1.485848734	1	Sprinter	ATTGTGCGCAAAGGAAATTATTCTAAGATCGAACACTGTTCAGCTCTTTTGTCTGGTGAT
217	-1.189274276	-1	Stayer	AACCAGACTGATGTTAACATCGCCACGTTCGAGTACCTGTGCTCAGCAACAAGATGGCTT
218	-1.370514328	-1	Stayer	AAGCCATCTTGTTGCTGAGCACAGGTACTCGAACACTGTTCAGCTCTTTTGTCTGGTGAT
219	1.232745812	1	Sprinter	AAATCAGAGAGACACTCTCTGGATGGTCTCGAACACTAGATCTTTGAGTCTAGTCTCTTT
220	-1.210232946	-1	Stayer	GAGTCTCTAGGTACCTGTCCGCTTCAGGTCGAGCATCTGGACTAATTTGTCCCGAGCTGC
221	-1.223286066	-1	Stayer	GAGTCTCTAGGTACCTGTCCGCTTCAGGTCGATAGAAATGAAGAGCTCAGCTGGGTGGCT
222	-1.250952065	-1	Stayer	GAGTCTCTAGGTACCTGTCCGCTTCAGGTCGATTTGGAGATGGTTGTACAATGCTATAAA
223	-1.236325525	-1	Stayer	AGGAAATGAACATCTAAATTCAAGAAGCTCGACAGTACTAGAAACCAACCCCTTCTCCCC
224	1.16341076	1	Sprinter	CTATTTCATGCTACGCCCTTGGGCTTTATCGAGAGTCTGCTGAATTTGTCTGCCACCTCT

225	-1.266532784	-1	Stayer	TAATTAAAATTTGATAATAAAGGCCTACTCGATGCCCTCCTTCTTGTACTCCTCCTGCTC
226	-1.505707053	-1	Stayer	CCTCCAGGAATTCTGTTAAGATGTATTTTCGAGTTAGAAAATTCCCCTCTATTTGTAGTT
227	1.205212661	1	Sprinter	ATAAAAAGCAAATAAGTGCTAGTGTTACTCGAAAAGTTGGCAGGTCTTAATCTACTGGAT
228	1.151900019	1	Sprinter	ATAAAAAGCAAATAAGTGCTAGTGTTACTCGAGGCTTACATTTCATCTGGGAAGTTTTTC
229	1.194746794	1	Sprinter	ATAAAAAGCAAATAAGTGCTAGTGTTACTCGAATACCACGTTTACTCAGACAAGAGAAAC
230	1.135671685	1	Sprinter	ATAAAAAGCAAATAAGTGCTAGTGTTACTCGAGCCTGTTGGGCGTGAGATAATCACCTTC
231	1.152730969	1	Sprinter	ATAAAAAGCAAATAAGTGCTAGTGTTACTCGAGCCTCCAGAACTCTGAGGAATAAATGTC
232	1.165040945	1	Sprinter	ATAAAAAGCAAATAAGTGCTAGTGTTACTCGAATTTCGTTTCTGCTAGTGCTTTAGCACA
233	-1.158877003	-1	Stayer	ATGTCCAGAGAATGGAAACAAACCTGACTCGAGGAATACGTGGGAAGAAATGGGGTACAG
234	-1.215690672	-1	Stayer	AATAACCAACATAACTAGAAAATTCTCCTCGAGGAATACGTGGGAAGAAATGGGGTACAG
235	-1.40675243	-1	Stayer	CTGTACCCCATTTCTTCCCACGTATTCCTCGAGAGCTATATCAAAAAGATTTTGGTATTT
236	-1.266337731	-1	Stayer	GACAGGGGTCTAGAATCATAGATTTCCCTCGATCTTGAGGTTGACAGTTACCACAATTAT
237	-1.350982072	-1	Stayer	GACAGGGGTCTAGAATCATAGATTTCCCTCGAATATGTAGTTGAGTCAGATCTGGGATTT
238	-1.311328555	-1	Stayer	GACAGGGGTCTAGAATCATAGATTTCCCTCGATACCCCAGTTTTCTTTTTGATCCCTTCA
239	1.192271822	1	Sprinter	GCTTCCAGAAATGAGAGCAGACTTCAAGTCGATATTTTGAATAAGGCTTACAGCAAGGGT
240	-1.152073379	-1	Stayer	GGTGTGTAGGCACAGGGGTTGGATCTCTTCGATTTTTATGGGTATCTCACTCTACAATTT
241	1.252054372	1	Sprinter	ACATGCTCAGAAATAAAAACATTAATTTTCGACAAATACTGTAGGATTTCAAGGGAAGAA
242	-1.171653431	-1	Stayer	TTAAAGCTATAGTGAATGAAGCAATATATCGAGTTGTCTTCTAAAAGACAGTCTAATAAT
243	-1.176939591	-1	Stayer	GAGTCTCTAGGTACCTGTCCGCTTCAGGTCGAGCTGTCAAGGGGCAAAAAAAAAAAAAAA
244	-1.229548609	-1	Stayer	AGGGCACTGCCCTTGATCAGGTAAATGTTCGACCTGAAGCGGACAGGTACCTAGAGACTC
245	-1.145576167	-1	Stayer	GAGTCTCTAGGTACCTGTCCGCTTCAGGTCGATGGTCGGCACATTTTCGTAGCCACCCTG
246	-1.282505466	-1	Stayer	GAGTCTCTAGGTACCTGTCCGCTTCAGGTCGAAATTAACAGACACATCTGTGTCTGCTCT
247	-1.257983837	-1	Stayer	GCGAGGTCATGAATGTACAAGTATAATGTCGAGTATAAGTTAAACGTGATTAAATGTAAG
248	-1.259633485	-1	Stayer	GCGAGGTCATGAATGTACAAGTATAATGTCGATTAAAATATTTTACTTTTCCTTAATTAC
249	1.263289306	1	Sprinter	ATGGGTATTGCTTTATGCCTGCTGTGTTTCGAATTGAATGGAGACGCCTTTTGGTAGGAT
250	-1.144092755	-1	Stayer	CTTACATTTAATCACGTTTAACTTATACTCGAGGTGCTCATCCCGAGGTACTTAGCGCCT
251	1.218623588	1	Sprinter	ATCCTACCAAAAGGCGTCTCCATTCAATTCGATTAAAATATTTTACTTTTCCTTAATTAC
252	-1.523013774	-1	Stayer	CAACGACACAAAGGTGTACACACAAACATCGATTTTTGCTAAGATGGTTGCAAATGATAG
253	-1.488754532	-1	Stayer	CAACGACACAAAGGTGTACACACAAACATCGAAAGAAAGATTTCTTTAGACTCTTAAGAT
254	-1.352418666	-1	Stayer	CAGCTGTACATTTTTAGTTGTGCGCACTTCGACGAGTCAAAACCGACGGAAGTCAGGCAG
255	-1.368213286	-1	Stayer	AATCTCACTAGAAGGTACAGGTGTCAAGTCGACGAGTCAAAACCGACGGAAGTCAGGCAG
256	-1.166429544	-1	Stayer	CTCAGGTTAAGTCCCCCTGTACCTGCTGTCGAGACAGACGTGTGCCTTCTTGAAAAAGCC

Table 33.d4

N	Probe Location					4 kb Sequence Location			
	Chr	Start1	End1	Start2	End2	Chr	Start1	End1	Start2
193	17	48760895	48760926	48985578	48985609	17	48756925	48760926	48985578
194	9	81548175	81548206	81579682	81579713	9	81544205	81548206	81579682
195	9	81540380	81540411	81579682	81579713	9	81540380	81544381	81579682
196	31	2794971	2795002	2851292	2851323	31	2791001	2795002	2851292
197	24	16803396	16803427	16918062	16918093	24	16803396	16807397	16914092
198	8	3352241	3352272	3404723	3404754	8	3352241	3356242	3404723
199	8	3439495	3439526	3479117	3479148	8	3435525	3439526	3475147
200	8	3439495	3439526	3469888	3469919	8	3435525	3439526	3469888
201	13	19588585	19588616	19619059	19619090	13	19584615	19588616	19615089
202	14	2229196	2229227	2274036	2274067	14	2229196	2233197	2274036
203	14	2229196	2229227	2401910	2401941	14	2229196	2233197	2401910
204	15	37903511	37903542	38029907	38029938	15	37903511	37907512	38029907
205	15	37903511	37903542	38069969	38070000	15	37903511	37907512	38069969
206	5	1010267	1010298	1038449	1038480	5	1006297	1010298	1034479
207	10	19508221	19508252	19593723	19593754	10	19508221	19512222	19589753
208	1	104992073	104992104	105164945	105164976	1	104992073	104996074	105160975
209	17	4337612	4337643	4528348	4528379	17	4333642	4337643	4524378
210	17	4418766	4418797	4517894	4517925	17	4414796	4418797	4513924
211	17	4418766	4418797	4528348	4528379	17	4414796	4418797	4524378

212	7	12601995	12602026	12717637	12717668	7	12601995	12605996	12713667
213	7	12717637	12717668	12737470	12737501	7	12713667	12717668	12737470
214	12	19894956	19894987	19974797	19974828	12	19894956	19898957	19970827
215	12	19992086	19992117	20053517	20053548	12	19992086	19996087	20049547
216	11	31942510	31942541	32032038	32032069	11	31942510	31946511	32032038
217	11	31953015	31953046	32042190	32042221	11	31953015	31957016	32038220
218	11	31953015	31953046	32032038	32032069	11	31953015	31957016	32032038
219	18	66450044	66450075	66500458	66500489	18	66446074	66450075	66496488
220	2	39767816	39767847	39804925	39804956	2	39763846	39767847	39804925
221	2	39767816	39767847	39839229	39839260	2	39763846	39767847	39835259
222	2	39767816	39767847	39835824	39835855	2	39763846	39767847	39835824
223	8	6868138	6868169	6923181	6923212	8	6868138	6872139	6923181
224	10	20037236	20037267	20084055	20084086	10	20037236	20041237	20080085
225	11	52882980	52883011	52915290	52915321	11	52882980	52886981	52911320
226	6	1098854	1098885	989242	989273	6	1098854	1102855	989242
227	11	17193641	17193672	17368932	17368963	11	17193641	17197642	17364962
228	11	17206623	17206654	17368932	17368963	11	17206623	17210624	17364962
229	11	17246461	17246492	17368932	17368963	11	17246461	17250462	17364962
230	11	17257199	17257230	17368932	17368963	11	17257199	17261200	17364962
231	11	17267739	17267770	17368932	17368963	11	17267739	17271740	17364962
232	11	17290815	17290846	17368932	17368963	11	17290815	17294816	17364962
233	1	61323595	61323626	61392274	61392305	1	61319625	61323626	61388304
234	1	61338770	61338801	61392274	61392305	1	61334800	61338801	61388304
235	1	61350438	61350469	61392274	61392305	1	61350438	61354439	61388304
236	1	109635329	109635360	109741316	109741347	1	109635329	109639330	109737346
237	1	109711483	109711514	109741316	109741347	1	109711483	109715484	109737346
238	1	109741316	109741347	109779877	109779908	1	109737346	109741347	109779877
239	25	25721432	25721463	25884535	25884566	25	25717462	25721463	25884535
240	11	22765246	22765277	22824653	22824684	11	22761276	22765277	22824653
241	23	34300375	34300406	34541066	34541097	23	34300375	34304376	34537096
242	23	34370479	34370510	34413070	34413101	23	34366509	34370510	34413070
243	2	39707018	39707049	39767816	39767847	2	39707018	39711019	39763846
244	2	39718640	39718671	39767816	39767847	2	39714670	39718671	39763846
245	2	39714609	39714640	39767816	39767847	2	39714609	39718610	39763846
246	2	39741527	39741558	39767816	39767847	2	39741527	39745528	39763846
247	2	66195314	66195345	66310948	66310979	2	66191344	66195345	66306978
248	2	66195314	66195345	66291709	66291740	2	66191344	66195345	66291709
249	2	66222272	66222303	66454370	66454401	2	66218302	66222303	66450400
250	2	66310948	66310979	66324859	66324890	2	66306978	66310979	66324859
251	2	66291709	66291740	66454370	66454401	2	66291709	66295710	66450400
252	16	35687870	35687901	35711378	35711409	16	35683900	35687901	35707408
253	16	35687870	35687901	35734783	35734814	16	35683900	35687901	35730813
254	11	25089999	25090030	25214955	25214986	11	25089999	25094000	25214955
255	11	25177016	25177047	25214955	25214986	11	25177016	25181017	25214955
256	21	5606382	5606413	5698848	5698879	21	5606382	5610383	5694878

Table 33.d5

N	**4 kb Sequence Location**		
	End2	Probe	Primer ID-1
193	48989579	LMO7_17_48756745_48760926_48985578_48994371_FR	OBD RD043.769
194	81583683	LY6D_9_81540380_81548206_81579682_81590550_FR	OBD RD043.773
195	81583683	LY6D_9_81540380_81548206_81579682_81590550_RR	OBD RD043.777
196	2855293	MAP3K4_31_2786762_2795002_2851292_2856203_FR	OBD RD043.781
197	16918093	MAP3K9_24_16803396_16807626_16910389_16918093_RF	OBD RD043.785

198	3408724	MAPK1_8_3352241_3355955_3404723_3412822_RR	OBD RD043.789
199	3479148	MAPK1_8_3435741_3439526_3469888_3479148_FF	OBD RD043.793
200	3473889	MAPK1_8_3435741_3439526_3469888_3479148_FR	OBD RD043.797
201	19619090	MAPK3_13_19583177_19588616_19608792_19619090_FF	OBD RD043.801
202	2278037	MAPK9_14_2229196_2237168_2274036_2279957_RR	OBD RD043.805
203	2405911	MAPK9_14_2229196_2237168_2401910_2410518_RR	OBD RD043.809
204	38033908	MDH1_15_37903511_37909683_38029907_38037711_RR	OBD RD043.813
205	38073970	MDH1_15_37903511_37909683_38069969_38081007_RR	OBD RD043.817
206	1038480	MDM4_5_1002213_1010298_1034976_1038480_FF	OBD RD043.821
207	19593754	MED25_10_19508221_19515457_19591613_19593754_RF	OBD RD043.825
208	105164976	MEF2A_1_104992073_105002150_105161756_105164976_RF	OBD RD043.829
209	4528379	MIPEP_17_4332285_4337643_4521242_4528379_FF	OBD RD043.833
210	4517925	MIPEP_17_4413535_4418797_4506914_4517925_FF	OBD RD043.837
211	4528379	MIPEP_17_4413535_4418797_4521242_4528379_FF	OBD RD043.841
212	12717668	MMP1_7_12601995_12610418_12711728_12717668_RF	OBD RD043.845
213	12741471	MMP1_7_12711728_12717668_12737470_12745025_FR	OBD RD043.849
214	19974828	MS4A2_12_19894956_19896244_19962410_19974828_RF	OBD RD043.853
215	20053548	MS4A2_12_19992086_20002065_20049543_20053548_RF	OBD RD043.857
216	32036039	MSI2_11_31942510_31947907_32032038_32042221_RR	OBD RD043.861
217	32042221	MSI2_11_31953015_31955643_32032038_32042221_RF	OBD RD043.865
218	32036039	MSI2_11_31953015_31955643_32032038_32042221_RR	OBD RD043.869
219	66500489	MSTN_18_66448734_66450075_66490497_66500489_FF	OBD RD043.873
220	39808926	MTHFR_2_39760745_39767847_39804925_39808549_FR	OBD RD043.877
221	39839260	MTHFR_2_39760745_39767847_39835824_39839260_FF	OBD RD043.881
222	39839825	MTHFR_2_39760745_39767847_39835824_39839260_FR	OBD RD043.885
223	6927182	MTMR3_8_6868138_6874813_6923181_6926871_RR	OBD RD043.889
224	20084086	MYBPC2_10_20037236_20038811_20080873_20084086_RF	OBD RD043.893
225	52915321	MYH1_11_52882980_52886797_52907287_52915321_RF	OBD RD043.897
226	993243	MYL1_6_1098854_1104299_989242_996235_RR	OBD RD043.901
227	17368963	MYL4_11_17193641_17194702_17358881_17368963_RF	OBD RD043.905
228	17368963	MYL4_11_17206623_17211708_17358881_17368963_RF	OBD RD043.909
229	17368963	MYL4_11_17246461_17251113_17358881_17368963_RF	OBD RD043.913
230	17368963	MYL4_11_17257199_17259878_17358881_17368963_RF	OBD RD043.917
231	17368963	MYL4_11_17267739_17271299_17358881_17368963_RF	OBD RD043.921
232	17368963	MYL4_11_17290815_17294484_17358881_17368963_RF	OBD RD043.925
233	61392305	MYOZ1_1_61314759_61323626_61385709_61392305_FF	OBD RD043.929
234	61392305	MYOZ1_1_61323626_61338801_61385709_61392305_FF	OBD RD043.933
235	61392305	MYOZ1_1_61350438_61357018_61385709_61392305_RF	OBD RD043.937
236	109741347	NDN_1_109635329_109640204_109733366_109741347_RF	OBD RD043.941
237	109741347	NDN_1_109711483_109720818_109733366_109741347_RF	OBD RD043.945
238	109783878	NDN_1_109733366_109741347_109779877_109789352_FR	OBD RD043.949
239	25888536	NDUFA8_25_25717207_25721463_25884535_25891335_FR	OBD RD043.953
240	22828654	NEUROD2_11_22762666_22765277_22824653_22836914_FR	OBD RD043.957
241	34541097	NFIB_23_34300375_34312881_34537544_34541097_RF	OBD RD043.961
242	34417071	NFIB_23_34364872_34370510_34413070_34423547_FR	OBD RD043.965
243	39767847	NPPA_2_39707018_39708108_39760745_39767847_RF	OBD RD043.969
244	39767847	NPPA_2_39714609_39718671_39760745_39767847_FF	OBD RD043.973
245	39767847	NPPA_2_39714609_39718671_39760745_39767847_RF	OBD RD043.977
246	39767847	NPPA_2_39741527_39742701_39760745_39767847_RF	OBD RD043.981
247	66310979	PALLD_2_66194319_66195345_66291709_66310979_FF	OBD RD043.985
248	66295710	PALLD_2_66194319_66195345_66291709_66310979_FR	OBD RD043.989
249	66454401	PALLD_2_66212034_66222303_66449615_66454401_FF	OBD RD043.993
250	66328860	PALLD_2_66291709_66310979_66324859_66327343_FR	OBD RD043.997
251	66454401	PALLD_2_66291709_66310979_66449615_66454401_RF	OBD RD043.1001
252	35711409	PCBP4_16_35681721_35687901_35707118_35711409_FF	OBD RD043.1005
253	35734814	PCBP4_16_35681721_35687901_35729420_35734814_FF	OBD RD043.1009
254	25218956	PHOSPHO1_11_25089999_25092180_25214955_25221072_RR	OBD RD043.1013

255	25218956	PHOSPHO1_11_25177016_25183355_25214955_25221072_RR	OBD RD043.1017
256	5698879	PIK3R1_21_5606382_5618174_5697527_5698879_RF	OBD RD043.1021

Table 33.d6

N	Primer Sequence	Primer ID-2	Primer Sequence
193	TTTTGTGTCCTAATGGAAGGCTGTGC	OBD RD043.771	CCCGAGTGCTCAGATTCTTGCTGG
194	GGCACTTCTGGTGTTTCAGCCTC	OBD RD043.775	CGGACGCTGGTTCCATAGTCGTG
195	CAGTGCGGTATCGGTGAAGGGAA	OBD RD043.779	CGGACGCTGGTTCCATAGTCGTG
196	CCTGCCACATCCGCTCTTGGTTG	OBD RD043.783	ACGAGCATTTATTGGGCACGGGC
197	CGTCTCCCCATTGTAAGGTAAACTCC	OBD RD043.787	TGAAAGCAAAGCACTTGGAAAGCATA
198	GTTGTGTGGAAACCTCTTCTGCCCCA	OBD RD043.791	GTAGATTTTGGACCTCGTGTCTCAGA
199	TGGTGTTGTGTGGAAACCTCTTCTGC	OBD RD043.795	ATGTGGCTATCCAACTATCCCAGCAC
200	CCCTTTTCATCAATGTTCGGGTG	OBD RD043.799	CCTGGGCGTCCTCAGACTGTCCG
201	CCGTGCCTTGGTTCTCTCTTCTG	OBD RD043.803	GCGGTGTTGTGGGCATCAAGGTG
202	GGCTGACTGAAGATACTTTGGCAT	OBD RD043.807	TTTTATCCTTGAAGCGTATTGAAT
203	CCTGGCTGACTGAAGATACTTTGGCA	OBD RD043.811	TAAGAGTTGGGAAGTGGTCAAGC
204	TACCCATAAATGTGTTTGCTGTTCAC	OBD RD043.815	CGGCAAGGGAGTAAACATCAGAGCAA
205	TACCCATAAATGTGTTTGCTGTTCAC	OBD RD043.819	CCCTTTGTCTCCTGAGCATCTGGTTT
206	GACACTTGGAGCCTGTTGTTTCT	OBD RD043.823	ACTCACATCAGTCAGCAGGAAGG
207	GAGTTGTAGTCCCCTGCCCACCT	OBD RD043.827	CGTGTATTCTGCTGTTTCCAGGTGG
208	CACCACGCAGCAGCCCGAAACAT	OBD RD043.831	GGGCAAGGAAACAGAGCCGTGTA
209	GGGAACTAACCCCACGACAAGAC	OBD RD043.835	GAGTCTCCCAGTCTCAGCCCATC
210	GACTCCCACGGATAAGATGCTCC	OBD RD043.839	GAGTCTCCCAGTCTCAGCCCATC
211	GGGAACTAACCCCACGACAAGAC	OBD RD043.843	GGCTCAGGGTTAGGTCAGGAGTC
212	GGATTTCCTATGGCAGCCTCCTTGGA	OBD RD043.847	CCCTTCTAACCACACACAAGTCCTTT
213	GGATTTCCTATGGCAGCCTCCTTGGA	OBD RD043.851	TACATTCAGGAGGACTGGAGACG
214	GCTTTCCCTATTTGATTTCAGAAG	OBD RD043.855	TAGGCAGGAACACTGTCTACTACA
215	GGGCTGTAACTGACCAGAATCTTTGA	OBD RD043.859	TTACACCCTTCGGAGGCACTGGAACA
216	CAAGGGTGGTGTGACAGGAAGTC	OBD RD043.863	GCGAGCCATCGGGAAAGAGCATC
217	TCAAGTCAGTGCCAGTCAAGGGC	OBD RD043.867	CTCCCCACCCAAGCCAAACAGGT
218	CTTTGTGGTTCATCCTCAGCCCC	OBD RD043.871	CTCCCCACCCAAGCCAAACAGGT
219	GGATAGTCTGTGGCAGGCTGGCTTTT	OBD RD043.875	TTCTCTGCTCCTTCCTTTCCAAACTG
220	TGGCTACGGCTGTGAGAGATGGA	OBD RD043.879	AGAGGAGGAAATGGCAGGCAGCC
221	TCACCCAAACCGTAGAGACAGGAGTG	OBD RD043.883	TATCCCTAAATGTCCCTTTTCACAGC
222	GTGGCTACGGCTGTGAGAGATGG	OBD RD043.887	CCTGCGTTTCTCCAAGGATGGTC
223	GGAACACCAATAAGTGGGCTAATACA	OBD RD043.891	CCCTGTGGCAAGTGATGGCAGTAGAA
224	GGGCAGAGAAAAGAGTCACTGTG	OBD RD043.895	TTCTGTGGTCCCTCCGCCTCCGC
225	CAGGGACTCCAGAATAACTGACCC	OBD RD043.899	GCAGTTCAACAGCCTGGAGCAGC
226	CTCAAACACTCCCAGCGTTGGCA	OBD RD043.903	GCCCTAACCTCTCCCCTTCACCA
227	GACTGTAAAGATGAAAGAAGATTC	OBD RD043.907	AGAAGAGACTTACTGTGCTATTTT
228	CAAAAGTCTGCCAAGTTATTCCTGGG	OBD RD043.911	TCAGACTCTAACCCACCTGTTCTTGG
229	GACTGTAAAGATGAAAGAAGATTC	OBD RD043.915	CTTGGTTTCCTTTGCCTTCCAGAA
230	CAAAAGTCTGCCAAGTTATTCCTGGG	OBD RD043.919	GGCTCTCACTCTTTCTCCTCAGCAGA
231	CAAAAGTCTGCCAAGTTATTCCTGGG	OBD RD043.923	GGCAGGATGGCATTCCACCTTATGTC
232	GACTGTAAAGATGAAAGAAGATTC	OBD RD043.927	GGTTGCTGTGACAAAATGCCATAG
233	GCTATTGTAAAGAGGCTATGCCAACT	OBD RD043.931	CATTCAACATACCCTCCTCCTCGCTG
234	CCATTCAACATACCCTCCTCCTCGC	OBD RD043.935	GGACATTATTCTCCAGGAAAGACCT
235	CATAAAGTAGAGGAGGACTGGTC	OBD RD043.939	TCCCATTCAACATACCCTCCTCC
236	GCCCTCTTGGGACTGAACTCTCT	OBD RD043.943	CGCCCCAACCTTGCTGGACATTG
237	CAGCCCTCTTGGGACTGAACTCTCTA	OBD RD043.947	CAGAAGAACTCCTGAAACGCCAAGAA
238	CAGCCCTCTTGGGACTGAACTCTCTA	OBD RD043.951	GCCAACACTGTGGAACTGAATCTAAG
239	TCATAGGCAATAGATTTCCTGGGAGC	OBD RD043.955	CAGCCGACAGTAGCCCTTAGATTGCT
240	GACAGCCAGACTGATGGGTGAGG	OBD RD043.959	CCACTCCCTTCCCATTCCTCCTT
241	CACTCGGCAGATGGCGTGGCATA	OBD RD043.963	TCTCTGCCCGTGACTTTGCTCCT
242	ATGTAACTGCCTACGAACCCTCCAGG	OBD RD043.967	AGATTAGGGTTGCTGAGTGGGTCAAT

243	GTGGCTACGGCTGTGAGAGATGG	OBD RD043.971	CAGGAACCTCTAATCCACGCCCT
244	TGGCTACGGCTGTGAGAGATGGA	OBD RD043.975	TTCCAGGACAACCGCATCCAGGG
245	GACCACCCCGCCCAGGCTGACCT	OBD RD043.979	ACGGCTGTGAGAGATGGAGAGTC
246	TGGCTACGGCTGTGAGAGATGGA	OBD RD043.983	AGGTGGCTTCCTGTGGGCTGAGA
247	GAGGAAGATTGGCAACAGATGCTA	OBD RD043.987	CCTCTATGTTTTCTCGTTCTTTTA
248	CCCACACACCACACCACTCATCA	OBD RD043.991	AGGCAGTCCACAAAGCCAGCGTG
249	GGCTTCTGGCACTTACTGAATGGCTT	OBD RD043.995	AGGTGGAAATGTAAGGCTGAGTAGGC
250	GAAAGAGAAATACACTCAACAGAGA	OBD RD043.999	TCCTCTATGTTTTCTCGTTCTTTTA
251	TCCAGAGGGCTGAAGACTTGAGAAAG	OBD RD043.1003	GGGACTCATAGGGAGACACATTA
252	TAGGTCCTTGGCATACGCATTGA	OBD RD043.1007	CTAAATAAAAGAGCACTACTGCCAGA
253	GAGTCTACGCTACAGATACAAGGG	OBD RD043.1011	AGAATCCACAAATCCATACTGATA
254	ATGGTCTGTGCCCCTGGTGCCTA	OBD RD043.1015	ATTGGGCAGGAGGTGAGGAACTG
255	CACCTCACATTCTAACATCTCAGTCT	OBD RD043.1019	TTGATGCTCTGGATTGGGCAGGAGGT
256	CCAGACAGGAGGAGAGAACAGATTTC	OBD RD043.1023	GTTTTGTTCCCAAGTGCCTCTGACAG

Table 33.d7

N	Probe	Marker
193	LMO7	OBD RD043.769.771
194	LY6D	OBD RD043.773.775
195	LY6D	OBD RD043.777.779
196	MAP3K4	OBD RD043.781.783
197	MAP3K9	OBD RD043.785.787
198	MAPK1	OBD RD043.789.791
199	MAPK1	OBD RD043.793.795
200	MAPK1	OBD RD043.797.799
201	MAPK3	OBD RD043.801.803
202	MAPK9	OBD RD043.805.807
203	MAPK9	OBD RD043.809.811
204	MDH1	OBD RD043.813.815
205	MDH1	OBD RD043.817.819
206	MDM4	OBD RD043.821.823
207	MED25	OBD RD043.825.827
208	MEF2A	OBD RD043.829.831
209	MIPEP	OBD RD043.833.835
210	MIPEP	OBD RD043.837.839
211	MIPEP	OBD RD043.841.843
212	MMP1	OBD RD043.845.847
213	MMP1	OBD RD043.849.851
214	MS4A2	OBD RD043.853.855
215	MS4A2	OBD RD043.857.859
216	MSI2	OBD RD043.861.863
217	MSI2	OBD RD043.865.867
218	MSI2	OBD RD043.869.871
219	MSTN	OBD RD043.873.875
220	MTHFR	OBD RD043.877.879
221	MTHFR	OBD RD043.881.883
222	MTHFR	OBD RD043.885.887
223	MTMR3	OBD RD043.889.891
224	MYBPC2	OBD RD043.893.895
225	MYH1	OBD RD043.897.899
226	MYL1	OBD RD043.901.903
227	MYL4	OBD RD043.905.907
228	MYL4	OBD RD043.909.911
229	MYL4	OBD RD043.913.915
230	MYL4	OBD RD043.917.919

231	MYL4	OBD RD043.921.923
232	MYL4	OBD RD043.925.927
233	MYOZ1	OBD RD043.929.931
234	MYOZ1	OBD RD043.933.935
235	MYOZ1	OBD RD043.937.939
236	NDN	OBD RD043.941.943
237	NDN	OBD RD043.945.947
238	NDN	OBD RD043.949.951
239	NDUFA8	OBD RD043.953.955
240	NEUROD2	OBD RD043.957.959
241	NFIB	OBD RD043.961.963
242	NFIB	OBD RD043.965.967
243	NPPA	OBD RD043.969.971
244	NPPA	OBD RD043.973.975
245	NPPA	OBD RD043.977.979
246	NPPA	OBD RD043.981.983
247	PALLD	OBD RD043.985.987
248	PALLD	OBD RD043.989.991
249	PALLD	OBD RD043.993.995
250	PALLD	OBD RD043.997.999
251	PALLD	OBD RD043.1001.1003
252	PCBP4	OBD RD043.1005.1007
253	PCBP4	OBD RD043.1009.1011
254	PHOSPHO1	OBD RD043.1013.1015
255	PHOSPHO1	OBD RD043.1017.1019
256	PIK3R1	OBD RD043.1021.1023

Table 33.d8

N	Probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig
257	PLXDC1_11_23117935_23125158_23188757_23196195_RR	PLXDC1	1	27
258	PRKAG2_4_103028895_103043216_103233754_103234780_RF	PRKAG2	2	177
259	PRKAG2_4_103028895_103043216_103342192_103345172_RR	PRKAG2	2	177
260	PRKCA_11_13786370_13794644_13849517_13854647_RF	PRKCA	1	60
261	PRKCB_13_23475428_23483033_23690253_23695272_RF	PRKCB	2	19
262	PRKCB_13_23532412_23540462_23690253_23695272_RF	PRKCB	2	19
263	RAB33B_2_91817483_91819013_91968018_91981648_FF	RAB33B	2	45
264	RAB33B_2_91817483_91819013_91968018_91981648_RR	RAB33B	2	45
265	RAG2_12_2995445_3004477_3070874_3072970_RF	RAG2	3	49
266	RAG2_12_2995445_3004477_3070874_3072970_RR	RAG2	3	49
267	RAG2_12_2995445_3004477_3124836_3128121_RF	RAG2	3	49
268	RASSF5_5_2727413_2732312_2768970_2779500_FF	RASSF5	3	31
269	RASSF5_5_2727413_2732312_2857276_2865680_FF	RASSF5	3	31
270	RASSF5_5_2752106_2755183_2768970_2779500_FF	RASSF5	3	31
271	RBPJL_22_34286715_34290143_34327562_34334894_FR	RBPJL	2	28
272	RBPJL_22_34286715_34290143_34327562_34334894_RR	RBPJL	2	28
273	SCN10A_16_46394076_46405616_46559136_46563398_RF	SCN10A	3	120
274	SCN10A_16_46394076_46405616_46644599_46646012_RF	SCN10A	3	120
275	SCN10A_16_46542432_46554053_46644599_46646012_RF	SCN10A	3	120
276	SCN2B_7_25981242_25985420_26023779_26030228_FF	SCN2B	2	31
277	SCN2B_7_25981242_25985420_26102356_26109968_FF	SCN2B	2	31
278	SCN4B_7_25954012_25959734_25981242_25985420_RF	SCN4B	1	31
279	SCN5A_16_46559136_46563398_46724067_46732988_FF	SCN5A	2	30
280	SCN5A_16_46559136_46563398_46724067_46732988_FR	SCN5A	2	30
281	SELL_5_6104471_6117065_6186372_6188629_FR	SELL	1	111

282	SEPT7_4_65366992_65373527_65534812_65540822_RF	SEPT7	1	127
283	SGCA_11_25806231_25808754_26000893_26002740_RF	SGCA	2	13
284	SGCA_11_25806231_25808754_26000893_26002740_RR	SGCA	2	13
285	SIK2_7_20268830_20278159_20296076_20300289_FR	SIK2	4	204
286	SIK2_7_20268830_20278159_20375473_20380173_FF	SIK2	4	204
287	SIK2_7_20268830_20278159_20391427_20402715_FR	SIK2	4	204
288	SIK2_7_20268830_20278159_20407650_20411122_FR	SIK2	4	204
289	SNAP29_8_3045435_3054804_3164300_3172603_FF	SNAP29	2	50
290	SNAP29_8_3117316_3123446_3164300_3172603_FF	SNAP29	2	50
291	SPRED1_1_149873033_149876737_150087432_150097168_RF	SPRED1	8	166
292	SPRED1_1_149873033_149876737_150099832_150110035_RF	SPRED1	8	166
293	SPRED1_1_149910043_149913663_150087432_150097168_RF	SPRED1	8	166
294	SPRED1_1_149910043_149913663_150099832_150110035_RF	SPRED1	8	166
295	SPRED1_1_149923380_149924915_150099832_150110035_RF	SPRED1	8	166
296	SPRED1_1_150016977_150019540_150099832_150110035_RF	SPRED1	8	166
297	SPRED1_1_150032266_150036031_150087432_150097168_RF	SPRED1	8	166
298	SPRED1_1_150068252_150074099_150099832_150110035_RF	SPRED1	8	166
299	SRC_22_27681702_27686300_27826003_27831147_FR	SRC	1	28
300	SRF_20_42097551_42100241_42177997_42186255_FR	SRF	1	31
301	STAT1_18_67266270_67281181_67315145_67320245_RF	STAT1	3	37
302	STAT1_18_67266270_67281181_67340514_67345500_RF	STAT1	3	37
303	STAT1_18_67266270_67281181_67404406_67407824_RR	STAT1	3	37
304	STAT3_11_20601546_20610244_20625038_20630547_FF	STAT3	2	28
305	STAT3_11_20601546_20610244_20625038_20630547_RF	STAT3	2	28
306	STAT5A_11_20625038_20630547_20748936_20755885_FF	STAT5A	1	30
307	STXBP4_11_29798087_29803880_29820062_29826392_RF	STXBP4	2	58
308	STXBP4_11_29820062_29826392_29856303_29862822_FR	STXBP4	2	58
309	TGFBR1_25_5777848_5781338_5953575_5963779_RF	TGFBR1	2	29
310	TGFBR1_25_5838527_5844153_5953575_5963779_RF	TGFBR1	2	29
311	TMEM156_3_88174369_88185533_88338789_88351273_FF	TMEM156	1	90
312	TOB1_11_26381091_26387145_26421158_26424834_RR	TOB1	2	31
313	TOB1_11_26381091_26387145_26552180_26554959_RR	TOB1	2	31
314	TSPAN3_1_117377450_117387477_117527452_117533304_RF	TSPAN3	2	53
315	TSPAN3_1_117501086_117515708_117527452_117533304_RF	TSPAN3	2	53
316	TSPAN5_3_40723323_40732311_40838443_40842795_RF	TSPAN5	1	176
317	VAV1_7_4248599_4253460_4432636_4444354_FF	VAV1	1	38
318	VEGFC_27_31943096_31950700_31994751_32003367_RR	VEGFC	2	54
319	VEGFC_27_31943096_31950700_32006848_32015827_RR	VEGFC	2	54
320	ZFHX3_3_20954370_20958861_21248124_21260027_FF	ZFHX3	1	141

Table 33.e1

N	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr
257	0.178891485	0.267074007	3.7	-0.498546573	8.334899675
258	0.248623084	0.310300562	1.13	-0.938829032	8.830030136
259	0.248623084	0.310300562	1.13	-0.409357346	9.945611435
260	0.303088108	0.331342084	1.67	-0.32685719	9.445425416
261	0.009980432	0.049518297	10.53	-0.470343416	9.5078615
262	0.009980432	0.049518297	10.53	-0.310412046	10.44482443
263	0.046697041	0.122937109	4.44	-0.192180899	10.74179204
264	0.046697041	0.122937109	4.44	-0.354237277	9.242623502
265	0.006920652	0.037512367	6.12	0.358172408	9.004366375
266	0.006920652	0.037512367	6.12	0.207569755	9.114059545
267	0.006920652	0.037512367	6.12	0.274277591	8.211642632
268	0.001955877	0.014841655	9.68	-0.380422279	10.05354755
269	0.001955877	0.014841655	9.68	-0.379141769	10.15172147

270	0.001955877	0.014841655	9.68	-0.321187765	8.346983577
271	0.020494302	0.075554863	7.14	-0.418632216	9.712363657
272	0.020494302	0.075554863	7.14	0.256227174	9.629544001
273	0.059031661	0.137915817	2.5	-0.303249497	9.538210055
274	0.059031661	0.137915817	2.5	-0.392996971	10.12637726
275	0.059031661	0.137915817	2.5	-0.517204321	9.549017556
276	0.024599258	0.075554863	6.45	-0.330982641	8.754115738
277	0.024599258	0.075554863	6.45	-0.600780426	8.122591447
278	0.198752749	0.267074007	3.23	-0.513873909	8.171494225
279	0.023201487	0.075554863	6.67	-0.275782912	9.599314892
280	0.023201487	0.075554863	6.67	-0.332593132	9.221879302
281	0.368532709	0.369972517	0.9	-0.192237265	11.73871812
282	0.369595168	0.369972517	0.79	0.236701745	11.5277415
283	0.004781729	0.029373479	15.38	-0.299567355	9.597332982
284	0.004781729	0.029373479	15.38	-0.395116377	8.436344868
285	0.060939547	0.137915817	1.96	-0.250370376	8.821107854
286	0.060939547	0.137915817	1.96	-0.205233587	8.887500946
287	0.060939547	0.137915817	1.96	-0.328539529	8.245361941
288	0.060939547	0.137915817	1.96	-0.366691703	8.419551683
289	0.055461917	0.137588217	4	-0.245937866	10.96109836
290	0.055461917	0.137588217	4	-0.261369209	11.03851689
291	0.0000634628527405492	0.001364451	4.82	0.626539336	8.460307208
292	0.0000634628527405492	0.001364451	4.82	0.45135055	7.830572417
293	0.0000634628527405492	0.001364451	4.82	0.514959643	8.178202101
294	0.0000634628527405492	0.001364451	4.82	0.330234467	7.825606038
295	0.0000634628527405492	0.001364451	4.82	0.347918733	8.022790865
296	0.0000634628527405492	0.001364451	4.82	0.265700639	8.225367878
297	0.0000634628527405492	0.001364451	4.82	0.418287098	8.296113768
298	0.0000634628527405492	0.001364451	4.82	0.292449794	7.689848783
299	0.183998999	0.267074007	3.57	-0.257211227	8.96771926
300	0.198752749	0.267074007	3.23	-0.289791551	11.53768831
301	0.003219239	0.020764093	8.11	0.950923864	8.127367441
302	0.003219239	0.020764093	8.11	0.339957139	10.88074422
303	0.003219239	0.020764093	8.11	0.422734986	8.738942644
304	0.020494302	0.075554863	7.14	-0.34818003	9.404675926
305	0.020494302	0.075554863	7.14	-0.308351369	10.09067586
306	0.193928419	0.267074007	3.33	-0.327160983	10.04088364
307	0.070089709	0.151221234	3.45	0.301994949	8.888178828
308	0.070089709	0.151221234	3.45	0.297112393	8.516631477
309	0.02183283	0.075554863	6.9	-0.462921799	9.298865314
310	0.02183283	0.075554863	6.9	-0.502142385	8.308741006
311	0.355201455	0.369972517	1.11	-0.25947705	8.734272977
312	0.024599258	0.075554863	6.45	-0.67235893	8.052267141
313	0.024599258	0.075554863	6.45	-0.658106699	8.007819166
314	0.060873696	0.137915817	3.77	-0.576817806	8.097751634
315	0.060873696	0.137915817	3.77	-0.568732319	8.537384311
316	0.341994894	0.367644511	0.57	-0.456101192	9.282066601
317	0.23001238	0.297307866	2.63	-0.183925655	10.27585426
318	0.062698978	0.139451175	3.7	-0.51992089	8.803285229
319	0.062698978	0.139451175	3.7	-0.570858041	8.216821116
320	0.365633172	0.369972517	0.71	-0.359210093	10.90927278

Table 33.e2

N	t	P.Value	adj.P.Val	B	FC
257	-8.679819127	0.0000000466671136396821	0.000070018619349385	8.618875681	0.707819507
258	-12.72862254	0.000000000080568203541454	0.000000960392461716811	14.05544918	0.521656113
259	-7.136605672	0.00000846145358915483	0.000471545	5.94886147	0.752958707
260	-7.042847832	0.0000101943002074247	0.00053024	5.774815448	0.797271393
261	-7.060938638	0.00000983342866158556	0.000518381	5.808503626	0.721792764
262	-6.523007013	0.0000292622869023077	0.001037747	4.785416246	0.806411408
263	-6.177861318	0.0000601133616970513	0.001701441	4.106203741	0.875281571
264	-6.685600302	0.0000209595044430101	0.000822758	5.09928145	0.782283111
265	5.396796706	0.0000323877534937054	0.005178058	2.508645352	1.281801096
266	5.003725624	0.0000775486565602272	0.00961269	1.677385244	1.154741363
267	6.369772263	0.00000402056197173788	0.001307018	4.48601267	1.209388354
268	-5.516753496	0.0000248906319064535	0.004416684	2.75901438	0.768212701
269	-5.382597738	0.0000334164554567416	0.005277635	2.478900424	0.768894855
270	-5.006426169	0.0000770809956858349	0.009606804	1.683147538	0.800410631
271	-5.662219604	0.0000181264479152015	0.003741337	3.060319651	0.748133575
272	5.012432569	0.0000760511136821973	0.009570174	1.695961392	1.194351241
273	-6.533997102	0.00000286064608645947	0.001033276	4.806755937	0.810424954
274	-6.783534136	0.00000171722954949946	0.00071265	5.286406035	0.761545969
275	-7.367545782	0.00000053746105134074 9	0.00033823	6.371766941	0.698724522
276	-5.071224906	0.0000666805443887129	0.008670693	1.821215505	0.794994816
277	-6.716956804	0.00000196610975254916	0.0007907	5.159353307	0.659397158
278	-6.486863965	0.00000315305553468220	0.001088502	4.715109769	0.700339367
279	-6.351012197	0.00000418091312232632	0.00133884	4.449120217	0.826001948
280	-6.052890375	0.00000783121810960962	0.002092437	3.856049162	0.794107853
281	-5.560217945	0.0000226347401909662	0.004245102	2.849313135	0.875247375
282	5.779181792	0.0000140717989649137	0.003153542	3.300663941	1.178295788
283	-7.386976626	0.00000051749520319 2340	0.000336458	6.406972586	0.812496017
284	-6.766116831	0.00000177901940080403	0.000730522	5.253232767	0.760428033
285	-7.016707493	0.00000107401014567895	0.000532857	5.726048608	0.840680564
286	-5.060793325	0.0000682529865421064	0.00878729	1.799014592	0.867398235
287	-5.72356327	0.0000158691029014987	0.003458401	3.186592403	0.79634223
288	-7.062768364	0.000000979767285195514	0.000518381	5.81190808	0.775558922
289	-5.519623473	0.0000247348136116668	0.004416684	2.764983829	0.843267427
290	-5.324822449	0.0000379586640410418	0.005899472	2.357637174	0.834295744
291	8.610941071	0.0000000527587433889362	0.000076226614059348	8.507428978	1.543857222
292	8.317816898	0.0000000895362606598224	0.000094400257522694	8.025208094	1.367319647
293	5.398124663	0.0000322932145065220	0.005178058	2.51142608	1.428954167
294	5.241619663	0.0000456337287914882	0.006692375	2.18236792	1.257217681
295	5.310396024	0.0000391882227946439	0.00599503	2.327300642	1.272723241
296	5.519453444	0.0000247440170633763	0.004416684	2.764630201	1.202219761
297	7.351175156	0.00000055490107289 8733	0.00033823	6.342060509	1.336339985
298	5.014061752	0.0000757741890045537	0.009566185	1.699436487	1.224718167
299	-6.350304057	0.00000418709338863960	0.00133884	4.447726623	0.836703731
300	-5.771975103	0.0000142923844781131	0.003153542	3.285905862	0.818020242
301	6.786415088	0.00000170722463564491	0.00071265	5.291888693	1.933110174
302	5.902616329	0.0000107912833479968	0.002598568	3.552375976	1.265718991
303	5.329665604	0.0000375547764940088	0.005860047	2.367816494	1.340466334
304	-5.50999994	0.0000252612746619697	0.00443021	2.744963363	0.785574481
305	-6.758325987	0.00000180739710817034	0.000734443	5.238379279	0.807564071
306	-6.387863787	0.00000387192196030923	0.001269275	4.521541626	0.797103527
307	7.516520233	0.00000040259024645 1762	0.000285546	6.640189451	1.232848009
308	6.214597334	0.00000055638117296 5962	0.001607736	4.179317957	1.228682697
309	-5.501989713	0.0000257082159965563	0.004477132	2.728290772	0.725515429
310	-5.432137617	0.0000299655620481664	0.004995541	2.58258052	0.706057515
311	-5.691989465	0.0000169925238007217	0.003622286	3.121658976	0.835390678
312	-8.960872932	0.00000002846283234 41866	0.000048275438684640	9.066366288	0.627479865

313	-8.504782119	0.000000063816325217 2577	0.000078597025797400	8.334275623	0.633709391
314	-9.911052133	0.000000005743505393 40819	0.000013179655611580	10.49543486	0.670440958
315	-12.64601994	0.000000000098476540550 3011	0.000009603924617168 11	13.96387344	0.674208949
316	-7.115525574	0.000000882250643786341	0.000484741	5.909847949	0.728953558
317	-5.065028806	0.0000676100320214694	0.008756001	1.80802993	0.880304376
318	-6.932852329	0.0000012704004082 1895	0.00058998	5.568900951	0.697410075
319	-6.149465237	0.000006382538637612 45	0.001778449	4.049556555	0.673216275
320	-10.65803034	0.000000001754815480704 41	0.000005704612658523 24	11.5327881	0.779591306

Table 33.e3

N				Probe sequence
	FC_1	LS	Loop Detected	60 mer
257	-1.412789547	-1	Stayer	AGTATTTGTATTTATTCTGGGAGTTTCATCGAACTGGCTTCATGCCAGATGCTGGAATTG
258	-1.91697169	-1	Stayer	AAGTTAGTACTGCATTGTTAGTCAAGTGTCGAAATTGCTATGTATACCAAAGATTAAGGC
259	-1.328094078	-1	Stayer	GCCTTAATCTTTGGTATACATAGCAATTTCGACCCACACAGCTCAAGAAGCTAATGCGCA
260	-1.254278039	-1	Stayer	GTACAATATAGAGACATCATTCTCGTTATCGATTGGCGCACAAGTGCCAGGGACACCTGC
261	-1.385439215	-1	Stayer	GGAAGAGGAAAAGAGAACTTAAAGAAGATCGAGAGAAAAGAAGGACAGACGAGGCTTCCA
262	-1.240061822	-1	Stayer	GGAAGAGGAAAAGAGAACTTAAAGAAGATCGACGGCAGCATAGCCTCTGAGCTGGACAGG
263	-1.142489494	-1	Stayer	TACAGGTGCCGTGTACCACTTTGATAAGTCGAACATTTGTTATTTTTTGTCTTGGTAATT
264	-1.278309587	-1	Stayer	AAAACTTTCATCGCAAATGTACTAGCTGTCGAAAACAGCACAGCTTTTTGAGCCAGAAAA
265	1.281801096	1	Sprinter	GTGCTTCTTTAAGATACCAGATAATTGATCGATACGACAGAACCTAGAAAAAGTTCCGAG
266	1.154741363	1	Sprinter	CTCGGAACTTTTTCTAGGTTCTGTCGTATCGATTCAATTCGTATATCTCCCTCTTTCTCA
267	1.209388354	1	Sprinter	GGTCTACCCGTGCGTGTTAACGCCGGGGTCGATACGACAGAACCTAGAAAAAGTTCCGAG
268	-1.301722815	-1	Stayer	CGGCAGAGCTCACTGCAGTCAATTGGAATCGAACACTATGATAATTCTTTCCCAGATTCA
269	-1.300567943	-1	Stayer	CGGCAGAGCTCACTGCAGTCAATTGGAATCGAGTTTATGCCTATCATAGGACTTGAACAG
270	-1.249358718	-1	Stayer	TCTTCATTTATTTAGTGCTCACAAAAACTCGAACACTATGATAATTCTTTCCCAGATTCA
271	-1.3366597	-1	Stayer	GGGCGTATTGCTATGGTTATGCCCCAGCTCGATTGTCTTATTTTTATTTATTTCTATCAC
272	1.194351241	1	Sprinter	CTTTTTTACAAATCCTAAAGGATGCCCCTCGATTGTCTTATTTTTATTTATTTCTATCAC
273	-1.233920543	-1	Stayer	ACCAGTGTCATCAGTACCCTAGAGGGCTTCGATGTTGTCTGCCTTTTTAATTTTTAACCA
274	-1.313118369	-1	Stayer	CCTTTGAGTCTCTGGTCAAGATTCTGGCTCGATGTTGTCTGCCTTTTTAATTTTTAACCA
275	-1.431179196	-1	Stayer	CCTTTGAGTCTCTGGTCAAGATTCTGGCTCGAAGATTAGAAATATTTGGATATATTTCTA
276	-1.257869837	-1	Stayer	GTGCGCTGCGCAGCTTAAACAGCAGAATTCGATGATTCTTGCCCGAGTCATATTTCACTA
277	-1.516536715	-1	Stayer	GTGCGCTGCGCAGCTTAAACAGCAGAATTCGATCTTAAATTTATTGTATTTTGTTTGCAT
278	-1.427879178	-1	Stayer	GTGCGCTGCGCAGCTTAAACAGCAGAATTCGACAAGGATCAGATATCATTAAGTCAAGTT
279	-1.210650898	-1	Stayer	ACCAGTGTCATCAGTACCCTAGAGGGCTTCGAATGTTGAAACATACTCTCCAGTGTGATG
280	-1.25927479	-1	Stayer	ACCAGTGTCATCAGTACCCTAGAGGGCTTCGAAACAAATGCTTTATATACTTACATCATC
281	-1.142534132	-1	Stayer	AGTATTGGGAAGGAGTCACGGTCAGTAATCGAGAGCAGCATGTTAGCTCTCCGCCTTCGG
282	1.178295788	1	Sprinter	CCCCTGCCTTACTCCCAGGGGCCGCCATTCGATGGGGGCACCGGGCAAGTCACTCACCCT
283	-1.230775265	-1	Stayer	AAGGGGAAAAAATAAAAATAGAAGACCATCGAATCCGGTACTTTCTGGCCTTCCAAAAAG
284	-1.315048836	-1	Stayer	CTTTTTGGAAGGCCAGAAAGTACCGGATTCGACCGTGGTGTATAATCCTTTTAATATACT
285	-1.189512454	-1	Stayer	ATAAGTTTGTTCTGTAACCGTAATTAAGTCGAAGGATGTTGGTCCTAGACCCATCCAAAC
286	-1.152872993	-1	Stayer	ATAAGTTTGTTCTGTAACCGTAATTAAGTCGAATAGCCCACGTTCAAGTGGAGAGGAATT
287	-1.255741517	-1	Stayer	ATAAGTTTGTTCTGTAACCGTAATTAAGTCGACAAATTCTATCAACTGATGAATTTATAA
288	-1.289392684	-1	Stayer	ATAAGTTTGTTCTGTAACCGTAATTAAGTCGAAGCTAAAAATATGCTTTAGTTTAAAATT
289	-1.185863426	-1	Stayer	GCAAAGAAATATCTTTTATTTGCAAAATTCGAGATCTGGGGGTACTGGGTGGACTCTGGG
290	-1.198615727	-1	Stayer	ACAAAGATTCTGTGGTTCCTTACCTTCTTCGAGATCTGGGGGTACTGGGTGGACTCTGGG
291	1.543857222	1	Sprinter	GTTTGAAGTTTTGATTATTGCATGTAATTCGACTCTAGAAAAGTCTTTGAAAGATAAAAG
292	1.367319647	1	Sprinter	TCAGTTATGGACATGTCTTGAAGTTAAATCGACTCTAGAAAAGTCTTTGAAAGATAAAAG
293	1.428954167	1	Sprinter	GTTTGAAGTTTTGATTATTGCATGTAATTCGATCAAACATTATTCTGGATGTTTAAGTGA
294	1.257217681	1	Sprinter	TCAGTTATGGACATGTCTTGAAGTTAAATCGATCAAACATTATTCTGGATGTTTAAGTGA

295	1.272723241	1	Sprinter	TCAGTTATGGACATGTCTTGAAGTTAAATCGAATACACAGGGTGTGAGATTAAGAGAAGA
296	1.202219761	1	Sprinter	TCAGTTATGGACATGTCTTGAAGTTAAATCGAGAAATGTGACGCAATAAATTTCCGTTGT
297	1.336339985	1	Sprinter	GTTTGAAGTTTTGATTATTGCATGTAATTCGAAAGCCCAGGTTGTCACTGGGCTTCTGAC
298	1.224718167	1	Sprinter	TCAGTTATGGACATGTCTTGAAGTTAAATCGAATATTACCTAAATTTTATCTATATAGAA
299	-1.195166178	-1	Stayer	GGGAGCTAAAAGTACAATTTTTAAAGAGTCGATCCGTCACGTAGCAATATCAGCTGTGCG
300	-1.222463636	-1	Stayer	TGCCAGTGTACCCAATAGGTACGGCCCGTCGAGTCACCCCAGTTCTGAGTCACCCCACTT
301	1.933110174	1	Sprinter	AAAACCCAAGTAAATGTCCTTGATTATTTCGAGGGTTTTTTTTTTTTTTAATTGGTTTTA
302	1.265718991	1	Sprinter	TAAAACCCAAAGACTTCAGCTTTCCCTCTCGAGGGTTTTTTTTTTTTTTAATTGGTTTTA
303	1.340466334	1	Sprinter	TAAAACCAATTAAAAAAAAAAAAAACCCTCGAGTCTCTTAACCAATTACATGTGTGTTGG
304	-1.272953774	-1	Stayer	ATGGCCCAATGGAATCAGCTGCAGCAGCTCGATGACCTGCACTAGGTACCGCAATGACCT
305	-1.238291841	-1	Stayer	AGGTCATTGCGGTACCTAGTGCAGGTCATCGAGCCTGATTGTAATTTATAGACTGAACAG
306	-1.254542185	-1	Stayer	AGGTCATTGCGGTACCTAGTGCAGGTCATCGAGCATGCGCTGCTTGAGCGTCCGCGGCAG
307	1.232848009	1	Sprinter	ATTGCTTAAAAGTAAAAGTGCCATTGAGTCGAAAAACTTTTGAGGCATCCACTGAAAAGC
308	1.228682697	1	Sprinter	ATTGCTTAAAAGTAAAAGTGCCATTGAGTCGAATATTAATGTTTTCCAACAACAGATTTA
309	-1.378330439	-1	Stayer	AGCTGATTTTACTCTTGGATTTATTTCATCGACTGCGAACTCCGTGGAGCTCTAGAGAGA
310	-1.416315213	-1	Stayer	AGCTGATTTTACTCTTGGATTTATTTCATCGACTAATAAAGTAGCATCAAAATATATAAG
311	-1.19704472	-1	Stayer	GGTTCACAATGTAGCTATTTCCAAGCGATCGATTCAGTTCCACCTAAGTTCTTACTGATA
312	-1.593676636	-1	Stayer	TCATCCATGGAATGTAATGACTATGAGATCGAATTAATACCTTTTGAAAAAAACTTAGCA
313	-1.578010384	-1	Stayer	TCATCCATGGAATGTAATGACTATGAGATCGACTCTATGCTCCAGTCATTTAAAAATAGT
314	-1.491555651	-1	Stayer	TAGTGACTTTCCCCAAAATAAAGTACATTCGATATTTGGCCAGATTTCCTGGCTAAAGTT
315	-1.483219708	-1	Stayer	TAGTGACTTTCCCCAAAATAAAGTACATTCGAGATTTTCCTGACAAGGTACCACCCAAGC
316	-1.371829506	-1	Stayer	ATATTTGTACTGGCAAACTGTTCTTTACTCGATACAGTCAGCTCCCTGTACACTCAGGAA
317	-1.135970725	-1	Stayer	ATGGAGTACCTGAGAAGGTGATGTTAGCTCGAAAAAATATCTGCCAAGAGTGTGGTACTT
318	-1.433876619	-1	Stayer	GCTCAATGAAAGGGTTCCAAATCATTGATCGATCACTGACACTGCTCACTGTGATCTCTT
319	-1.485406752	-1	Stayer	GCTCAATGAAAGGGTTCCAAATCATTGATCGATTTGGACCTTGAGTGCGCAGTGTCTGTG
320	-1.282723386	-1	Stayer	ATTATGATTGTGGCAATGCTTCGGAAGGTCGAAACCACCCTTTAAAAAAACATTTTTTTA

Table 33.e4

N	Probe Location					4 kb Sequence Location			
	Chr	Start1	End1	Start2	End2	Chr	Start1	End1	Start2
257	11	23117935	23117966	23188757	23188788	11	23117935	23121936	23188757
258	4	103028895	103028926	103234749	103234780	4	103028895	103032896	103230779
259	4	103028895	103028926	103342192	103342223	4	103028895	103032896	103342192
260	11	13786370	13786401	13854616	13854647	11	13786370	13790371	13850646
261	13	23475428	23475459	23695241	23695272	13	23475428	23479429	23691271
262	13	23532412	23532443	23695241	23695272	13	23532412	23536413	23691271
263	2	91818982	91819013	91981617	91981648	2	91815012	91819013	91977647
264	2	91817483	91817514	91968018	91968049	2	91817483	91821484	91968018
265	12	2995445	2995476	3072939	3072970	12	2995445	2999446	3068969
266	12	2995445	2995476	3070874	3070905	12	2995445	2999446	3070874
267	12	2995445	2995476	3128090	3128121	12	2995445	2999446	3124120
268	5	2732281	2732312	2779469	2779500	5	2728311	2732312	2775499
269	5	2732281	2732312	2865649	2865680	5	2728311	2732312	2861679
270	5	2755152	2755183	2779469	2779500	5	2751182	2755183	2775499
271	22	34290112	34290143	34327562	34327593	22	34286142	34290143	34327562
272	22	34286715	34286746	34327562	34327593	22	34286715	34290716	34327562
273	16	46394076	46394107	46563367	46563398	16	46394076	46398077	46559397
274	16	46394076	46394107	46645981	46646012	16	46394076	46398077	46642011
275	16	46542432	46542463	46645981	46646012	16	46542432	46546433	46642011
276	7	25985389	25985420	26030197	26030228	7	25981419	25985420	26026227
277	7	25985389	25985420	26109937	26109968	7	25981419	25985420	26105967
278	7	25954012	25954043	25985389	25985420	7	25954012	25958013	25981419
279	16	46563367	46563398	46732957	46732988	16	46559397	46563398	46728987
280	16	46563367	46563398	46724067	46724098	16	46559397	46563398	46724067
281	5	6117034	6117065	6186372	6186403	5	6113064	6117065	6186372

282	4	65366992	65367023	65540791	65540822	4	65366992	65370993	65536821
283	11	25806231	25806262	26002709	26002740	11	25806231	25810232	25998739
284	11	25806231	25806262	26000893	26000924	11	25806231	25810232	26000893
285	7	20278128	20278159	20296076	20296107	7	20274158	20278159	20296076
286	7	20278128	20278159	20380142	20380173	7	20274158	20278159	20376172
287	7	20278128	20278159	20391427	20391458	7	20274158	20278159	20391427
288	7	20278128	20278159	20407650	20407681	7	20274158	20278159	20407650
289	8	3054773	3054804	3172572	3172603	8	3050803	3054804	3168602
290	8	3123415	3123446	3172572	3172603	8	3119445	3123446	3168602
291	1	149873033	149873064	150097137	150097168	1	149873033	149877034	150093167
292	1	149873033	149873064	150110004	150110035	1	149873033	149877034	150106034
293	1	149910043	149910074	150097137	150097168	1	149910043	149914044	150093167
294	1	149910043	149910074	150110004	150110035	1	149910043	149914044	150106034
295	1	149923380	149923411	150110004	150110035	1	149923380	149927381	150106034
296	1	150016977	150017008	150110004	150110035	1	150016977	150020978	150106034
297	1	150032266	150032297	150097137	150097168	1	150032266	150036267	150093167
298	1	150068252	150068283	150110004	150110035	1	150068252	150072253	150106034
299	22	27686269	27686300	27826003	27826034	22	27682299	27686300	27826003
300	20	42100210	42100241	42177997	42178028	20	42096240	42100241	42177997
301	18	67266270	67266301	67320214	67320245	18	67266270	67270271	67316244
302	18	67266270	67266301	67345469	67345500	18	67266270	67270271	67341499
303	18	67266270	67266301	67404406	67404437	18	67266270	67270271	67404406
304	11	20610213	20610244	20630516	20630547	11	20606243	20610244	20626546
305	11	20601546	20601577	20630516	20630547	11	20601546	20605547	20626546
306	11	20630516	20630547	20755854	20755885	11	20626546	20630547	20751884
307	11	29798087	29798118	29826361	29826392	11	29798087	29802088	29822391
308	11	29826361	29826392	29856303	29856334	11	29822391	29826392	29856303
309	25	5777848	5777879	5963748	5963779	25	5777848	5781849	5959778
310	25	5838527	5838558	5963748	5963779	25	5838527	5842528	5959778
311	3	88185502	88185533	88351242	88351273	3	88181532	88185533	88347272
312	11	26381091	26381122	26421158	26421189	11	26381091	26385092	26421158
313	11	26381091	26381122	26552180	26552211	11	26381091	26385092	26552180
314	1	117377450	117377481	117533273	117533304	1	117377450	117381451	117529303
315	1	117501086	117501117	117533273	117533304	1	117501086	117505087	117529303
316	3	40723323	40723354	40842764	40842795	3	40723323	40727324	40838794
317	7	4253429	4253460	4444323	4444354	7	4249459	4253460	4440353
318	27	31943096	31943127	31994751	31994782	27	31943096	31947097	31994751
319	27	31943096	31943127	32006848	32006879	27	31943096	31947097	32006848
320	3	20958830	20958861	21259996	21260027	3	20954860	20958861	21256026

Table 33.e5

N	**4 kb Sequence Location**		
	End2	Probe	Primer ID-1
257	23192758	PLXDC1_11_23117935_23125158_23188757_23196195_RR	OBD RD043.1025
258	103234780	PRKAG2_4_103028895_103043216_103233754_103234780_RF	OBD RD043.1029
259	103346193	PRKAG2_4_103028895_103043216_103342192_103345172_RR	OBD RD043.1033
260	13854647	PRKCA_11_13786370_13794644_13849517_13854647_RF	OBD RD043.1037
261	23695272	PRKCB_13_23475428_23483033_23690253_23695272_RF	OBD RD043.1041
262	23695272	PRKCB_13_23532412_23540462_23690253_23695272_RF	OBD RD043.1045
263	91981648	RAB33B_2_91817483_91819013_91968018_91981648_FF	OBD RD043.1049
264	91972019	RAB33B_2_91817483_91819013_91968018_91981648_RR	OBD RD043.1053
265	3072970	RAG2_12_2995445_3004477_3070874_3072970_RF	OBD RD043.1057
266	3074875	RAG2_12_2995445_3004477_3070874_3072970_RR	OBD RD043.1061
267	3128121	RAG2_12_2995445_3004477_3124836_3128121_RF	OBD RD043.1065

268	2779500	RASSF5_5_2727413_2732312_2768970_2779500_FF	OBD RD043.1069
269	2865680	RASSF5_5_2727413_2732312_2857276_2865680_FF	OBD RD043.1073
270	2779500	RASSF5_5_2752106_2755183_2768970_2779500_FF	OBD RD043.1077
271	34331563	RBPJL_22_34286715_34290143_34327562_34334894_FR	OBD RD043.1081
272	34331563	RBPJL_22_34286715_34290143_34327562_34334894_RR	OBD RD043.1085
273	46563398	SCN10A_16_46394076_46405616_46559136_46563398_RF	OBD RD043.1089
274	46646012	SCN10A_16_46394076_46405616_46644599_46646012_RF	OBD RD043.1093
275	46646012	SCN10A_16_46542432_46554053_46644599_46646012_RF	OBD RD043.1097
276	26030228	SCN2B_7_25981242_25985420_26023779_26030228_FF	OBD RD043.1101
277	26109968	SCN2B_7_25981242_25985420_26102356_26109968_FF	OBD RD043.1105
278	25985420	SCN4B_7_25954012_25959734_25981242_25985420_RF	OBD RD043.1109
279	46732988	SCN5A_16_46559136_46563398_46724067_46732988_FF	OBD RD043.1113
280	46728068	SCN5A_16_46559136_46563398_46724067_46732988_FR	OBD RD043.1117
281	6190373	SELL_5_6104471_6117065_6186372_6188629_FR	OBD RD043.1121
282	65540822	SEPT7_4_65366992_65373527_65534812_65540822_RF	OBD RD043.1125
283	26002740	SGCA_11_25806231_25808754_26000893_26002740_RF	OBD RD043.1129
284	26004894	SGCA_11_25806231_25808754_26000893_26002740_RR	OBD RD043.1133
285	20300077	SIK2_7_20268830_20278159_20296076_20300289_FR	OBD RD043.1137
286	20380173	SIK2_7_20268830_20278159_20375473_20380173_FF	OBD RD043.1141
287	20395428	SIK2_7_20268830_20278159_20391427_20402715_FR	OBD RD043.1145
288	20411651	SIK2_7_20268830_20278159_20407650_20411122_FR	OBD RD043.1149
289	3172603	SNAP29_8_3045435_3054804_3164300_3172603_FF	OBD RD043.1153
290	3172603	SNAP29_8_3117316_3123446_3164300_3172603_FF	OBD RD043.1157
291	150097168	SPRED1_1_149873033_149876737_150087432_150097168_RF	OBD RD043.1161
292	150110035	SPRED1_1_149873033_149876737_150099832_150110035_RF	OBD RD043.1165
293	150097168	SPRED1_1_149910043_149913663_150087432_150097168_RF	OBD RD043.1169
294	150110035	SPRED1_1_149910043_149913663_150099832_150110035_RF	OBD RD043.1173
295	150110035	SPRED1_1_149923380_149924915_150099832_150110035_RF	OBD RD043.1177
296	150110035	SPRED1_1_150016977_150019540_150099832_150110035_RF	OBD RD043.1181
297	150097168	SPRED1_1_150032266_150036031_150087432_150097168_RF	OBD RD043.1185
298	150110035	SPRED1_1_150068252_150074099_150099832_150110035_RF	OBD RD043.1189
299	27830004	SRC_22_27681702_27686300_27826003_27831147_FR	OBD RD043.1193
300	42181998	SRF_20_42097551_42100241_42177997_42186255_FR	OBD RD043.1197
301	67320245	STAT1_18_67266270_67281181_67315145_67320245_RF	OBD RD043.1201
302	67345500	STAT1_18_67266270_67281181_67340514_67345500_RF	OBD RD043.1205
303	67408407	STAT1_18_67266270_67281181_67404406_67407824_RR	OBD RD043.1209
304	20630547	STAT3_11_20601546_20610244_20625038_20630547_FF	OBD RD043.1213
305	20630547	STAT3_11_20601546_20610244_20625038_20630547_RF	OBD RD043.1217
306	20755885	STAT5A_11_20625038_20630547_20748936_20755885_FF	OBD RD043.1221
307	29826392	STXBP4_11_29798087_29803880_29820062_29826392_RF	OBD RD043.1225
308	29860304	STXBP4_11_29820062_29826392_29856303_29862822_FR	OBD RD043.1229
309	5963779	TGFBR1_25_5777848_5781338_5953575_5963779_RF	OBD RD043.1233
310	5963779	TGFBR1_25_5838527_5844153_5953575_5963779_RF	OBD RD043.1237
311	88351273	TMEM156_3_88174369_88185533_88338789_88351273_FF	OBD RD043.1241
312	26425159	TOB1_11_26381091_26387145_26421158_26424834_RR	OBD RD043.1245
313	26556181	TOB1_11_26381091_26387145_26552180_26554959_RR	OBD RD043.1249
314	117533304	TSPAN3_1_117377450_117387477_117527452_117533304_RF	OBD RD043.1253
315	117533304	TSPAN3_1_117501086_117515708_117527452_117533304_RF	OBD RD043.1257
316	40842795	TSPAN5_3_40723323_40732311_40838443_40842795_RF	OBD RD043.1261
317	4444354	VAV1_7_4248599_4253460_4432636_4444354_FF	OBD RD043.1265
318	31998752	VEGFC_27_31943096_31950700_31994751_32003367_RR	OBD RD043.1269
319	32010849	VEGFC_27_31943096_31950700_32006848_32015827_RR	OBD RD043.1273
320	21260027	ZFHX3_3_20954370_20958861_21248124_21260027_FF	OBD RD043.1277

Table 33.e6

N	Primer Sequence	Primer ID-2	Primer Sequence
257	AAGCCACATCCTTCCCACCCAGC	OBD RD043.1027	GGAGAGCAAGGTCCTGGGAGTTA
258	GGAAGAGTCCTGACGACATCCTG	OBD RD043.1031	GAAGAAATGGTAGTGCCCGCCCC
259	GGGCTGCGGATGCTGTTCCTTGA	OBD RD043.1035	GGAAGAGTCCTGACGACATCCTG
260	GTCAACATTTCACTCCGTCGGGC	OBD RD043.1039	GGCGAGGCTCTCTCATCTCTCTC
261	CGCCTCAGCGACACAGAGAACAA	OBD RD043.1043	CCGTCATAGTTCCCGTCCTGAGG
262	CGCCTCAGCGACACAGAGAACAA	OBD RD043.1047	CTGGAGACACGCTGAGGATTGGC
263	AATGCCCTTCCCTAACTCTGAACG	OBD RD043.1051	AAACTACAATGAGATAACCACCCT
264	CCAAACTTTTCTGTGGAATACACG	OBD RD043.1055	CATAATGAGACTAAATAACTTGTCC
265	CCTGAGCGAGGTCACACTGTTCA	OBD RD043.1059	TCCAGAGTGCTTCCTGCCCCAAG
266	TGAGAGCCGCTGGTGTAGATACG	OBD RD043.1063	TCCAGAGTGCTTCCTGCCCCAAG
267	GGTGGTGGCTACCCTGAAACTCATTG	OBD RD043.1067	TAACAGGTGTGTGTGTAAGAGAGGGA
268	TCCCCTCTCTGGTGCTCCTGACA	OBD RD043.1071	ACCCCAGGTTCACGAAAGTCAGG
269	TCCCCTCTCTGGTGCTCCTGACA	OBD RD043.1075	AAGGCAGGGAGAGCCAGAGAAGA
270	ACCTTCTGAGCACCTCCCACAGC	OBD RD043.1079	GTTTATGTCTTGTTTCTCCTGGACG
271	CTCTGAGTTGCTTACTGCCTCCTGC	OBD RD043.1083	CCATTCTGGAAACAATCTGGCAGTA
272	GACAACATACACCTCTCAGACGATGC	OBD RD043.1087	CCATTCTGGAAACAATCTGGCAGTA
273	TAGTTTTAGGGCTGGGCACACAGGA	OBD RD043.1091	AAAGACAGTAGACACTTCACCAATGA
274	AAGGTGGAGGGTTCAGATGGGCTCAT	OBD RD043.1095	AGACTGGCAGGAAATAAACCAAGTTG
275	TCAACAATGCTAAATCACCAAGGG	OBD RD043.1099	AGACAGTAGACACTTCACCAATGA
276	TAAGACACAACCCCTGCCACGGG	OBD RD043.1103	CCAGGTAACAGGATGGCTCAAGG
277	TAAGACACAACCCCTGCCACGGG	OBD RD043.1107	CTCTGTGGTGTCATTGCCCCTTC
278	AGAAGAGTAAGACACAACCCCTGCCA	OBD RD043.1111	TGGTCCTGAGACGACTACCTTGAAGT
279	TAGTTTTAGGGCTGGGCACACAGGAG	OBD RD043.1115	CTTTAGAGCATACAGTAAGCCAATGG
280	ATGAGAAGGGCAGGACAGGGCTG	OBD RD043.1119	CCACCTTTCCGCAGTATCCTCAC
281	GTGATAAGATGGAAGCCAAGACAAAA	OBD RD043.1123	GGACGCAGCCATCTTGCCCCGAA
282	TTCCTCTTACCGTCTCTTGCGAT	OBD RD043.1127	GTAGAAGTGGGTTTTAGAGAGGGT
283	GCAAGGTTAGTGAGTGGCGAGGT	OBD RD043.1131	TGGCTGGACCTGCCTCTCCTTTC
284	TGGCTGGACCTGCCTCTCCTTTC	OBD RD043.1135	CAGACCAGCAGCCCTTATGGACA
285	GCAAAATGGGCAGGAAGGACATACAA	OBD RD043.1139	GGTTTAGAGGTCCTGATTTGTTCTCC
286	AATGGGCAGGAAGGACATACAAAATA	OBD RD043.1143	TGACACTTCTCCCATCAAGAGGG
287	GCAAAATGGGCAGGAAGGACATACAA	OBD RD043.1147	CTTGCCCTTGTGGATAGAGAGTAGGC
288	TGGGCAGGAAGGACATACAAAATA	OBD RD043.1151	GGGAGATTGGCAACAGATGTAAGC
289	TGTGGAAACAGGAAGGGCACGAC	OBD RD043.1155	TCCACCGCATCAGCACCTTCCCA
290	CAGAAGCAACACTTAGGCACCCAG	OBD RD043.1159	TCCACCGCATCAGCACCTTCCCA
291	CGCTTTCCTGACCTCCTACCCATCAA	OBD RD043.1163	TTTTCATACTTTCCTCTCCTTGCCCC
292	GACAGCCCATAGGTTAGGGACACC	OBD RD043.1167	GCTTCCGCCTCCAAATGGCATCT
293	GACAGCCCATAGGTTAGGGACACCAA	OBD RD043.1171	TTTTCATACTTTCCTCTCCTTGCCCC
294	CCGCTTTCCTGACCTCCTACCCA	OBD RD043.1175	GAGTTCCTTCTTGCTCACGGGTG
295	GACAGCCCATAGGTTAGGGACACC	OBD RD043.1179	GAGTTCCTTCTTGCTCACGGGTG
296	GTTAGGGACACCAAATAGTATGCT	OBD RD043.1183	TTGAAAGAAATGCCAACAAATGAT
297	GACAGCCCATAGGTTAGGGACACC	OBD RD043.1187	GGGCAGAAGTTGAAGCCATCCTG
298	GCTTTCCTGACCTCCTACCCATC	OBD RD043.1191	CCCTCTCACATCCCTTGCCCTGT
299	ATCATCCATCCTCACTTGGGCACA	OBD RD043.1195	CTTTTGTTAGACAGAAGTTATCAAT
300	TCAAAGCCCAGAATCTCCAGCAT	OBD RD043.1199	TACGGGATGAAGTCTGGAGGCAT
301	GCACTAAGAATCAAAGTCGCCTTCCA	OBD RD043.1203	CCCAAAAGGCTTCTGACCAACACCTC
302	AAGGCTTCTGACCAACACCTCTGAGA	OBD RD043.1207	GAGAATAAATAGGTGATGTGGGAGGC
303	AGGCTGCTGAAGTCCCCGTAGGG	OBD RD043.1211	CAAACTCAAGACCTCACATTGTCAGG
304	CCAAGGTGAGTGCCCATCCTCTG	OBD RD043.1215	GGTTTGGTGACTTGCTGAAGGGC
305	TACAGTTGGGACCCCTGATTCCG	OBD RD043.1219	CCAAGGTGAGTGCCCATCCTCTG
306	CCAAGGTGAGTGCCCATCCTCTG	OBD RD043.1223	AGGACCTCAAGGACTTCATCCGC
307	GACTGACCTATGTTGGGAAAAGCAAA	OBD RD043.1227	CTAAACAGCATAATACTACTTGCCTC
308	ATGTATGTTTATGTATGACTTCCT	OBD RD043.1231	GAATAAAGTAATGTAACAGGAAGA
309	TTTTGCTTGGCTTGCTTCCTTTGGA	OBD RD043.1235	ATGTTACTCCGATACTGCTTTCTT
310	GGTTTTCAGCAGATTCTTCCTTGAGG	OBD RD043.1239	AGCGGAAGTGCCCCTGCTTTGGTTTA
311	GAACTGCCTACTGCTATGTGAGGATG	OBD RD043.1243	GGATGTGTCCAATAACTGGTGGCTGT
312	GGGTGAGGAAGGGACACAGGCAT	OBD RD043.1247	GAGAGGGAAGGAGGAAACGAAGC

313	GGGTGAGGAAGGGACACAGGCAT	OBD RD043.1251	CTATGTGCTGTGCCAGAGATGGG
314	GAAGTTAGTCCTCACTCTCCTCCC	OBD RD043.1255	TCTCCGCCTTGCCAACCCCATCA
315	AAGTTAGTCCTCACTCTCCTCCCA	OBD RD043.1259	AAAGTGAGACATTTTAGTGCTCCG
316	CTGCCAATGGAGCAAGAACTTCAAAA	OBD RD043.1263	ACAGAACCCGAACAGTCAGACGCTCT
317	GCACCTATTGCCTGTCAAGCCTC	OBD RD043.1267	TGGCACCACATCACTCCTGCTGC
318	CGGCTATGTCACTCACTACCTGG	OBD RD043.1271	CACTCCACCCTGGCGTGTTTTCC
319	CACCTACGGTCTGATGGTATGTTA	OBD RD043.1275	TTTCAGGGCAGAATAAAGATACAT
320	GACACAAATACCAAGGAGAGAAAGGC	OBD RD043.1279	CAGAACCTGACTATGTAGGCACGCTG

Table 33.e7

N	Probe	Marker
257	PLXDC1	OBD RD043.1025.1027
258	PRKAG2	OBD RD043.1029.1031
259	PRKAG2	OBD RD043.1033.1035
260	PRKCA	OBD RD043.1037.1039
261	PRKCB	OBD RD043.1041.1043
262	PRKCB	OBD RD043.1045.1047
263	RAB33B	OBD RD043.1049.1051
264	RAB33B	OBD RD043.1053.1055
265	RAG2	OBD RD043.1057.1059
266	RAG2	OBD RD043.1061.1063
267	RAG2	OBD RD043.1065.1067
268	RASSF5	OBD RD043.1069.1071
269	RASSF5	OBD RD043.1073.1075
270	RASSF5	OBD RD043.1077.1079
271	RBPJL	OBD RD043.1081.1083
272	RBPJL	OBD RD043.1085.1087
273	SCN10A	OBD RD043.1089.1091
274	SCN10A	OBD RD043.1093.1095
275	SCN10A	OBD RD043.1097.1099
276	SCN2B	OBD RD043.1101.1103
277	SCN2B	OBD RD043.1105.1107
278	SCN4B	OBD RD043.1109.1111
279	SCN5A	OBD RD043.1113.1115
280	SCN5A	OBD RD043.1117.1119
281	SELL	OBD RD043.1121.1123
282	SEPT7	OBD RD043.1125.1127
283	SGCA	OBD RD043.1129.1131
284	SGCA	OBD RD043.1133.1135
285	SIK2	OBD RD043.1137.1139
286	SIK2	OBD RD043.1141.1143
287	SIK2	OBD RD043.1145.1147
288	SIK2	OBD RD043.1149.1151
289	SNAP29	OBD RD043.1153.1155
290	SNAP29	OBD RD043.1157.1159
291	SPRED1	OBD RD043.1161.1163
292	SPRED1	OBD RD043.1165.1167
293	SPRED1	OBD RD043.1169.1171
294	SPRED1	OBD RD043.1173.1175
295	SPRED1	OBD RD043.1177.1179
296	SPRED1	OBD RD043.1181.1183
297	SPRED1	OBD RD043.1185.1187
298	SPRED1	OBD RD043.1189.1191
299	SRC	OBD RD043.1193.1195
300	SRF	OBD RD043.1197.1199

301	STAT1	OBD RD043.1201.1203
302	STAT1	OBD RD043.1205.1207
303	STAT1	OBD RD043.1209.1211
304	STAT3	OBD RD043.1213.1215
305	STAT3	OBD RD043.1217.1219
306	STAT5A	OBD RD043.1221.1223
307	STXBP4	OBD RD043.1225.1227
308	STXBP4	OBD RD043.1229.1231
309	TGFBR1	OBD RD043.1233.1235
310	TGFBR1	OBD RD043.1237.1239
311	TMEM156	OBD RD043.1241.1243
312	TOB1	OBD RD043.1245.1247
313	TOB1	OBD RD043.1249.1251
314	TSPAN3	OBD RD043.1253.1255
315	TSPAN3	OBD RD043.1257.1259
316	TSPAN5	OBD RD043.1261.1263
317	VAV1	OBD RD043.1265.1267
318	VEGFC	OBD RD043.1269.1271
319	VEGFC	OBD RD043.1273.1275
320	ZFHX3	OBD RD043.1277.1279

Table 33.e8

N	Marker with Dilution	Marker	Freq	Rank Sum	Rank Mean	Rank Median
1	OBD142_437.439_1.2x	OBD142_437.439	1000	198	1.98	2
2	OBD142_025.027_1x	OBD142_025.027	1000	1224.5	12.245	8.5
3	OBD142_417.419_1x	OBD142_417.419	1000	1369	13.69	13
4	OBD142_517.519_1.2x	OBD142_517.519	1000	1251.5	12.515	13
5	OBD142_065.067_1x	OBD142_065.067	971	3903	39.03	35.5
6	OBD142_513.515_1.2x	OBD142_513.515	971	3903	39.03	35.5
7	OBD142_017.019_1x	OBD142_017.019	977	4446	44.46	40
8	OBD142_029.031_1x	OBD142_029.031	972	4681.5	46.815	40.5
9	OBD142_069.071_1.2x	OBD142_069.071	972	5103.5	51.035	40
10	OBD142_085.087_1.2x	OBD142_085.087	972	4667	46.67	41
11	OBD142_093.095_1x	OBD142_093.095	1000	3945	39.45	40
12	OBD142_117.119_1.2x	OBD142_117.119	1000	4206.5	42.065	38.5
13	OBD142_125.127_1.2x	OBD142_125.127	977	4446	44.46	40
14	OBD142_157.159_1.4x	OBD142_157.159	1000	3707.5	37.075	38
15	OBD142_233.235_1.4x	OBD142_233.235	1000	3707.5	37.075	38
16	OBD142_285.287_1.4x	OBD142_285.287	975	4749	47.49	37.75
17	OBD142_325.327_1.4x	OBD142_325.327	1000	4206.5	42.065	38.5
18	OBD142_449.451_1x	OBD142_449.451	1000	3738	37.38	38.25
19	OBD142_461.463_1.4x	OBD142_461.463	972	4667	46.67	41
20	OBD142_469.471_1x	OBD142_469.471	975	4749	47.49	37.75
21	OBD142_133.135_1x	OBD142_133.135	504	14009	140.09	86.5
22	OBD142_181.183_1.4x	OBD142_181.183	504	14009	140.09	86.5
23	OBD142_397.399_1x	OBD142_397.399	504	14009	140.09	86.5
24	OBD142_253.255_1.2x	OBD142_253.255	867	7643	76.43	109.25
25	OBD142_181.183_1.4x	OBD142_181.183	504	14009	140.09	86.5
26	OBD142_037.039_1x	OBD142_037.039	779	8626.5	86.265	113
27	OBD142_353.355_1x	OBD142_353.355	699	8585.5	85.855	113
28	OBD142_005.007_1x	OBD142_005.007	527	12594.5	125.945	76.5

29	OBD142_009.011_1.4x	OBD142_009.011	737	9784	97.84	44.5
30	OBD142_025.027_1.2x	OBD142_025.027	1000	11604	116.04	42
31	OBD142_029.031_1.4x	OBD142_029.031	1000	2760.5	27.605	38
32	OBD142_041.043_1.2x	OBD142_041.043	737	9784	97.84	44.5
33	OBD142_045.047_1x	OBD142_045.047	525	13251.5	132.515	77.5
34	OBD142_057.059_1.8x	OBD142_057.059	715	11959.5	119.595	51.5
35	OBD142_061.063_1.4x	OBD142_061.063	814	10698.5	106.985	44.5
36	OBD142_065.067_1.2x	OBD142_065.067	1000	859.5	8.595	9.5
37	OBD142_069.071_1.2x	OBD142_069.071	967	10625.5	106.255	43
38	OBD142_081.083_1.4x	OBD142_081.083	1000	2686	26.86	34
39	OBD142_097.099_1.8x	OBD142_097.099	1000	11838	118.38	51.5
40	OBD142_101.103_1x	OBD142_101.103	1000	5050	50.5	70
41	OBD142_109.111_1.2x	OBD142_109.111	1000	11604	116.04	42
42	OBD142_121.123_1.8x	OBD142_121.123	814	10698.5	106.985	44.5
43	OBD142_133.135_1.8x	OBD142_133.135	737	9784	97.84	44.5
44	OBD142_137.139_1.2x	OBD142_137.139	1000	3052	30.52	39
45	OBD142_141.143_1.4x	OBD142_141.143	737	9784	97.84	44.5
46	OBD142_145.147_1.4x	OBD142_145.147	523	12431.5	124.315	81.5
47	OBD142_153.155_1.4x	OBD142_153.155	1000	914	9.14	10
48	OBD142_157.159_1.4x	OBD142_157.159	514	13293.5	132.935	83.5
49	OBD142_165.167_1x	OBD142_165.167	1000	4818.5	48.185	69.5
50	OBD142_185.187_1.4x	OBD142_185.187	1000	3161	31.61	39
51	OBD142_189.191_1x	OBD142_189.191	1000	2760.5	27.605	38
52	OBD142_197.199_1.4x	OBD142_197.199	1000	2795	27.95	38
53	OBD142_201.203_1.4x	OBD142_201.203	1000	2903.5	29.035	38.5
54	OBD142_213.215_1.4x	OBD142_213.215	151	19515.5	195.155	212
55	OBD142_233.235_1.2x	OBD142_233.235	505	12737	127.37	81.5
56	OBD142_241.243_1x	OBD142_241.243	1000	2820.5	28.205	38
57	OBD142_253.255_1.2x	OBD142_253.255	1000	5334.5	53.345	70
58	OBD142_257.259_1.2x	OBD142_257.259	1000	11995.5	119.955	51.5
59	OBD142_261.263_1x	OBD142_261.263	1000	5144	51.44	69.5
60	OBD142_265.267_1.4x	OBD142_265.267	967	9975.5	99.755	41.5
61	OBD142_273.275_1.4x	OBD142_273.275	962	12527	125.27	51.5
62	OBD142_277.279_1.2x	OBD142_277.279	1000	3060	30.6	38.5
63	OBD142_297.299_1.2x	OBD142_297.299	1000	847.5	8.475	9.5
64	OBD142_309.311_1.4x	OBD142_309.311	806	9550	95.5	42
65	OBD142_313.315_1x	OBD142_313.315	1000	2760.5	27.605	38
66	OBD142_321.323_1.2x	OBD142_321.323	1000	11995.5	119.955	51.5
67	OBD142_325.327_1.2x	OBD142_325.327	1000	4958.5	49.585	69.5
68	OBD142_329.331_1.4x	OBD142_329.331	1000	2795	27.95	38
69	OBD142_337.339_1x	OBD142_337.339	817	10759.5	107.595	43
70	OBD142_357.359_1.4x	OBD142_357.359	962	12527	125.27	51.5
71	OBD142_361.363_1.2x	OBD142_361.363	932	11406.5	114.065	43
72	OBD142_373.375_1x	OBD142_373.375	1000	2903.5	29.035	38.5
73	OBD142_393.395_1.2x	OBD142_393.395	1000	921.5	9.215	10.5
74	OBD142_401.403_1x	OBD142_401.403	1000	2820.5	28.205	38
75	OBD142_405.407_1x	OBD142_405.407	537	11739.5	117.395	73.5
76	OBD142_413.415_1.2x	OBD142_413.415	638	10473	104.73	45.5
77	OBD142_433.435_1x	OBD142_433.435	1000	2969.5	29.695	39
78	OBD142_437.439_1x	OBD142_437.439	1000	5144	51.44	69.5
79	OBD142_445.447_1.2x	OBD142_445.447	752	10351.5	103.515	45
80	OBD142_457.459_1x	OBD142_457.459	1000	3016	30.16	38.5

81	OBD142_469.471_1.2x	OBD142_469.471	1000	2829	28.29	38.5
82	OBD142_477.479_1.2x	OBD142_477.479	752	10351.5	103.515	45
83	OBD142_489.491_1x	OBD142_489.491	937	9975.5	99.755	41.5
84	OBD142_501.503_1x	OBD142_501.503	537	11739.5	117.395	73.5
85	OBD142_509.511_1.8x	OBD142_509.511	970	11725.5	117.255	43.25
86	OBD142_517.519_1x	OBD142_517.519	1000	914	9.14	10

Table 34.a

N	Mean p value	Median p value	Classification
1	0.01576	0.01562	Present in Strength Training
2	0.08678	0.09375	Present in Strength Training
3	0.09328	0.125	Present in Strength Training
4	0.09312	0.125	Present in Strength Training
5	0.20758	0.13696	Present in Strength Training
6	0.20758	0.13696	Present in Strength Training
7	0.23382	0.28125	Present in Strength Training
8	0.23992	0.28125	Present in Strength Training
9	0.26566	0.28125	Present in Strength Training
10	0.24252	0.28125	Present in Strength Training
11	0.22246	0.28125	Present in Strength Training
12	0.23621	0.28125	Present in Strength Training
13	0.23382	0.28125	Present in Strength Training
14	0.22324	0.28125	Present in Strength Training
15	0.22324	0.28125	Present in Strength Training
16	0.24953	0.28125	Present in Strength Training
17	0.23621	0.28125	Present in Strength Training
18	0.21652	0.28125	Present in Strength Training
19	0.24252	0.28125	Present in Strength Training
20	0.24953	0.28125	Present in Strength Training
21	0.60112	0.34375	Present in Strength Training
22	0.60112	0.34375	Present in Strength Training
23	0.60112	0.34375	Present in Strength Training
24	0.62216	0.34375	Present in Strength Training
25	0.60112	0.34375	Present in Strength Training
26	0.35984	0.45312	Present in Strength Training
27	0.35078	0.45312	Present in Strength Training
28	0.57	0.28906	Present in Endurance Training
29	0.4475	0.1875	Present in Endurance Training
30	0.53687	0.1875	Present in Endurance Training
31	0.13594	0.1875	Present in Endurance Training
32	0.4475	0.1875	Present in Endurance Training
33	0.60297	0.28906	Present in Endurance Training
34	0.55312	0.1875	Present in Endurance Training
35	0.49625	0.1875	Present in Endurance Training
36	0.05469	0.07031	Present in Endurance Training
37	0.48812	0.1875	Present in Endurance Training
38	0.13008	0.1875	Present in Endurance Training
39	0.545	0.1875	Present in Endurance Training
40	0.21125	0.28906	Present in Endurance Training

41	0.53687	0.1875	Present in Endurance Training
42	0.49625	0.1875	Present in Endurance Training
43	0.4475	0.1875	Present in Endurance Training
44	0.14414	0.1875	Present in Endurance Training
45	0.4475	0.1875	Present in Endurance Training
46	0.56711	0.28906	Present in Endurance Training
47	0.05781	0.07031	Present in Endurance Training
48	0.6025	0.28906	Present in Endurance Training
49	0.20031	0.28906	Present in Endurance Training
50	0.15117	0.1875	Present in Endurance Training
51	0.13594	0.1875	Present in Endurance Training
52	0.13711	0.1875	Present in Endurance Training
53	0.1418	0.1875	Present in Endurance Training
54	0.90047	1	Present in Endurance Training
55	0.57758	0.28906	Present in Endurance Training
56	0.13828	0.1875	Present in Endurance Training
57	0.22125	0.28906	Present in Endurance Training
58	0.55312	0.1875	Present in Endurance Training
59	0.21031	0.28906	Present in Endurance Training
60	0.46375	0.1875	Present in Endurance Training
61	0.58562	0.1875	Present in Endurance Training
62	0.14766	0.1875	Present in Endurance Training
63	0.05531	0.07031	Present in Endurance Training
64	0.43937	0.1875	Present in Endurance Training
65	0.13594	0.1875	Present in Endurance Training
66	0.55312	0.1875	Present in Endurance Training
67	0.20344	0.28906	Present in Endurance Training
68	0.13711	0.1875	Present in Endurance Training
69	0.49625	0.1875	Present in Endurance Training
70	0.58562	0.1875	Present in Endurance Training
71	0.52875	0.1875	Present in Endurance Training
72	0.1418	0.1875	Present in Endurance Training
73	0.05781	0.07031	Present in Endurance Training
74	0.13828	0.1875	Present in Endurance Training
75	0.5257	0.28906	Present in Endurance Training
76	0.48812	0.1875	Present in Endurance Training
77	0.14297	0.1875	Present in Endurance Training
78	0.21031	0.28906	Present in Endurance Training
79	0.48	0.1875	Present in Endurance Training
80	0.14414	0.1875	Present in Endurance Training
81	0.13594	0.1875	Present in Endurance Training
82	0.48	0.1875	Present in Endurance Training
83	0.46375	0.1875	Present in Endurance Training
84	0.5257	0.28906	Present in Endurance Training
85	0.545	0.1875	Present in Endurance Training
86	0.05781	0.07031	Present in Endurance Training

Table 34.b

N	Equine Marker	Exact_Boschloo_p.value
1	OBD154_001/OBD154_003_1:2x	0.597203758
2	OBD154_009/OBD154_011_1:2x	0.180069259

3	OBD154_013/OBD154_015_1x	0.050106528
4	OBD154_033/OBD154_035_1:4x	0.283703806
5	OBD154_037/OBD154_039_1:8x	0.523402567
6	OBD154_041/OBD154_043_1x	0.64299739
7	OBD154_045/OBD154_047_1x	0.180069259
8	OBD154_049/OBD154_051_1:4x	0.11992508
9	OBD154_053/OBD154_055_1:2x	0.597203758
10	OBD154_057/OBD154_059_1:2x	0.663949317
11	OBD154_061/OBD154_063_1x	0.663949317
12	OBD154_069/OBD154_071_1x	0.23718116
13	OBD154_073/OBD154_075_1x	0.125083174
14	OBD154_077/OBD154_079_1x	0.422463565
15	OBD154_085/OBD154_087_1:2x	0.038860637
16	OBD154_093/OBD154_095_1:2x	0.075142123
17	OBD154_097/OBD154_099_1x	0.523402567
18	OBD154_105/OBD154_107_1:2x	0.210490032
19	OBD154_109/OBD154_111_1:2x	0.387940572
20	OBD154_113/OBD154_115_1:4x	0.523402567
21	OBD154_117/OBD154_119_1x	0.659282164
22	OBD154_121/OBD154_123_1x	0.659282164
23	OBD154_125/OBD154_127_1:2x	0.006313179
24	OBD154_133/OBD154_135_1:2x	0.32961205
25	OBD154_137/OBD154_139_1x	0.663949317
26	OBD154_141/OBD154_143_1x	0.180069259
27	OBD154_149/OBD154_151_1:2x	0.678620772
28	OBD154_153/OBD154_155_1:8x	0.523402567
29	OBD154_157/OBD154_159_1:2x	0.038860637
30	OBD154_161/OBD154_163_1:2x	0.422463565
31	OBD154_165/OBD154_167_1x	0.180069259
32	OBD154_169/OBD154_171_1:4x	0.283703806
33	OBD154_177/OBD154_179_1x	0.23718116
34	OBD154_185/OBD154_187_1x	0.64299739
35	OBD154_201/OBD154_203_1x	0.11992508
36	OBD154_205/OBD154_207_1:2x	0.125083174
37	OBD154_209/OBD154_211_1:2x	0.253032887
38	OBD154_213/OBD154_215_1:2x	0.180069259
39	OBD154_217/OBD154_219_1x	0.387940572
40	OBD154_229/OBD154_231_1x	0.054191604
41	OBD154_237/OBD154_239_1x	0.23718116
42	OBD154_245/OBD154_247_1x	0.050106528

Table 35

N	Marker for Human	Training	Odds Ratio	Combined	Cardio	Strength
1	OBD142_029.031_1x	Any	7.2	0.01668097	0.066688	0.01613009
2	OBD142_061.063_1.8x	Any	8.2	0.01851064	0.11741215	0.10680154
3	OBD142_069.071_1.2x	Any	8	0.00255609	0.066688	0.05766889
4	OBD142_089.091_1x	Any	2.9	0.12375267	0.40122897	0.18059725
5	OBD142_137.139_1.2x	Any	8	0.06270144	0.11741215	0.18262433
6	OBD142_081.083_1.4x	Endurance	6	0.13923948	0.070484	0.7999889
7	OBD142_189.191_1x	Endurance	4.5	0.11969458	0.11741215	0.84528948

8	OBD142_213.215_1.4x	Endurance	2.25	1	0.69409048	0.13523206
9	OBD142_017.019_1.2x	Strength	4	0.72495046	0.54542431	0.28124028
10	OBD142_037.039_1x	Strength	12	0.15251771	1	0.02525659
11	OBD142_065.067_1x	Strength	5	0.13191103	0.54542431	0.05766889
12	OBD142_133.135_1x	Strength	4	0.46156086	1	0.01613009
13	OBD142_253.255_1.2x	Strength	12	0.44960749	0.61010368	0.02421162
14	OBD142_353.355_1x	Strength	9	0.11969458	1	0.01615402
15	OBD142_477.479_1x	Strength	9	0.42751765	1	0.02525659
16	OBD142_181.183_1.4x	Strength	2	0.75595814	0.74070856	0.17780781
17	OBD142_397.399_1x	Strength	2	0.15163712	0.66842823	0.09667637

Table 36. Top Human Markers (from I to IIIB)

Table 37 is shown below. Some parts of the table have been left out which relate to information shown in other tables.

	probe	GeneLocus	Loop detected
1	ACACB_12_109146008_109150083_109185066_109187324_RR	ACACB	E_Trn
2	ACBD6_1_180269638_180272765_180371571_180375410_RR	ACBD6	E_Trn
3	ACBD6_1_180337907_180340909_180371571_180375410_FR	ACBD6	E_Trn
4	ADRB3_8_37962724_37965269_37984580_37986052_FF	ADRB3	Str_Trn
5	ADRB3_8_37962724_37965269_37996522_37999233_FR	ADRB3	Str_Trn
6	ALDH1A2_15_58053198_58062371_58157807_58162832_RR	ALDH1A2	Str_Trn
7	ALDH1A2_15_58053198_58062371_58229591_58234474_RF	ALDH1A2	E_Trn
8	ANO2_12_5767708_5775129_5922387_5930466_RR	ANO2	Str_Trn
9	ANO2_12_5872622_5877860_5922387_5930466_RR	ANO2	Str_Trn
10	B3GAT1_11_134376219_134382136_134419343_134423366_FF	B3GAT1	Str_Trn
11	B3GAT2_6_70837358_70839856_70855194_70857991_FR	B3GAT2	E_Trn
12	B3GAT2_6_70837358_70839856_70933019_70941366_FF	B3GAT2	Str_Ctrl
13	BMP7_20_57274840_57277666_57290751_57294583_RF	BMP7	E_Ctrl
14	C1GALT1_7_7113076_7114831_7258228_7260668_FF	C1GALT1	E_Trn
15	CALCR_7_93553156_93563952_93593898_93597071_RF	CALCR	E_Ctrl
16	CARD11_7_2966372_2970772_3066095_3073017_RR	CARD11	E_Trn
17	CASP9_1_15526774_15533191_15569002_15572579_FR	CASP9	E_Trn
18	CBL_11_119249760_119252653_119294588_119299643_RF	CBL	E_Trn
19	CD36_7_80539507_80544315_80603212_80611693_FR	CD36	E_Ctrl
20	CD36_7_80539507_80544315_80679651_80687690_FR	CD36	Str_Ctrl
21	COL13A1_10_69769669_69775141_69840301_69843474_RF	COL13A1	E_Trn
22	COL25A1_4_109024771_109031337_109090838_109104305_RR	COL25A1	E_Ctrl
23	COL25A1_4_109090838_109104305_109307411_109309712_RF	COL25A1	E_Ctrl
24	COL4A2_13_110272408_110277108_110487749_110493325_FR	COL4A2	E_Trn
25	COL5A1_9_134738485_134741113_134811418_134816113_RR	COL5A1	Str_Trn
26	CYGB_17_76511049_76513649_76555120_76557454_RF	CYGB	Str_Trn
27	CYGB_17_76533052_76534398_76555120_76557454_RF	CYGB	Str_Trn
28	CYGB_17_76555120_76557454_76593886_76595265_FF	CYGB	Str_Trn
29	CYGB_17_76555120_76557454_76593886_76595265_FR	CYGB	Str_Trn

Table 37.A1

30	DGKH_13_42011104_42015078_42235825_42240914_RR	DGKH	E_Trn
31	DIAPH3_13_59818047_59823591_59854837_59860534_RR	DIAPH3	E_Ctrl
32	DKK3_11_11956071_11968035_11984245_11993733_FR	DKK3	Str_Trn
33	DKK3_11_11956071_11968035_12010923_12019458_FF	DKK3	Str_Trn
34	DKK3_11_11956071_11968035_12010923_12019458_FR	DKK3	Str_Trn
35	DKK3_11_11956071_11968035_12048403_12051930_FR	DKK3	Str_Trn
36	DLK1_14_100687837_100692867_100749541_100751577_RF	DLK1	Str_Trn
37	DOK5_20_54466479_54470848_54572383_54577350_RF	DOK5	Str_Ctrl
38	EGR3_8_22681793_22682820_22737091_22739184_FF	EGR3	E_Trn
39	EHD1_11_64868178_64874017_64914431_64916090_RF	EHD1	E_Trn
40	EMCN_4_100525710_100532027_100732651_100738720_RR	EMCN	Str_Ctrl
41	ETS1_11_128476761_128480323_128561632_128566579_RR	ETS1	E_Trn
42	EYA1_8_71216399_71218728_71261816_71267769_RR	EYA1	Str_Trn
43	FBLN2_3_13512352_13515076_13582406_13590343_RF	FBLN2	E_Trn
44	FBXO32_8_123526212_123527874_123555254_123559065_FR	FBXO32	E_Trn
45	FOXO1_13_40524349_40526124_40688580_40690771_RR	FOXO1	Str_Ctrl
46	FOXO3_6_108603215_108604436_108629992_108635481_FR	FOXO3	E_Trn_
47	FTO_16_53844989_53854574_54045378_54052319_RF	FTO	E_Trn
48	GPC5_13_91724432_91728749_91910388_91925040_FR	GPC5	E_Trn
49	GPC5_13_91794062_91815301_91953115_91957441_RR	GPC5	E_Trn
50	GPC6_13_94054831_94060621_94121445_94133208_RF	GPC6	Str_Ctrl
51	GPC6_13_94121445_94133208_94296633_94304225_FF	GPC6	Str_Ctrl
52	GRB10_7_50706363_50709345_50775503_50780905_RF	GRB10	E_Trn
53	GSN_9_121177548_121180410_121268506_121274144_FR	GSN	E_Trn
54	GSN_9_121182946_121189020_121239116_121243347_FF	GSN	Str_Ctrl
55	GSN_9_121227501_121232628_121268506_121274144_FR	GSN	E_Trn
56	GSN_9_121239116_121243347_121268506_121274144_FR	GSN	E_Trn
57	GSN_9_121253564_121256485_121268506_121274144_RR	GSN	Str_Trn
58	HDAC9_7_18055950_18064786_18135886_18142010_RF	HDAC9	E_Ctrl
59	HOXC6_12_53956382_53960014_53992251_53994278_FF	HOXC6	Str_Trn

Table 37.B1

60	IGF1R_15_98659065_98662585_98893484_98899517_FR	IGF1R	E_Trn
61	IL1RAP_3_190465562_190469171_190489665_190498302_RF	IL1RAP	E_Trn
62	IL1RAP_3_190489665_190498302_190560851_190563356_FR	IL1RAP	E_Ctrl
63	KDM1A_1_23064655_23070269_23096951_23098159_FR	KDM1A	Str_Ctrl
64	LAMA2_6_128920996_128927003_129105731_129113311_FF	LAMA2	E_Trn
65	LAMA2_6_129342029_129351351_129383008_129389769_FR	LAMA2	E_Trn
66	LCK_1_32214585_32217213_32237144_32241139_RF	LCK	E_Ctrl
67	LDB2_4_16489298_16494220_16535160_16542582_RR	LDB2	E_Ctrl
68	LMO4_1_87315524_87318670_87343110_87349940_FF	LMO4	E_Trn
69	LMO4_1_87315524_87318670_87355277_87360229_FR	LMO4	Str_Trn
70	MAPK10_4_86572598_86581486_86617317_86621940_FF	MAPK10	E_Trn_
71	MBNL1_3_152229500_152234786_152252961_152257281_FR	MBNL1	E_Trn
72	MBNL1_3_152229500_152234786_152281057_152285843_FR	MBNL1	Str_Trn
73	MYBPC1_12_101527342_101530065_101646571_101655128_RF	MYBPC1	Str_Ctrl
74	MYH1_17_10491098_10496051_10520297_10523271_RR	MYH1	Str_Trn
75	MYH1_17_10523271_10524567_10560779_10565755_FF	MYH1	E_Ctrl

76	MYO18B_22_26004818_26009467_26030914_26037279_FF	MYO18B	E_Trn
77	NCAM1_11_113019160_113028536_113163748_113168132_FR	NCAM1	E_Trn
78	NECTIN2_19_44815042_44816736_44827160_44828776_RR	NECTIN2	E_Ctrl
79	NFKB1_4_102504137_102509238_102557818_102560252_FF	NFKB1	Str_Ctrl
80	NFKB1_4_102557818_102560252_102627099_102634363_FR	NFKB1	E_Trn
81	NFKB1_4_102599188_102601960_102627099_102634363_FR	NFKB1	E_Trn
82	NR4A1_12_51995149_51997631_52041793_52046779_RR	NR4A1	Str_Trn
83	NRXN1_2_50580957_50583587_50867546_50884047_RF	NRXN1	E_Ctrl
84	NTRK2_9_84804816_84814325_84917519_84924935_FR	NTRK2	E_Ctrl
85	NTRK2_9_84804816_84814325_84934592_84942655_RF	NTRK2	E_Ctrl
86	PAG1_8_81007411_81018107_81069439_81070856_FR	PAG1	E_Trn
87	PAG1_8_81007411_81018107_81126745_81129448_FR	PAG1	E_Trn
88	PCK1_20_57527297_57530814_57551578_57557205_RR	PCK1	E_Trn
89	PCK1_20_57527297_57530814_57570220_57572870_RR	PCK1	E_Trn

Table 37.C1

90	PCK1_20_57527297_57530814_57579772_57583521_RR	PCK1	E_Trn
91	PCK1_20_57527297_57530814_57583521_57585923_RR	PCK1	Str_Trn
92	PDK3_X_24441637_24447950_24480152_24481252_FR	PDK3	E_Trn
93	PDK3_X_24441637_24447950_24490440_24491541_FR	PDK3	E_Trn
94	PHTF2_7_77800747_77805972_77956111_77960107_RR	PHTF2	E_Trn
95	PHTF2_7_77846910_77851576_77956111_77960107_RR	PHTF2	Str_Ctrl
96	PIK3C3_18_42033052_42039159_42070009_42072187_RF	PIK3C3	Str_Ctrl
97	PIK3C3_18_42070009_42072187_42088671_42094691_FF	PIK3C3	E_Ctrl
98	PIK3R1_5_68187850_68194388_68237549_68241297_FF	PIK3R1	E_Trn
99	PIK3R1_5_68203536_68213336_68237549_68241297_FR	PIK3R1	E_Trn
100	PLCXD2_3_111719030_111722119_111809065_111815838_RR	PLCXD2	E_Ctrl
101	PPARGC1A_4_23871872_23880181_23925180_23932379_FF	PPARGC1A	E_Ctrl
102	PPP3CA_4_101055418_101067369_101247819_101259416_RR	PPP3CA	E_Trn
103	PRDX6_1_173434669_173438537_173475099_173476805_FR	PRDX6	E_Trn
104	PRDX6_1_173434669_173438537_173477717_173485417_FR	PRDX6	E_Trn
105	PRDX6_1_173450908_173452763_173477717_173485417_FR	PRDX6	Str_Trn
106	PRKCQ_10_6432893_6439235_6488207_6489596_FF	PRKCQ	E_Trn
107	PTPRC_1_198595771_198598296_198659753_198666156_RF	PTPRC	E_Ctrl
108	PTPRC_1_198631562_198634915_198659753_198666156_RF	PTPRC	E_Ctrl
109	PTPRC_1_198659753_198666156_198697386_198704777_FR	PTPRC	E_Ctrl
110	PTPRC_1_198659753_198666156_198704777_198709653_FR	PTPRC	E_Ctrl
111	PTPRC_1_198659753_198666156_198721093_198724578_FF	PTPRC	E_Ctrl
112	PTPRC_1_198659753_198666156_198768850_198775826_FF	PTPRC	E_Ctrl
113	PYGM_11_64747174_64749438_64762879_64765587_RF	PYGM	E_Trn
114	RGS6_14_72139099_72144564_72213251_72222544_FR	RGS6	Str_Ctrl
115	RORA_15_60902137_60909221_61019417_61030714_RR	RORA	E_Trn
116	RUNX3_1_24920810_24923822_24973522_24976037_RF	RUNX3	Str_Ctrl
117	RYR1_19_38410632_38413089_38495982_38499305_RR	RYR1	Str_Ctrl
118	SGCZ_8_14631157_14642508_14656955_14664444_RF	SGCZ	E_Trn
119	SLC35B1_17_49700402_49702340_49724264_49725934_RR	SLC35B1	Str_Trn

120	SLC35D1_1_66998822_67004850_67070417_67074223_FR	SLC35D1	E_Ctrl
121	SMAD7_18_48917335_48920290_48969505_48974578_RF	SMAD7	Str_Ctrl
122	STIM1_11_4071215_4074242_4084365_4091420_FR	STIM1	E_Trn
123	STK39_2_167959346_167965882_168109573_168114525_FF	STK39	E_Trn
124	STK39_2_168057412_168062336_168109573_168114525_FF	STK39	E_Trn
125	STXBP4_17_55035186_55042800_55142272_55149288_FR	STXBP4	E_Trn
126	SULF2_20_47663998_47665865_47797013_47801718_FR	SULF2	Str_Trn
127	SYK_9_90789107_90793598_90876350_90879196_RF	SYK	E_Trn
128	SYK_9_90816328_90822228_90832284_90836084_RR	SYK	E_Ctrl
129	SYK_9_90816328_90822228_90836573_90843345_FR	SYK	E_Trn
130	SYK_9_90816328_90822228_90836573_90843345_RR	SYK	E_Ctrl
131	SYK_9_90816328_90822228_90872966_90875740_RR	SYK	E_Ctrl
132	TBX21_17_47685438_47687129_47704291_47707744_FR	TBX21	Str_Trn
133	TGFB2_1_218317687_218325587_218386401_218389011_FR	TGFB2	E_Trn
134	TGFBR2_3_30563062_30565548_30608158_30611268_FF	TGFBR2	E_Trn
135	TGFBR2_3_30566144_30567439_30633318_30636860_RR	TGFBR2	Str_Ctrl
136	TGFBR2_3_30566144_30567439_30694718_30698514_RR	TGFBR2	Str_Ctrl
137	TGFBR2_3_30641481_30645057_30688470_30694718_FF	TGFBR2	E_Trn
138	THADA_2_43260154_43263093_43324949_43335508_FF	THADA	Str_Trn
139	THADA_2_43260154_43263093_43415062_43421910_FF	THADA	Str_Trn
140	THNSL2_2_88139809_88146295_88161717_88164554_FF	THNSL2	E_Ctrl
141	THNSL2_2_88139809_88146295_88161717_88164554_FR	THNSL2	E_Ctrl
142	TLR2_4_153659613_153661830_153693586_153700349_RF	TLR2	Str_Ctrl
143	TNFRSF25_1_6481328_6484248_6494588_6498048_FR	TNFRSF25	Str_Trn
144	TTN_2_178554164_178555670_178788193_178796485_FR	TTN	E_Ctrl
145	UACA_15_70715123_70719636_70780754_70784668_RF	UACA	E_Trn
146	WASL_7_123664155_123666896_123763390_123768284_RF	WASL	E_Trn
147	ZEB1_10_31273317_31275631_31437913_31439545_RF	ZEB1	E_Ctrl
148	ZEB1_10_31273317_31275631_31507470_31524442_FF	ZEB1	E_Ctrl
149	ZEB1_10_31437913_31439545_31458964_31462037_FR	ZEB1	E_Ctrl

150	ZEB1_10_31437913_31439545_31463562_31470397_FR	ZEB1	E_Ctrl
151	ZFHX3_16_73147488_73153243_73182254_73184585_FF	ZFHX3	Str_Trn
152	ADRB3_8_37962724_37965269_37987735_37989039_FR	ADRB3	Str_Trn
153	ADRB3_8_37962724_37965269_38014799_38016599_FR	ADRB3	Str_Trn
154	AGT_1_230717799_230719628_230752057_230757333_RF	AGT	Str_Trn
155	AGT_1_230724515_230729957_230752057_230757333_RF	AGT	Str_Trn
156	BMPR1B_4_94967703_94973952_95026184_95035151_FR	BMPR1B	Str_Trn
157	HTR2A_13_46860092_46866824_46904346_46907815_RF	HTR2A	Str_Trn
158	PPARA_22_46101029_46102611_46241078_46244347_FR	PPARA	E_Trn
159	SOS1_2_38982199_38993639_39061418_39066028_FF	SOS1	Str_Trn
160	SVEP1_9_110493529_110499578_110527410_110532406_FR	SVEP1	Str_Trn
161	UBE3A_15_25355032_25368345_25399797_25404434_FF	UBE3A	Str_Trn
162	UBE3A_15_25355032_25368345_25457129_25464700_FR	UBE3A	Str_Trn
163	ACBD6_1_180431719_180434683_180541491_180549122_RR	ACBD6	E_Trn
164	BMPR1B_4_94821712_94826817_94866803_94871889_FF	BMPR1B	Str_Trn
165	HADHA_2_26188355_26191067_26247231_26249308_FR	HADHA	Str_Trn
166	HADHA_2_26188355_26191067_26280650_26284864_FF	HADHA	Str_Trn
167	MTFR1_8_65658401_65661888_65780891_65782535_RF	MTFR1	E_Trn
168	MYBPC1_12_101567479_101571538_101655128_101656342_RF	MYBPC1	Str_Trn
169	MYH1_17_10502067_10505465_10533547_10534931_RF	MYH1	Str_Trn
170	MYL1_2_210288997_210291732_210359762_210362293_FF	MYL1	E_Trn
171	MYOD1_11_17685862_17689487_17729653_17733608_FR	MYOD1	E_Trn
172	NECTIN3_3_111028574_111034204_111209684_111210764_FR	NECTIN3	Str_Trn
173	PON1_7_95303795_95305644_95332254_95337348_RF	PON1	Str_Trn
174	ACACB_12_109146008_109150083_109236052_109237242_RR	ACACB	E_Ctrl
175	ACACB_12_109236052_109237242_109268078_109273323_RR	ACACB	E_Ctrl
176	COL1A2_7_94359704_94366215_94394399_94397338_RF	COL1A2	E_Ctrl
177	COX6A1_12_120397017_120399520_120449180_120450939_RF	COX6A1	E_Ctrl
178	GGPS1_1_235284158_235288561_235306299_235310474_FR	GGPS1	E_Ctrl
179	GSN_9_121182946_121189020_121323589_121328431_FF	GSN	Str_Trn_

Table 37.E1

180	HTR2A_13_46847106_46857832_46938758_46942222_RF	HTR2A	E_Ctrl
181	HTR2A_13_46877712_46880636_46938758_46942222_FF	HTR2A	E_Ctrl
182	IGF1R_15_98652565_98657862_98731539_98737034_RF	IGF1R	Str_Trn
183	MUSK_9_110648469_110652659_110747866_110751903_FR	MUSK	Str_Trn_
184	MYOT_5_137829466_137834410_137882068_137884626_RR	MYOT	E_Ctrl
185	PPARA_22_46128634_46134707_46231440_46235124_FR	PPARA	Str_Trn
186	PPP1R9A_7_94903925_94908776_94951930_94967018_RF	PPP1R9A	E_Ctrl
187	PPP1R9A_7_94951930_94967018_95061734_95065150_FR	PPP1R9A	E_Ctrl
188	PPP1R9A_7_94951930_94967018_95258927_95267729_FF	PPP1R9A	E_Ctrl
189	RB1_13_48378062_48381344_48486008_48495146_FF	RB1	E_Ctrl
190	SLC25A13_7_96209525_96214524_96295606_96302029_FF	SLC25A13	E_Ctrl
191	ACE2_X_15558483_15561359_15624288_15632375_RR	ACE2	E_Ctrl
192	DNAH5_5_13907228_13913186_13947622_13950495_FR	DNAH5	E_Ctrl
193	EMCN_4_100636305_100649860_100744427_100745788_RR	EMCN	E_Ctrl

194	ITGAV_2_186622411_186639782_186682119_186696186_RR	ITGAV	E_Ctrl
195	MSTN_2_190044593_190053476_190068550_190073029_FR	MSTN	E_Ctrl
196	PLCXD2_3_111633890_111638317_111672672_111677327_FR	PLCXD2	E_Ctrl
197	SGCZ_8_14631157_14642508_14778176_14785491_FF	SGCZ	E_Ctrl
198	SLC25A13_7_96178122_96182739_96295606_96302029_RF	SLC25A13	E_Ctrl
199	SOCS7_17_38347510_38348776_38360864_38363420_FR	SOCS7	E_Ctrl
200	SRI_7_88199682_88203042_88229166_88237101_RF	SRI	E_Ctrl
201	STXBP4_17_55035186_55042800_55117598_55123347_RR	STXBP4	E_Ctrl
202	SVEP1_9_110397951_110405969_110503630_110509758_FF	SVEP1	E_Ctrl

Table 37.F2

Table 38 is below. Some parts of the table have been left out which relates to information in other tables.

	Probe	GeneLocus	Loop Detected
1	C1GALT1_7_7113076_7114831_7258228_7260668_FF	C1GALT1	E_Trn
2	DKK3_11_11956071_11968035_11984245_11993733_FR	DKK3	Str_Trn
3	FBXO32_8_123526212_123527874_123555254_123559065_FR	FBXO32	E_Trn
4	GPC6_13_94054831_94060621_94121445_94133208_RF	GPC6	Str_Ctrl
5	GSN_9_121177548_121180410_121268506_121274144_FR	GSN	E_Trn
6	LMO4_1_87315524_87318670_87343110_87349940_FF	LMO4	E_Trn
7	MAPK10_4_86572598_86581486_86617317_86621940_FF	MAPK10	E_Trn
8	MBNL1_3_152229500_152234786_152281057_152285843_FR	MBNL1	Str_Trn
9	PCK1_20_57527297_57530814_57579772_57583521_RR	PCK1	E_Trn
10	PIK3C3_18_42070009_42072187_42088671_42094691_FF	PIK3C3	E_Ctrl
11	PTPRC_1_198595771_198598296_198659753_198666156_RF	PTPRC	E_Ctrl
12	RGS6_14_72139099_72144564_72213251_72222544_FR	RGS6	Str_Ctrl
13	RUNX3_1_24920810_24923822_24973522_24976037_RF	RUNX3	Str_Ctrl
14	ZFHX3_16_73147488_73153243_73182254_73184585_FF	ZFHX3	Str_Trn
15	MYOT_5_137829466_137834410_137882068_137884626_RR	MYOT	Str_Ctrl
16	AGT_1_230724515_230729957_230752057_230757333_RF	AGT	Str_Trn
17	MYL1_2_210288997_210291732_210359762_210362293_FF	MYL1	E_Trn
18	SRI_7_88199682_88203042_88229166_88237101_RF	SRI	E_Ctrl

Table 38.a

		Inner_primers
	Probe	**PCR-Primer1_ID**
1	C1GALT1_7_7113076_7114831_7258228_7260668_FF	OBD142_025
2	DKK3_11_11956071_11968035_11984245_11993733_FR	OBD142_061
3	FBXO32_8_123526212_123527874_123555254_123559065_FR	OBD142_089
4	GPC6_13_94054831_94060621_94121445_94133208_RF	OBD142_109
5	GSN_9_121177548_121180410_121268506_121274144_FR	OBD142_117
6	LMO4_1_87315524_87318670_87343110_87349940_FF	OBD142_145
7	MAPK10_4_86572598_86581486_86617317_86621940_FF	OBD142_153
8	MBNL1_3_152229500_152234786_152281057_152285843_FR	OBD142_157
9	PCK1_20_57527297_57530814_57579772_57583521_RR	OBD142_189
10	PIK3C3_18_42070009_42072187_42088671_42094691_FF	OBD142_213
11	PTPRC_1_198595771_198598296_198659753_198666156_RF	OBD142_233
12	RGS6_14_72139099_72144564_72213251_72222544_FR	OBD142_245
13	RUNX3_1_24920810_24923822_24973522_24976037_RF	OBD142_253
14	ZFHX3_16_73147488_73153243_73182254_73184585_FF	OBD142_325

15	MYOT_5_137829466_137834410_137882068_137884626_RR	OBD142_341
16	AGT_1_230724515_230729957_230752057_230757333_RF	OBD142_365
17	MYL1_2_210288997_210291732_210359762_210362293_FF	OBD142_449
18	SRI_7_88199682_88203042_88229166_88237101_RF	OBD142_509

Table 38.g

	Inner_primers			Category
	PCR_Primer1	**PCR-Primer2_ID**	**PCR_Primer2**	**High or Low Responder**
1	CACCTCAAAAGACAACCCCAGACCCA	OBD142_027	CCCTCACTTTCCTTCTACTCTTCAAG	Presence in strength high responder
2	GCTCCACATTTCCCAATCTAACCTGC	OBD142_063	GTCAGAGTTGCCGATAGGTCTTGCTA	Presence in strength high responder
3	AATCTCTGTCCCCAACTGTATCTGGC	OBD142_091	ACATCTATCTTGCCCCTCACTCAGGT	Presence in strength high responder
4	GAGTATTTACGATGGTCAGGTGCTGC	OBD142_111	ATCCAAACACAGGACGAGAATAAAGC	Presence in strength high responder
5	GACCTGTGGTTCTGACTGTCCAG	OBD142_119	TATCGTCCAGGAGGCAAGGGTCC	Presence in strength high responder
6	GCAACCTGGTCTCCTACCTGCTTCTA	OBD142_147	GATGAGGTAACCAAAGTTCAGGGAGA	Presence in strength high responder
7	TAGCAGACAATCAGAGGGTTTTGC	OBD142_155	CTCTCTCCTCATCCTCCCTCCTAATA	Presence in strength high responder
8	GCTGGTAGTTGGCTTTTGGGAAGAAC	OBD142_159	GGGAGCCAGAAAGATAGCAATGCCTA	Presence in strength high responder
9	TTCTCCCTCGGACGCTCATCCTC	OBD142_191	GAGGAGGAGAAACTCAGAAGCCC	Presence in strength high responder
10	CTGGAACTTGTTTAGGCACTGAAGCA	OBD142_215	GCACAAGACCTCACATTCTGATGGGC	Presence in strength high responder
11	GCAAAGGGCAGGTCATCATCATTCAA	OBD142_235	CTCTCCTTTATCCCCTACCCTGCTCA	Presence in strength high responder
12	CCCCGATGAATGTTACCCTGTCCC	OBD142_247	CAGAGAAAGGGAGTTTGGAGGGC	Presence in strength high responder
13	CTGAAATCCCATAGTGAGATGCCTTC	OBD142_255	CCCCAAACTCCCAGACACATCAGAGA	Presence in strength high responder
14	CCTGGATGTTCATTCCCACCTGG	OBD142_327	AGAGGGAAAGGCAGGTCGTGAGC	Presence in strength high responder
15	GCAGATTCCACAGGGCTTAC	OBD142_343	GCTGGTCTCAAACTCCTGGG	Presence in strength high responder
16	ACCCAACCCTGCTATACAATTCCA	OBD142_367	GGGCATCTTTCCTCTTATTCAAGGT	Presence in strength high responder
17	ACAGTCAGTGATTGGCACAGAGTAA	OBD142_451	AGGAAATAGCCCAAATGCAACTGAA	Presence in strength high responder
18	GAATGAAACTCTGAGGCCGG	OBD142_511	CCCATTCGTCTCTCTGAGCTG	Presence in strength high responder

Table 38.h

	Probe	GeneLocus	
1	THNSL2_2_88139809_88146295_88161717_88164554_FR	THNSL2	E_Ctrl
2	IGF1R_15_98652565_98657862_98731539_98737034_RF	IGF1R	Str_Ctrl
3	DKK3_11_11956071_11968035_11984245_11993733_FR	DKK3	Str_Trn
4	CBL_11_119249760_119252653_119294588_119299643_RF	CBL	E_Trn
5	EYA1_8_71216399_71218728_71261816_71267769_RR	EYA1	Str_Trn
6	ACACB_12_109236052_109237242_109268078_109273323_RR	ACACB	E_Ctrl
7	PTPRC_1_198595771_198598296_198659753_198666156_RF	PTPRC	E_Ctrl

Table 39.a

CV Only	Gene
OBD142_513.515	SRI
Shared	
OBD142_261.263	SMAD7
OBD142_313.315	WASL
OBD142_021.023	B3GAT2
Strength_Only	
OBD142_473.475	RB1
OBD142_389.391	MTFR1
OBD142_301.303	TLR2
OBD142_169.171	NFKB1
OBD142_173.175	NTRK2
OBD142_489.491	ITGAV
OBD142_457.459	PPARA

Table 40

No.	Probe	Loci	
1	CBL_11_119249760_119252653_119294588_119299643_RF	CBL	Present in Endurance
2	DKK3_11_11956071_11968035_11984245_11993733_FR	DKK3	Present in Strength
3	DKK3_11_11956071_11968035_12048403_12051930_FR	DKK3	Present in Strength
4	FBXO32_8_123526212_123527874_123555254_123559065_FR	FBXO32	Present in Endurance
5	KDM1A_1_23064655_23070269_23096951_23098159_FR	KDM1A	Present in Strength
6	EYA1_8_71216399_71218728_71261816_71267769_RR	EYA1	Present in Strength
7	PCK1_20_57527297_57530814_57579772_57583521_RR	PCK1	Present in Endurance
8	PIK3C3_18_42070009_42072187_42088671_42094691_FF	PIK3C3	Present in Endurance
9	ALDH1A2_15_58053198_58062371_58157807_58162832_RR	ALDH1A2	Present in Strength
10	CD36_7_80539507_80544315_80679651_80687690_FR	CD36	Present in Strength

11	DKK3_11_11956071_11968035_12010923_12019458_FF	DKK3	Present in Strength
12	IL1RAP_3_190489665_190498302_190560851_190563356_FR	IL1RAP	Present in Endurance
13	RUNX3_1_24920810_24923822_24973522_24976037_RF	RUNX3	Present in Strength
14	PPARA_22_46101029_46102611_46241078_46244347_FR	PPARA	Present in Endurance
15	SLC25A13_7_96209525_96214524_96295606_96302029_FF	SLC25A13	Present in Endurance
16	PCK1_20_57527297_57530814_57551578_57557205_RR	PCK1	Present in Endurance
17	MYL1_2_210288997_210291732_210359762_210362293_FF	MYL1	Present in Endurance
18	C1GALT1_7_7113076_7114831_7258228_7260668_FF	C1GALT1	Present in Endurance
19	COL25A1_4_109024771_109031337_109090838_109104305_RR	COL25A1	Present in Endurance
20	COL5A1_9_134738485_134741113_134811418_134816113_RR	COL5A1	Present in Strength
21	DIAPH3_13_59818047_59823591_59854837_59860534_RR	DIAPH3	Present in Endurance
22	FBLN2_3_13512352_13515076_13582406_13590343_RF	FBLN2	Present in Endurance
23	GPC6_13_94121445_94133208_94296633_94304225_FF	GPC6	Present in Strength
24	GSN_9_121177548_121180410_121268506_121274144_FR	GSN	Present in Endurance
25	GSN_9_121227501_121232628_121268506_121274144_FR	GSN	Present in Endurance
26	GSN_9_121239116_121243347_121268506_121274144_FR	GSN	Present in Endurance
27	LCK_1_32214585_32217213_32237144_32241139_RF	LCK	Present in Endurance
28	LMO4_1_87315524_87318670_87343110_87349940_FF	LMO4	Present in Endurance
29	MAPK10_4_86572598_86581486_86617317_86621940_FF	MAPK10	Present in Endurance
30	MBNL1_3_152229500_152234786_152281057_152285843_FR	MBNL1	Present in Strength
31	NCAM1_11_113019160_113028536_113163748_113168132_FR	NCAM1	Present in Endurance
32	PCK1_20_57527297_57530814_57570220_57572870_RR	PCK1	Present in Endurance
33	PDK3_X_24441637_24447950_24480152_24481252_FR	PDK3	Present in Endurance
34	PDK3_X_24441637_24447950_24490440_24491541_FR	PDK3	Present in Endurance
35	PTPRC_1_198595771_198598296_198659753_198666156_RF	PTPRC	Present in Endurance

36	PTPRC_1_198659753_198666156_198721093_198724578_FF	PTPRC	Present in Endurance
37	RYR1_19_38410632_38413089_38495982_38499305_RR	RYR1	Present in Strength
38	THNSL2_2_88139809_88146295_88161717_88164554_FR	THNSL2	Present in Endurance
39	UACA_15_70715123_70719636_70780754_70784668_RF	UACA	Present in Endurance
40	ZEB1_10_31273317_31275631_31507470_31524442_FF	ZEB1	Present in Endurance
41	ZFHX3_16_73147488_73153243_73182254_73184585_FF	ZFHX3	Present in Strength
42	ADRB3_8_37962724_37965269_37987735_37989039_FR	ADRB3	Present in Strength
43	AGT_1_230724515_230729957_230752057_230757333_RF	AGT	Present in Strength
44	HTR2A_13_46860092_46866824_46904346_46907815_RF	HTR2A	Present in Strength
45	SOS1_2_38982199_38993639_39061418_39066028_FF	SOS1	Present in Strength
46	ACBD6_1_180431719_180434683_180541491_180549122_RR	ACBD6	Present in Endurance
47	MYH1_17_10502067_10505465_10533547_10534931_RF	MYH1	Present in Endurance
48	MYOD1_11_17685862_17689487_17729653_17733608_FR	MYOD1	Present in Endurance
49	NECTIN3_3_111028574_111034204_111209684_111210764_FR	NECTIN3	Present in Endurance
50	ACACB_12_109146008_109150083_109236052_109237242_RR	ACACB	Present in Endurance
51	ACACB_12_109236052_109237242_109268078_109273323_RR	ACACB	Present in Endurance
52	IGF1R_15_98652565_98657862_98731539_98737034_RF	IGF1R	Present in Strength
53	SOCS7_17_38347510_38348776_38360864_38363420_FR	SOCS7	Present in Endurance
54	STXBP4_17_55035186_55042800_55117598_55123347_RR	STXBP4	Present in Endurance
55	SVEP1_9_110397951_110405969_110503630_110509758_FF	SVEP1	Present in Endurance
56	EMCN_4_100636305_100649860_100744427_100745788_RR	EMCN	Present in Endurance
57	ACACB_12_109146008_109150083_109185066_109187324_RR	ACACB	Present in Endurance
58	FOXO1_13_40524349_40526124_40688580_40690771_RR	FOXO1	Present in Strength
59	FOXO3_6_108603215_108604436_108629992_108635481_FR	FOXO3	Present in Endurance
60	FTO_16_53844989_53854574_54045378_54052319_RF	FTO	Present in Endurance
61	GPC6_13_94054831_94060621_94121445_94133208_RF	GPC6	Present in Strength

62	PPP3CA_4_101055418_101067369_101247819_101259416_RR	PPP3CA	Present in Endurance
63	SMAD7_18_48917335_48920290_48969505_48974578_RF	SMAD7	Present in Strength
64	SYK_9_90816328_90822228_90832284_90836084_RR	SYK	Present in Endurance
65	SYK_9_90816328_90822228_90872966_90875740_RR	SYK	Present in Endurance
66	TGFB2_1_218317687_218325587_218386401_218389011_FR	TGFB2	Present in Endurance
67	TGFBR2_3_30566144_30567439_30694718_30698514_RR	TGFBR2	Present in Strength
68	TLR2_4_153659613_153661830_153693586_153700349_RF	TLR2	Present in Strength
69	SVEP1_9_110493529_110499578_110527410_110532406_FR	SVEP1	Present in Strength
70	MTFR1_8_65658401_65661888_65780891_65782535_RF	MTFR1	Present in Endurance
71	GSN_9_121182946_121189020_121323589_121328431_FF	GSN	Present in Strength
72	MUSK_9_110648469_110652659_110747866_110751903_FR	MUSK	Present in Strength
73	PPARA_22_46128634_46134707_46231440_46235124_FR	PPARA	Present in Strength
74	PPP1R9A_7_94903925_94908776_94951930_94967018_RF	PPP1R9A	Present in Endurance
75	PLCXD2_3_111633890_111638317_111672672_111677327_FR	PLCXD2	Present in Endurance
76	SGCZ_8_14631157_14642508_14778176_14785491_FF	SGCZ	Present in Endurance
77	SRI_7_88199682_88203042_88229166_88237101_RF	SRI	Present in Endurance

Table 41 shows markers identified in the human study, which are preferably used to type humans.

CLAIMS

1. A process for detecting a chromosome state which represents a subgroup in a population comprising determining whether a chromosome interaction relating to that chromosome state is present or absent within a defined region of the genome, wherein said subgroup relates to physical performance in an individual; and

- wherein said chromosome interaction has optionally been identified by a method of determining which chromosomal interactions are relevant to a chromosome state corresponding to a physical performance 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 pattern of hybridisation between the first and second set of nucleic acids allows a determination of which chromosomal interactions are specific to a physical performance subgroup; and

- wherein the chromosome interaction either:

(i) corresponds to any one of the chromosome interactions shown in any of Tables 3, 7, 8, 9, 25 and 30; and/or

(ii) corresponds to any one of the chromosome interactions shown in any of Tables 13, 14, 18, 22, 23 and 24; and/or

(iii) corresponds to any one of the chromosome interactions shown in Table 31 or 32; and/or

(iv) is present in a 4,000 base region which comprises or which flanks (i), (ii) or (iii); and/or

(v) is present in any one of the regions or genes listed in Table 21, 24, 25, 30, 31 or 32.

2. A process according to claim 1 wherein:

- the individual is a human and the subgroup is a human subgroup
- the individual is a horse and the subgroup is a horse subgroup, and

wherein optionally:

(i) the process is carried out to determine physical performance ability, and/or

(ii) the process is carried out to detect responsiveness to a stimulus relating to physical performance, which is preferably physical training, and optionally strength or endurance training; and/or

(iii) the process is carried out to select an individual suitable for a physical activity, which is preferably a sport; and/or

(iv) the process is carried out to select a stimulus relating to physical performance to give to the individual, wherein said stimulus is a type of physical training.

3. A process according to claim 1 or 2 wherein a specific combination of chromosome interactions are typed:

(i) comprising all of the chromosome interactions represented in any of Tables 3, 7, 8, 9, 25 and 30 or any of Tables 13, 14, 18, 22, 23; and/or

(ii) comprising at least 10%, 20%, 50%, or 80% of the chromosome interactions in any of Tables 3, 7, 8, 9, 25 and 30 or any of Tables 13, 14, 18, 22, 23; and/or

(iii) which together are present in at least 10, 50 or 100 of the regions or genes listed in any of Tables 21, 24, 25 or 30; and/or

(iv) wherein at least 10, 50, 100, 150, 200 or 300 chromosome interactions are typed which are present in a 4,000 base region which comprises or which flanks the chromosome interactions represented in any of Tables 3, 7, 8, 9, 25 and 30 or any of Tables 13, 14, 18, 22, 23.

4. A process according to any one of the preceding claims wherein a specific combination of chromosome interactions are typed:

(i) comprising all of the chromosome interactions represented in Table 31 or 32; and/or

(ii) comprising at least 10%, 20%, 50%, or 80% of the chromosome interactions in Table 31 or 32; and/or

(iii) which together are present in at least 5 of the regions or genes listed in Table 31 or 32; and/or

(iv) wherein at least 5 chromosome interactions are typed which are present in a 4,000 base region which comprises or which flanks the chromosome interactions represented in Table 31 or 32.

5. A process according to any one of the preceding claims in which 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 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, wherein detection of the ligated nucleic acid is preferably by using either:

(i) a probe that has at least 70% identity to any of the specific probe sequences mentioned in Table 24, 25, 30, 31 or 32 and/or (ii) by a primer pair which has at least 70% identity to any primer pair in Table 24, 25, 30, 31 or 32.

6. A process according to any one of the preceding claims, wherein:

- the second set of nucleic acids is from a larger group of individuals than the first set of nucleic acids; and/or
- the first set of nucleic acids is from at least 8 individuals; and/or
- the first set of nucleic acids is from at least 4 individuals from a first subgroup and at least 4 individuals from a second subgroup which is preferably non-overlapping with the first subgroup.

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

- the second set of nucleic acids represents an unselected group; and/or

- wherein the second set of nucleic acids is bound to an array at defined locations; and/or

- wherein the second set of nucleic acids represents chromosome interactions in least 100 different genes; and/or

- wherein the second set of nucleic acids comprises at least 1,000 different nucleic acids representing at least 1,000 different chromosome interactions; and/or

- wherein the first set of nucleic acids and the second set of nucleic acids comprise at least 100 nucleic acids with length 10 to 100 nucleotide bases.

8. A process according to any one of the preceding claims, wherein the first set of nucleic acids is obtainable in a process comprising the steps of: -

(i) cross-linking of chromosome regions which have come together in a chromosome interaction;

(ii) subjecting said cross-linked regions to cleavage, optionally by restriction digestion cleavage with an enzyme; and

(iii) ligating said cross-linked cleaved DNA ends to form the first set of nucleic acids (in particular comprising ligated DNA).

9. A process according to any one of the preceding claims:

- wherein at least 10 to 50 different chromosome interactions are typed, preferably in 10 to 50 different regions or genes optionally as defined in Table 21, 24, 25, 30, 31 or 32;

and/or

- which is:

(i) carried out on a human or horse athlete; and/or

(ii) carried out as part of a training regime, preferably after the start of the training regime; and/or

(iii) carried out on a Thoroughbred horse, preferably a racing horse; or

(iv) carried out on a human individual of who is less than 20 years old or is carried out on a horse that is less than 18 months old, and/or

(v) which is carried out at multiple time points to assess physical performance characteristics at specific time points, wherein the process is optionally carried out at at least 3 time points, which are preferably at least 30 days apart from each other.

10. A process according to any one of the preceding claims wherein said defined region of the genome:
(i) comprises a single nucleotide polymorphism (SNP); and/or
(ii) expresses a microRNA (miRNA); and/or
(iii) expresses a non-coding RNA (ncRNA); and/or
(iv) expresses a nucleic acid sequence encoding at least 10 contiguous amino acid residues; and/or
(v) expresses a regulating element; and/or
(vi) comprises a CTCF binding site.

11. A process according to any one of the preceding claims:
- which is carried out to identify an individual that is suited to endurance training, and preferably the identified individual is then subject to endurance training, which optionally occurs on at least 100 days out of the next 365 days after the identification; or
- which is carried out to identify an individual that is suited to strength training, and preferably the identified individual is then subject to strength training, which optionally occurs on at least 100 days out of the next 365 days after the identification.

12. A process according to any one of the preceding claims which is carried out to select the individual for racing.

13. A process according to any one of the preceding claims wherein a specific combination of chromosome interactions are typed:
(i) comprising all of the chromosome interactions represented in any of Tables 33, 34, 35, 36, 37, 38, 39, 40 or 41, or in any of Figures 16, 17 or 18; and/or
(ii) comprising at least 10%, 20%, 50%, or 80% of the chromosome interactions in any of Tables 33, 34, 35, 36, 37, 38, 39, 40 or 41, or in any of Figures 16, 17 or 18; and/or
(iii) which together are present in at least 10 of the regions or genes listed in any of Tables 33, 34, 35, 36, 37, 38, 39, 40 or 41, or in any of Figures 16, 17 or 18; and/or
(iv) wherein at least 10 chromosome interactions are typed which are present in a 4,000 base region which comprises or which flanks the chromosome interactions represented in any of Tables 33, 34, 35, 36, 37, 38, 39, 40 or 41, or in any of Figures 16, 17 or 18.

14. A process according to any one of the preceding claims which is carried out to identify or design a an agent that affects physical performance, wherein said process is used to detect whether a candidate agent is able to cause a change to a chromosome state which is associated with a different physical performance state; wherein

- the chromosomal interaction is any specific interaction or combination of interactions defined in any preceding claim and/or is present in any one of the regions or genes listed in Table 21, 24, 25, 30, 31 or 32; and/or

- the change in chromosomal interaction is monitored using (i) a probe that has at least 70% identity to any of the specific probe sequences mentioned in Table 24, 25, 30, 31 or 32 and/or (ii) by a primer pair which has at least 70% identity to any primer pair in Table 24, 25, 30, 31 or 32.

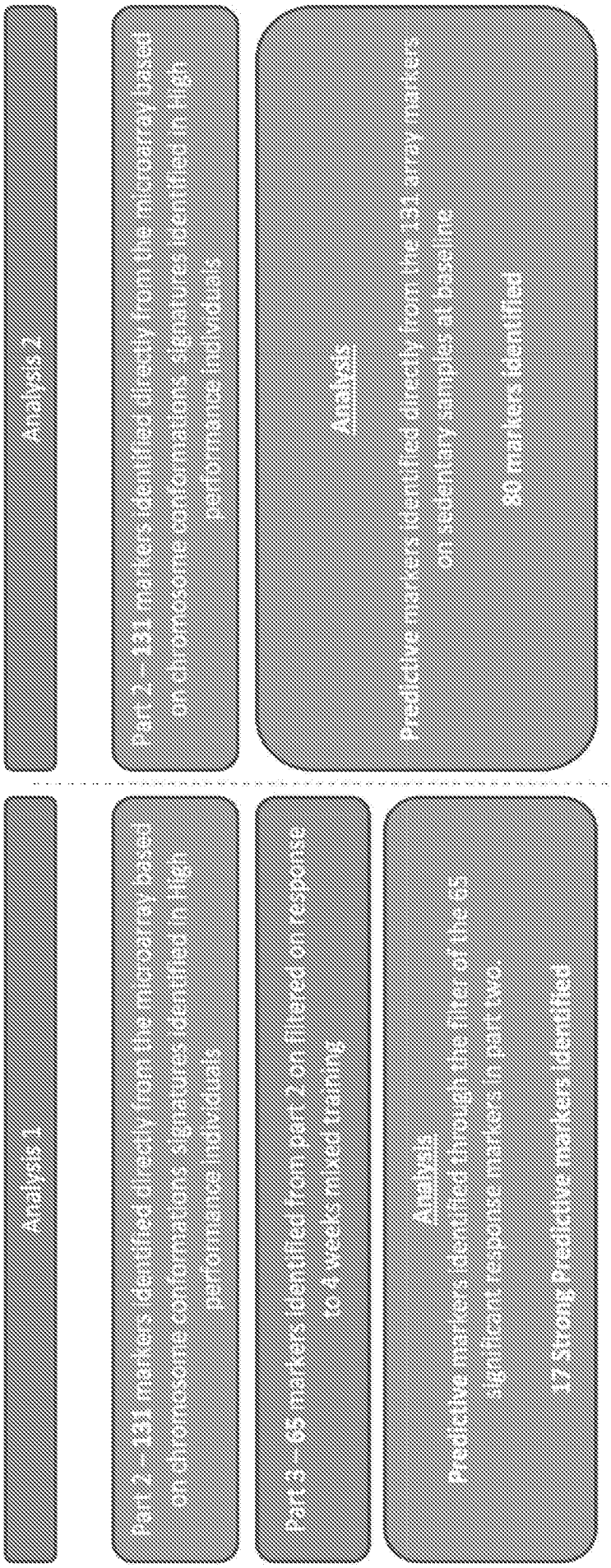
15. A process according to claim 14 which comprises selecting a target based on detection of chromosome interactions, and preferably screening for a modulator of the target to identify an agent which affects physical performance, wherein said target is optionally a protein.

16. A process 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
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.

17. A process according to any one of the proceeding claims which further comprises:

- producing a report on the physical performance characteristics of the individual based on the results of the process, or
- inputting the results of the process into a database, or
- assigning a specific fitness or training regime to the individual based on the results of the process, or
- designing a specific fitness or training regime for the individual based on the results of the process.

Figure 1


Analysis 1
Part 2 – 131 markers identified directly from the microarray based on chromosome conformations signatures identified in High performance individuals
Part 3 – 65 markers identified from part 2 on filtered on response to 4 weeks mixed training
Analysis
Predictive markers identified through the filter of the 65 significant response markers in part two.
17 Strong Predictive markers identified
Analysis 2
Part 2 – 131 markers identified directly from the microarray based on chromosome conformations signatures identified in High performance individuals
Analysis
Predictive markers identified directly from the 131 array markers on sedentary samples at baseline
80 markers identified

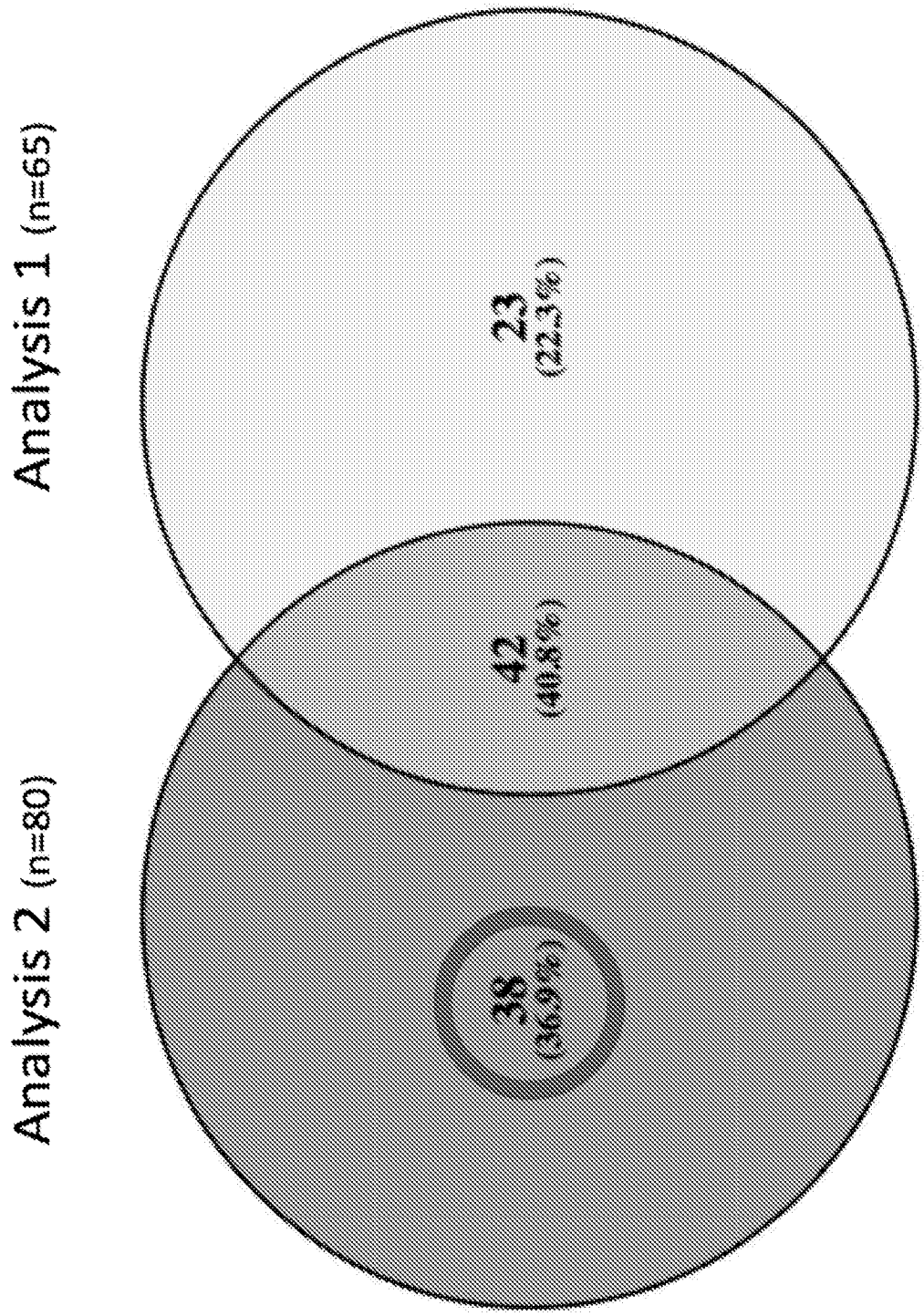
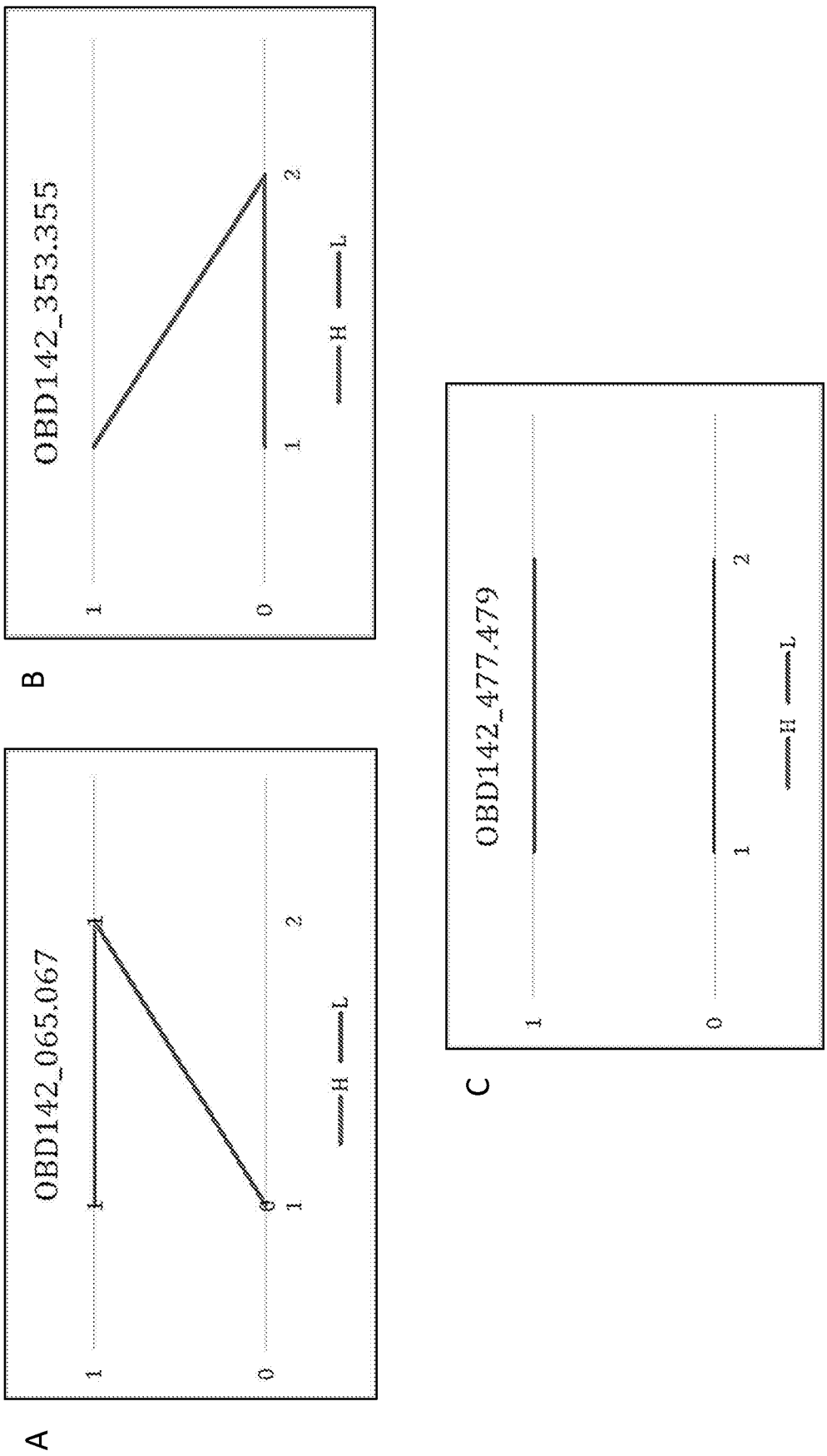


Figure 2

Figure 3


A
OBD142_065.067
1
0
1
2
H
L
B
OBD142_353.355
1
0
1
2
H
L
C
OBD142_477.479
1
0
1
2
H
L

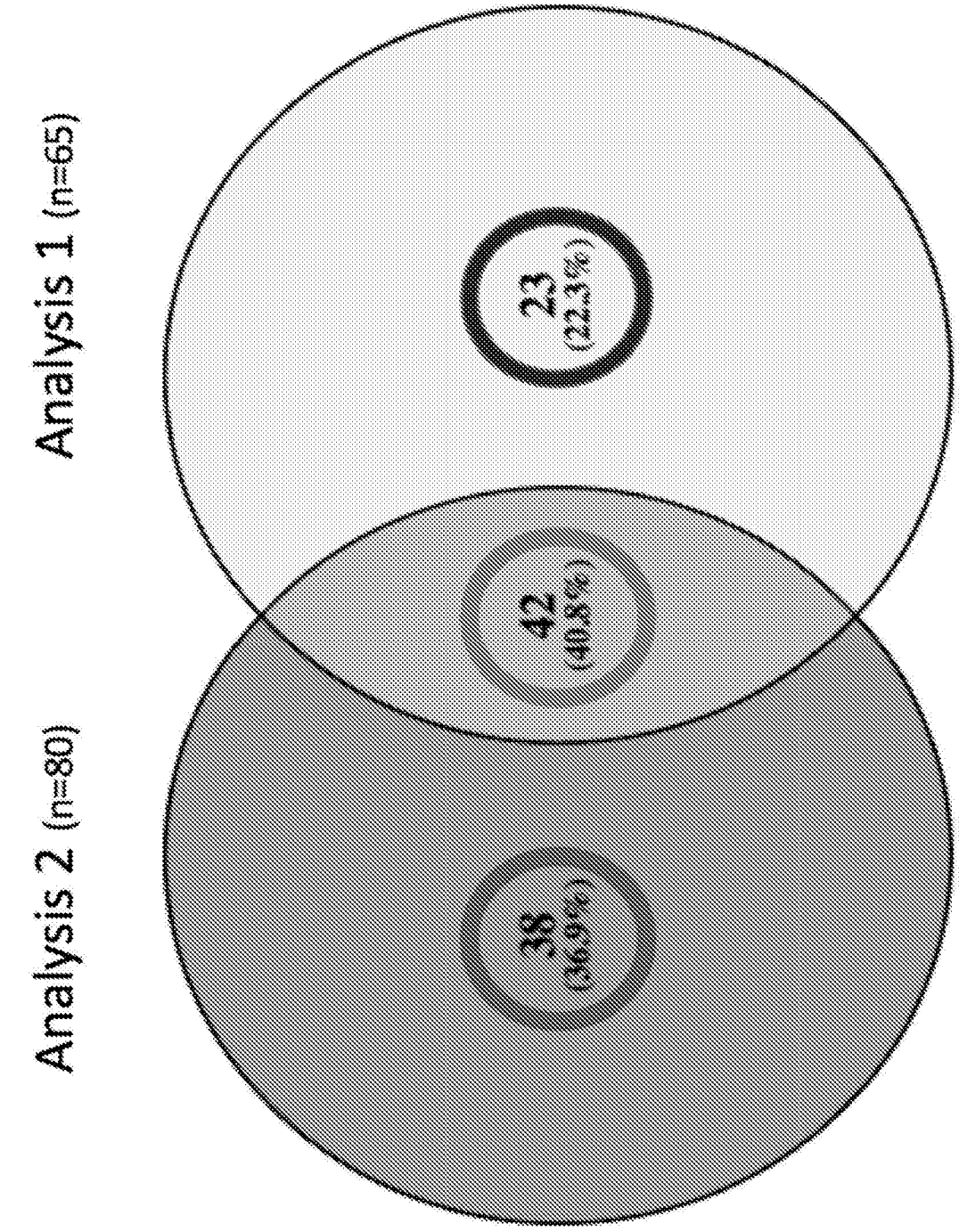


Figure 4

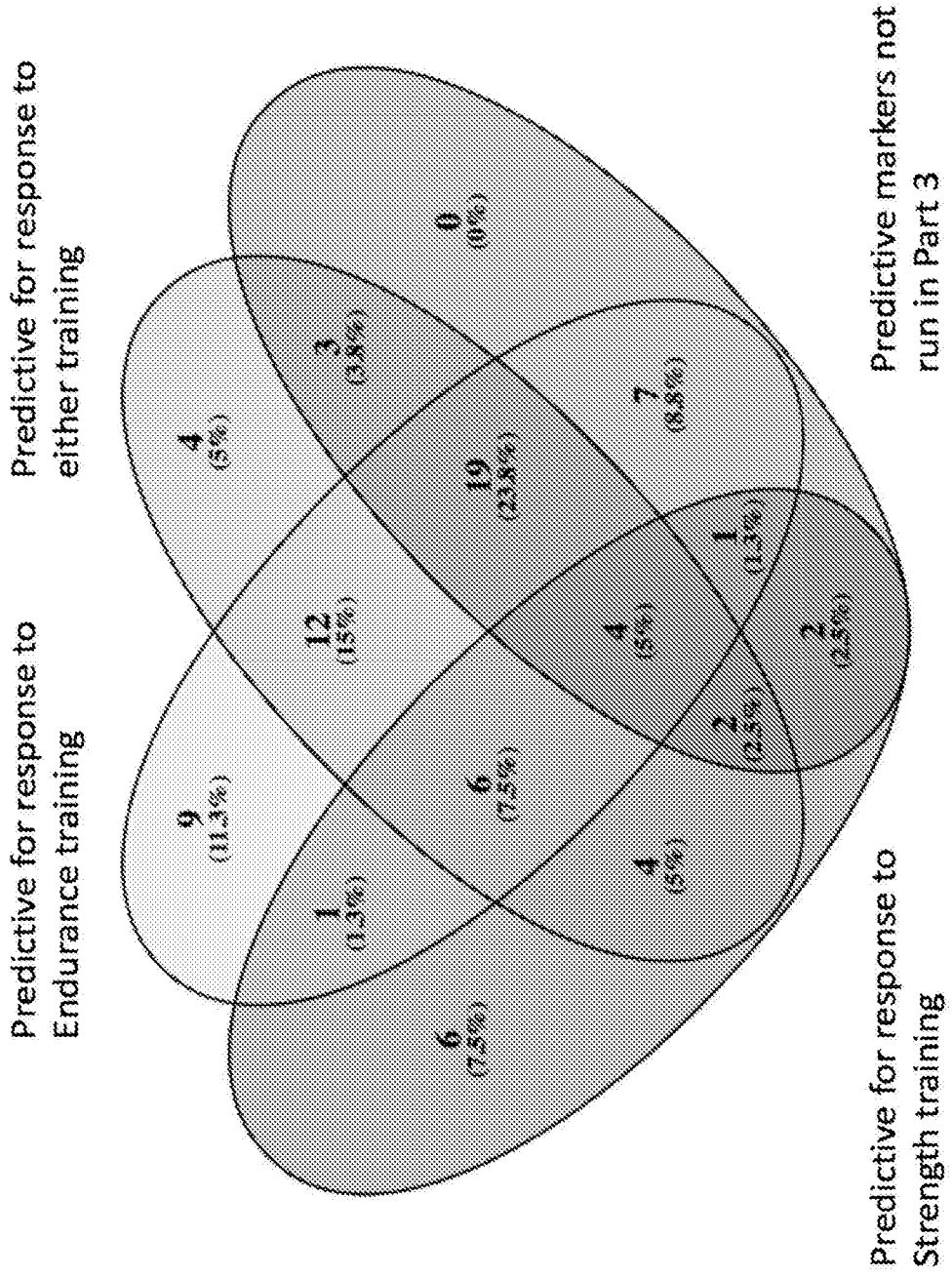

Predictive for response to Endurance training
Predictive for response to either training
Predictive markers not run in Part 3
Predictive for response to Strength training
0 (0%)
3 (3.8%)
7 (8.8%)
4 (5%)
19 (23.8%)
1 (1.3%)
12 (15%)
4 (5%)
2 (2.5%)
2 (2.5%)
9 (11.3%)
6 (7.5%)
1 (1.3%)
4 (5%)
6 (7.5%)

Figure 5

Figure 6

```
Confusion Matrix and Statistics

          Reference
Prediction  0  1
         0 15  1
         1  1 15

               Accuracy : 0.9375
                 95% CI : (0.7919, 0.9923)
    No Information Rate : 0.5
    P-Value [Acc > NIR] : 1.232e-07

                  Kappa : 0.875
 Mcnemar's Test P-Value : 1

            Sensitivity : 0.9375
            Specificity : 0.9375
         Pos Pred Value : 0.9375
         Neg Pred Value : 0.9375
             Prevalence : 0.5000
         Detection Rate : 0.4688
   Detection Prevalence : 0.5000
      Balanced Accuracy : 0.9375

       'Positive' Class : 0
```

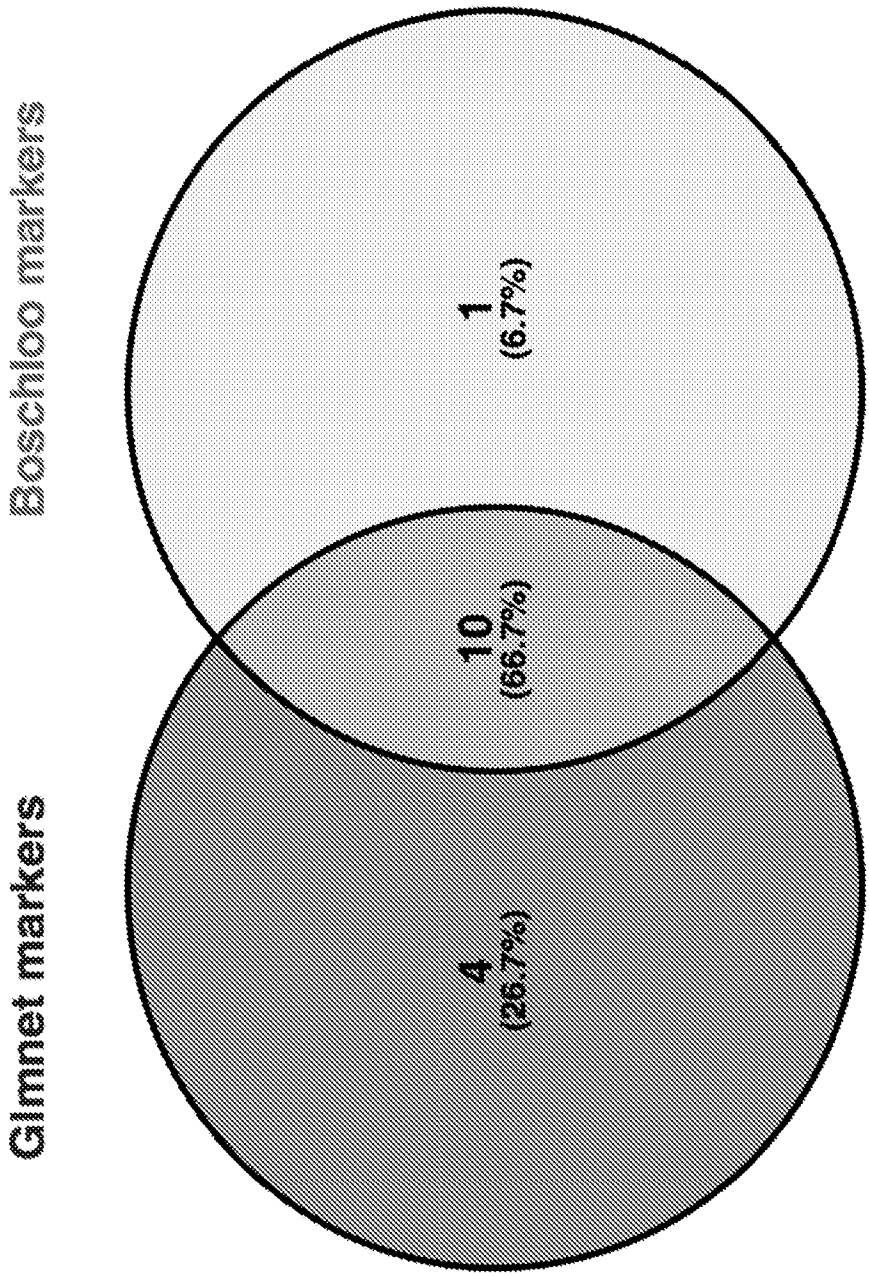


Figure 7

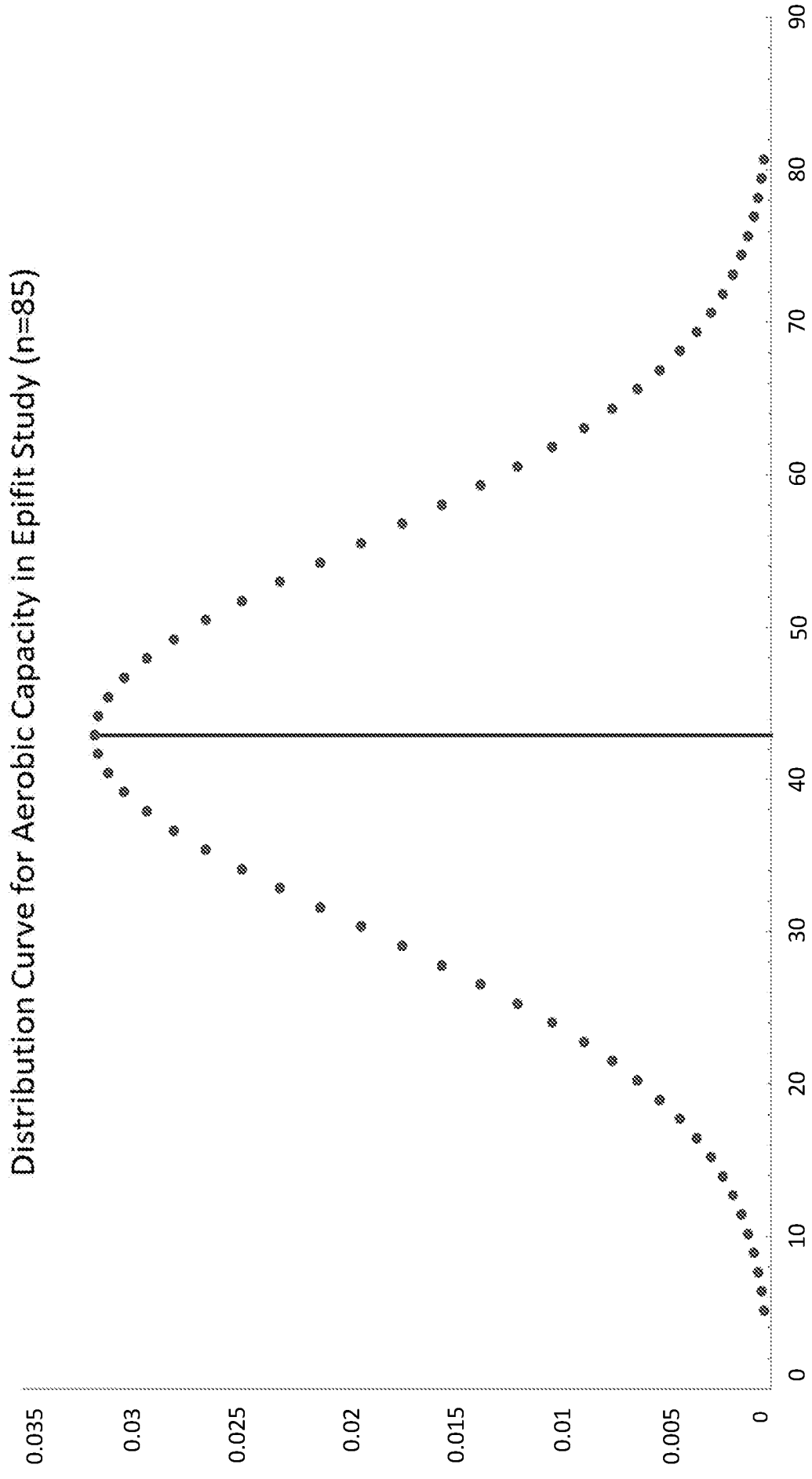
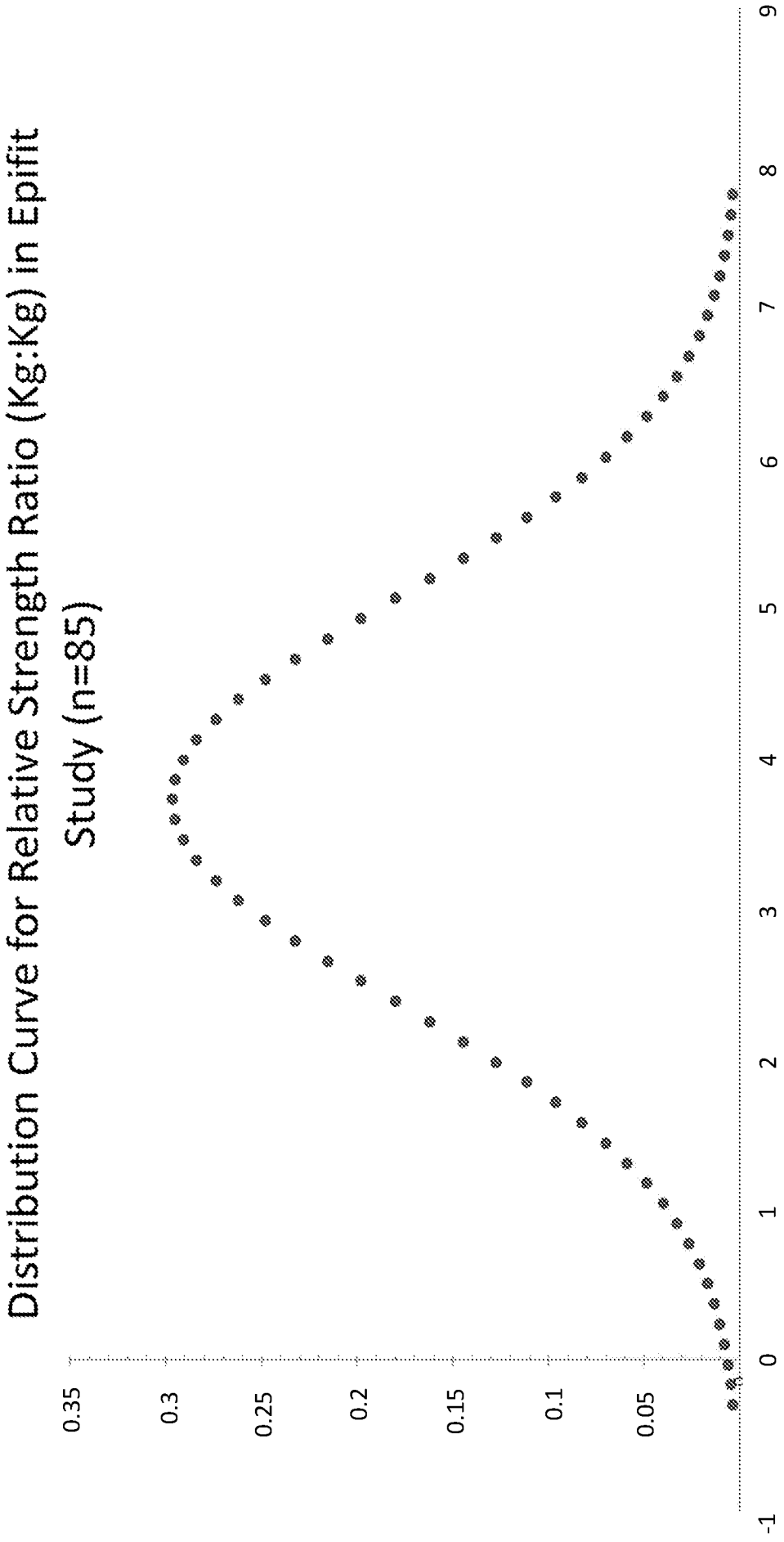

Distribution Curve for Aerobic Capacity in Epifit Study (n=85)
0.035
0.03
0.025
0.02
0.015
0.01
0.005
0
0
10
20
30
40
50
60
70
80
90

Figure 8

Figure 9


Distribution Curve for Relative Strength Ratio (Kg:Kg) in Epifit Study (n=85)
0.35
0.3
0.25
0.2
0.15
0.1
0.05
-1
0
1
2
3
4
5
6
7
8
9

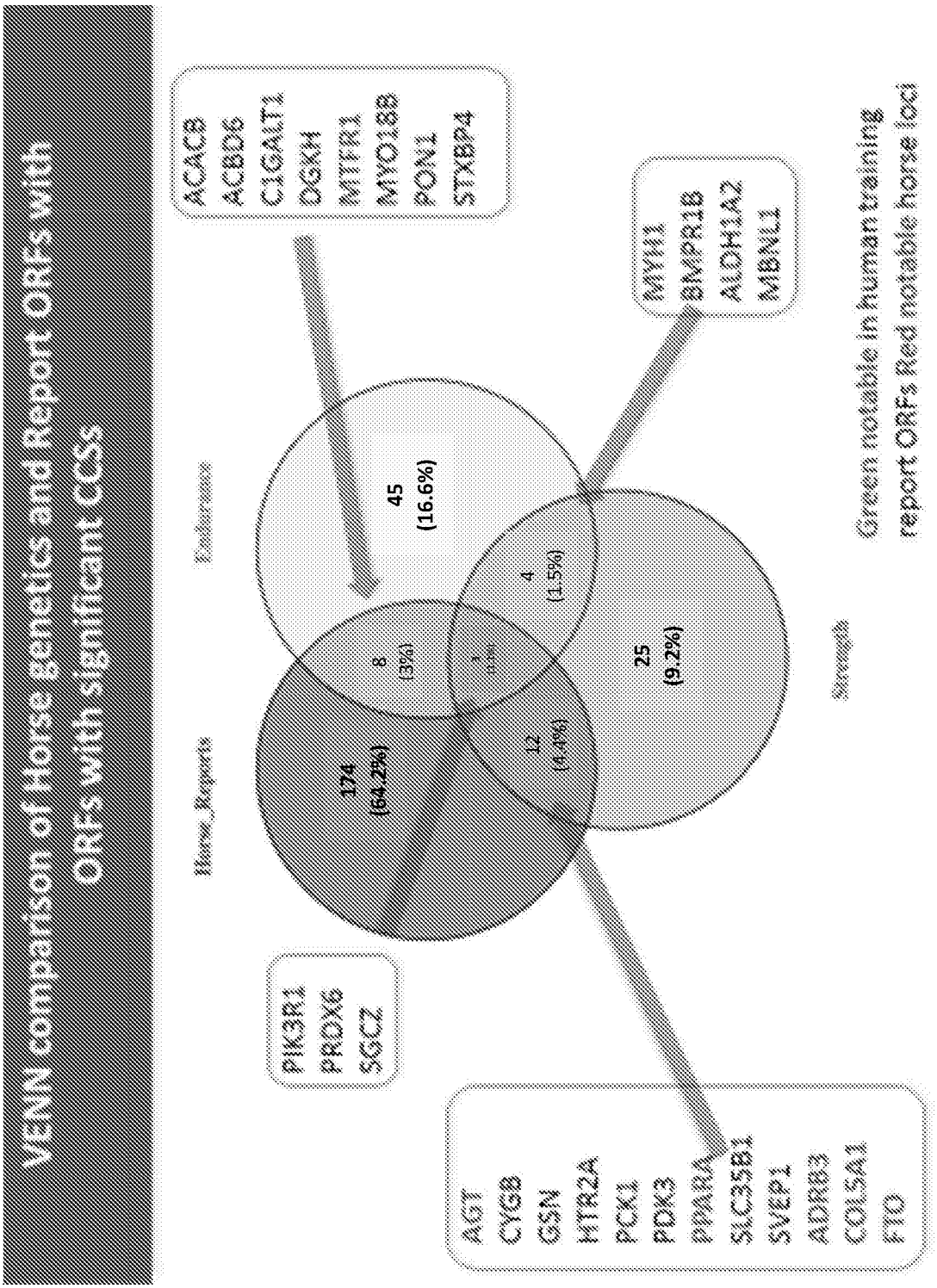

VENN comparison of Horse genetics and Report ORFs with ORFs with significant CCSs
ACACB
ACBD6
CIGALT1
DGKH
MTFR1
MYO18B
PON1
STXBP4
PIK3R1
PRDX6
SGCZ
AGT
CYGB
GSN
HTR2A
PCK1
PDK3
PPARA
SLC35B1
SVEP1
ADRB3
COL5A1
FTO
MYH1
BMPR1B
ALDH1A2
MBNL1
45
(16.6%)
174
(64.2%)
8
(3%)
4
(1.5%)
12
(4.4%)
25
(9.2%)
Green notable in human training
report ORFs Red notable horse loci

Figure 10

Figure 11

VENN diagram of the top 250 loops in sedentary subjects compared to the 2 athletic groups
Endurance_Ctrl
Strength_Ctrl
75
23.3%
175
(54.3%)
72
(22.4%)
This shows that 175 CCSs are shared in the sedentary subjects compared to the 2 athlete groups. These are loops present in sedentary but absent in training. There are 75 unique CCSs in the comparison to Endurance and 72 to strength

VENN comparison of Horse genetics and Report ORFs with
ORFs with significant common CCS in sedentary subjects
ACAC8
ACSS1
B4GALT5
C1GALT1
CACNA1E
DGKH
DOK5
EIF4E
EMCN
GLRX2
GSN
HSDL2
HTR2A
LCP1
MMP28
MTFR1
MUSK
NPL
PIK3C3
PPP1R9A
PRDX6
SGCZ
SOAT1
SRI
STXBP4
SUCLA2
SVEP1
UGCG
VEGFC
LIPC
MSTN
PPARGC1A
SOD2
Horse_Reports
Common_Ctrl
164
61%
33
(12.3%)
72
(26.8%)
Green notable in human training
report ORFs Red notable horse loci

Figure 12

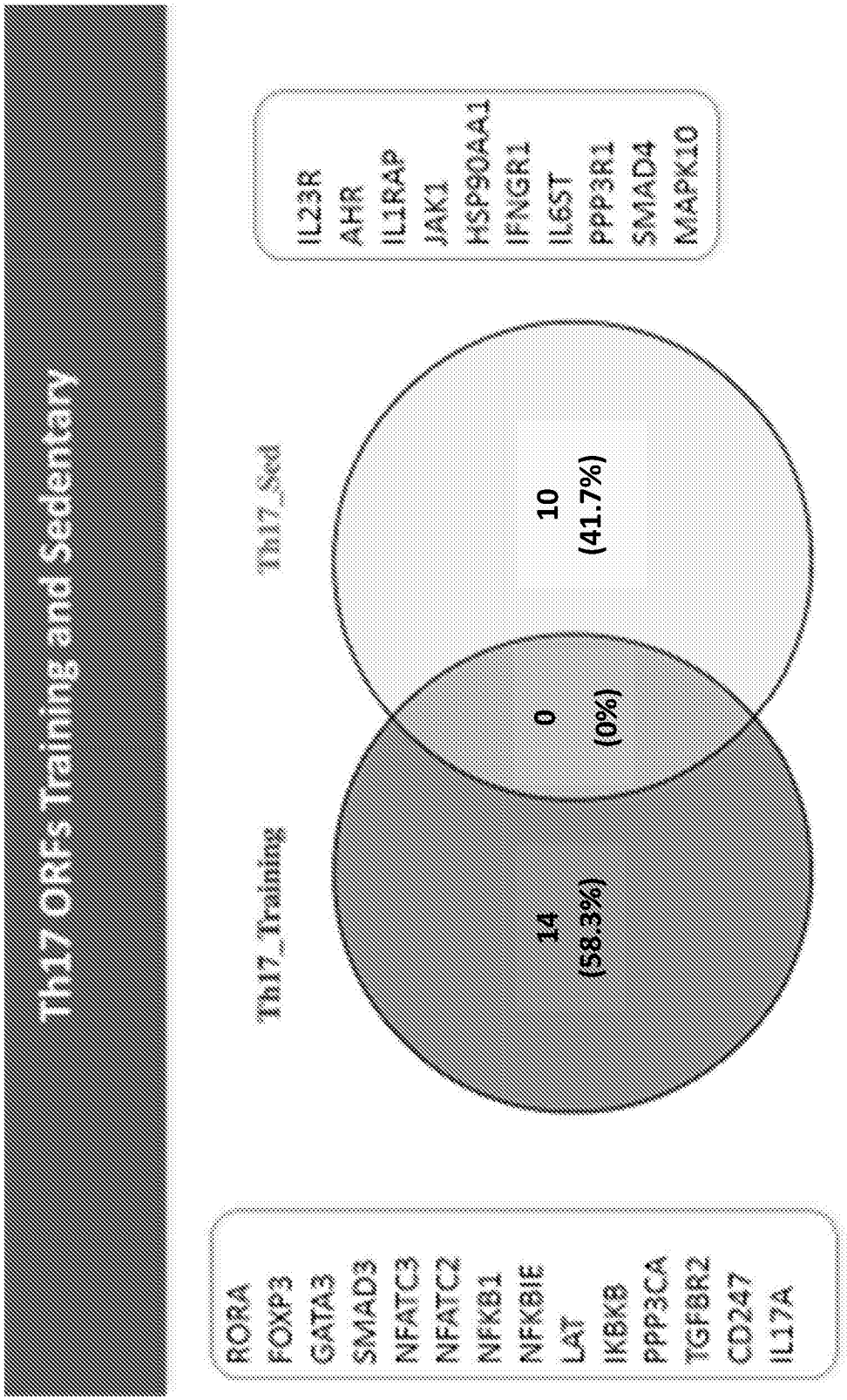
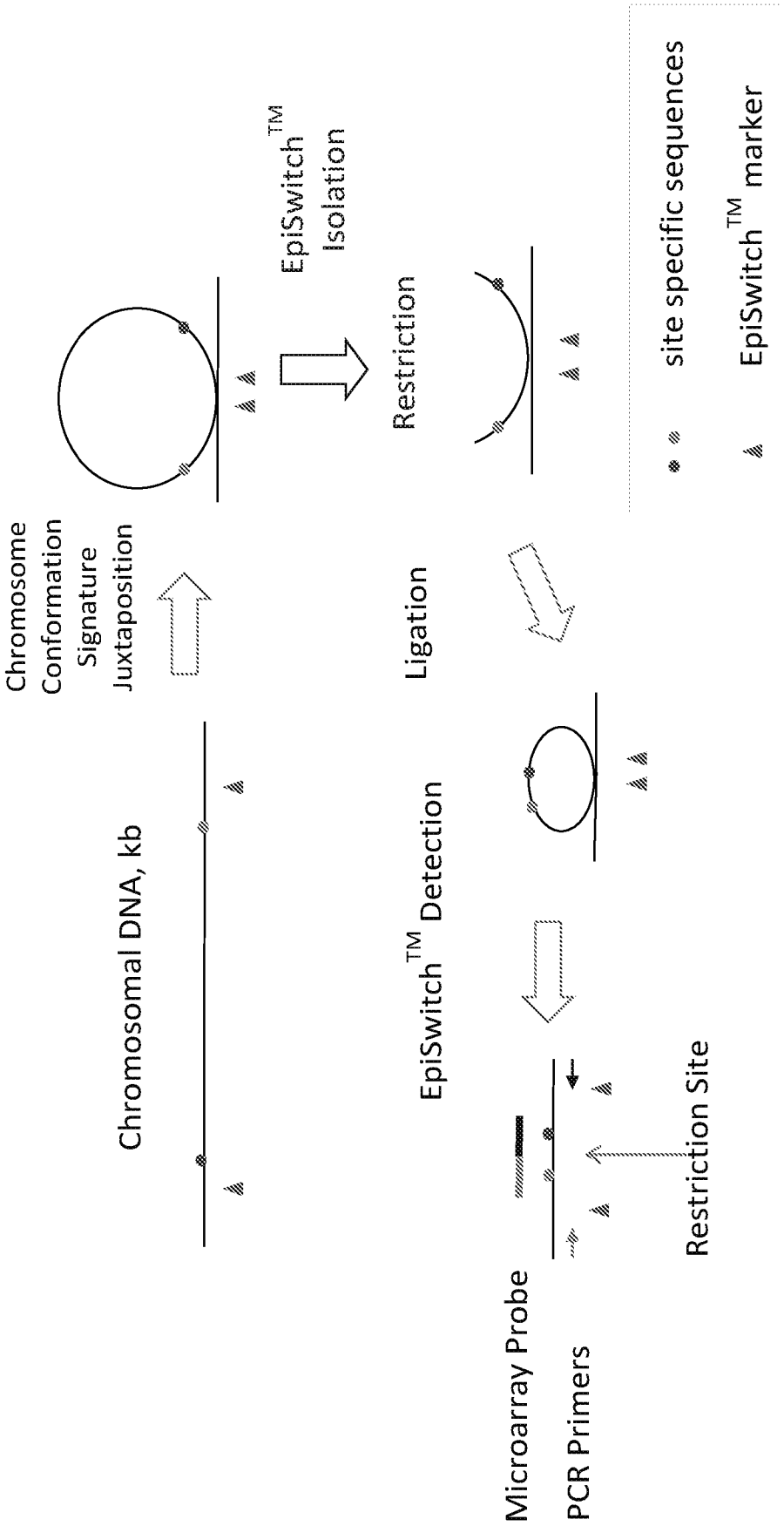

Th17 ORFs Training and Sedentary
Th17_Training
Th17_Sed
14
(58.3%)
0
(0%)
10
(41.7%)
RORA
FOXP3
GATA3
SMAD3
NFATC3
NFATC2
NFKB1
NFKBIE
LAT
IKBKB
PPP3CA
TGFBR2
CD247
IL17A
IL23R
AHR
IL1RAP
JAK1
HSP90AA1
IFNGR1
IL6ST
PPP3R1
SMAD4
MAPK10

Figure 13

Figure 14


Chromosome Conformation Signature Juxtaposition
EpiSwitch™ Isolation
Restriction
Ligation
EpiSwitch™ Detection
Chromosomal DNA, kb
Microarray Probe
PCR Primers
Restriction Site
site specific sequences
EpiSwitch™ marker

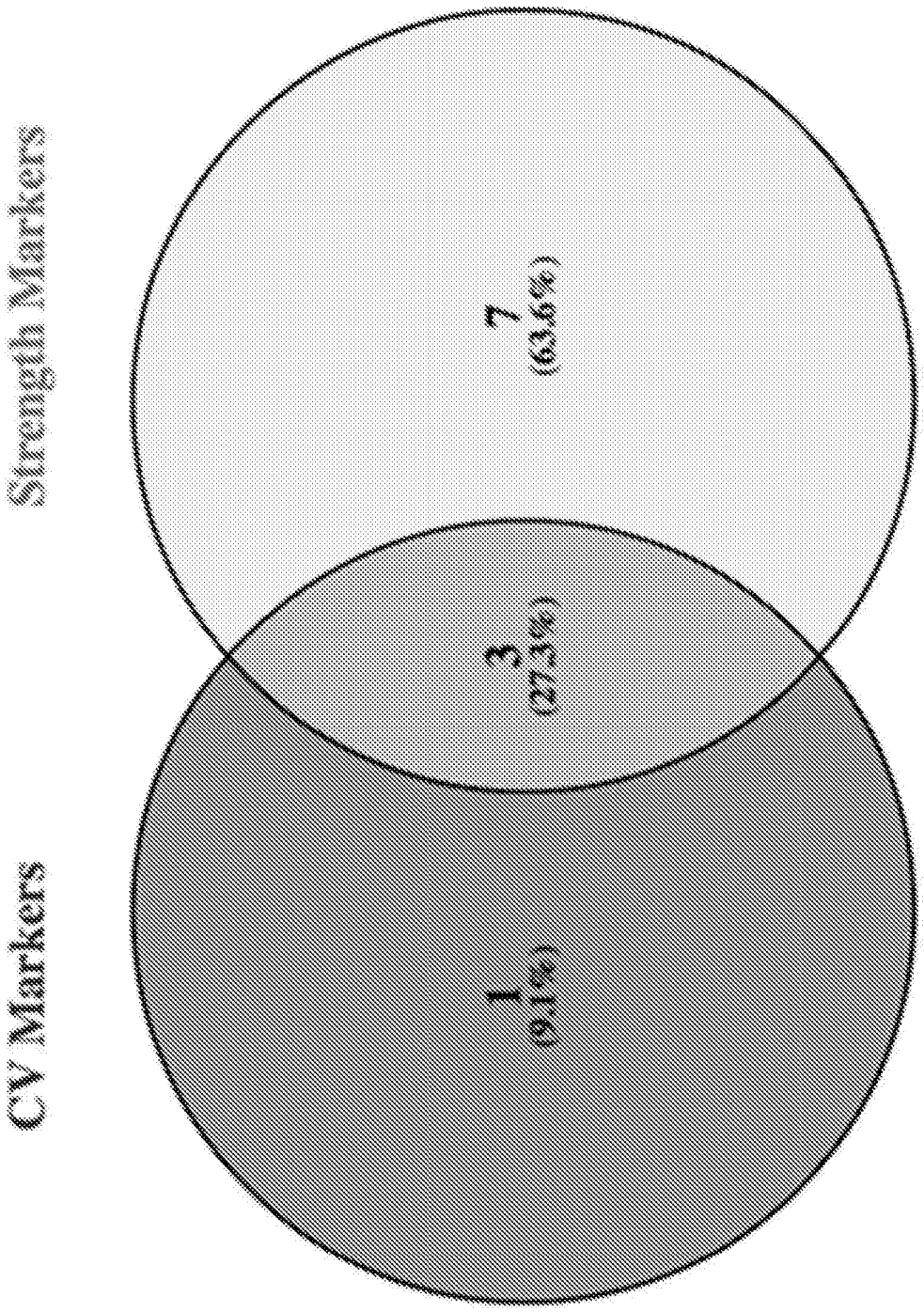


Figure 15

	A	B	C	D
1	Marker	Stats_CV	Stats_CS	Marker
2	OBD142_433.435	0.01290572	0.328290877	OBD142_433.435
3	OBD142_353.355	0.02356851	0.201245427	OBD142_353.355
4	OBD142_261.263	0.03096974	0.08554256	OBD142_261.263
5	OBD142_513.515	0.03583026	1	OBD142_513.515
6	OBD142_021.023	0.06817021	0.08653307	OBD142_021.023
7	OBD142_313.315	0.06915879	0.024329662	OBD142_313.315
8	OBD142_073.075	0.09839179	0.014782786	OBD142_073.075
9	Group_s2	0.09839179	0.077405989	Group_v2
10	OBD142_205.207	0.09164972	1	OBD142_205.207
11	OBD142_461.463	0.09164972	0.01770556	OBD142_461.463
12	OBD142_497.499	0.09164972	0.247600428	OBD142_497.499

Figure 16

	A	B	C	D
1	Marker	Stats_CS	Stats_CV	Marker
2	OBD142_073.075	0.014782786	0.08839179	OBD142_073.075
3	OBD142_029.031	0.01770556	1	OBD142_029.031
4	OBD142_461.463	0.01770556	0.09164972	OBD142_461.463
5	OBD142_169.171	0.02169621	1	OBD142_169.171
6	OBD142_429.431	0.023549199	1	OBD142_429.431
7	OBD142_313.315	0.024329662	0.06915879	OBD142_313.315
8	OBD142_493.495	0.030273855	0.686083314	OBD142_493.495
9	OBD142_457.459	0.043391466	0.69003797	OBD142_457.459
10	OBD142_277.279	0.048135281	0.21510564	OBD142_277.279
11	OBD142_021.023	0.065754175	0.15236533	OBD142_021.023
12	OBD142_209.211	0.065754175	0.50892571	OBD142_209.211
13	OBD142_389.391	0.065754175	1	OBD142_389.391
14	OBD142_397.399	0.065754175	1	OBD142_397.399
15	Group_v2	0.077405989	0.08839179	Group_s2
16	OBD142_261.263	0.085542256	0.03096974	OBD142_261.263
17	OBD142_345.347	0.085542256	1	OBD142_345.347
18	OBD142_077.079	0.09653307	1	OBD142_077.079
19	OBD142_109.111	0.109796792	1	OBD142_109.111
20	OBD142_273.275	0.110314369	0.50892571	OBD142_273.275
21	OBD142_473.475	0.110314369	1	OBD142_473.475

Figure 17

Figure 18

	A	B	C	D	E	F	G
1	Probe	Chr	Horse_Genomic		Human_Genomic		Marker_Type
2	OBD154_013.015_1x	ORF37_7_82005043_82035799_82946828_82948039_FF	AMPP	ARNTL	DKK3		Sprinter
3	OBD154_041.043_1.4x	ORF24_7_26919921_26921163_26962320_26963327_RF	TAGLN		CBL	MCAM	Stayer
4	OBD154_049.051_1.4x	ORF1_3_36982976_36984987_36937821_36902754_RR	MC1R		NFKB1		Stayer
5	OBD154_073.075_1x	ORF12_28_42033251_42034839_42111316_42112829_FR	PPARA		PPARA		Stayer
6	OBD154_085.087_1.2x	ORF31_24_18025107_18025879_18089550_18090204_FR	SYNJ2BP	DKK2	RGS6		Sprinter
7	OBD154_093.095_1.2x	ORF28_19_27971050_27974189_28029396_28030610_FR	TFRC	MIR1248	ILIRAP		Sprinter
8	OBD154_125.127_1.2x	ORF51_4_788561_790967_729450_732106_FR	CCDC136		CD36		Sprinter
9	OBD154_157.159_1.2x	ORF86_19_45853761_45861211_45775880_45782396_RR	EEF1A1		PLCXD2	PHLDB2	Stayer
10	OBD154_229.231_1x	ORF73_16_84538528_84540820_84582113_84585716_FR			MBNL1		Sprinter
11	OBD154_245.247_1x	ORF88_3_100800317_100801373_100744664_100751637_FF MIR218			PPARGC1A		Sprinter

INTERNATIONAL SEARCH REPORT

International application No
PCT/GB2019/052996

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12Q1/6876
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, WPI Data, BIOSIS, Sequence Search, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Bing Yu ET AL: "Genetics of Athletic Performance" In: "ENCYCLOPEDIA OF LIFE SCIENCES", 17 June 2010 (2010-06-17), John Wiley & Sons, Ltd, Chichester, XP055558481, ISBN: 978-0-470-01590-2 DOI: 10.1002/9780470015902.a0022400, page 6, left-hand column ----- -/--	1-17

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
19 December 2019	10/01/2020

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Gabriels, Jan

1

Form PCT/ISA/210 (second sheet) (April 2005)

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	N.C. CRAIG SHARP: "The Human Genome and Sport, Including Epigenetics, Gene Doping, and Athleticogenomics", ENDOCRINOLOGY AND METABOLISM CLINICS OF NORTH AMERICA., vol. 39, no. 1, 1 March 2010 (2010-03-01), pages 201-215, XP055558468, PHILADELPHIA ISSN: 0889-8529, DOI: 10.1016/j.ecl.2009.10.010 the whole document	1-17
A	JOÃO PAULO LIMONGI FRANÇA GUILHERME ET AL: "Genetics and sport performance: current challenges and directions to the future", REVISTA BRASILEIRA DE EDUCAÇÃO FÍSICA E ESPORTE, vol. 28, no. 1, 1 March 2014 (2014-03-01), pages 177-193, XP055558473, DOI: 10.1590/S1807-55092014000100177 page 187 - page 188	1-17
A	ELAINE A. OSTRANDER ET AL: "Genetics of Athletic Performance", ANNUAL REVIEW OF GENOMICS AND HUMAN GENETICS, vol. 10, no. 1, 1 September 2009 (2009-09-01), pages 407-429, XP055558459, US ISSN: 1527-8204, DOI: 10.1146/annurev-genom-082908-150058 the whole document	1-17
A	WO 2016/207661 A1 (OXFORD BIODYNAMICS LTD [GB]) 29 December 2016 (2016-12-29) page 6 - page 7; claim 1	1

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/GB2019/052996

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2016207661 A1	29-12-2016	AU 2016281766 A1	01-02-2018
		AU 2016281772 A1	01-02-2018
		AU 2016281776 A1	08-02-2018
		AU 2019219864 A1	12-09-2019
		CA 2988673 A1	29-12-2016
		CA 2988674 A1	29-12-2016
		CN 108138222 A	08-06-2018
		CN 108138223 A	08-06-2018
		CN 108377651 A	07-08-2018
		EP 3314014 A1	02-05-2018
		EP 3314015 A1	02-05-2018
		EP 3314018 A1	02-05-2018
		JP 2018518203 A	12-07-2018
		JP 2018518992 A	19-07-2018
		JP 2018527016 A	20-09-2018
		KR 20180039629 A	18-04-2018
		KR 20180039631 A	18-04-2018
		KR 20180040575 A	20-04-2018
		US 2018274015 A1	27-09-2018
		US 2019071715 A1	07-03-2019
		WO 2016207647 A1	29-12-2016
		WO 2016207653 A1	29-12-2016
		WO 2016207661 A1	29-12-2016
		ZA 201708230 B	31-07-2019