Innovation, Sciences et
Développement économique Canada
Office de la Propriété Intellectuelle du Canada

Innovation, Science and
Economic Development Canada
Canadian Intellectual Property Office

CA 3078675 A1 2019/05/09

(21) 3 078 675

(12) DEMANDE DE BREVET CANADIEN
CANADIAN PATENT APPLICATION

(13) A1

(86) Date de dépôt PCT/PCT Filing Date: 2018/11/02
(87) Date publication PCT/PCT Publication Date: 2019/05/09
(85) Entrée phase nationale/National Entry: 2020/04/07
(86) N° demande PCT/PCT Application No.: GB 2018/053196
(87) N° publication PCT/PCT Publication No.: 2019/086898
(30) Priorités/Priorities: 2017/11/03 (US62/581,287);
2018/10/03 (GB PCT/GB2018/052818)

(51) Cl.Int./Int.Cl. *C12Q 1/6886* (2018.01)
(71) Demandeur/Applicant:
OXFORD BIODYNAMICS LIMITED, GB
(72) Inventeurs/Inventors:
AKOULITCHEV, ALEXANDRE, GB;
RAMADASS, AROUL SELVAM, GB;
HUNTER, EWAN, GB
(74) Agent: DEETH WILLIAMS WALL LLP

(54) Titre : REGULATION GENETIQUE
(54) Title: GENETIC REGULATION

(57) Abrégé/Abstract:

A process for analysing chromosome regions and interactions relating to immunoresponsiveness.

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

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
09 May 2019 (09.05.2019)

WIPO | PCT

(10) International Publication Number
WO 2019/086898 A3

(51) International Patent Classification:
C12Q 1/6886 (2018.01)

(21) International Application Number:
PCT/GB2018/053196

(22) International Filing Date:
02 November 2018 (02.11.2018)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/581,287 03 November 2017 (03.11.2017) US
PCT/GB2018/052818
03 October 2018 (03.10.2018) GB

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

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

(74) Agent: **AVIDITY IP**; Broers Building, Hauser Forum, 21 J J Thomson Avenue, 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))*
- *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*

(88) **Date of publication of the international search report:**
13 June 2019 (13.06.2019)

(54) **Title:** GENETIC REGULATION OF IMMUNORESPONSE BY CHROMOSOME INTERACTIONS

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

GENETIC REGULATION

Field of the Invention

The invention relates to detecting chromosome interactions.

Background of the Invention

Disease processes are complex and outcomes cannot be predicted using available methods. In particular it is difficult to predict how patients will react to specific therapies.

Summary of the Invention

Specific Chromosome Conformation Signatures (CCSs) at loci either exist or are absent due to the regulatory epigenetic control settings associated with pathology or treatment. CCSs have mild off-rates and when representing a particular phenotype or pathology, they will only change with a physiologically signalled transition to a new phenotype, or as a result of external intervention. In addition, the measurement of these events is binary, and so this read-out is in stark contrast to the continuum readout of varying levels of DNA methylation, histone modifications and most of the non-coding RNAs. The continuum read-out used for most molecular biomarkers to date offers a challenge to data analysis, in that the magnitude of change for particular biomarkers varies greatly from patient to patient, which causes problems for classification statistics when they are used to stratify cohorts of patients. These classification statistics are better-suited to using biomarkers that are absent of magnitude and offer just a "yes or no" binary score of phenotypic differences - signifying that chromosome conformation (*EpiSwitch*™) biomarkers are an excellent resource for potential diagnostic, prognostic and predictive biomarkers.

The inventors have identified regions of the genome with chromosomal interactions relevant to immunoresponsiveness using an approach which allows identification of subgroups in a population. The identified regions, genes and specific chromosome interactions from two separate studies using different therapies to treat two different conditions have been found to determine general immunoresponsiveness in a patient, including through the immune response regulating cell surface signalling pathway and regulation of T cell activation. The inventors' work allows changes in immunoresponsiveness to be followed, for example during the course of disease or therapy.

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 how immunoresponsive individuals are; 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 an immunoresponsive 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 an immunoresponsive subgroup; and
- wherein the chromosome interaction:

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

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

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

The invention also 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 how immunoresponsive individuals are; 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 an immunoresponsive 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 an immunoresponsive subgroup; and
- wherein the chromosome interaction:

a) is present in any one of the regions or genes listed in Table 13; and/or

b) corresponds to any one of the chromosome interactions represented by any probe shown in Table 13, and/or

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

The invention further 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 how immunoresponsive individuals are; 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 an immunoresponsive 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 an immunoresponsive subgroup; and
- wherein the chromosome interaction:

(α) is present in any one of the regions or genes listed in Table 16; and/or

(β) corresponds to any one of the chromosome interactions represented by any probe shown in Table 16, and/or

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

Detailed Description of the Invention

Aspects of the Invention

The inventions concerns a panel of epigenetic markers which relate to the regulation of the immune system, in particular via cell surface signalling pathways and T cell activation.

The invention also includes monitoring the state of the immune system to determine its responsiveness to particular therapies. That means appropriate therapies can be given to a patient, and whether or not the patient is retaining or losing 'responder' status can be determined. The invention therefore provides in one embodiment a 'live' ongoing readout of 'responder' status allowing a personalised therapy to be given to the patient which accurately reflects the patient's needs.

Immunoresponsiveness

The invention relates to determining immunoresponsiveness. This is preferably responsiveness to a therapy which comprises a molecule or cell that is relevant to the immune system, such as administration of a composition that comprises an antibody or immune cell (for example a T cell or dendritic cell) or administration of any therapeutic substance mentioned herein. It may be responsiveness to a substance that modulates or stimulates the immune system, such as a vaccine therapy. The immunoresponsiveness is thus preferably the responsiveness to an immunotherapy. The immunotherapy may modulate, block or stimulate an immune checkpoint, and thus may target or modulate PD-L1, PD-L2 or CTLA4 or any other immune checkpoint molecule disclosed herein, and thus may be an immunocheckpoint therapy. Preferably the immunoresponsiveness is responsiveness to an antibody therapy, or to any specific therapy disclosed herein (see specific drugs in later sections). The therapy may be a combination therapy.

In one embodiment immunoresponsiveness to responsiveness to a PD-1 inhibitor or PD-L1 inhibitor, including an antibody specific for PD-1 or PD-L1. PD-1 is 'programmed cell death protein' and PD-L1 is 'programmed death-ligand 1'.

The immunoresponsiveness is preferably to a cancer therapy, and so typically is relevant to whether a specific individual is responsive to the therapy, where the individual may or may not have cancer, or may be at risk of cancer. The cancer is typically any cancer mentioned herein, and for example is melanoma, lung cancer, non-small cell lung carcinoma (NSCLC), diffuse large B-cell lymphoma, liver cancer, hepatocellular carcinoma, prostate cancer, breast cancer, leukaemia, acute myeloid leukaemia, pancreatic cancer, thyroid cancer, nasal cancer, brain cancer, bladder cancer, cervical cancer, non-Hodgkin lymphoma, ovarian cancer, colorectal cancer or kidney cancer.

The term 'antibody' includes all fragments and derivatives of an antibody that retain the ability to bind the antigen target, for example single chain scFV's or Fab's.

As will be discussed later immunoresponsiveness can be determined for any therapy, cell or drug which is mentioned herein. In some embodiments any therapy, cell or drug that is mentioned herein may be administered to individuals whose immunoresponsiveness has been determined.

The Process of the Invention

The process of the invention comprises a typing system for detecting chromosome interactions relevant to immunoresponsiveness. 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 refers 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 in response to change of the physiological conditions. 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 immunoresponsiveness) 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. Thus the process of the invention is able to detect early stages of a biological process. This allows early intervention (for example treatment) which may as a consequence be more effective. Chromosome interactions also reflect the current state of the individual and therefore can be used to assess changes to immunoresponsiveness. 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. Further 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. It should further be noted that the inventors have discovered that epigenetic interactions in all regions are equally important in determining the status of the chromosomal locus. These interactions are not necessarily in the coding region of a particular gene located at the locus and 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 1. However it may also be upstream or downstream of the gene, for example up to 50,000, up to 30,000, up to 20,000, up to 10,000 or up to 5000 bases upstream or downstream from the gene or from the coding sequence.

The chromosome interaction which is detected is preferably within any of the genes mentioned in Table 13. However it may also be upstream or downstream of the gene, for example up to 50,000, up to 30,000, up to 20,000, up to 10,000 or up to 5000 bases upstream or downstream from the gene or from the coding sequence.

The chromosome interaction which is detected is preferably within any of the genes mentioned in Table 16. However it may also be upstream or downstream of the gene, for example up to 50,000, up to 30,000, up to 20,000, up to 10,000 or up to 5000 bases upstream or downstream from the gene or from the coding sequence.

Subgroups, Time Points and Personalised Treatment

The aim of the present invention is to determine the level of immunoresponsiveness. This may be at one or more defined time points, for example at at least 1, 2, 5, 8 or 10 different time points. The durations between at least 1, 2, 5 or 8 of the time points may be at least 5, 10, 20, 50, 80 or 100 days. Typically at least 1, 2 or 5 time points are before therapy begins and/or at least 1, 2 or 5 time points are after the beginning of therapy.

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 particular animal such as a particular eukaryote, or mammal (e.g. human, non-human, non-human primate, or rodent e.g. mouse or rat). Most preferably, a "subgroup" refers to a subgroup in the human population.

The invention includes detecting and treating particular subgroups in a population. The inventors have discovered that chromosome interactions differ between subsets (for example at least two subsets) in a given population. Identifying these differences will allow physicians to categorize their patients as a part of one subset of the population as described in the process. The invention therefore provides physicians with a process of personalizing medicine for the patient based on their epigenetic chromosome interactions.

In one embodiment the invention relates to testing whether an individual is a 'responder'. Once a person is found to be a 'responder' they can be given the relevant therapy which is typically a therapy that targets an immune checkpoint molecule such as PD-1, PD-L1 or CTLA4. In one embodiment if an individual is found to be a non-responder then they will be given a combination therapy, such as any combination therapy listed herein. Typically a combination therapy comprises an antibody and a small molecule.

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^{TM} 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 4 are used in the PCR reaction. In other embodiments at least 1, 2 or 3 primers or primer pairs as shown in Table 13 are used in the PCR reaction. In other embodiments at least 1, 2 or 3 primers or primer pairs as shown in Table 17 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, such as tissues relevant to disease. For certain conditions, such as cancer, genetic noise due to mutations can affect the chromosome interaction 'signal' in the relevant tissues and therefore using blood is advantageous.

Properties of Nucleic Acids of the Invention

The invention relates to certain nucleic acids, such as the ligated nucleic acids which are described herein as being used or generated in the process of the invention. These may be the same as, or have any of the properties of, the first and second nucleic acids mentioned herein. The nucleic acids of the invention typically comprise two portions each comprising sequence from one of the two regions of the chromosome which come together in the chromosome interaction. Typically each portion is at least 8, 10, 15, 20, 30 or 40 nucleotides in length, for example 10 to 40 nucleotides in length. Preferred nucleic acids comprise sequence from any of the genes mentioned in any of the tables. Typically preferred nucleic acids comprise the specific probe sequences mentioned in Table 1; or fragments and/or homologues of such sequences. The preferred nucleic acids may comprise the specific probe sequences mentioned in Table 13; or fragments and/or homologues of such sequences. The preferred nucleic acids may comprise the specific probe sequences mentioned in Table 16; 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. 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 4 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 4; or fragments and/or homologues of any sequence shown in Table 4. The primers shown in Table 13 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 13; or fragments and/or homologues of any sequence shown in Table 13. The primers shown in Table 17 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 17; or fragments and/or homologues of any sequence shown in Table 17.

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 disease state (typically relevant to diagnosis or prognosis) in a species. The second set of nucleic acids typically comprises sequences representing epigenetic interactions both relevant and not relevant to an immunoresponsiveness 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 immunoresponsiveness. 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.

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 immunoresponsiveness in an individual. Preferably the chromosome interactions are those in any of the genes mentioned herein. In one embodiment the chromosome interactions which are typed are those represented by the nucleic acids in Table 1. In another embodiment the chromosome interactions are those represented in Table 13. In another embodiment the chromosome interactions are those represented in Table 16. The column titled 'Loop Detected' in the tables shows which subgroup is detected (i.e. responder or non-responder) by each probe.

The Individual that is Tested

Examples of the species that the individual who is tested is from are mentioned herein. In addition the individual that is tested in the process of the invention may have been selected in some way. The individual may be susceptible to any condition mentioned herein and/or may be in need of any therapy mentioned in. The individual may be receiving any therapy mentioned herein.

In one embodiment the individual that is tested has shown a lack of response to therapy, and the purpose of testing them is to discover whether they are a 'pseudo-progressor' that will respond to therapy in the second stage of disease, though they have not responded at an earlier stage.

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 Table 1. Typically in the processes of the invention chromosome interactions are detected from at least 1, 2, 10, 50, 100, 150, 200 or 300 of the relevant genes listed in Table 1. Preferably the presence or absence of at least 1, 2, 10, 50, 100, 150, 200 or 300 of the relevant specific chromosome interactions represented by the probe sequences in Table 1 are detected. 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, 15, 20 or all of the chromosome interactions in Table 1.a are typed. In one embodiment at least 5, 10, 15, 20 or all of the chromosome interactions in Table 1.b are typed. In one embodiment at least 5, 10, 15, 20 or all of the chromosome interactions in Table 1.c are typed. In one embodiment at least 5, 10, 15, 20 or all of the chromosome interactions in Table 1.d are typed. In one embodiment at least 5, 10, 15, 20 or all of the chromosome interactions in Table 1.e are typed. In one embodiment at least 5, 10, 15, 20 or all of the chromosome interactions in Table 1.f are typed. In one embodiment at least 5, 10, 15, 20 or all of the chromosome interactions in Table 1.g 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, 100, 200, 300 or all of the genes mentioned in Table 2. Typically the chromosome interactions which are typed are present in at least 10, 20, 50, 70 or all of the genes mentioned in Table 3.

For all aspects of the invention preferred gene regions, loci, genes and chromosome interactions are mentioned in Table 13. Typically in the processes of the invention chromosome interactions are detected from at least 1, 2, 10, 50, 100, 150, 200 or 300 of the relevant genes listed in Table 13. Preferably the presence or absence of at least 1, 2, 10, 50, 100, 150, 200 or 300 of the relevant specific chromosome interactions represented by the probe sequences in Table 13 are detected. 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, 15, 20 or all of the chromosome interactions in Table 13.a are typed. In one embodiment at least 5, 10, 15, 20 or all of the chromosome interactions in Table 13.b are typed. In one embodiment at least 5, 10, 15, 20 or all of the chromosome interactions in Table 13.c are typed. In one embodiment at least 5, 10, 15, 20 or all of the chromosome interactions in Table 13.d are typed. In one embodiment at least 5, 10, 15, 20 or all of the chromosome interactions in Table 13.e are typed. In one embodiment at least 5, 10, 15, 20 or all of the chromosome interactions in Table 13.f are typed. In one embodiment at least 5, 10, 15, 20 or all of the chromosome interactions in Table 13.g are typed. In one embodiment at least 5, 10, 15, 20 or all of the chromosome interactions in Table 13.h are typed. In one embodiment at least 5, 10, 15, 20 or all of the chromosome interactions in Table 13.i 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, 100, 200, 300 or all of the genes mentioned in Table 13. Typically the chromosome interactions which are typed are present in at least 10, 20, 50, 70 or all of the genes mentioned in Table 13.

For all aspects of the invention preferred gene regions, loci, genes and chromosome interactions are mentioned in Table 16. Typically in the processes of the invention chromosome interactions are detected from at least 1, 2, 10, 20. 30 or 40 of the relevant genes listed in Table 16. Preferably the presence or absence of at least 1, 2, 10, 20, 30 or 40 of the relevant specific chromosome interactions represented by the probe sequences in Table 16 are detected. 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 15 or all of the chromosome interactions in Table 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, 100, 200, 300 or all of the genes mentioned in Table 13. Typically the chromosome interactions which are typed are present in at least 10, 20, 50, 70 or all of the genes mentioned in Table 13.

In one embodiment at least 5, 10, 15, 20, 30, 40 or 70 different chromosome interactions are typed from those defined in any of Tables 1, 13 and 16. In another embodiment at least 50%, 80% or all of the chromosome interactions which are typed are from Tables 1, 13 and 16.

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 1. 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 13.

In one embodiment the chromosome interactions which are detected are present at any of the gene regions shown Table 13. In the case where a ligated nucleic acid is detected in the process then sequence shown in any of the probe sequences in Table 13 may be detected.

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

Table 1 shows probe (Episwitch™ marker) data and gene data representing chromosome interactions relevant to immunoresponsiveness. 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

Table 1 shows genes where a relevant chromosome interaction has been found to occur. Other tables show similar data. 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 LS column shows presence or absence of the relevant interaction with that particular responder status.

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)).

Tables 1 and 4 relates to detection of immunoresponsiveness. Table 2 shows the overlap between the two studies that were done, and Table 3 shows the overlap with markers relating to interferon gamma. The invention can be carried out using markers as disclosed/represented in any of the tables. Other tables, including Tables 13 and 1, can be interpreted in a similar manner as set out for Table 1 above.

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 25 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 Table 1, and/or

- wherein the chromosomal interaction may be any of the chromosome interactions mentioned herein or corresponding to any of the probes disclosed in Table 1, and/or

- wherein the ligated product may have or comprise (i) sequence which is the same as or homologous to any of the probe sequences disclosed in Table 1; or (ii) sequence which is complementary to (ii).

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 immunoresponsiveness, and/or
- the chromosome state may be at any locus, region or gene mentioned in Table 1; and/or
- the chromosome interaction may be any of those mentioned in Table 1 or corresponding to any of the probes disclosed in 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 Table 13, and/or

- wherein the chromosomal interaction may be any of the chromosome interactions mentioned herein or corresponding to any of the probes disclosed in Table 13, and/or

- wherein the ligated product may have or comprise (i) sequence which is the same as or homologous to any of the probe sequences disclosed in Table 13; 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 immunoresponsiveness, and/or
- the chromosome state may be at any locus, region or gene mentioned in Table 13; and/or
- the chromosome interaction may be any of those mentioned in Table 13 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 Table 16, and/or

- wherein the chromosomal interaction may be any of the chromosome interactions mentioned herein or corresponding to any of the probes disclosed in Table 16, and/or

- wherein the ligated product may have or comprise (i) sequence which is the same as or homologous to any of the probe sequences disclosed in Table 16; 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 immunoresponsiveness, and/or
- the chromosome state may be at any locus, region or gene mentioned in Table 16; and/or
- the chromosome interaction may be any of those mentioned in Table 16 or corresponding to any of the probes disclosed in that table.

The invention includes detecting chromosome interactions at any locus, gene or regions mentioned Table 1. 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 4 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 13. 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 13 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 16. 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 17 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 Treatments

Knowledge of chromosome interactions can be used to identify new treatments for conditions. The invention provides methods and uses of chromosomes interactions defined herein to identify or design new therapeutic agents, for example relating to immunotherapy.

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.

Therapeutic Agents (for which responsiveness is determined or which are selected based on testing according to the invention)

Therapeutic agents are mentioned herein. The invention provides such agents for use in preventing or treating a disease condition in certain individuals, for example those identified by a process of the invention. This may comprise administering to an individual in need a therapeutically effective amount of the agent. The invention provides use of the agent in the manufacture of a medicament to prevent or treat a condition in certain individuals.

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

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

In one embodiment the invention comprises detecting responsiveness to a therapeutic agent, for example any therapeutic agent mentioned herein. This may be before treatment has started and/or during the course of therapy.

The therapy may be mono or combination therapy, for example with immunocheckpoint modulators (inhibitors) for PD-1 and or its ligand, PD-L1. The therapy could be a combination of an anti-PD-1 or anti-PD-L1 combined with another drug that targets a checkpoint like CTLA4 (Ipilimumab/Yervoy) or small molecules. The PD-1 inhibitors could be pembrolizumab (Keytruda) or nivolumab (Opdivo). The modulator of PD-L1 or therapeutic agent could be Atezolizumab (Tecentriq), Avelumab (Bavencio), Durvalumab (Imfinzi), CA-170, Ipilimumab, Tremelimumab, Nivolumab, Pembrolizumab, Pidilizumab, BMS935559, GVAXMPDL3280A, MEDI4736, MSB0010718C, MDX-1105/BMS-936559, AMP-224, MEDI0680.

The therapy may comprise administering agents that target and/or modulate interferon gamma or the JAK-START pathway.

The therapeutic agent may be any such agent disclosed in any table herein (for example in Table 9, 10 or 11), or may target any 'target' disclosed herein, including any protein disclosed herein in any table (including Table 1, 13 or 16). It is understood that any agent that is disclosed in a combination should be seen as also disclosed for administration individually.

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 immunoresponsiveness. 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 the Figures, including any or all genes mentioned in Figures 2 and 4.

In one embodiment none of the chromosome interactions represented by the probes or primers of any or all of Tables 5 to 7 are typed. In another embodiment no chromosome interactions present in any of the genes listed in any or all of Tables 5 to 7 are typed. In a further embodiment no chromosome interactions present in any of the regions listed in any or all of Tables 5 to 7 are typed.

In one embodiment the immunoresponsiveness does not relate to antibody therapy. In another embodiment the immunoresponsiveness does not relate to anti-PD-1 therapy, for example anti-PD-1 therapy of melanoma. In another embodiment the immunoresponsiveness does not relate to therapy one or more of the following: a blood cancer, leukaemia, prostate cancer, breast cancer, diffuse large B cell lymphoma.

Screening method

The invention provides a method of determining which chromosomal interactions are relevant to a chromosome state corresponding to an immunoresponsive 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 an immunoresponsive subgroup. The subgroup may be any of the specific subgroups defined herein, for example with reference to particular conditions or therapies.

Publications

The contents of all publications mentioned herein are incorporated by reference into the present specification and may be used to further define the features relevant to the invention.

Tables

Table 1 shows the final set of markers for testing immunoresponsiveness.

Table 2 shows the shared markers between the anti-PD-1 and anti-PD-L1 studies.

Table 3 shows markers which overlap with interferon gamma activated ORF's.

Table 4 shows primer pairs that can be used to detect markers relating to immunoresponsiveness.

Tables 5 to 7 show markers, genes and regions which are not included in certain embodiments.

Table 8 shows immune checkpoint molecules.

Table 9 provides example of cancer therapies.

Tables 10 and 11 show combination and mono therapies for certain embodiments of the invention. In some embodiments these are the therapies for which responsiveness is tested. In other embodiments these therapies are given to the patient depending on the outcome of testing according to the invention.

Table 12 provides a description of genes relevant to the invention.

Table 13 shows a further set of markers for testing immunoresponsiveness.

Tables 14 and 15 describe genes that relate to embodiments of the invention.

Tables 16 to 18 shows markers for testing immunoresponsiveness.

Embodiments of the Invention

Paragraph A. 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 how immunoresponsive individuals are; 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 an immunoresponsive 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 an immunoresponsive subgroup; and

- wherein the chromosome interaction either:

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

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

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

or

a) is present in any one of the regions or genes listed in Table 13; and/or

b) corresponds to any one of the chromosome interactions represented by any probe shown in Table 13, and/or

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

Paragraph B. A process according to paragraph A wherein a specific combination of chromosome interactions are typed:

(i) comprising all of the chromosome interactions represented by the probes in Table 1; and/or

(ii) comprising at least 10, 50, 100, 150, 200 or 300 of the chromosome interactions represented by the probes in Table 1; and/or

(iii) which together are present in at least 10, 50, 100, 150 or 200 of the regions or genes listed in Table 1; 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 by the probes in Table 1.

Paragraph C. A process according to paragraph A wherein a specific combination of chromosome interactions are typed:

(i) comprising all of the chromosome interactions represented by the probes in Table 13; and/or

(ii) comprising at least 10, 50, 100, 150, 200 or 300 of the chromosome interactions represented by the probes in Table 13; and/or

(iii) which together are present in at least 10, 50, 100, 150 or 200 of the regions or genes listed in Table 13; 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 by the probes in Table 13.

D. 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 1, and/or (ii) by a primer pair which has at least 70% identity to any primer pair in Table 4; or

(a) a probe that has at least 70% identity to any of the specific probe sequences mentioned in Table 13, and/or (b) by a primer pair which has at least 70% identity to any primer pair in Table 13.

E. 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; and/or

- the process is carried out to select an individual for a medical treatment; and/or

- the immunoresponsiveness is responsiveness to immunotherapy or an immunocheckpoint therapy; and/or

- the immunoresponsiveness is responsiveness to cancer immunotherapy, and/or

- the process is carried out to determine immunoresponsiveness at one or more defined time points, wherein optionally at least one of the time points is during the course of therapy.

F. 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.

G. 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).

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

- wherein at least 10 to 200 different chromosome interactions are typed, preferably in 10 to 200 different regions or genes; and optionally (a) 50 to 100 different chromosome interactions are typed each of which is in a different gene and/or a different region as defined in Table 1; or (b) 50 to 100 different chromosome interactions are typed each of which is in a different gene and/or a different region as defined in Table 13;

and/or

- which is carried out to select whether or not an individual will receive an immunotherapy, wherein the immunotherapy preferably comprises a small molecule immunotherapy, antibody immunotherapy or cell immunotherapy.

I. 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.

J. A process according to any one of the preceding paragraphs which is carried out to identify or design a therapeutic agent for immunotherapy;

- wherein preferably 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 level of immunoresponsiveness;

- wherein the chromosomal interaction is represented by any probe in Table 1; and/or

- the chromosomal interaction is present in any region or gene listed in Table 1;

and wherein optionally:

- the chromosomal interaction has been identified by the method of determining which chromosomal interactions are relevant to a chromosome state as defined in claim 1, and/or

- the change in chromosomal interaction is monitored using (i) a probe that has at least 70% identity to any of the probe sequences mentioned in Table 1, and/or (ii) by a primer pair which has at least 70% identity to any primer pair in Table 4.

K. A process according to any one of the preceding paragraphs which is carried out to identify or design a therapeutic agent for immunotherapy;

- wherein preferably 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 level of immunoresponsiveness;

- wherein the chromosomal interaction is represented by any probe in Table 13; and/or

- the chromosomal interaction is present in any region or gene listed in Table 13;

and wherein optionally:

- the chromosomal interaction has been identified by the method of determining which chromosomal interactions are relevant to a chromosome state as defined in claim 1, and/or
- the change in chromosomal interaction is monitored using (i) a probe that has at least 70% identity to any of the probe sequences mentioned in Table 13, and/or (ii) by a primer pair which has at least 70% identity to any primer pair in Table 13.

L. A process according to paragraph J or K which comprises selecting a target based on detection of chromosome interactions, and preferably screening for a modulator of the target to identify a therapeutic agent for immunotherapy, wherein said target is optionally a protein.

M. A therapeutic agent for use in a method of immunotherapy in an individual that has been identified as being in need of the therapeutic agent by a process according to any one of paragraphs A to

I.

N. A process according to any one of paragraphs A to K or a therapeutic agent for use according to paragraph M, 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.

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.

Examples

In the first study patients with melanoma were treated with anti-PD-1 (Pembrolizumab) for 12 weeks. Their epigenetic status, measured by EpiSwitch was assessed first at baseline prior to treatment and then at 12 weeks, along with clinical readout of response or no-response. We then screened, evaluated and validated parts of 3D genome architecture profiles, chromosome conformation signatures, at base line to identify profiles conducive to response or no-response to treatment at over 332 genetic locations across the genome. These were evaluate on an EpiSwitch array looking at local multiple 3C interactions at those genetic locations in technical and biological repeats, comparing samples from responders and non-responders at base line. Over 14,000 EpiSwitch markers were directly evaluated on the array. The best markers were translated into PCR and evaluated on the independent patient cohort.

Figure 1 shows an example of clinical annotations of patients used in the study. Colour coded markings: patients listed in red were used in array screening. Patients in blue were used as part of independent cohort for validation - those patient were not used for marker selection, which is important in development of robust biomarkers. Clinical assessment of response or no-response was defined by the standard RESIST 1.1 criteria.

Stage 1 consist of the initial array screening and evaluation for the 14,000 marker leads (all predicted by pattern recognition). Stage 2 is the translation of statistically significant marker leads from array into PCR. Further evaluation by PCR of the markers by regression analysis for reduction of the final marker number in the final signature. Stage 3 is validation of the final signature of 6 best biomarkers (shown in Figure 2). The table in Figure 2 shows the names for the best biomarkers and the genetic loci in which they are positioned, i.e. in this loci they contribute in a particular way to the overall regulation.

Figure 3 shows the Venn diagram for the best predictive biomarkers from array analysis (comparing baseline for responders and non-responders) and best response biomarkers (comparing responders at baseline and at 12 weeks). The overlap gives not only good response biomarkers that are present at the start for response, but also could be monitored over 12 weeks.

Figure 4 is an example of a binary PCR readout on individual patients for some of the final signature biomarkers: 1 CCs is present, 0 CCS is absent. One can see visually the difference in profiles for responders and non-responders. R is a responder. NR is a non-responder.

Figure 5 shows two groups of patients with lung cancer who were treated with anti-PD-L1 monoclonal antibody. Blood was collected at baseline prior to treatment (BL) and at two weeks after the start of treatment (2W). The identity of the two groups for response was established but in the original study had been blinded into group I and group II. The top best 30 PCR-based marker leads predictive for response from anti-PD-1 from the first study (see above) were evaluated on all the patients listed.

Figure 6 show statistical analysis of the best top 13 statistically significant markers discriminating between groups I and II. PDCD1LG2 and STAT5 are also the top discriminating markers in the original anti-PD-1 study: PDCD1LG2 for non-responders, STAT5B for responders. This helps to identify the groups I and II as responder and non-responder groups correctly. The biomarkers monitor deregulation in the same immunotherapies checkpoint cellular network, triggered either by PD-1 in the first study or by its ligand PD-L1 in the second study, and thus have shared features with overlap on the same markers - 6 non-response markers, 7 response markers from the first study on PD-1 still being valid in the second study with PD-L1.

Figure 7 shows a principle component analysis (PCA) of the top 13 markers selected from the PD-L1 cohort. This is a 3D PCA that shows on the three first components of stratification a good separation of responders and non-responders. Noticeably, non-responders (dark triangles) also separate between for the same patients for baseline (A) and 2 weeks (B) of treatment. This is a separate feature related to how tight the epigenetic profiles are controlled in responders and non-responders.

Figure 8 show how in a separate , third study, conducted on lung cancer patients with a different anti-PD-L1 monoclonal, 15 patient baseline samples were provided as blinded on annotation for response/no-response to treatment. Combining the first and the second study, using 8 patients from the first (PD-1 treatment in melanoma) and 24 from the second (a different PD-L1 in lung cancer) a pool of markers was evaluated and the top 5 markers on statistical significance (listed in the table) were then used for classification of 15 blinded samples.

Figure 9 shows how a Random Forest Classifier built on the listed 5 markers produces predicted calls for each of the 15 samples (column predicted). Figure 10 shows predicted calls for each sample compared against unblinded validations (column actual). The stratification efficiency is listed in the table. Sensitivity 71%, Specificity 87.5%, Positive predictive value 83% (important in this context of patient selection), negative predictive value 77%.

Figure 11 shows the standard rOC curve for the classifier. AUC = 0.786

Figure 12 shows a principle component analysis for all the samples used in this analysis: 8 from the first study, 24 from the second, 15 from the validation. On the first principle components the separation for responders and non-responders is already obvious. There are only two miscalled samples in the open classifier for all 47 samples.

The third study relates to anti-PD-L1 treatment in lung cancer. At the array stage of screening 12 responders and 12 non-responders were compared at base line on the array for a total of 180,000 readouts (in technical and biological repeats). There was then PCR translation for the top 100 marker leads from the array followed by validation.

There was a comparison of marker leads from the arrays for the PD-1 (study I), PD-L1 (study II) with the PD-L1 study III. Figure 13 shows the overlap of a common 2522 leads for responders. Figure 14 shows the same, but now looking at the most statistically significant - 276 common significant leads for both studies for responders (study I on the left, study II on the right). Figure 15 shows the same, but for non-responders of which there is only one (study I on the left, study II on the right).

Figure 16 shows how the genetic loci for array reads for response and non-response markers (Studies I and III) overlap with genes involved in interferon gamma pathway. Interferon gamma treatment can increase PD-L1 expression, which is a clinical observation for predisposition for response to treatment. Figure 17 shows the same, but for statistical significant data only. Figure 18 shows the same, but for all studies I-III.

Figure 19 shows Venn diagrams across four cohorts: gene loci (ORFs) for INFG pathway, anti-PD-L1 responders and non-responders, all anti-PD-1.

Figure 20 shows Venn diagrams across four cohorts: gene loci (ORFs) for INFG pathway, anti-PD-1 responders and non-responders, all anti-PD-L1

Figure 21 shows all gene loci for responders markers shared between studies I-III and INFG genes. Figure 22 shows the same, but with the list of 95 loci that contain some of the significant response EpiSwitch markers shared between all three studies I-III. Figure 23 shows the loci list from Figure 22 showing the number of significant marker leads and total number of marker leads when these loci were evaluated on array. Figure 24 shows Interferon Signaling Pathway Matched to aPD-L1 significant EpiSwitch™ CCSs associated ORFs.

Having established common epigenetic settings as markers for responders in PD-1 and PD-L1 treatments, we followed the genetic locations observed under control of epigenetic settings to their protein products and investigated the network relationship for those proteins in the context of known protein-protein networks and their functional roles. Over-imposing the genetic loci affected by EpiSwitch markers of response onto the String database network shows that epigenetically controlled proteins in responders are involved in the close network associated with the two functions: Immune response-regulating cell surface receptor singling pathway and regulation of T-cell activation.

Specific Conclusions

Markers have been identified that have statistically significant disseminating powers to identify in baseline patients those who are set up for good response to immunotherapies (including immunocheckpoint therapies), i.e. responders, and those who are not, i.e. non-responders, or progressors. The markers of Table 1 represent a common universal profile of responders across three independent cohorts with either melanoma or lung cancer (NSCLC). Melanoma patients were treated with PD-1 (pembrolizumab), NSCLC with two different PD-L1. These are agnostic makers predictive of treatment and present across different types of cancers. There is also one important agnostic and universal predictive marker for non-response, located between PD-L1 and PD-L2 loci.

The list of markers in Table 1 reflects a common network regulation in responders. These can be used as agnostic markers to monitor response/non-response across various treatments and conditions, including in response to treatments targeting standard immunocheckpoint molecules controlling the immunological network response.

Further Work

Continuing the goal of identifying epigenetic changes based on chromosome conformation signatures (CCSs) that will be able to select a priori patients who will respond to anti PD-1 therapy, either alone or in combination, for the treatment of non-small cell lung cancer (NSCLC). The discovered EpiSwitch™ markers from this array screen were then screened and validated using the EpiSwitch™ PCR platform using three immunotherapies cohorts, two anti-PD-L1 therapies and one anti-PD-1 therapy (Pembrolizumab) in baseline patients' samples. The two anti-PD-L1 response CCSs were developed on NSCLC patients and the Pembrolizumab response CCSs on melanoma patients and further validated on NSCLC patients. Tables 13, 16 and 18 provide the results of further work, and shows a further set of markers that can be used to determine immunoresponsiveness.

Study Designs

In the metastatic melanoma study, a total number of 32 peripheral blood mononuclear cells (PBMC) samples from 16 patients with metastatic melanoma were studied. These patients had received anti-PD1 therapy. The patients were assessed at 2 time-points, baseline and 12-week tumour assessment. A total number of 16 samples were used for the discovery stage using the EpiSwitch Array. The top 100 EpiSwitch Markers identified from the array screening were verified in the baseline and 12 week samples to identify response to anti-PD1 therapy and pharmacodynamics effects. The top EpiSwitch markers were classified into two group of responders and non-responders to anti-PD-1 therapy.

In the NSCLC study a total number of 16 baseline PBMCs from non-small-cell lung carcinoma (NSCLC) patients treated with an anti-PD-L1 therapy were studied. 30 EpiSwitch™ predictive markers were evaluated. The aim of this project was to confirm predictive capability of EpiSwitch markers common for an anti-PD-1 and anti-PD-L1 predictive profile in baseline NSCLC patients who have been treated with anti-PD-L1 therapy.

	probe	GeneLocus	Probe_Count_Total
1	ORF293_6_32634077_32639503_32662361_32664960_FR	HLA-DQA1	28
2	ORF241_10_88946200_88948398_88998943_89014190_FF	FAS	50
3	ORF293_6_32626930_32634077_32662361_32664960_RR	HLA-DQA1	28
4	ORF38_13_111255999_111262146_111317973_111320769_FF	ARHGEF7	122
5	ORF226_1_94522204_94526809_94565070_94571537_RR	F3	36
6	ORF553_7_6325447_6327369_6392091_6396545_RR	RAC1	64
7	ORF705_9_114882931_114894596_114957908_114962933_FR	TNFSF8	50
8	ORF441_5_68187850_68194388_68215410_68221074_FR	PIK3R1	148
9	IKBKB_8_42264241_42271203_42302441_42304680_FF	IKBKB	46
10	ORF703_1_6461604_6466207_6481328_6484248_FF	TNFRSF25	68
11	ORF38_13_111170222_111182176_111317973_111320769_FF	ARHGEF7	122
12	PRR5_22_44662780_44666500_44696835_44701888_FF	PRR5	64
13	ORF531_22_44662780_44666500_44696835_44701888_FF	PRR5	64
14	ORF501_5_68215410_68221074_68272048_68277769_RF	PIK3R1	148
15	TNFRSF25_1_6461604_6466207_6481328_6484248_FF	TNFRSF25	68
16	C8A_1_56824227_56829583_56902220_56908104_FR	C8A	166
17	ORF76_2_241559192_241566423_241577996_241581000_RR	BOK	44
18	IKBKB_8_42264241_42271203_42331044_42332799_FR	IKBKB	46
19	BOK_2_241559192_241566423_241577996_241581000_RR	BOK	44
20	ORF464_6_44270723_44274914_44307667_44312139_RF	NFKBIE	44
21	TNFRSF25_1_6461604_6466207_6514024_6515315_FR	TNFRSF25	68
22	PIK3R1_5_68195469_68198352_68215410_68221074_RR	PIK3R1	148
23	ORF698_18_62330039_62332469_62356961_62362521_FR	TNFRSF11A	58
24	ORF307_8_42264241_42271203_42331044_42332799_FR	IKBKB	46
25	CD82_11_44526701_44529279_44592038_44600902_RF	CD82	50
26	ORF703_1_6461604_6466207_6494588_6498048_FF	TNFRSF25	68
27	ORF307_8_42264241_42271203_42302441_42304680_FF	IKBKB	46
28	TNFRSF25_1_6461604_6466207_6494588_6498048_FF	TNFRSF25	68
29	CASP6_4_109703339_109705583_109735036_109741090_RF	CASP6	28

Table 1.a1

	Probe_Count_Sig	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr
1	4	0.178427395	0.954389149	14.29	-0.64455528	-0.64455528
2	8	0.041957105	0.555032562	16	-0.625760222	-0.625760222
3	4	0.178427395	0.954389149	14.29	-0.491099473	-0.491099473
4	6	0.928958915	0.99999793	4.92	-0.47329526	-0.47329526
5	2	0.791365183	0.99999793	5.56	-0.436454288	-0.436454288
6	2	0.967461559	0.99999793	3.12	-0.432758998	-0.432758998
7	4	0.568728839	0.99999793	8	-0.415876997	-0.415876997
8	12	0.513477047	0.99999793	8.11	-0.396269087	-0.396269087
9	12	0.00018363	0.010627608	26.09	-0.393553534	-0.393553534
10	16	6.44E-05	0.004967399	23.53	-0.391557328	-0.391557328
11	6	0.928958915	0.99999793	4.92	-0.390398405	-0.390398405
12	4	0.7582782	0.99999793	6.25	-0.385982839	-0.385982839
13	4	0.7582782	0.99999793	6.25	-0.38593493	-0.38593493
14	12	0.513477047	0.99999793	8.11	-0.384094729	-0.384094729
15	16	6.44E-05	0.004967399	23.53	-0.375198131	-0.375198131
16	8	0.957766442	0.99999793	4.82	-0.374033997	-0.374033997
17	10	0.001969408	0.075986326	22.73	-0.367707426	-0.367707426

18	12	0.00018363	0.010627608	26.09	-0.363126662	-0.363126662
19	10	0.001969408	0.075986326	22.73	-0.362483584	-0.362483584
20	4	0.466402982	0.99999793	9.09	-0.361055592	-0.361055592
21	16	6.44E-05	0.004967399	23.53	-0.358891419	-0.358891419
22	12	0.513477047	0.99999793	8.11	-0.356573442	-0.356573442
23	4	0.686266831	0.99999793	6.9	-0.351747423	-0.351747423
24	12	0.00018363	0.010627608	26.09	-0.348439424	-0.348439424
25	6	0.203083688	0.988148592	12	-0.348220668	-0.348220668
26	16	6.44E-05	0.004967399	23.53	-0.347052896	-0.347052896
27	12	0.00018363	0.010627608	26.09	-0.346675126	-0.346675126
28	16	6.44E-05	0.004967399	23.53	-0.342250575	-0.342250575
29	2	0.663352621	0.99999793	7.14	-0.339412631	-0.339412631

Table 1.a2

	t	P.Value	adj.P.Val	B	FC	FC_1
1	-2.980618242	0.01344665400	0.040517443	-3.620544416	0.639689949	-1.563257327
2	-6.24344027	0.00008620000	0.001125209	1.58573085	0.648078185	-1.543023701
3	-3.580221478	0.00482085800	0.018832070	-2.583272553	0.711482673	-1.405515606
4	-22.94378205	0.00000000038	0.000001590	13.50068753	0.72031744	-1.388276813
5	-6.068793285	0.00010890800	0.001320738	1.342264192	0.738948493	-1.353274294
6	-5.571884831	0.00021663700	0.002075220	0.625787741	0.740843647	-1.34981248
7	-6.927544857	0.00003590000	0.000632929	2.498799383	0.749563705	-1.33410942
8	-16.24057806	0.00000001200	0.000010700	10.48782055	0.759820695	-1.316099977
9	-17.46788221	0.00000000585	0.000010100	11.15054812	0.761252236	-1.313625041
10	-9.736436082	0.00000168000	0.000107198	5.651749271	0.762306283	-1.311808681
11	-17.0031469	0.00000000765	0.000010700	10.90661915	0.762918893	-1.310755324
12	-17.18527923	0.00000000688	0.000010600	11.00320387	0.765257487	-1.30674971
13	-15.39183699	0.00000002050	0.000013100	9.992593359	0.765282901	-1.306706316
14	-16.16361934	0.00000001260	0.000010700	10.44421723	0.766259665	-1.305040636
15	-11.77686613	0.00000027700	0.000044500	7.465604014	0.770999521	-1.297017667
16	-10.68867959	0.00000070000	0.000068900	6.540229405	0.771621904	-1.295971504
17	-11.11416276	0.00000048300	0.000057900	6.912800589	0.775013085	-1.290300795
18	-16.40706083	0.00000001090	0.000010700	10.58128991	0.777477774	-1.286210402
19	-10.9324899	0.00000056500	0.000062000	6.755470255	0.77782441	-1.285637205
20	-19.65763701	0.00000000180	0.000005770	12.19684795	0.778594689	-1.284365299
21	-10.66682351	0.00000071300	0.000069500	6.520700487	0.779763527	-1.282440079
22	-14.85687535	0.00000002900	0.000015300	9.663464141	0.78101738	-1.280381239
23	-2.587519517	0.02657975500	0.067536623	-4.295830899	0.783634368	-1.276105338
24	-16.6498587	0.00000000942	0.000010700	10.71553998	0.785433249	-1.273182669
25	-12.64682486	0.00000014000	0.000033200	8.144494866	0.785552353	-1.272989631
26	-12.44559121	0.00000016300	0.000035700	7.991924175	0.786188466	-1.271959642
27	-16.03607714	0.00000001370	0.000010900	10.37139589	0.786394357	-1.271626622
28	-12.06306132	0.00000022000	0.000039400	7.6945755	0.788809824	-1.26773269
29	-13.55417084	0.00000007120	0.000022100	8.801357166	0.790363029	-1.265241367

Table 1.a3

			Probe sequence
	LS	Loop detected	**60 mer**
1	-1	PD-L1 responder	CCCGTCTTCCCCAAAATCTATGTGGTCCTCGAAGTCTTGGATTAAGGTTCATTCAACAAA

2	-1	PD-L1 responder	GTAATATTATGTAAAATTGCATTTGGTATCGAACAAAGCCTTTAACTTGACTTAGTGTCA
3	-1	PD-L1 responder	GTTTATCAGCCAGGCTGGTAAGAAAATGTCGAAGTCTTGGATTAAGGTTCATTCAACAAA
4	-1	PD-L1 responder	GTAAATGAATTTGAAATATTACAAAAGATCGACTCACCTGCGCCTCACATCCCAGGCGGG
5	-1	PD-L1 responder	TTAGCATCACTTGAAAGCTAGTTAAAAATCGATTGCAAATGATATGACAGAATTGCTTTG
6	-1	PD-L1 responder	GGATGTATATATATATACTATTTTTATATCGAGCGCTTAATTAGTGCATGTTACCTATGG
7	-1	PD-L1 responder	TGAAACTTAGACATACTTAAGCATTTCTTCGAAAGCTAATGAGGTATGAGGGGAGAATAC
8	-1	PD-L1 responder	CTGAGTCTTCATTACCAAAAAAAAAAGTTCGACCTCCCCGAACCCCTCCGCCTCTGCGCT
9	-1	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGACAGTCCCAAGAGGTCAGAACTGGCTTCC
10	-1	PD-L1 responder	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGAGGCTTTCAAGGGATCCAGGGTGGGGTGC
11	-1	PD-L1 responder	CGCAGCAGTCTCGTTGATCTTCACGGTGTCGACTCACCTGCGCCTCACATCCCAGGCGGG
12	-1	PD-L1 responder	CCAAACTGGCAATCAACCCAGATAGTCTTCGACCCCGGCCCCGGAGGTCTCCCTCCACAG
13	-1	PD-L1 responder	CCAAACTGGCAATCAACCCAGATAGTCTTCGACCCCGGCCCCGGAGGTCTCCCTCCACAG
14	-1	PD-L1 responder	GCAGTCAATCACCGAGTTATATGAGGTCTCGACCTCCCCGAACCCCTCCGCCTCTGCGCT
15	-1	PD-L1 responder	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGAGGCTTTCAAGGGATCCAGGGTGGGGTGC
16	-1	PD-L1 responder	GGTGACTGCTCAGAAGAGCAGTACTCATTCGACCTTATGCTAAGCCTAAACTTGCCTTCC
17	-1	PD-L1 responder	GTTTGCTCCGGGGCCGCCGGGCCCGCCCTCGATTTTAACACCACCATGGTTTGAATGAAT
18	-1	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGACCCCCTGACATGGGGCTGCCTGGAGCAG
19	-1	PD-L1 responder	GTTTGCTCCGGGGCCGCCGGGCCCGCCCTCGATTTTAACACCACCATGGTTTGAATGAAT
20	-1	PD-L1 responder	TTTCAAAGAAGGTATGATGGGAAAGGTCTCGACGCGCCCCCTCTACGCCATGTCCCCCCC
21	-1	PD-L1 responder	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGAGAAGCATAAAGCAGGGACAGGTATGGAG
22	-1	PD-L1 responder	AAATCATAATTGTGCAGATGATTTGCCTTCGACCTCCCCGAACCCCTCCGCCTCTGCGCT
23	-1	PD-L1 responder	GAGAATCAATTCCATTTTTAAAGCTTAGTCGATTTTGAGGGCTTCTCACAACTCTAGATT
24	-1	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGACCCCCTGACATGGGGCTGCCTGGAGCAG
25	-1	PD-L1 responder	CACAGCTTCTAAATGGTAGGTGTGGGACTCGACCCGCTTTCCTCCCCGCCCCCTCATCCG
26	-1	PD-L1 responder	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGATGTGTTGGAAGTCAGGGCGGCGGTGCCC
27	-1	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGACAGTCCCAAGAGGTCAGAACTGGCTTCC

28	-1	PD-L1 responder	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGATGTGTTGGAAGTCAGGGCGGCGGTGCCC
29	-1	PD-L1 responder	GGGGCCTCCAGAGTCCCCTTTACAGGCATCGACGCCCCCTGCCTACCTGCCGGGTGCCCC

Table 1.a4

	Probe Location					4 kb Sequence Location		
	Chr	Start1	End1	Start2	End2	Chr	Start1	End1
1	6	32639472	32639501	32662363	32662392	6	32635502	32639501
2	10	88948367	88948396	89014159	89014188	10	88944397	88948396
3	6	32626932	32626961	32662363	32662392	6	32626932	32630931
4	13	111262115	111262144	111320738	111320767	13	111258145	111262144
5	1	94522206	94522235	94565072	94565101	1	94522206	94526205
6	7	6325449	6325478	6392093	6392122	7	6325449	6329448
7	9	114894565	114894594	114957910	114957939	9	114890595	114894594
8	5	68194357	68194386	68215412	68215441	5	68190387	68194386
9	8	42271172	42271201	42304649	42304678	8	42267202	42271201
10	1	6466176	6466205	6484217	6484246	1	6462206	6466205
11	13	111182145	111182174	111320738	111320767	13	111178175	111182174
12	22	44666469	44666498	44701857	44701886	22	44662499	44666498
13	22	44666469	44666498	44701857	44701886	22	44662499	44666498
14	5	68215412	68215441	68277738	68277767	5	68215412	68219411
15	1	6466176	6466205	6484217	6484246	1	6462206	6466205
16	1	56829552	56829581	56902222	56902251	1	56825582	56829581
17	2	241559194	241559223	241577998	241578027	2	241559194	241563193
18	8	42271172	42271201	42331046	42331075	8	42267202	42271201
19	2	241559194	241559223	241577998	241578027	2	241559194	241563193
20	6	44270725	44270754	44312108	44312137	6	44270725	44274724
21	1	6466176	6466205	6514026	6514055	1	6462206	6466205
22	5	68195471	68195500	68215412	68215441	5	68195471	68199470
23	18	62332438	62332467	62356963	62356992	18	62328468	62332467
24	8	42271172	42271201	42331046	42331075	8	42267202	42271201
25	11	44526703	44526732	44600871	44600900	11	44526703	44530702
26	1	6466176	6466205	6498017	6498046	1	6462206	6466205
27	8	42271172	42271201	42304649	42304678	8	42267202	42271201
28	1	6466176	6466205	6498017	6498046	1	6462206	6466205
29	4	109703341	109703370	109741059	109741088	4	109703341	109707340

Table 1.a5

	4 kb Sequence Location	
	Start2	End2
1	32662363	32666362
2	89010189	89014188
3	32662363	32666362
4	111316768	111320767
5	94565072	94569071
6	6392093	6396092
7	114957910	114961909
8	68215412	68219411
9	42300679	42304678
10	6480247	6484246
11	111316768	111320767

12	44697887	44701886
13	44697887	44701886
14	68273768	68277767
15	6480247	6484246
16	56902222	56906221
17	241577998	241581997
18	42331046	42335045
19	241577998	241581997
20	44308138	44312137
21	6514026	6518025
22	68215412	68219411
23	62356963	62360962
24	42331046	42335045
25	44596901	44600900
26	6494047	6498046
27	42300679	42304678
28	6494047	6498046
29	109737089	109741088

Table 1.a6

	probe	GeneLocus	Probe_Count_Total
30	ORF567_11_65634932_65641044_65653258_65654626_RF	RELA	56
31	PIK3R1_5_68187850_68194388_68215410_68221074_FR	PIK3R1	148
32	TNFRSF25_1_6450603_6452273_6494588_6498048_RF	TNFRSF25	68
33	IKBKB_8_42264241_42271203_42290979_42292124_FF	IKBKB	46
34	ORF703_1_6461604_6466207_6514024_6515315_FR	TNFRSF25	68
35	CD6_11_60938640_60941215_60977084_60983727_RF	CD6	56
36	PIK3R1_5_68215410_68221074_68272048_68277769_RF	PIK3R1	148
37	ORF703_1_6450603_6452273_6494588_6498048_RF	TNFRSF25	68
38	ORF703_1_6461604_6466207_6494588_6498048_FR	TNFRSF25	68
39	ORF454_2_105728227_105741825_105841316_105844511_FF	NCK2	66
40	IKBKB_8_42264241_42271203_42290979_42292124_FR	IKBKB	46
41	IKBKB_8_42241866_42245619_42264241_42271203_RF	IKBKB	46
42	ORF529_10_6432893_6439235_6460245_6464187_RF	PRKCQ	106
43	ORF114_16_28959098_28963335_28975508_28978445_RF	CD19	56
44	NFKBIE_6_44270723_44274914_44307667_44312139_RF	NFKBIE	44
45	ORF104_17_36075902_36084513_36095759_36100192_FR	CCL18	42
46	ORF307_8_42264241_42271203_42281222_42285075_FR	IKBKB	46
47	ORF307_8_42241866_42245619_42264241_42271203_RF	IKBKB	46
48	TNFRSF25_1_6494588_6498048_6514024_6515315_FR	TNFRSF25	68
49	ORF540_12_112418669_112423831_112478543_112482415_RR	PTPN11	56
50	ORF329_5_132472660_132477912_132495376_132497062_FF	IRF1	42
51	ORF22_14_104800011_104801022_104839372_104843321_FF	AKT1	60
52	BOK_2_241514645_241518779_241559192_241566423_RR	BOK	44
53	ORF703_1_6461604_6466207_6494588_6498048_RF	TNFRSF25	68
54	ORF307_8_42264241_42271203_42290979_42292124_FR	IKBKB	46
55	ORF703_1_6494588_6498048_6514024_6515315_FR	TNFRSF25	68
56	PTPN11_12_112418669_112423831_112478543_112482415_RR	PTPN11	56
57	ITGAM_16_31214801_31216194_31318595_31324659_RF	ITGAM	50
58	IKBKB_8_42264241_42271203_42281222_42285075_FR	IKBKB	46
59	ORF130_11_60938640_60941215_60977084_60983727_RF	CD6	56
60	ORF703_1_6461604_6466207_6481328_6484248_RF	TNFRSF25	68

61	IKBKB_8_42264241_42271203_42302441_42304680_FR	IKBKB	46
62	ORF368_1_32254316_32257966_32298315_32301756_FR	LCK	46
63	ORF712_9_120913546_120919710_120936524_120940468_RF	TRAF1	42
64	IRF1_5_132472660_132477912_132495376_132497062_FF	IRF1	42
65	ORF307_8_42264241_42271203_42302441_42304680_FR	IKBKB	46
66	ORF673_6_149314242_149316764_149361564_149369248_RF	TAB2	151
67	TNFRSF25_1_6481328_6484248_6494588_6498048_FF	TNFRSF25	68
68	CRADD_12_93830263_93837995_93848656_93851009_FR	CRADD	231
69	ORF708_1_3611941_3615812_3638742_3642185_FR	TP73	32
70	ORF130_11_60938640_60941215_61017867_61025585_RF	CD6	56
71	ORF307_8_42264241_42271203_42290979_42292124_FF	IKBKB	46
72	ORF715_11_36467487_36469166_36503363_36509375_FR	TRAF6	60
73	TNFRSF25_1_6461604_6466207_6494588_6498048_RF	TNFRSF25	68
74	ORF501_5_68215410_68221074_68258878_68268897_RF	PIK3R1	148
75	ORF464_6_44253666_44257911_44307667_44312139_RF	NFKBIE	44
76	ORF657_2_191108390_191117485_191184623_191189153_RR	STAT4	58
77	LYN_8_55939615_55941582_55961822_55966587_RR	LYN	48
78	ORF76_2_241535460_241542885_241559192_241566423_RR	BOK	44
79	ORF76_2_241514645_241518779_241559192_241566423_RR	BOK	44

Table 1.b1

	Probe_Count_Sig	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr
30	2	0.94351322	0.99999793	3.57	-0.335793252	-0.335793252
31	12	0.513477047	0.99999793	8.11	-0.331665721	-0.331665721
32	16	6.44E-05	0.004967399	23.53	-0.330748028	-0.330748028
33	12	0.00018363	0.010627608	26.09	-0.325741973	-0.325741973
34	16	6.44E-05	0.004967399	23.53	-0.324809038	-0.324809038
35	14	9.03E-05	0.005970563	25	-0.321565937	-0.321565937
36	12	0.513477047	0.99999793	8.11	-0.31812964	-0.31812964
37	16	6.44E-05	0.004967399	23.53	-0.316909254	-0.316909254
38	16	6.44E-05	0.004967399	23.53	-0.316023276	-0.316023276
39	4	0.779227696	0.99999793	6.06	-0.308568317	-0.308568317
40	12	0.00018363	0.010627608	26.09	-0.307578042	-0.307578042
41	12	0.00018363	0.010627608	26.09	-0.304258892	-0.304258892
42	2	0.998452566	0.99999793	1.89	-0.301937872	-0.301937872
43	4	0.659150649	0.99999793	7.14	-0.295598703	-0.295598703
44	4	0.466402982	0.99999793	9.09	-0.293579626	-0.293579626
45	8	0.016095432	0.256971894	19.05	-0.291933406	-0.291933406
46	12	0.00018363	0.010627608	26.09	-0.291439389	-0.291439389
47	12	0.00018363	0.010627608	26.09	-0.291244548	-0.291244548
48	16	6.44E-05	0.004967399	23.53	-0.282267049	-0.282267049
49	6	0.283634013	0.99999793	10.71	-0.281116435	-0.281116435
50	8	0.016095432	0.256971894	19.05	-0.279967907	-0.279967907
51	4	0.711822793	0.99999793	6.67	-0.279823808	-0.279823808
52	10	0.001969408	0.075986326	22.73	-0.269875843	-0.269875843
53	16	6.44E-05	0.004967399	23.53	-0.269533141	-0.269533141
54	12	0.00018363	0.010627608	26.09	-0.269116289	-0.269116289
55	16	6.44E-05	0.004967399	23.53	-0.268243062	-0.268243062
56	6	0.283634013	0.99999793	10.71	-0.266902081	-0.266902081
57	8	0.041957105	0.555032562	16	-0.266411523	-0.266411523
58	12	0.00018363	0.010627608	26.09	-0.265642352	-0.265642352
59	14	9.03E-05	0.005970563	25	-0.262767321	-0.262767321

60	16	6.44E-05	0.004967399	23.53	-0.262221662	-0.262221662
61	12	0.00018363	0.010627608	26.09	-0.258543002	-0.258543002
62	4	0.501622356	0.99999793	8.7	-0.256759221	-0.256759221
63	6	0.112492545	0.789152247	14.29	-0.255423865	-0.255423865
64	8	0.016095432	0.256971894	19.05	-0.25495765	-0.25495765
65	12	0.00018363	0.010627608	26.09	-0.254863767	-0.254863767
66	4	0.998322979	0.99999793	2.65	-0.254467168	-0.254467168
67	16	6.44E-05	0.004967399	23.53	-0.253550906	-0.253550906
68	4	0.999992975	0.99999793	1.73	-0.249667458	-0.249667458
69	4	0.246707931	0.99999793	12.5	-0.248090073	-0.248090073
70	14	9.03E-05	0.005970563	25	-0.24505568	-0.24505568
71	12	0.00018363	0.010627608	26.09	-0.244420225	-0.244420225
72	2	0.957059624	0.99999793	3.33	-0.241600331	-0.241600331
73	16	6.44E-05	0.004967399	23.53	-0.240482211	-0.240482211
74	12	0.513477047	0.99999793	8.11	-0.240064228	-0.240064228
75	4	0.466402982	0.99999793	9.09	-0.239598775	-0.239598775
76	2	0.950729209	0.99999793	3.45	-0.238303306	-0.238303306
77	2	0.903339407	0.99999793	4.17	-0.237388831	-0.237388831
78	10	0.001969408	0.075986326	22.73	-0.235455099	-0.235455099
79	10	0.001969408	0.075986326	22.73	-0.233288241	-0.233288241

Table 1.b2

	t	P.Value	adj.P.Val	B	FC	FC_1
30	-14.59846809	0.00000003440	0.000016100	9.499491123	0.792348352	-1.262071156
31	-11.91788456	0.00000024800	0.000042600	7.579137577	0.794618496	-1.258465547
32	-18.17630665	0.00000000394	0.000008640	11.50694716	0.79512411	-1.257665297
33	-15.03154881	0.00000002580	0.000014100	9.772437866	0.79788793	-1.253308845
34	-10.99489816	0.00000053500	0.000060300	6.809806578	0.79840406	-1.252498641
35	-13.11065547	0.00000009840	0.000026300	8.486465281	0.800200848	-1.249686254
36	-14.30149147	0.00000004210	0.000017200	9.306864203	0.802109086	-1.246713219
37	-18.81843594	0.00000000279	0.000006830	11.81480874	0.802787883	-1.245659061
38	-9.967999414	0.00000135000	0.000094900	5.875116011	0.803281037	-1.24489432
39	-13.88505293	0.00000005630	0.000020400	9.028942709	0.807442641	-1.238478065
40	-13.22491838	0.00000009050	0.000025200	8.56869633	0.807997065	-1.237628258
41	-11.89187759	0.00000025300	0.000042700	7.5583041	0.809858131	-1.234784169
42	-16.13705896	0.00000001280	0.000010700	10.42910997	0.811162087	-1.232799235
43	-10.15502575	0.00000113000	0.000085500	6.052012506	0.814734156	-1.227394227
44	-14.68901883	0.00000003240	0.000015800	9.557329978	0.815875189	-1.225677668
45	-10.89682004	0.00000058300	0.000063200	6.724276277	0.816806693	-1.224279879
46	-11.64817138	0.00000030800	0.000046400	7.360765169	0.817086438	-1.223860725
47	-11.89788921	0.00000025200	0.000042600	7.56312403	0.817196796	-1.223695449
48	-15.53979703	0.00000001860	0.000012900	10.08124721	0.822297844	-1.216104368
49	-10.51176015	0.00000081900	0.000072900	6.381022079	0.822953925	-1.215134857
50	-13.66679402	0.00000006570	0.000021400	8.879509786	0.823609338	-1.214167875
51	-6.169801402	0.00009510000	0.001205431	1.483598722	0.823691606	-1.214046607
52	-13.95705976	0.00000005350	0.000019800	9.077666225	0.829390919	-1.205704062
53	-8.821110144	0.00000419000	0.000175127	4.718854863	0.829587958	-1.205417689
54	-12.17892232	0.00000020100	0.000038100	7.78566957	0.829827694	-1.205069446
55	-15.17179069	0.00000002360	0.000013500	9.858864135	0.83033012	-1.204340269
56	-10.63311125	0.00000073500	0.000070500	6.490501331	0.831102269	-1.203221357
57	-9.608582862	0.00000190000	0.000114103	5.526310904	0.831384915	-1.202812298
58	-11.56467535	0.00000033000	0.000048300	7.292110963	0.831828285	-1.202171191

59	-9.763551812	0.00000164000	0.000106067	5.678158075	0.833487622	-1.199777866
60	-7.729993148	0.00001380000	0.000350395	3.491591234	0.833802925	-1.199324169
61	-12.34378327	0.00000017600	0.000037000	7.913735609	0.835931712	-1.196269965
62	-12.17180037	0.00000020200	0.000038100	7.780096223	0.836965917	-1.194791783
63	-10.52329131	0.00000081100	0.000072800	6.391477553	0.837740969	-1.193686398
64	-13.36737718	0.00000008150	0.000024000	8.670136499	0.838011734	-1.193300714
65	-9.902604635	0.00000144000	0.000098100	5.812528625	0.838066269	-1.193223062
66	-8.107409551	0.00000900000	0.000268320	3.931310999	0.838296687	-1.192895088
67	-9.140567696	0.00000302000	0.000145043	5.053843186	0.838829261	-1.192137716
68	-9.588148198	0.00000194000	0.000115278	5.506120648	0.841090265	-1.188933034
69	-8.279478026	0.00000745000	0.000241272	4.126320504	0.842010382	-1.187633812
70	-9.532818868	0.00000205000	0.000117891	5.451255469	0.84378323	-1.18513851
71	-14.00748875	0.00000005160	0.000019700	9.111620951	0.844154968	-1.184616614
72	-14.96153336	0.00000002710	0.000014500	9.728935581	0.845806568	-1.182303422
73	-10.36380562	0.00000093600	0.000078800	6.245881241	0.846462341	-1.181387466
74	-7.872213087	0.00001170000	0.000314692	3.659255262	0.846707616	-1.18104524
75	-11.49610245	0.00000035000	0.000050100	7.235348626	0.846980832	-1.180664264
76	-5.423526716	0.00026779500	0.002394757	0.404995163	0.84774172	-1.179604562
77	-9.072038739	0.00000324000	0.000150461	4.982857006	0.848279245	-1.178857087
78	-9.387573754	0.00000236000	0.000128993	5.305841842	0.849417008	-1.177278052
79	-13.63209575	0.00000006730	0.000021500	8.855508119	0.85069375	-1.175511164

Table 1.b3

			Probe sequence
	LS	Loop detected	**60 mer**
30	-1	PD-L1 responder	GTTCAGCAGCTGCTGAAACTCGGAGTTGTCGACACCCCTCTCTCCCCTCCCTGTTTTTCC
31	-1	PD-L1 responder	CTGAGTCTTCATTACCAAAAAAAAAAGTTCGACCTCCCCGAACCCCTCCGCCTCTGCGCT
32	-1	PD-L1 responder	GGGCACCGCCGCCCTGACTTCCAACACATCGAAGAATGGGTGGGGCCTTGCACCTCATAC
33	-1	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAAGTGCTGTTGAGTTCCCCCATCTCTCAT
34	-1	PD-L1 responder	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGAGAAGCATAAAGCAGGGACAGGTATGGAG
35	-1	PD-L1 responder	TTAATGCTGATACAATTCTATTGGATAATCGACACTTCGGCTCCCTGCACCTCCCATGCC
36	-1	PD-L1 responder	GCAGTCAATCACCGAGTTATATGAGGTCTCGACCTCCCCGAACCCCTCCGCCTCTGCGCT
37	-1	PD-L1 responder	GGGCACCGCCGCCCTGACTTCCAACACATCGAAGAATGGGTGGGGCCTTGCACCTCATAC
38	-1	PD-L1 responder	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGACAATGTTATTCTTTGTTTCTCTTACCAA
39	-1	PD-L1 responder	TCTTTGCAGATGTTGTAAGATAAGGATGTCGACTTCATAATCCGCCCGCCTCAGCCTCCC
40	-1	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGATTTCCAAAAGCTCACACATGGGTGCACA
41	-1	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAACTAATATTAGAGGAGAGAGGTCAGTTA
42	-1	PD-L1 responder	TCACAACCTGGGAAAACTGTCGCCTTGCTCGACTCCTGCTTCCCTCCCCTCATCTTTAAA

43	-1	PD-L1 responder	CCTGCACTTCCTCACGCCTGCTCACCCCTCGAGTGAGTGGGAGAGATGGCTCTCCACGCC
44	-1	PD-L1 responder	TTTCAAAGAAGGTATGATGGGAAAGGTCTCGACGCGCCCCCTCTACGCCATGTCCCCCCC
45	-1	PD-L1 responder	TCCAGCCTTGCCTGGAGCTAGGGCCACCTCGATCTTGGCTCACCGCAACCTTGGCCTCCC
46	-1	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAGGGCCTGGCAAGAAGACAGAAGCCGACT
47	-1	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAACTAATATTAGAGGAGAGAGGTCAGTTA
48	-1	PD-L1 responder	GGGCACCGCCGCCCTGACTTCCAACACATCGAGAAGCATAAAGCAGGGACAGGTATGGAG
49	-1	PD-L1 responder	CACCGACCCGTCCGGGCCCGCTGCCACATCGAATAGCTTCTTTTGCTATGTCTCCAAGTT
50	-1	PD-L1 responder	GTGTCTCGGCCCCCTGGGGCCCCACCCTTCGATTTCCCTGTTGCCGCCGCGTTTGCAAGA
51	-1	PD-L1 responder	CCCGCGGCGGAGCTGCTACTGTTTACTTTCGAAGCTTCTTCCTTTCGGCCCCCAGGCCTA
52	-1	PD-L1 responder	TCTCCTGCCTACCACACTGTGAGAAAGCTCGAGGGCGGGCCCGGCGGCCCCGGAGCAAAC
53	-1	PD-L1 responder	GGGCACCGCCGCCCTGACTTCCAACACATCGATCTCTGCCTCGCGCAGCCCCAGCGTGCG
54	-1	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGATTTCCAAAAGCTCACACATGGGTGCACA
55	-1	PD-L1 responder	GGGCACCGCCGCCCTGACTTCCAACACATCGAGAAGCATAAAGCAGGGACAGGTATGGAG
56	-1	PD-L1 responder	CACCGACCCGTCCGGGCCCGCTGCCACATCGAATAGCTTCTTTTGCTATGTCTCCAAGTT
57	-1	PD-L1 responder	CAAATCCCGGCTATCTCTTAGAATTGCATCGACGCGCCCGTGACAGCCGAGTGCGGCCAC
58	-1	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAGGGCCTGGCAAGAAGACAGAAGCCGACT
59	-1	PD-L1 responder	TTAATGCTGATACAATTCTATTGGATAATCGACACTTCGGCTCCCTGCACCTCCCATGCC
60	-1	PD-L1 responder	GCACCCCACCCTGGATCCCTTGAAAGCCTCGATCTCTGCCTCGCGCAGCCCCAGCGTGCG
61	-1	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAAGGCTGGACTTAAAAGAGCAGATGCAAG
62	-1	PD-L1 responder	TAATGCTTTTTTTTTTGTTCTCTCTGTGTCGACCTCAGATGATCGCCTGCCTCGGCCTCC
63	-1	PD-L1 responder	TATGAGTAATAATTACAATTTCCCCCTTTCGACCTCCAGGTCCCCCGCCACTTCCACGGC
64	-1	PD-L1 responder	GTGTCTCGGCCCCCTGGGGCCCCACCCTTCGATTTCCCTGTTGCCGCCGCGTTTGCAAGA
65	-1	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAAGGCTGGACTTAAAAGAGCAGATGCAAG
66	-1	PD-L1 responder	ATAAAAATAAGGTGGGTAGTTTTCAACTTCGAACCTAATCTATTTCATGTACCTGCTAGA
67	-1	PD-L1 responder	GCACCCCACCCTGGATCCCTTGAAAGCCTCGATGTGTTGGAAGTCAGGGCGGCGGTGCCC
68	-1	PD-L1 responder	ACAGTTTTATTGTTGACCTTCCATGGACTCGAGATGCGCCACGCCCTGTTCCTCCTTCAT

69	-1	PD-L1 responder	GCTTCTCCCCTCTTTATCCCACCTGGCCTCGACTCACCCTGCAGACAAGCTTTCGGGTAT
70	-1	PD-L1 responder	CAATATGACGGTGACATTAATGATAGCTTCGACACTTCGGCTCCCTGCACCTCCCATGCC
71	-1	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAAGTGCTGTTGAGTTCCCCCATCTCTCAT
72	-1	PD-L1 responder	AGTGTTGGTGAGATATTGTCTCTCAGTTTCGACTCACTGCAACCCCCGCCTCTGGGTTCT
73	-1	PD-L1 responder	GGGCACCGCCGCCCTGACTTCCAACACATCGATCTCTGCCTCGCGCAGCCCCAGCGTGCG
74	-1	PD-L1 responder	CCCACACACCGCTGGTGCCCAAGGACTGTCGACCTCCCCGAACCCCTCCGCCTCTGCGCT
75	-1	PD-L1 responder	TTTCAAAGAAGGTATGATGGGAAAGGTCTCGAGTGCCCCTGTCCCACCTGGCTCCCCCTG
76	-1	PD-L1 responder	TCATCTTTAATGAACAAGACTGTCACTATCGAATTTCCACAAGTGGGTGCCAACCACGGT
77	-1	PD-L1 responder	GCGGCCAACCCACAGCGCACCGGGCCGCTCGACCTCTGAGAGGAAACTTGCTAGCCCCAG
78	-1	PD-L1 responder	GACCCCCGGGAATTGGCTCCAGCACATCTCGAGGGCGGGCCCGGCGGCCCCGGAGCAAAC
79	-1	PD-L1 responder	TCTCCTGCCTACCACACTGTGAGAAAGCTCGAGGGCGGGCCCGGCGGCCCCGGAGCAAAC

Table 1.b4

	Probe Location					**4 kb Sequence Location**	
	Chr	**Start1**	**End1**	**Start2**	**End2**	**Chr**	**Start1**
30	11	65634934	65634963	65654595	65654624	11	65634934
31	5	68194357	68194386	68215412	68215441	5	68190387
32	1	6450605	6450634	6498017	6498046	1	6450605
33	8	42271172	42271201	42292093	42292122	8	42267202
34	1	6466176	6466205	6514026	6514055	1	6462206
35	11	60938642	60938671	60983696	60983725	11	60938642
36	5	68215412	68215441	68277738	68277767	5	68215412
37	1	6450605	6450634	6498017	6498046	1	6450605
38	1	6466176	6466205	6494590	6494619	1	6462206
39	2	105741794	105741823	105844480	105844509	2	105737824
40	8	42271172	42271201	42290981	42291010	8	42267202
41	8	42241868	42241897	42271172	42271201	8	42241868
42	10	6432895	6432924	6464156	6464185	10	6432895
43	16	28959100	28959129	28978414	28978443	16	28959100
44	6	44270725	44270754	44312108	44312137	6	44270725
45	17	36084482	36084511	36095761	36095790	17	36080512
46	8	42271172	42271201	42281224	42281253	8	42267202
47	8	42241868	42241897	42271172	42271201	8	42241868
48	1	6498017	6498046	6514026	6514055	1	6494047
49	12	112418671	112418700	112478545	112478574	12	112418671
50	5	132477881	132477910	132497031	132497060	5	132473911
51	14	104800991	104801020	104843290	104843319	14	104797021
52	2	241514647	241514676	241559194	241559223	2	241514647
53	1	6461606	6461635	6498017	6498046	1	6461606
54	8	42271172	42271201	42290981	42291010	8	42267202
55	1	6498017	6498046	6514026	6514055	1	6494047

56	12	112418671	112418700	112478545	112478574	12	112418671
57	16	31214803	31214832	31324628	31324657	16	31214803
58	8	42271172	42271201	42281224	42281253	8	42267202
59	11	60938642	60938671	60983696	60983725	11	60938642
60	1	6461606	6461635	6484217	6484246	1	6461606
61	8	42271172	42271201	42302443	42302472	8	42267202
62	1	32257935	32257964	32298317	32298346	1	32253965
63	9	120913548	120913577	120940437	120940466	9	120913548
64	5	132477881	132477910	132497031	132497060	5	132473911
65	8	42271172	42271201	42302443	42302472	8	42267202
66	6	149314244	149314273	149369217	149369246	6	149314244
67	1	6484217	6484246	6498017	6498046	1	6480247
68	12	93837964	93837993	93848658	93848687	12	93833994
69	1	3615781	3615810	3638744	3638773	1	3611811
70	11	60938642	60938671	61025554	61025583	11	60938642
71	8	42271172	42271201	42292093	42292122	8	42267202
72	11	36469135	36469164	36503365	36503394	11	36465165
73	1	6461606	6461635	6498017	6498046	1	6461606
74	5	68215412	68215441	68268866	68268895	5	68215412
75	6	44253668	44253697	44312108	44312137	6	44253668
76	2	191108392	191108421	191184625	191184654	2	191108392
77	8	55939617	55939646	55961824	55961853	8	55939617
78	2	241535462	241535491	241559194	241559223	2	241535462
79	2	241514647	241514676	241559194	241559223	2	241514647

Table 1.b5

	4 kb Sequence Location		
	End1	Start2	End2
30	65638933	65650625	65654624
31	68194386	68215412	68219411
32	6454604	6494047	6498046
33	42271201	42288123	42292122
34	6466205	6514026	6518025
35	60942641	60979726	60983725
36	68219411	68273768	68277767
37	6454604	6494047	6498046
38	6466205	6494590	6498589
39	105741823	105840510	105844509
40	42271201	42290981	42294980
41	42245867	42267202	42271201
42	6436894	6460186	6464185
43	28963099	28974444	28978443
44	44274724	44308138	44312137
45	36084511	36095761	36099760
46	42271201	42281224	42285223
47	42245867	42267202	42271201
48	6498046	6514026	6518025
49	112422670	112478545	112482544
50	132477910	132493061	132497060
51	104801020	104839320	104843319
52	241518646	241559194	241563193
53	6465605	6494047	6498046

54	42271201	42290981	42294980
55	6498046	6514026	6518025
56	112422670	112478545	112482544
57	31218802	31320658	31324657
58	42271201	42281224	42285223
59	60942641	60979726	60983725
60	6465605	6480247	6484246
61	42271201	42302443	42306442
62	32257964	32298317	32302316
63	120917547	120936467	120940466
64	132477910	132493061	132497060
65	42271201	42302443	42306442
66	149318243	149365247	149369246
67	6484246	6494047	6498046
68	93837993	93848658	93852657
69	3615810	3638744	3642743
70	60942641	61021584	61025583
71	42271201	42288123	42292122
72	36469164	36503365	36507364
73	6465605	6494047	6498046
74	68219411	68264896	68268895
75	44257667	44308138	44312137
76	191112391	191184625	191188624
77	55943616	55961824	55965823
78	241539461	241559194	241563193
79	241518646	241559194	241563193

Table 1.b6

	probe	GeneLocus	Probe_Count_Total
80	TNFRSF25_1_6486023_6490057_6514024_6515315_FR	TNFRSF25	68
81	ORF544_1_198595771_198598296_198619087_198627361_RF	PTPRC	214
82	TRAF1_9_120913546_120919710_120936524_120940468_RF	TRAF1	42
83	ORF479_8_81007411_81018107_81053410_81059648_FR	PAG1	144
84	ORF463_4_102557818_102560252_102627099_102634363_FR	NFKB1	64
85	ITK_5_157225228_157231430_157263646_157266576_RF	ITK	26
86	ORF479_8_80968986_80975857_81095100_81099880_RR	PAG1	144
87	ORF335_16_31331188_31333058_31344274_31352361_RF	ITGAM	50
88	ORF57_19_48955700_48958764_48973070_48975293_RR	BAX	52
89	BOK_2_241559192_241566423_241589009_241592694_RF	BOK	44
90	ORF401_4_86098061_86104840_86327055_86336679_RF	MAPK10	186
91	ORF305_15_98652565_98657862_98893484_98899517_RR	IGF1R	104
92	CD6_11_60922069_60925026_61017867_61025585_RR	CD6	56
93	AKT1_14_104800011_104801022_104839372_104843321_FF	AKT1	60
94	ORF479_8_81007411_81018107_81095100_81099880_FR	PAG1	144
95	PVRL1_11_119705149_119706599_119729288_119738834_FR	PVRL1	96
96	ITGAM_16_31331188_31333058_31344274_31352361_RF	ITGAM	50
97	ITGAX_16_31331188_31333058_31344274_31352361_RF	ITGAX	41
98	ORF58_19_47214451_47217416_47236830_47241014_RF	BBC3	56
99	HLA-DQA1_6_32634077_32639503_32662361_32664960_FF	HLA-DQA1	28
100	ORF703_1_6481328_6484248_6494588_6498048_FF	TNFRSF25	68
101	ORF209_4_109875299_109879120_110005130_110011368_FF	EGF	48

102	ORF307_8_42231188_42234849_42264241_42271203_RF	IKBKB	46
103	ORF76_2_241559192_241566423_241589009_241592694_RF	BOK	44
104	MAPKAP1_9_125549822_125553339_125631239_125635100_RF	MAPKAP1	52
105	PTPN11_12_112418669_112423831_112508400_112510869_RR	PTPN11	56
106	CD6_11_60938640_60941215_61017867_61025585_RF	CD6	56
107	MTOR_1_11162452_11169997_11281372_11283081_FR	MTOR	60
108	ORF538_8_140725196_140731179_140877455_140883144_RF	PTK2	248
109	PIK3R1_5_68215410_68221074_68258878_68268897_RF	PIK3R1	148
110	IRF2_4_184439815_184446749_184518370_184519514_RF	IRF2	38
111	ORF336_16_31344274_31352361_31385398_31389135_FF	ITGAX	41
112	MYC_8_127691489_127694045_127732337_127733526_FF	MYC	42
113	ITK_5_157178319_157181048_157266725_157271762_RR	ITK	26
114	ORF703_1_6486023_6490057_6514024_6515315_FR	TNFRSF25	68
115	ORF406_1_150570652_150572543_150615513_150618018_RR	MCL1	77
116	TNFRSF1A_12_6358656_6362143_6379726_6384063_FF	TNFRSF1A	46
117	ORF76_2_241535460_241542885_241589009_241592694_FR	BOK	44
118	ORF712_9_120888366_120893320_120919710_120922922_FR	TRAF1	42
119	PTPN6_12_6934234_6935639_6946597_6948368_RR	PTPN6	46
120	ORF99_3_105803937_105818229_105883590_105884656_RF	CBLB	182
121	ORF712_9_120888366_120893320_120913546_120919710_FR	TRAF1	42
122	NFKBIE_6_44253666_44257911_44307667_44312139_RF	NFKBIE	44
123	ORF703_1_6461604_6466207_6486023_6490057_RR	TNFRSF25	68
124	PTPN6_12_6934234_6935639_6965161_6966968_RR	PTPN6	46
125	FAS_10_88953662_88956472_88985428_88990419_FF	FAS	50
126	ORF401_4_86050968_86053502_86086215_86098061_RF	MAPK10	186
127	ORF305_15_98886232_98891127_98957432_98962130_FR	IGF1R	104
128	FAS_10_88940885_88944343_88985428_88990419_FF	FAS	50
129	ITK_5_157249288_157254103_157266725_157271762_RR	ITK	26
130	PTPN11_12_112418669_112423831_112499733_112502544_RF	PTPN11	56
131	ORF293_6_32634077_32639503_32662361_32664960_FF	HLA-DQA1	28
132	ORF299_19_10230936_10232348_10245172_10246736_FF	ICAM1	63
133	RPTOR_17_80636056_80643737_80661868_80664436_RR	RPTOR	86
134	ORF336_16_31318595_31324659_31385398_31389135_FF	ITGAX	41
135	TRAF2_9_136904007_136906211_136939587_136941363_RF	TRAF2	46
136	MYC_8_127691489_127694045_127738939_127740424_FR	MYC	42
137	ORF670_9_90789107_90793598_90816328_90822228_RF	SYK	78
138	ORF173_4_77503292_77510413_77602626_77605431_RR	CXCL13	108
139	ORF544_1_198591683_198595771_198619087_198627361_FR	PTPRC	214

Table 1.c1

	Probe_Count_Sig	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr
80	16	6.44E-05	0.004967399	23.53	-0.23286156	-0.23286156
81	10	0.978491243	0.99999793	4.67	-0.230147469	-0.230147469
82	6	0.112492545	0.789152247	14.29	-0.22976066	-0.22976066
83	12	0.474481533	0.99999793	8.33	-0.229747184	-0.229747184
84	6	0.398773743	0.99999793	9.38	-0.229043922	-0.229043922
85	10	1.57E-05	0.002607465	38.46	-0.226854713	-0.226854713
86	12	0.474481533	0.99999793	8.33	-0.226025291	-0.226025291
87	8	0.041957105	0.555032562	16	-0.224585718	-0.224585718
88	2	0.925958703	0.99999793	3.85	-0.224267121	-0.224267121
89	10	0.001969408	0.075986326	22.73	-0.223699232	-0.223699232
90	10	0.931377207	0.99999793	5.38	-0.223280405	-0.223280405

91	16	0.007797893	0.171924974	15.38	-0.222320696	-0.222320696
92	14	9.03E-05	0.005970563	25	-0.21998431	-0.21998431
93	4	0.711822793	0.99999793	6.67	-0.219972658	-0.219972658
94	12	0.474481533	0.99999793	8.33	-0.219792116	-0.219792116
95	8	0.497039718	0.99999793	8.33	-0.21590346	-0.21590346
96	8	0.041957105	0.555032562	16	-0.215030115	-0.215030115
97	8	0.013975308	0.239650655	19.51	-0.212953478	-0.212953478
98	8	0.073465475	0.710624303	14.29	-0.211934778	-0.211934778
99	4	0.178427395	0.954389149	14.29	-0.211239457	-0.211239457
100	16	6.44E-05	0.004967399	23.53	-0.210801738	-0.210801738
101	2	0.903339407	0.99999793	4.17	-0.210308957	-0.210308957
102	12	0.00018363	0.010627608	26.09	-0.209493573	-0.209493573
103	10	0.001969408	0.075986326	22.73	-0.209408376	-0.209408376
104	6	0.229017635	0.99999793	11.54	-0.208545117	-0.208545117
105	6	0.283634013	0.99999793	10.71	-0.207915939	-0.207915939
106	14	9.03E-05	0.005970563	25	-0.207569599	-0.207569599
107	4	0.711822793	0.99999793	6.67	-0.206498971	-0.206498971
108	12	0.979779286	0.99999793	4.84	-0.205518478	-0.205518478
109	12	0.513477047	0.99999793	8.11	-0.20551606	-0.20551606
110	2	0.815788109	0.99999793	5.26	-0.204963087	-0.204963087
111	8	0.013975308	0.239650655	19.51	-0.204949768	-0.204949768
112	4	0.430324418	0.99999793	9.52	-0.204707302	-0.204707302
113	10	1.57E-05	0.002607465	38.46	-0.204619133	-0.204619133
114	16	6.44E-05	0.004967399	23.53	-0.202040567	-0.202040567
115	2	0.987032863	0.99999793	2.6	-0.200905599	-0.200905599
116	2	0.889742685	0.99999793	4.35	-0.200276865	-0.200276865
117	10	0.001969408	0.075986326	22.73	-0.199287717	-0.199287717
118	6	0.112492545	0.789152247	14.29	-0.199273043	-0.199273043
119	4	0.501622356	0.99999793	8.7	-0.198832502	-0.198832502
120	2	0.999995464	0.99999793	1.1	-0.197007746	-0.197007746
121	6	0.112492545	0.789152247	14.29	-0.196616458	-0.196616458
122	4	0.466402982	0.99999793	9.09	-0.195945166	-0.195945166
123	16	6.44E-05	0.004967399	23.53	-0.195455805	-0.195455805
124	4	0.501622356	0.99999793	8.7	-0.1942843	-0.1942843
125	8	0.041957105	0.555032562	16	-0.194159165	-0.194159165
126	10	0.931377207	0.99999793	5.38	-0.193852528	-0.193852528
127	16	0.007797893	0.171924974	15.38	-0.193623643	-0.193623643
128	8	0.041957105	0.555032562	16	-0.193599779	-0.193599779
129	10	1.57E-05	0.002607465	38.46	-0.191450511	-0.191450511
130	6	0.283634013	0.99999793	10.71	-0.190144577	-0.190144577
131	4	0.178427395	0.954389149	14.29	-0.188169485	-0.188169485
132	2	0.96511521	0.99999793	3.17	-0.188079391	-0.188079391
133	6	0.687444338	0.99999793	6.98	-0.187583846	-0.187583846
134	8	0.013975308	0.239650655	19.51	-0.187127305	-0.187127305
135	2	0.889742685	0.99999793	4.35	-0.18670662	-0.18670662
136	4	0.430324418	0.99999793	9.52	-0.186601169	-0.186601169
137	6	0.592795697	0.99999793	7.69	-0.186508136	-0.186508136
138	14	0.046569042	0.598929617	12.96	-0.18577624	-0.18577624
139	10	0.978491243	0.99999793	4.67	-0.185177032	-0.185177032

Table 1.c2

	t	P.Value	adj.P.Val	B	FC	FC_1
80	-9.606130665	0.00000191000	0.000114201	5.523890109	0.850945382	-1.175163555
81	-3.148603455	0.01006256300	0.032644588	-3.329509766	0.852547742	-1.17295484
82	-9.762488772	0.00000164000	0.000106067	5.677124024	0.852776354	-1.172640394
83	-5.910931698	0.00013500300	0.001520418	1.118479259	0.85278432	-1.172629441
84	-4.146762666	0.00188918300	0.009492832	-1.621910593	0.853200123	-1.172057966
85	-7.188770374	0.00002600000	0.000519842	2.830950394	0.854495789	-1.170280782
86	-8.99633921	0.00000350000	0.000158450	4.90389231	0.854987189	-1.169608168
87	-9.432629187	0.00000226000	0.000125198	5.351165953	0.855840752	-1.168441673
88	-9.299564365	0.00000258000	0.000135935	5.216740329	0.856029772	-1.168183669
89	-11.48918083	0.00000035200	0.000050200	7.229600039	0.856366798	-1.167723926
90	-6.056778408	0.00011069000	0.001332889	1.325356439	0.856615445	-1.167384975
91	-9.042592259	0.00000334000	0.000153695	4.952209419	0.857185472	-1.166608666
92	-6.891261434	0.00003750000	0.000650749	2.451958669	0.858574774	-1.164720919
93	-4.996552469	0.00050161400	0.003704426	-0.24806514	0.858581708	-1.164711512
94	-8.380946819	0.00000667000	0.000227068	4.239758043	0.85868916	-1.164565767
95	-6.141683115	0.00009870000	0.001232539	1.444399249	0.861006802	-1.161431011
96	-9.152973735	0.00000298000	0.000144884	5.066643761	0.861528176	-1.160728143
97	-9.692570589	0.00000175000	0.000109375	5.608883602	0.862769165	-1.159058576
98	-11.61300437	0.00000031700	0.000047500	7.331910669	0.86337859	-1.158240442
99	-3.939059704	0.00265151700	0.012158182	-1.970945908	0.863794804	-1.157682352
100	-9.768060356	0.00000163000	0.000106067	5.682542516	0.864056922	-1.15733116
101	-10.40736882	0.00000090000	0.000077000	6.285863051	0.864352108	-1.156935918
102	-7.675120855	0.00001470000	0.000366068	3.426254482	0.864840762	-1.156282225
103	-11.65447319	0.00000030700	0.000046400	7.3659264	0.864891836	-1.156213943
104	-7.711401904	0.00001410000	0.000355136	3.469495184	0.865409512	-1.155522312
105	-6.889497379	0.00003760000	0.000651415	2.449676896	0.86578701	-1.155018484
106	-8.105335573	0.00000902000	0.000268394	3.928939971	0.86599488	-1.154741238
107	-2.697141397	0.02197855000	0.058573399	-4.108873892	0.866637776	-1.153884619
108	-7.923787367	0.00001100000	0.000303945	3.719464345	0.867226966	-1.153100675
109	-8.305090458	0.00000725000	0.000237593	4.155062284	0.867228419	-1.153098743
110	-3.763496869	0.00354591900	0.015017871	-2.269233273	0.867560884	-1.152656855
111	-11.39755162	0.00000038000	0.000051600	7.153167186	0.867568894	-1.152646213
112	-8.414783357	0.00000643000	0.000223311	4.277331934	0.867714714	-1.15245251
113	-9.041273175	0.00000334000	0.000153695	4.950834477	0.867767745	-1.152382081
114	-9.244873048	0.00000272000	0.000138639	5.160989094	0.869320116	-1.150324239
115	-4.428242487	0.00120416000	0.006890615	-1.156604974	0.870004278	-1.149419635
116	-7.487088438	0.00001830000	0.000418541	3.199585235	0.870383513	-1.148918821
117	-8.006905671	0.00001010000	0.000287708	3.815843073	0.870980475	-1.148131363
118	-6.213719238	0.00008970000	0.001156677	1.544601478	0.870989334	-1.148119685
119	-10.70312653	0.00000069100	0.000068700	6.553116754	0.87125534	-1.147769149
120	-4.723247929	0.00075994900	0.004919307	-0.679565911	0.872358022	-1.14631834
121	-6.590704313	0.00005480000	0.000830816	2.057190334	0.872594655	-1.146007478
122	-9.511762166	0.00000209000	0.000119285	5.430299258	0.873000772	-1.14547436
123	-8.372647173	0.00000673000	0.000228439	4.230522364	0.873296943	-1.145085882

124	-10.52136039	0.00000081200	0.000072800	6.389727527	0.87400637	-1.144156421
125	-8.590649368	0.00000533000	0.000200984	4.470605821	0.874082182	-1.144057184
126	-7.722891129	0.00001390000	0.000352401	3.483155256	0.874267983	-1.143814047
127	-4.845372443	0.00063036800	0.004341248	-0.485478626	0.874406698	-1.143632594
128	-5.573764843	0.00021606000	0.002072157	0.628565303	0.874421161	-1.143613677
129	-6.961093779	0.00003440000	0.000618186	2.541955486	0.87572481	-1.141911236
130	-9.052077707	0.00000330000	0.000152860	4.962091343	0.876517878	-1.140878041
131	-3.287365783	0.00792963500	0.027297251	-3.089016199	0.877718679	-1.139317214
132	-9.516115389	0.00000208000	0.000119006	5.434635159	0.877773493	-1.139246068
133	-5.431560127	0.00026471700	0.002374878	0.417032009	0.878075047	-1.138854821
134	-10.29247019	0.00000099900	0.000081400	6.180062011	0.878352958	-1.138494487
135	-5.163579985	0.00039119800	0.003113294	0.010501538	0.87860912	-1.138162554
136	-8.01397424	0.00000998000	0.000286168	3.824002229	0.878673343	-1.138079365
137	-5.46686154	0.00025163400	0.002300079	0.469815665	0.878730006	-1.138005978
138	-6.120444196	0.00010159100	0.001258366	1.414716294	0.879175909	-1.1374288
139	-3.18372378	0.00947264400	0.031204399	-3.26862691	0.879541141	-1.13695648

Table 1.c3

			Probe sequence
	LS	Loop detected	**60 mer**
80	-1	PD-L1 responder	GCGCAGCCTCTGGCGCCCCCTGCCGGCCTCGAGAAGCATAAAGCAGGGACAGGTATGGAG
81	-1	PD-L1 responder	AGGAAGTATGTTTGATTTAGAATGTTATTCGAAGATCATTGTCTCATTTTTTTACTTGTT
82	-1	PD-L1 responder	TATGAGTAATAATTACAATTTCCCCCTTTCGACCTCCAGGTCCCCCGCCACTTCCACGGC
83	-1	PD-L1 responder	TCAGATAAGTAACTTCCTGATAATTAACTCGAGAAATGGATTCATATTTCCATGGCTTAC
84	-1	PD-L1 responder	GAATTAGCAATAGTGTGTTACTTCTTTCTCGATATTTTACATGGAATCTTTCCCTTTTTA
85	-1	PD-L1 responder	GGCCGCGAGCCCGGCAGCGGCGACATCCTCGAGAAATTCTCCCGCTTTAGCCTCCCAAAG
86	-1	PD-L1 responder	CTTTTTAAAAATTATCTTTTTATTTGCTTCGATGCCAATCCACGTCATTAGATGAGGACC
87	-1	PD-L1 responder	AGTGGTCTCACCATGGCTTTCTTCCAATTCGAGGTCCCCAACCCCCTGCCGCTCATCGTG
88	-1	PD-L1 responder	CGGGTGCCTCCCCCCCCATTCGCCCTGCTCGAGGGAGGGAAATGATTGGATTACGGGGGT
89	-1	PD-L1 responder	CACTTCCCCAACATAAGCCTCGGTCTCTTCGAGGGCGGGCCCGGCGGCCCCGGAGCAAAC
90	-1	PD-L1 responder	TATTCCATATTTCTGCTCAACATTCTCCTCGAGTAATTTAAATCAACAAAGCCATAGACA
91	-1	PD-L1 responder	TCTTAGAGTTGAACTTTTCTAATCTTTTTCGAGTGTAAAAGGGCTTTTACTGGTGCACAC
92	-1	PD-L1 responder	CTGGCGTTCCAGCCCTCGCACCTTGGCCTCGAGCACCTCTTCAGGGGAGGATTACTGCAA
93	-1	PD-L1 responder	CCCGCGGCGGAGCTGCTACTGTTTACTTTCGAAGCTTCTTCCTTTCGGCCCCCAGGCCTA
94	-1	PD-L1 responder	TCAGATAAGTAACTTCCTGATAATTAACTCGATGCCAATCCACGTCATTAGATGAGGACC

95	-1	PD-L1 responder	AGAAAATATAGTATTGATTGCTTTCAAGTCGATGCGCGCCCGCCGGGGCCCGGTCGGAGC
96	-1	PD-L1 responder	AGTGGTCTCACCATGGCTTTCTTCCAATTCGAGGTCCCCAACCCCCTGCCGCTCATCGTG
97	-1	PD-L1 responder	AGTGGTCTCACCATGGCTTTCTTCCAATTCGAGGTCCCCAACCCCCTGCCGCTCATCGTG
98	-1	PD-L1 responder	CGTGGATCCAGACTGGGAGCCCCCAGCCTCGAGCAGTTGCACTCCAGCCTAGGCAACAAG
99	-1	PD-L1 responder	CCCGTCTTCCCCAAAATCTATGTGGTCCTCGACAGCGACGTGGGGGTGTACCGCGCGGTG
100	-1	PD-L1 responder	GCACCCCACCCTGGATCCCTTGAAAGCCTCGATGTGTTGGAAGTCAGGGCGGCGGTGCCC
101	-1	PD-L1 responder	CAGGCTATTGTAGTGCTCTTCCTGGCCCTCGACACCCCCTTCAAGGGTCTGTGTCCCATA
102	-1	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAGGTGGCTTGGGTCTTAGTCTTCCAGGCA
103	-1	PD-L1 responder	CACTTCCCCAACATAAGCCTCGGTCTCTTCGAGGGCGGGCCCGGCGGCCCCGGAGCAAAC
104	-1	PD-L1 responder	CACTAATCTTTACTCTTTTTCCACTTATTCGACCCTCCCCTTCCAGCTGGGCACAGGTGG
105	-1	PD-L1 responder	CACCGACCCGTCCGGGCCCGCTGCCACATCGAGGTGAAGTTTTAAAAAAAAAGTTGTGGA
106	-1	PD-L1 responder	CAATATGACGGTGACATTAATGATAGCTTCGACACTTCGGCTCCCTGCACCTCCCATGCC
107	-1	PD-L1 responder	ATTCCCAATGTTTCCTGAGTAGAACTGTTCGACTGCGAGCTCCCTCCCTGCAGTCAGGGA
108	-1	PD-L1 responder	CTTTCAAACAAATGACCTTCACCACTGTTCGATCACGGCTCACTGCAGCCTTGGCCTCCT
109	-1	PD-L1 responder	CCCACACACCGCTGGTGCCCAAGGACTGTCGACCTCCCCGAACCCCTCCGCCTCTGCGCT
110	-1	PD-L1 responder	TTATGATATTGTAAATTATTTTTAATATTCGAGCAAACTGACTTGGGGCCCCTATGTGTG
111	-1	PD-L1 responder	AGTGGTCTCACCATGGCTTTCTTCCAATTCGATTCACCCTCCTCAGCCTCCCAAAGTGCT
112	-1	PD-L1 responder	AGGGAGAACAAAAGAAGTTCCATCCATCTCGATCCCCCCGGGCTCAAAGCAAACCTCCTA
113	-1	PD-L1 responder	CAAAATCAAACACAAATCTAATCAAACTTCGATGTTTGGGGGCGGAGGGCTTTGATGAGA
114	-1	PD-L1 responder	GCGCAGCCTCTGGCGCCCCCTGCCGGCCTCGAGAAGCATAAAGCAGGGACAGGTATGGAG
115	-1	PD-L1 responder	AATTTATGGATTGTATGTTACTACTGTATCGAGATCTTCCTACCTCACCGTCCCAAGTAG
116	-1	PD-L1 responder	TCCAGGGATGGCAGAGTCTCTGGCAGCCTCGATGCGGGGCGGGAGGGGCGGCCGGGAAAG
117	-1	PD-L1 responder	GGGTTTCACCCTGTTGGCCAGGCTGGTCTCGAGACCGGCCTGGCCAACATGGTGAAACCC
118	-1	PD-L1 responder	ATAAAATGGGGAGGCCTTCCAGAAGCTCTCGACCGCCACCTCCTCCAGGAAGCCCTGCCT
119	-1	PD-L1 responder	CTGACCCCTCCAGGGGAGGCCCGGCCCCTCGAGGAGGAAGTGGCTGATTACTGAGCGGTT
120	-1	PD-L1 responder	CCTAATATTTCATTATGATAAGAAAGATTCGAGAGTAAGTTTCTTCTGTTCACTCAGGAG

121	-1	PD-L1 responder	ATAAAATGGGGAGGCCTTCCAGAAGCTCTCGACCTCCAGGTCCCCCGCCACTTCCACGGC
122	-1	PD-L1 responder	TTTCAAAGAAGGTATGATGGGAAAGGTCTCGAGTGCCCCTGTCCCACCTGGCTCCCCCTG
123	-1	PD-L1 responder	CGCACGCTGGGGCTGCGCGAGGCAGAGATCGATCCCCGCCCAGCCCTGGGGGTGCCCACT
124	-1	PD-L1 responder	CTGACCCCTCCAGGGGAGGCCCGGCCCCTCGAGAACTCAGGGCCAGCCTTCCCAGCTTGG
125	-1	PD-L1 responder	CGTGAATATATTGGGCTCTAATGGATAATCGAGAGCCGGCCTCCTGCCCTTTCTAAAGGC
126	-1	PD-L1 responder	ATTGACCTGTTAAAGACTTGATTTAGTGTCGAAGGAATTCAGCTTTCAAAATGCACCTAA
127	-1	PD-L1 responder	TCCTAGGAGAGACTGAACTTTAAAGATATCGACCTGCTGATCCTTGGATCCTGAATCTGT
128	-1	PD-L1 responder	GTCTTTGTGTAAATAAATAAGGTAACCCTCGAGAGCCGGCCTCCTGCCCTTTCTAAAGGC
129	-1	PD-L1 responder	TACAGACTTTTTTTCTCTTCTCAGAAAATCGATGTTTGGGGGCGGAGGGCTTTGATGAGA
130	-1	PD-L1 responder	GTTCATGGATTACTTTGAAGTCAGGAGTTCGATGTGGCAGCGGGCCCGGACGGGTCGGTG
131	-1	PD-L1 responder	CCCGTCTTCCCCAAAATCTATGTGGTCCTCGACAGCGACGTGGGGGTGTACCGCGCGGTG
132	-1	PD-L1 responder	TGCGGAAATGATGGACACTACACCTTCATCGAGATCTTGGTTCACTGCAACCTCTGTCTC
133	-1	PD-L1 responder	AGCTGGAGTCTTGATTAACACAAAAATCTCGAGATTCACTGCGCTGCACACCAGGGCCTC
134	-1	PD-L1 responder	CAAATCCCGGCTATCTCTTAGAATTGCATCGATTCACCCTCCTCAGCCTCCCAAAGTGCT
135	-1	PD-L1 responder	CCGCCTCACCTCCCGCATGGTCTTGAGGTCGAGCATGCAGCGCATCTGAGCAGTGAGGCT
136	-1	PD-L1 responder	AGGGAGAACAAAAGAAGTTCCATCCATCTCGACGGAGTCCTCCCCGCAGGGCAGCCCCGA
137	-1	PD-L1 responder	TTTTACTGTTTTTGTAAGAGATATGTTTTCGAAACTCTCTCCAATGAAACAATTCTTTGA
138	-1	PD-L1 responder	GTATTTTGATGATAAAAGCTGAACAACTTCGATTCCAAAGTGAAGCAAAAAAAAAACTTC
139	-1	PD-L1 responder	TGTTTTTTATTGTTTGATGTCCAATGTATCGAGTTTCAGTGTATTTGACATGTTATTCCA

Table 1.c4

	Probe Location					**4 kb Sequence Location**	
	Chr	**Start1**	**End1**	**Start2**	**End2**	**Chr**	**Start1**
80	1	6490026	6490055	6514026	6514055	1	6486056
81	1	198595773	198595802	198627330	198627359	1	198595773
82	9	120913548	120913577	120940437	120940466	9	120913548
83	8	81018076	81018105	81053412	81053441	8	81014106
84	4	102560221	102560250	102627101	102627130	4	102556251
85	5	157225230	157225259	157266545	157266574	5	157225230
86	8	80968988	80969017	81095102	81095131	8	80968988
87	16	31331190	31331219	31352330	31352359	16	31331190
88	19	48955702	48955731	48973072	48973101	19	48955702
89	2	241559194	241559223	241592663	241592692	2	241559194
90	4	86098063	86098092	86336648	86336677	4	86098063

91	15	98652567	98652596	98893486	98893515	15	98652567
92	11	60922071	60922100	61017869	61017898	11	60922071
93	14	104800991	104801020	104843290	104843319	14	104797021
94	8	81018076	81018105	81095102	81095131	8	81014106
95	11	119706568	119706597	119729290	119729319	11	119702598
96	16	31331190	31331219	31352330	31352359	16	31331190
97	16	31331190	31331219	31352330	31352359	16	31331190
98	19	47214453	47214482	47240983	47241012	19	47214453
99	6	32639472	32639501	32664929	32664958	6	32635502
100	1	6484217	6484246	6498017	6498046	1	6480247
101	4	109879089	109879118	110011337	110011366	4	109875119
102	8	42231190	42231219	42271172	42271201	8	42231190
103	2	241559194	241559223	241592663	241592692	2	241559194
104	9	125549824	125549853	125635069	125635098	9	125549824
105	12	112418671	112418700	112508402	112508431	12	112418671
106	11	60938642	60938671	61025554	61025583	11	60938642
107	1	11169966	11169995	11281374	11281403	1	11165996
108	8	140725198	140725227	140883113	140883142	8	140725198
109	5	68215412	68215441	68268866	68268895	5	68215412
110	4	184439817	184439846	184519483	184519512	4	184439817
111	16	31352330	31352359	31389104	31389133	16	31348360
112	8	127694014	127694043	127733495	127733524	8	127690044
113	5	157178321	157178350	157266727	157266756	5	157178321
114	1	6490026	6490055	6514026	6514055	1	6486056
115	1	150570654	150570683	150615515	150615544	1	150570654
116	12	6362112	6362141	6384032	6384061	12	6358142
117	2	241542854	241542883	241589011	241589040	2	241538884
118	9	120893289	120893318	120919712	120919741	9	120889319
119	12	6934236	6934265	6946599	6946628	12	6934236
120	3	105803939	105803968	105884625	105884654	3	105803939
121	9	120893289	120893318	120913548	120913577	9	120889319
122	6	44253668	44253697	44312108	44312137	6	44253668
123	1	6461606	6461635	6486025	6486054	1	6461606
124	12	6934236	6934265	6965163	6965192	12	6934236
125	10	88956441	88956470	88990388	88990417	10	88952471
126	4	86050970	86050999	86098030	86098059	4	86050970
127	15	98891096	98891125	98957434	98957463	15	98887126
128	10	88944312	88944341	88990388	88990417	10	88940342
129	5	157249290	157249319	157266727	157266756	5	157249290
130	12	112418671	112418700	112502513	112502542	12	112418671
131	6	32639472	32639501	32664929	32664958	6	32635502
132	19	10232317	10232346	10246705	10246734	19	10228347
133	17	80636058	80636087	80661870	80661899	17	80636058
134	16	31324628	31324657	31389104	31389133	16	31320658
135	9	136904009	136904038	136941332	136941361	9	136904009
136	8	127694014	127694043	127738941	127738970	8	127690044
137	9	90789109	90789138	90822197	90822226	9	90789109
138	4	77503294	77503323	77602628	77602657	4	77503294
139	1	198595740	198595769	198619089	198619118	1	198591770

Table 1.c5

	4 kb Sequence Location		
	End1	Start2	End2
80	6490055	6514026	6518025
81	198599772	198623360	198627359
82	120917547	120936467	120940466
83	81018105	81053412	81057411
84	102560250	102627101	102631100
85	157229229	157262575	157266574
86	80972987	81095102	81099101
87	31335189	31348360	31352359
88	48959701	48973072	48977071
89	241563193	241588693	241592692
90	86102062	86332678	86336677
91	98656566	98893486	98897485
92	60926070	61017869	61021868
93	104801020	104839320	104843319
94	81018105	81095102	81099101
95	119706597	119729290	119733289
96	31335189	31348360	31352359
97	31335189	31348360	31352359
98	47218452	47237013	47241012
99	32639501	32660959	32664958
100	6484246	6494047	6498046
101	109879118	110007367	110011366
102	42235189	42267202	42271201
103	241563193	241588693	241592692
104	125553823	125631099	125635098
105	112422670	112508402	112512401
106	60942641	61021584	61025583
107	11169995	11281374	11285373
108	140729197	140879143	140883142
109	68219411	68264896	68268895
110	184443816	184515513	184519512
111	31352359	31385134	31389133
112	127694043	127729525	127733524
113	157182320	157266727	157270726
114	6490055	6514026	6518025
115	150574653	150615515	150619514
116	6362141	6380062	6384061
117	241542883	241589011	241593010
118	120893318	120919712	120923711
119	6938235	6946599	6950598
120	105807938	105880655	105884654
121	120893318	120913548	120917547
122	44257667	44308138	44312137
123	6465605	6486025	6490024
124	6938235	6965163	6969162
125	88956470	88986418	88990417
126	86054969	86094060	86098059
127	98891125	98957434	98961433
128	88944341	88986418	88990417
129	157253289	157266727	157270726

130	112422670	112498543	112502542
131	32639501	32660959	32664958
132	10232346	10242735	10246734
133	80640057	80661870	80665869
134	31324657	31385134	31389133
135	136908008	136937362	136941361
136	127694043	127738941	127742940
137	90793108	90818227	90822226
138	77507293	77602628	77606627
139	198595769	198619089	198623088

Table 1.c6

	probe	GeneLocus	Probe_Count_Total
140	CD2_1_116707374_116708774_116735758_116740399_FR	CD2	34
141	PVRL1_11_119671081_119677815_119729288_119738834_RR	PVRL1	96
142	ORF401_4_86120725_86131416_86336679_86343485_FF	MAPK10	186
143	ORF611_20_1891489_1897350_1924633_1930962_RR	SIRPA	56
144	ORF338_5_157249288_157254103_157266725_157271762_RR	ITK	26
145	IGF2_11_2113132_2119465_2180328_2182624_RR	IGF2	32
146	ORF631_15_67098632_67101498_67199584_67204251_RR	SMAD3	34
147	ITGAM_16_31278026_31284381_31331188_31333058_RR	ITGAM	50
148	ORF538_8_140715391_140725081_140877455_140883144_FR	PTK2	248
149	CD14_5_140643798_140647427_140670568_140672728_FF	CD14	62
150	IGF1R_15_98731539_98737034_98785670_98790114_FF	IGF1R	104
151	ORF113_5_67178844_67182260_67233989_67237362_FR	CD180	38
152	ORF130_11_60922069_60925026_60977084_60983727_RR	CD6	56
153	ORF490_16_2500832_2504754_2543954_2548518_RF	PDPK1	60
154	BID_22_17731946_17735544_17804446_17806939_FF	BID	42
155	ORF642_16_29613904_29616227_29630194_29632081_RF	SPN	56
156	ORF223_11_124746039_124755799_124783109_124787738_RF	ESAM	32
157	ORF456_11_119671081_119677815_119700077_119705149_FF	PVRL1	96
158	ORF138_3_122014664_122021863_122097537_122100802_RF	CD86	46
159	ITK_5_157178319_157181048_157266725_157271762_FR	ITK	26
160	IRF3_19_49654782_49660360_49691432_49693107_RR	IRF3	30
161	SHH_7_155794440_155798922_155840981_155842935_RF	SHH	36
162	ORF224_6_151870936_151873891_151985888_151997878_FF	ESR1	198
163	PDPK1_16_2500832_2504754_2543954_2548518_RF	PDPK1	60
164	ORF305_15_98779700_98784973_98893484_98899517_FR	IGF1R	104
165	ORF22_14_104760238_104764613_104839372_104843321_RF	AKT1	60
166	ORF542_12_6934234_6935639_6965161_6966968_RR	PTPN6	46
167	ORF86_1_56934234_56943891_56962729_56967106_FR	C8A	166
168	ORF544_1_198591683_198595771_198735456_198749256_FF	PTPRC	214
169	SPN_16_29613904_29616227_29630194_29632081_RF	SPN	56
170	PTPRA_20_2816709_2821045_2963104_2968013_RF	PTPRA	82
171	CD6_11_60977084_60983727_60996251_60998956_FR	CD6	56
172	ORF95_2_201261158_201267239_201286114_201291036_FF	CASP8	41
173	BBC3_19_47236830_47241014_47256212_47257706_FR	BBC3	56
174	TRAF1_9_120888366_120893320_120913546_120919710_FR	TRAF1	42
175	ORF538_8_140715391_140725081_140781905_140783960_FF	PTK2	248
176	IRF1_5_132472660_132477912_132536450_132537922_FR	IRF1	42
177	ORF642_16_29613904_29616227_29686079_29687229_RF	SPN	56

178	ORF403_9_125608173_125614421_125631239_125635100_RF	MAPKAP1	52
179	ORF124_12_6767426_6773999_6796695_6798393_FR	CD4	42
180	CD82_11_44561823_44564856_44624533_44629606_FF	CD82	50
181	ORF311_5_149378172_149380861_149421073_149426819_RR	IL17B	44
182	C8B_1_56959632_56962729_56991331_56998079_FF	C8B	151
183	ORF538_8_140715391_140725081_140763162_140771406_FF	PTK2	248
184	ORF73_10_96186298_96190208_96274838_96286475_RF	BLNK	66
185	ORF331_19_49654782_49660360_49691432_49693107_RR	IRF3	30
186	ORF305_15_98893484_98899517_98957432_98962130_RR	IGF1R	104
187	BAX_19_48955700_48958764_48973070_48975293_RR	BAX	52
188	ORF317_14_23324243_23329232_23356396_23359421_RF	IL25	74
189	CD6_11_60932387_60933682_61017867_61025585_FR	CD6	56
190	ORF501_5_68203536_68213336_68272048_68277769_FF	PIK3R1	148
191	ORF167_5_132051982_132053273_132068115_132074991_FF	CSF2	36
192	ORF540_12_112418669_112423831_112478543_112482415_RF	PTPN11	56
193	ORF456_11_119671081_119677815_119729288_119738834_RR	PVRL1	96
194	ORF306_11_2113132_2119465_2180328_2182624_RR	IGF2	32
195	ICOSLG_21_44243731_44245588_44267559_44270033_RR	ICOSLG	40
196	ORF55_11_64267793_64269811_64292591_64296924_FF	BAD	70
197	TNFRSF19_13_23627958_23632852_23678002_23680230_RR	TNFRSF19	60
198	ORF112_5_140643798_140647427_140670568_140672728_FF	CD14	62
199	ORF479_8_81007411_81018107_81077565_81079322_FR	PAG1	144

Table 1.d1

	Probe_Count_Sig	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr
140	2	0.764125503	0.99999793	5.88	-0.18498091	-0.18498091
141	8	0.497039718	0.99999793	8.33	-0.184910905	-0.184910905
142	10	0.931377207	0.99999793	5.38	-0.18453906	-0.18453906
143	4	0.659150649	0.99999793	7.14	-0.183746617	-0.183746617
144	10	1.57E-05	0.002607465	38.46	-0.180610127	-0.180610127
145	6	0.037675475	0.528598335	18.75	-0.180180699	-0.180180699
146	2	0.764125503	0.99999793	5.88	-0.180175335	-0.180175335
147	8	0.041957105	0.555032562	16	-0.179650611	-0.179650611
148	12	0.979779286	0.99999793	4.84	-0.179032383	-0.179032383
149	6	0.369692981	0.99999793	9.68	-0.178209877	-0.178209877
150	16	0.007797893	0.171924974	15.38	-0.178097117	-0.178097117
151	4	0.356577228	0.99999793	10.53	-0.176986579	-0.176986579
152	14	9.03E-05	0.005970563	25	-0.176532216	-0.176532216
153	6	0.340695433	0.99999793	10	-0.176282137	-0.176282137
154	2	0.857080857	0.99999793	4.76	-0.1760267	-0.1760267
155	4	0.659150649	0.99999793	7.14	-0.175972335	-0.175972335
156	2	0.733846963	0.99999793	6.25	-0.175898715	-0.175898715
157	8	0.497039718	0.99999793	8.33	-0.175584682	-0.175584682
158	2	0.889742685	0.99999793	4.35	-0.17550915	-0.17550915
159	10	1.57E-05	0.002607465	38.46	-0.17535973	-0.17535973
160	2	0.700318757	0.99999793	6.67	-0.175351435	-0.175351435
161	6	0.062022042	0.70039526	16.67	-0.174771304	-0.174771304
162	4	0.999928673	0.99999793	2.02	-0.174094119	-0.174094119
163	6	0.340695433	0.99999793	10	-0.172705626	-0.172705626
164	16	0.007797893	0.171924974	15.38	-0.171537182	-0.171537182
165	4	0.711822793	0.99999793	6.67	-0.17111407	-0.17111407
166	4	0.501622356	0.99999793	8.7	-0.170682414	-0.170682414

167	8	0.957766442	0.99999793	4.82	-0.170673324	-0.170673324
168	10	0.978491243	0.99999793	4.67	-0.170660074	-0.170660074
169	4	0.659150649	0.99999793	7.14	-0.169924144	-0.169924144
170	8	0.325435728	0.99999793	9.76	-0.169491925	-0.169491925
171	14	9.03E-05	0.005970563	25	-0.169304269	-0.169304269
172	4	0.412035429	0.99999793	9.76	-0.168954906	-0.168954906
173	8	0.073465475	0.710624303	14.29	-0.166543413	-0.166543413
174	6	0.112492545	0.789152247	14.29	-0.165440732	-0.165440732
175	12	0.979779286	0.99999793	4.84	-0.165036217	-0.165036217
176	8	0.016095432	0.256971894	19.05	-0.165001138	-0.165001138
177	4	0.659150649	0.99999793	7.14	-0.16436617	-0.16436617
178	6	0.229017635	0.99999793	11.54	-0.163709607	-0.163709607
179	6	0.112492545	0.789152247	14.29	-0.163562981	-0.163562981
180	6	0.203083688	0.988148592	12	-0.162924558	-0.162924558
181	4	0.466402982	0.99999793	9.09	-0.162260458	-0.162260458
182	9	0.85591599	0.99999793	5.96	-0.161358241	-0.161358241
183	12	0.979779286	0.99999793	4.84	-0.161243979	-0.161243979
184	4	0.779227696	0.99999793	6.06	-0.160877914	-0.160877914
185	2	0.700318757	0.99999793	6.67	-0.160722895	-0.160722895
186	16	0.007797893	0.171924974	15.38	-0.160584806	-0.160584806
187	2	0.925958703	0.99999793	3.85	-0.15962933	-0.15962933
188	2	0.983929844	0.99999793	2.7	-0.159277184	-0.159277184
189	14	9.03E-05	0.005970563	25	-0.159211463	-0.159211463
190	12	0.513477047	0.99999793	8.11	-0.158345461	-0.158345461
191	2	0.791365183	0.99999793	5.56	-0.158073637	-0.158073637
192	6	0.283634013	0.99999793	10.71	-0.158042348	-0.158042348
193	8	0.497039718	0.99999793	8.33	-0.157293527	-0.157293527
194	6	0.037675475	0.528598335	18.75	-0.156852321	-0.156852321
195	8	0.012066038	0.223463015	20	-0.156295949	-0.156295949
196	8	0.18964104	0.954389149	11.43	-0.155897691	-0.155897691
197	8	0.100733588	0.781478358	13.33	-0.155472557	-0.155472557
198	6	0.369692981	0.99999793	9.68	-0.154642066	-0.154642066
199	12	0.474481533	0.99999793	8.33	-0.154283407	-0.154283407

Table 1.d2

	t	P.Value	adj.P.Val	B	FC	FC_1
140	-9.04469975	0.00000333000	0.000153670	4.954405786	0.879660716	-1.13680193
141	-5.863852649	0.00014402900	0.001584971	1.05105187	0.879703401	-1.13674677
142	-3.956476668	0.00257667000	0.011877700	-1.941508536	0.879930168	-1.136453819
143	-7.539838325	0.00001720000	0.000403646	3.263611548	0.880413629	-1.135829759
144	-7.561434137	0.00001670000	0.000397765	3.289725067	0.882329773	-1.133363092
145	-8.22189382	0.00000793000	0.000252813	4.061431872	0.882592444	-1.133025789
146	-8.471609217	0.00000605000	0.000215806	4.34015114	0.882595726	-1.133021576
147	-8.796652754	0.00000430000	0.000176706	4.692775469	0.882916793	-1.132609559
148	-4.998863428	0.00049987800	0.003693568	-0.24446078	0.883295225	-1.132124314
149	-7.696109127	0.00001430000	0.000359185	3.451288223	0.883798951	-1.131479053
150	-7.086728608	0.00002950000	0.000560642	2.702258066	0.88386803	-1.131390622
151	-9.75949409	0.00000165000	0.000106067	5.674210448	0.884548664	-1.13052005
152	-5.770771019	0.00016383700	0.001725769	0.916804544	0.884827288	-1.13016406
153	-6.7528275	0.00004460000	0.000732249	2.271638916	0.884980679	-1.129968172
154	-8.001384234	0.00001010000	0.000288637	3.809465717	0.885137383	-1.129768123
155	-7.054965999	0.00003060000	0.000572312	2.661925201	0.885170738	-1.129725551

156	-8.062849839	0.00000946000	0.000276188	3.880260462	0.885215909	-1.129667903
157	-8.22019318	0.00000795000	0.000252897	4.059509833	0.885408616	-1.129422034
158	-7.944299089	0.00001080000	0.000298984	3.743323414	0.885454973	-1.129362905
159	-7.936893754	0.00001090000	0.000300885	3.734715272	0.885546684	-1.129245942
160	-7.320634642	0.00002220000	0.000473074	2.995279965	0.885551776	-1.12923945
161	-4.501723442	0.00107250100	0.006331857	-1.036726499	0.885907942	-1.128785456
162	-5.359979733	0.00029353100	0.002553248	0.309452325	0.886323875	-1.128255741
163	-7.348002424	0.00002150000	0.000464745	3.029109603	0.887177311	-1.127170396
164	-4.993189956	0.00050415200	0.003717896	-0.253310928	0.88789613	-1.126257866
165	-3.519797341	0.00533871900	0.020318036	-2.68729466	0.888156569	-1.125927607
166	-7.967884713	0.00001050000	0.000294299	3.7706972	0.888422346	-1.125590778
167	-6.912341375	0.00003650000	0.000639759	2.47919335	0.888427944	-1.125583686
168	-4.143646897	0.00189873700	0.009528203	-1.627112625	0.888436104	-1.125573349
169	-7.327193408	0.00002210000	0.000471182	3.003395936	0.888889417	-1.124999331
170	-6.725576504	0.00004620000	0.000751090	2.235840762	0.889155761	-1.124662342
171	-9.223976152	0.00000278000	0.000140257	5.139609489	0.889271424	-1.124516063
172	-5.086671011	0.00043842800	0.003367258	-0.108066516	0.889486795	-1.124243783
173	-6.557217188	0.00005720000	0.000856101	2.012450668	0.890974834	-1.122366157
174	-5.606610708	0.00020624200	0.002008025	0.677010146	0.891656084	-1.121508638
175	-6.152539392	0.00009730000	0.001222803	1.459547106	0.891906129	-1.121194224
176	-9.029584345	0.00000338000	0.000154851	4.938642975	0.891927816	-1.121166963
177	-7.773176867	0.00001310000	0.000338569	3.542755797	0.892320463	-1.120673616
178	-3.931754114	0.00268358500	0.012258029	-1.983302218	0.892726646	-1.120163719
179	-6.094548905	0.00010519100	0.001290304	1.378439476	0.892817381	-1.120049879
180	-4.377302648	0.00130537400	0.007284682	-1.240107008	0.89321256	-1.119554343
181	-7.4412892	0.00001930000	0.000434267	3.143716166	0.893623817	-1.119039109
182	-2.947668664	0.01423557000	0.042361163	-3.677544832	0.894182836	-1.118339516
183	-7.690183808	0.00001440000	0.000361067	3.444226195	0.894253659	-1.118250946
184	-4.458017464	0.00114886400	0.006651262	-1.10794705	0.894480593	-1.11796724
185	-7.035502311	0.00003140000	0.000581633	2.637144966	0.894576711	-1.117847121
186	-5.690028109	0.00018339000	0.001862995	0.799345244	0.89466234	-1.11774013
187	-6.204852631	0.00009070000	0.001165246	1.532307434	0.895255058	-1.117000111
188	-5.699454074	0.00018098300	0.001844393	0.813105827	0.895473607	-1.116727498
189	-8.406010145	0.00000650000	0.000223939	4.267601817	0.8955144	-1.116676627
190	-4.255312553	0.00158598400	0.008382570	-1.441362142	0.896052109	-1.116006524
191	-5.410812733	0.00027274400	0.002422901	0.3859262	0.896220954	-1.115796272
192	-5.030639438	0.00047664400	0.003574555	-0.194976515	0.896240392	-1.115772073
193	-7.050761716	0.00003080000	0.000573918	2.656576685	0.8967057	-1.11519309
194	-6.511242084	0.00006070000	0.000890100	1.950776985	0.896979973	-1.114852093
195	-6.247769863	0.00008570000	0.001121376	1.591712007	0.897325957	-1.114422236
196	-6.419907226	0.00006840000	0.000962212	1.827393464	0.8975737	-1.11411464
197	-8.514647533	0.00000578000	0.000210469	4.387493728	0.897838236	-1.113786381
198	-5.287869683	0.00032596900	0.002741288	0.20033182	0.898355228	-1.113145412
199	-3.020061123	0.01256025500	0.038539753	-3.552262166	0.89857859	-1.112868714

Table 1.d3

			Probe sequence
	LS	Loop detected	**60 mer**
140	-1	PD-L1 responder	ATTTGACAACGCTGGCACGGAGGCAAGATCGACCTCCCTGTCCCTCCTGGGCCTCTCCGG

141	-1	PD-L1 responder	TCTTCTCTCCCTCACTCAGTATCCTCACTCGATGCGCGCCCGCCGGGGCCCGGTCGGAGC
142	-1	PD-L1 responder	GAGGATTTAATAAAACCCAAACTGTATTTCGAGAAAATAGTGTTTTGCTATTTAGATAAG
143	-1	PD-L1 responder	GCGCCCTATTTCCACCTTGTGCCTTCTGTCGAGACATCTAAGAAGGTCCAGCCAGATGTT
144	-1	PD-L1 responder	TACAGACTTTTTTTCTCTTCTCAGAAAATCGATGTTTGGGGGCGGAGGGCTTTGATGAGA
145	-1	PD-L1 responder	GTGACAATTAAGAGTGTGACATTGCTTCTCGAGGACTCACTGGGCCTGCAGGGGGGCAGC
146	-1	PD-L1 responder	GTGGCAGGAGAAAAACGCGGCCCCACCCTCGAAAATACTAGAATTATGCCGCACAGTCAG
147	-1	PD-L1 responder	ACATCGCTACCAGGCCGATGTGCTGATATCGAGGTCCCCAACCCCCTGCCGCTCATCGTG
148	-1	PD-L1 responder	AAGTCTTTTGTTTGGTTATTGTGCTGTATCGAATCAAAGCTGTGTCACAAACTATGTAAC
149	-1	PD-L1 responder	GCGGGGGCTTCCCTCAACTTCAGGGAGGTCGAGGCGCGGCGCGCAGGCCGCCATCGCCAC
150	-1	PD-L1 responder	CGTAGAACTAAGATGTATTCAAAGTCAGTCGAAATCACCTGTCCCGGCCTCTTTCCAAAC
151	-1	PD-L1 responder	GACCTAAGGATTAAGAAGATTAATGGAGTCGAGCATCCTCTACCTCTATCTCCAACCCCT
152	-1	PD-L1 responder	CTGGCGTTCCAGCCCTCGCACCTTGGCCTCGAACTTTACAGAGGGATCTAGAATGAGTGA
153	-1	PD-L1 responder	ACATGACCGTGATACCTCTGTCACTCTGTCGATGGGGACCTGAACCGGGGCCGCACAAGC
154	-1	PD-L1 responder	TGGAAGCAGCTATACAGCTGTGACCACATCGACGCCCCTGTCACGGGCCCTGTTATTCAA
155	-1	PD-L1 responder	AGGCGACACTCTTGTCCCCGCCATCTTTTCGAAGGCCCCCGTCCTCCTGCGCCATGGAGA
156	-1	PD-L1 responder	AATAAACATCTTTTTGCTCATACATTATTCGAATCCCCAGCCCTTCCCTCTGCCCACCCT
157	-1	PD-L1 responder	GGACCTTGTCATCCTGCCCCTTCTTGGCTCGAGCCCTGCCTGGCCAGCACACACTGCATC
158	-1	PD-L1 responder	CATCATAGCAACCCATTGTAACTAGACTTCGAATAGATACTTCAGGAAAGAAATGTATAT
159	-1	PD-L1 responder	ATCCCAACAAAAGAGAAGAACTTCTCCCTCGATGTTTGGGGGCGGAGGGCTTTGATGAGA
160	-1	PD-L1 responder	GCAGCCAGCCCGGTGGGGGTGGGGGGGGTCGACGCTCGCCTCCGCTCACAGCCTCAGCAT
161	-1	PD-L1 responder	ACATGAGATGTCCTTCAAGTGAAACTGTTCGACCATGCCCGGGCAGGTGGCTGAGACCTC
162	-1	PD-L1 responder	TAAACCATAGTTAATTTTATGTAAATATTCGAATCTTTTCAGGATGGTAGCATCTTTAAA
163	-1	PD-L1 responder	ACATGACCGTGATACCTCTGTCACTCTGTCGATGGGGACCTGAACCGGGGCCGCACAAGC
164	-1	PD-L1 responder	TGACTGTATTTACAACATGTCTAGATTTTCGAGTGTAAAAGGGCTTTTACTGGTGCACAC
165	-1	PD-L1 responder	TAGGCCTGGGGGCCGAAAGGAAGAAGCTTCGACTGAGGCGGGTCCCAGCCCCTCCAGGGA
166	-1	PD-L1 responder	CTGACCCCTCCAGGGGAGGCCCGGCCCCTCGAGAACTCAGGGCCAGCCTTCCCAGCTTGG

167	-1	PD-L1 responder	GTAGTTCACTCTGTCCCTTTTCCTATGATCGATTTTGCTCCCCCCACCTTACCCCCAGAG
168	-1	PD-L1 responder	TGTTTTTTATTGTTTGATGTCCAATGTATCGATAAACAAATTATACAACAAAAGTCTAAG
169	-1	PD-L1 responder	AGGCGACACTCTTGTCCCCGCCATCTTTTCGAAGGCCCCCGTCCTCCTGCGCCATGGAGA
170	-1	PD-L1 responder	TCCATTGTCTTATTCCAGTCTAGGCTTGTCGAACTGGCGGCAACCGCTGCAGCGCCTGCT
171	-1	PD-L1 responder	TTAATGCTGATACAATTCTATTGGATAATCGACGTGCCTTGGGGCCTCCCCTTTCCCTAT
172	-1	PD-L1 responder	TTTTTTTCCTCTCTTATCTTGATGCCTCTCGAGCTTCCTGGCCACTTTGTTTACCTACTC
173	-1	PD-L1 responder	CGTGGATCCAGACTGGGAGCCCCCAGCCTCGAACCACGCCAGGCTTCCAGGCGTCAGTGC
174	-1	PD-L1 responder	ATAAAATGGGGAGGCCTTCCAGAAGCTCTCGACCTCCAGGTCCCCCGCCACTTCCACGGC
175	-1	PD-L1 responder	AAGTCTTTTGTTTGGTTATTGTGCTGTATCGAAGTCTTGACCTCAGGTGATCCACCCACC
176	-1	PD-L1 responder	GTGTCTCGGCCCCCTGGGGCCCCACCCTTCGAGTGCATCCTGCAGCTGTTTGTCCAGAAG
177	-1	PD-L1 responder	CATCATCACAGTCTACGGCTGTTTCCTCTCGAAGGCCCCCGTCCTCCTGCGCCATGGAGA
178	-1	PD-L1 responder	CACTAATCTTTACTCTTTTTCCACTTATTCGAAGTTTCCAGAAAAGTCCTGAAGTTTTAA
179	-1	PD-L1 responder	CCGCCTCCGTCTGCGCCTGGGCCAGGCCTCGACCTGCCTGTCAATATTTGCAATCACTGC
180	-1	PD-L1 responder	ACGCCCGCCTCCATGAGATTCAGAGCCCTCGACTCCTTTCCCAGACACATTCAGCACGTG
181	-1	PD-L1 responder	TCCCACCCACTCTTAATCAACATTCCATTCGATTTAATCCTACATGCTCCTTTCTTATGT
182	-1	PD-L1 responder	ATTTTGACATCTGCATTTTACAGCAGCCTCGATGCGAGCTCGTGGTGGGTGCTCAAGACT
183	-1	PD-L1 responder	AAGTCTTTTGTTTGGTTATTGTGCTGTATCGATCCAGCTTTTTGACTCTAAAATGAGCTT
184	-1	PD-L1 responder	GGCAAATGCTACAAATCAGAGTTGTTTTTCGATCACACTGGGAGCTGCAGACCGGAGCTG
185	-1	PD-L1 responder	GCAGCCAGCCCGGTGGGGGTGGGGGGGGTCGACGCTCGCCTCCGCTCACAGCCTCAGCAT
186	-1	PD-L1 responder	GTGTGCACCAGTAAAAGCCCTTTTACACTCGACCTGCTGATCCTTGGATCCTGAATCTGT
187	-1	PD-L1 responder	CGGGTGCCTCCCCCCCCATTCGCCCTGCTCGAGGGAGGGAAATGATTGGATTACGGGGGT
188	-1	PD-L1 responder	CTCCATCTCCCTGCCCTCTGGATCCCCCTCGATTCTACAGTGGTTTTAACAGCAGGCCCC
189	-1	PD-L1 responder	GTGTGGGCCCCCCTGCTACCGCTGCGTATCGAGCACCTCTTCAGGGGAGGATTACTGCAA
190	-1	PD-L1 responder	CGTTGCAAATTGTACATCTTCTGCTATTTCGAGACCTCATATAACTCGGTGATTGACTGC
191	-1	PD-L1 responder	TAACAAGGAGTGGAGTATTCCTGGGATATCGACCCCACCCCCTAGATTAAGACATTCCTG
192	-1	PD-L1 responder	AACAAGGCAGGTAGTGTTCCTGCCCTCATCGATGTGGCAGCGGGCCCGGACGGGTCGGTG

193	-1	PD-L1 responder	TCTTCTCTCCCTCACTCAGTATCCTCACTCGATGCGCGCCCGCCGGGGCCCGGTCGGAGC
194	-1	PD-L1 responder	GTGACAATTAAGAGTGTGACATTGCTTCTCGAGGACTCACTGGGCCTGCAGGGGGGCAGC
195	-1	PD-L1 responder	AGGTGGAGATCAGAAGACCCCCACGCCCTCGAGTCACAGCTGTAGTGGGGTGGGGGGTGA
196	-1	PD-L1 responder	GCACTACCCCGGCCTGCCGGAGCCCCAGTCGAGTTGGTTTCTGGGTCCGCACCCCCTCCC
197	-1	PD-L1 responder	GAATGTTTACCTATTATAAAAATGAGGATCGAGCACAGCGCCGGCTGGGGTACCTGGCAC
198	-1	PD-L1 responder	GCGGGGGCTTCCCTCAACTTCAGGGAGGTCGAGGCGCGGCGCGCAGGCCGCCATCGCCAC
199	-1	PD-L1 responder	TCAGATAAGTAACTTCCTGATAATTAACTCGAAAAAACATTAATTTCTTCAGGTGTAAAG

Table 1.d4

	Probe Location					**4 kb Sequence Location**	
	Chr	**Start1**	**End1**	**Start2**	**End2**	**Chr**	**Start1**
140	1	116708743	116708772	116735760	116735789	1	116704773
141	11	119671083	119671112	119729290	119729319	11	119671083
142	4	86131385	86131414	86343454	86343483	4	86127415
143	20	1891491	1891520	1924635	1924664	20	1891491
144	5	157249290	157249319	157266727	157266756	5	157249290
145	11	2113134	2113163	2180330	2180359	11	2113134
146	15	67098634	67098663	67199586	67199615	15	67098634
147	16	31278028	31278057	31331190	31331219	16	31278028
148	8	140725050	140725079	140877457	140877486	8	140721080
149	5	140647396	140647425	140672697	140672726	5	140643426
150	15	98737003	98737032	98790083	98790112	15	98733033
151	5	67182229	67182258	67233991	67234020	5	67178259
152	11	60922071	60922100	60977086	60977115	11	60922071
153	16	2500834	2500863	2548487	2548516	16	2500834
154	22	17735513	17735542	17806908	17806937	22	17731543
155	16	29613906	29613935	29632050	29632079	16	29613906
156	11	124746041	124746070	124787707	124787736	11	124746041
157	11	119677784	119677813	119705118	119705147	11	119673814
158	3	122014666	122014695	122100771	122100800	3	122014666
159	5	157181017	157181046	157266727	157266756	5	157177047
160	19	49654784	49654813	49691434	49691463	19	49654784
161	7	155794442	155794471	155842904	155842933	7	155794442
162	6	151873860	151873889	151997847	151997876	6	151869890
163	16	2500834	2500863	2548487	2548516	16	2500834
164	15	98784942	98784971	98893486	98893515	15	98780972
165	14	104760240	104760269	104843290	104843319	14	104760240
166	12	6934236	6934265	6965163	6965192	12	6934236
167	1	56943860	56943889	56962731	56962760	1	56939890
168	1	198595740	198595769	198749225	198749254	1	198591770
169	16	29613906	29613935	29632050	29632079	16	29613906
170	20	2816711	2816740	2967982	2968011	20	2816711
171	11	60983696	60983725	60996253	60996282	11	60979726
172	2	201267208	201267237	201291005	201291034	2	201263238
173	19	47240983	47241012	47256214	47256243	19	47237013

174	9	120893289	120893318	120913548	120913577	9	120889319
175	8	140725050	140725079	140783929	140783958	8	140721080
176	5	132477881	132477910	132536452	132536481	5	132473911
177	16	29613906	29613935	29687198	29687227	16	29613906
178	9	125608175	125608204	125635069	125635098	9	125608175
179	12	6773968	6773997	6796697	6796726	12	6769998
180	11	44564825	44564854	44629575	44629604	11	44560855
181	5	149378174	149378203	149421075	149421104	5	149378174
182	1	56962698	56962727	56998048	56998077	1	56958728
183	8	140725050	140725079	140771375	140771404	8	140721080
184	10	96186300	96186329	96286444	96286473	10	96186300
185	19	49654784	49654813	49691434	49691463	19	49654784
186	15	98893486	98893515	98957434	98957463	15	98893486
187	19	48955702	48955731	48973072	48973101	19	48955702
188	14	23324245	23324274	23359390	23359419	14	23324245
189	11	60933651	60933680	61017869	61017898	11	60929681
190	5	68213305	68213334	68277738	68277767	5	68209335
191	5	132053242	132053271	132074960	132074989	5	132049272
192	12	112418671	112418700	112482384	112482413	12	112418671
193	11	119671083	119671112	119729290	119729319	11	119671083
194	11	2113134	2113163	2180330	2180359	11	2113134
195	21	44243733	44243762	44267561	44267590	21	44243733
196	11	64269780	64269809	64296893	64296922	11	64265810
197	13	23627960	23627989	23678004	23678033	13	23627960
198	5	140647396	140647425	140672697	140672726	5	140643426
199	8	81018076	81018105	81077567	81077596	8	81014106

Table 1.d5

	4 kb Sequence Location		
	End1	**Start2**	**End2**
140	116708772	116735760	116739759
141	119675082	119729290	119733289
142	86131414	86339484	86343483
143	1895490	1924635	1928634
144	157253289	157266727	157270726
145	2117133	2180330	2184329
146	67102633	67199586	67203585
147	31282027	31331190	31335189
148	140725079	140877457	140881456
149	140647425	140668727	140672726
150	98737032	98786113	98790112
151	67182258	67233991	67237990
152	60926070	60977086	60981085
153	2504833	2544517	2548516
154	17735542	17802938	17806937
155	29617905	29628080	29632079
156	124750040	124783737	124787736
157	119677813	119701148	119705147
158	122018665	122096801	122100800
159	157181046	157266727	157270726
160	49658783	49691434	49695433
161	155798441	155838934	155842933

162	151873889	151993877	151997876
163	2504833	2544517	2548516
164	98784971	98893486	98897485
165	104764239	104839320	104843319
166	6938235	6965163	6969162
167	56943889	56962731	56966730
168	198595769	198745255	198749254
169	29617905	29628080	29632079
170	2820710	2964012	2968011
171	60983725	60996253	61000252
172	201267237	201287035	201291034
173	47241012	47256214	47260213
174	120893318	120913548	120917547
175	140725079	140779959	140783958
176	132477910	132536452	132540451
177	29617905	29683228	29687227
178	125612174	125631099	125635098
179	6773997	6796697	6800696
180	44564854	44625605	44629604
181	149382173	149421075	149425074
182	56962727	56994078	56998077
183	140725079	140767405	140771404
184	96190299	96282474	96286473
185	49658783	49691434	49695433
186	98897485	98957434	98961433
187	48959701	48973072	48977071
188	23328244	23355420	23359419
189	60933680	61017869	61021868
190	68213334	68273768	68277767
191	132053271	132070990	132074989
192	112422670	112478414	112482413
193	119675082	119729290	119733289
194	2117133	2180330	2184329
195	44247732	44267561	44271560
196	64269809	64292923	64296922
197	23631959	23678004	23682003
198	140647425	140668727	140672726
199	81018105	81077567	81081566

Table 1.d6

	probe	GeneLocus	Probe_Count_Total
200	IKBKB_8_42231188_42234849_42264241_42271203_RF	IKBKB	46
201	SPN_16_29613904_29616227_29686079_29687229_RF	SPN	56
202	PTK2_8_140763162_140771406_141001274_141004301_FR	PTK2	248
203	ORF263_11_78304460_78312808_78374350_78382835_RF	GAB2	132
204	PVRL1_11_119711187_119714047_119729288_119738834_FR	PVRL1	96
205	CD6_11_60932387_60933682_60977084_60983727_FR	CD6	56
206	ORF490_16_2500832_2504754_2601193_2603749_RF	PDPK1	60
207	ORF456_11_119671081_119677815_119700077_119705149_FR	PVRL1	96
208	ORF712_9_120888366_120893320_120913546_120919710_RR	TRAF1	42
209	ORF104_17_36075902_36084513_36095759_36100192_RF	CCL18	42

210	BOK_2_241535460_241542885_241559192_241566423_RR	BOK	44
211	IRF1_5_132472660_132477912_132517598_132521351_FF	IRF1	42
212	ORF173_4_77534161_77541495_77571558_77583817_RF	CXCL13	108
213	ORF58_19_47236830_47241014_47256212_47257706_FR	BBC3	56
214	ORF55_11_64267793_64269811_64288581_64290103_FR	BAD	70
215	PTPN11_12_112418669_112423831_112478543_112482415_RF	PTPN11	56
216	CD82_11_44515603_44522167_44561823_44564856_RF	CD82	50
217	ORF104_17_36023309_36028028_36075902_36084513_FR	CCL18	42
218	ORF122_19_51189093_51190958_51254261_51263712_FR	CD33	32
219	ORF305_15_98652565_98657862_98874707_98883774_RR	IGF1R	104
220	ORF104_17_36051957_36057144_36075902_36084513_FR	CCL18	42
221	ITK_5_157225228_157231430_157266725_157271762_FR	ITK	26
222	EGF_4_109875299_109879120_110005130_110011368_FF	EGF	48
223	ORF293_6_32626930_32634077_32662361_32664960_RF	HLA-DQA1	28
224	ORF479_8_81053410_81059648_81095100_81099880_RR	PAG1	144
225	ORF130_11_60977084_60983727_60996251_60998956_FR	CD6	56
226	ORF108_6_167109295_167112439_167149742_167154610_FF	CCR6	46
227	ORF538_8_140715391_140725081_140891408_140893244_FF	PTK2	248
228	ORF55_11_64267793_64269811_64301867_64303120_FR	BAD	70
229	ORF544_1_198619087_198627361_198650099_198652874_FF	PTPRC	214
230	PDCD1_2_241872992_241878216_241891223_241897247_RR	PDCD1	36
231	SHH_7_155807951_155810124_155829183_155832221_FR	SHH	36
232	ORF670_9_90767553_90774633_90856872_90861170_RR	SYK	78
233	ORF546_19_44596239_44600261_44664293_44665588_FR	PVR	65
234	ORF403_9_125518474_125526994_125631239_125635100_RF	MAPKAP1	52
235	ORF544_1_198591683_198595771_198768850_198775826_FF	PTPRC	214
236	RPTOR_17_80636056_80643737_80661868_80664436_FR	RPTOR	86
237	ORF168_15_74772372_74779791_74801744_74804023_RF	CSK	48
238	NCK2_2_105715815_105716905_105886459_105893355_FR	NCK2	66
239	CD4_12_6767426_6773999_6813425_6817229_FR	CD4	42
240	ORF538_8_140763162_140771406_141001274_141004301_FR	PTK2	248
241	ORF250_2_215361328_215366837_215435722_215439709_FR	FN1	42
242	BAD_11_64267793_64269811_64292591_64296924_FF	BAD	70
243	ORF398_17_45280830_45283423_45297938_45303012_RR	MAP3K14	44
244	RPTOR_17_80636056_80643737_80793263_80796075_FF	RPTOR	86
245	ORF163_12_93752886_93759416_93791200_93797905_FF	CRADD	231
246	ORF95_2_201224034_201225522_201286114_201291036_FF	CASP8	41
247	ORF215_12_47728716_47732358_47745284_47751054_FR	ENDOU	26
248	ORF480_11_77430379_77437843_77514783_77519103_RF	PAK1	136
249	ORF306_11_2113132_2119465_2170498_2173159_RR	IGF2	32
250	CASP9_1_15520953_15524014_15542554_15547367_FR	CASP9	46
251	STAT5A_17_42251917_42254441_42312276_42316438_FR	STAT5A	99
252	SMAD3_15_67098632_67101498_67199584_67204251_RR	SMAD3	34
253	STAT3_17_42312276_42316438_42406596_42409990_RF	STAT3	100
254	PIK3R2_19_18105164_18110364_18179077_18180271_FR	PIK3R2	116
255	MCL1_1_150570652_150572543_150615513_150618018_RR	MCL1	77
256	ORF701_13_23612221_23617919_23627958_23632852_FF	TNFRSF19	60
257	ORF55_11_64267793_64269811_64317605_64318816_FR	BAD	70
258	ORF263_11_78204241_78207061_78304460_78312808_RR	GAB2	132
259	BBC3_19_47214451_47217416_47236830_47241014_RF	BBC3	56

Table 1.e1

	Probe_Count_Sig	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr
200	12	0.00018363	0.010627608	26.09	-0.153734995	-0.153734995
201	4	0.659150649	0.99999793	7.14	-0.153139995	-0.153139995
202	12	0.979779286	0.99999793	4.84	-0.152326374	-0.152326374
203	4	0.994374946	0.99999793	3.03	-0.152150489	-0.152150489
204	8	0.497039718	0.99999793	8.33	-0.15064075	-0.15064075
205	14	9.03E-05	0.005970563	25	-0.149724624	-0.149724624
206	6	0.340695433	0.99999793	10	-0.149355476	-0.149355476
207	8	0.497039718	0.99999793	8.33	-0.149050171	-0.149050171
208	6	0.112492545	0.789152247	14.29	-0.148665785	-0.148665785
209	8	0.016095432	0.256971894	19.05	-0.147845095	-0.147845095
210	10	0.001969408	0.075986326	22.73	-0.147733184	-0.147733184
211	8	0.016095432	0.256971894	19.05	-0.147678268	-0.147678268
212	14	0.046569042	0.598929617	12.96	-0.147196733	-0.147196733
213	8	0.073465475	0.710624303	14.29	-0.147180745	-0.147180745
214	8	0.18964104	0.954389149	11.43	-0.146341453	-0.146341453
215	6	0.283634013	0.99999793	10.71	-0.146237304	-0.146237304
216	6	0.203083688	0.988148592	12	-0.145793053	-0.145793053
217	8	0.016095432	0.256971894	19.05	-0.145522289	-0.145522289
218	4	0.246707931	0.99999793	12.5	-0.145368223	-0.145368223
219	16	0.007797893	0.171924974	15.38	-0.14534477	-0.14534477
220	8	0.016095432	0.256971894	19.05	-0.145186047	-0.145186047
221	10	1.57E-05	0.002607465	38.46	-0.144955613	-0.144955613
222	2	0.903339407	0.99999793	4.17	-0.144833276	-0.144833276
223	4	0.178427395	0.954389149	14.29	-0.144695604	-0.144695604
224	12	0.474481533	0.99999793	8.33	-0.143993345	-0.143993345
225	14	9.03E-05	0.005970563	25	-0.143973167	-0.143973167
226	4	0.501622356	0.99999793	8.7	-0.14391148	-0.14391148
227	12	0.979779286	0.99999793	4.84	-0.14318365	-0.14318365
228	8	0.18964104	0.954389149	11.43	-0.142614975	-0.142614975
229	10	0.978491243	0.99999793	4.67	-0.142566804	-0.142566804
230	2	0.791365183	0.99999793	5.56	-0.141810476	-0.141810476
231	6	0.062022042	0.70039526	16.67	-0.140520637	-0.140520637
232	6	0.592795697	0.99999793	7.69	-0.140441943	-0.140441943
233	2	0.969655536	0.99999793	3.08	-0.140409158	-0.140409158
234	6	0.229017635	0.99999793	11.54	-0.140408889	-0.140408889
235	10	0.978491243	0.99999793	4.67	-0.14040288	-0.14040288
236	6	0.687444338	0.99999793	6.98	-0.140265969	-0.140265969
237	6	0.178303905	0.954389149	12.5	-0.14006922	-0.14006922
238	4	0.779227696	0.99999793	6.06	-0.14004291	-0.14004291
239	6	0.112492545	0.789152247	14.29	-0.139921516	-0.139921516
240	12	0.979779286	0.99999793	4.84	-0.13991747	-0.13991747
241	4	0.430324418	0.99999793	9.52	-0.139856487	-0.139856487
242	8	0.18964104	0.954389149	11.43	-0.139786492	-0.139786492
243	2	0.874387211	0.99999793	4.55	-0.139621418	-0.139621418
244	6	0.687444338	0.99999793	6.98	-0.139084539	-0.139084539
245	4	0.999992975	0.99999793	1.73	-0.138988579	-0.138988579
246	4	0.412035429	0.99999793	9.76	-0.138820075	-0.138820075
247	2	0.622797749	0.99999793	7.69	-0.138484187	-0.138484187
248	6	0.963851563	0.99999793	4.41	-0.138029302	-0.138029302
249	6	0.037675475	0.528598335	18.75	-0.137735512	-0.137735512

250	2	0.889742685	0.99999793	4.35	-0.137531489	-0.137531489
251	3	0.987493488	0.99999793	3.03	-0.137312489	-0.137312489
252	2	0.764125503	0.99999793	5.88	-0.13672288	-0.13672288
253	3	0.988282647	0.99999793	3	-0.136436646	-0.136436646
254	8	0.71102088	0.99999793	6.9	-0.136435703	-0.136435703
255	2	0.987032863	0.99999793	2.6	-0.136350796	-0.136350796
256	8	0.100733588	0.781478358	13.33	-0.136324733	-0.136324733
257	8	0.18964104	0.954389149	11.43	-0.135663101	-0.135663101
258	4	0.994374946	0.99999793	3.03	-0.13560486	-0.13560486
259	8	0.073465475	0.710624303	14.29	-0.135407703	-0.135407703

Table 1.e2

	t	P.Value	adj.P.Val	B	FC	FC_1
200	-7.304936683	0.00002260000	0.000477724	2.975832882	0.898920232	-1.11244576
201	-6.667140097	0.00004970000	0.000781417	2.158738806	0.899291043	-1.111987056
202	-7.625429518	0.00001550000	0.000380419	3.366772483	0.899798349	-1.111360118
203	-4.577281937	0.00095286200	0.005814117	-0.914179847	0.899908054	-1.111224636
204	-6.783904683	0.00004290000	0.000712857	2.312341711	0.900850275	-1.110062379
205	-8.117825922	0.00000890000	0.000266511	3.943211829	0.901422506	-1.109357702
206	-7.836679042	0.00001220000	0.000321613	3.617589371	0.901653186	-1.109073883
207	-6.891048765	0.00003750000	0.000650749	2.451683607	0.901844015	-1.108839204
208	-4.410767412	0.00123791600	0.007019121	-1.185214291	0.902084331	-1.108543809
209	-4.251334919	0.00159613900	0.008419218	-1.447954133	0.902597636	-1.107913382
210	-6.666436335	0.00004980000	0.000781822	2.15780744	0.902667654	-1.107827445
211	-6.626064358	0.00005240000	0.000805791	2.104266413	0.902702014	-1.107785276
212	-5.836984087	0.00014946900	0.001619866	1.012428105	0.903003364	-1.107415586
213	-6.340071543	0.00007590000	0.001036334	1.718599523	0.903013371	-1.107403314
214	-5.009008006	0.00049233200	0.003660595	-0.228647352	0.903538855	-1.106759266
215	-4.993800795	0.00050369000	0.003715147	-0.252357852	0.903604084	-1.106679372
216	-5.45369143	0.00025643200	0.002326445	0.450144339	0.903882374	-1.106338644
217	-6.211155845	0.00009000000	0.001158865	1.541048326	0.904052031	-1.106131026
218	-5.088815906	0.00043703100	0.003357770	-0.104748419	0.90414858	-1.106012908
219	-5.753969471	0.00016771300	0.001754983	0.892439998	0.904163278	-1.105994929
220	-7.577635502	0.00001640000	0.000394253	3.309278087	0.904262758	-1.105873255
221	-8.636856152	0.00000508000	0.000194036	4.520831371	0.904407203	-1.105696634
222	-7.422808069	0.00001970000	0.000439652	3.121097762	0.904483898	-1.105602877
223	-3.861408042	0.00301392500	0.013289266	-2.102539121	0.904570214	-1.105497379
224	-4.923920109	0.00055958200	0.004010305	-0.361729876	0.905010637	-1.104959388
225	-8.04914211	0.00000960000	0.000278481	3.864510034	0.905023296	-1.104943933
226	-7.030078326	0.00003160000	0.000584325	2.630230616	0.905061993	-1.104896689
227	-8.097864547	0.00000910000	0.000269771	3.920394803	0.905518706	-1.104339417
228	-6.189561727	0.00009260000	0.001182316	1.511079783	0.90587571	-1.103904199
229	-4.553892926	0.00098831100	0.005962042	-0.952034894	0.905905957	-1.103867341
230	-5.565131269	0.00021872300	0.002087609	0.615805718	0.906381	-1.103288794
231	-6.954162178	0.00003470000	0.000620295	2.533051066	0.907191711	-1.102302841
232	-3.707755589	0.00389163500	0.016071261	-2.3644857	0.907241196	-1.102242716
233	-7.239219785	0.00002450000	0.000501173	2.894081942	0.907261813	-1.102217668
234	-5.951614421	0.00012769200	0.001464818	1.176490654	0.907261983	-1.102217462
235	-5.186348648	0.00037827900	0.003044422	0.045441754	0.907265761	-1.102212872
236	-6.28050969	0.00008210000	0.001088928	1.636855792	0.907351864	-1.102108277
237	-6.053728742	0.00011114700	0.001336285	1.321061584	0.907475614	-1.101957986
238	-6.51116257	0.00006070000	0.000890100	1.95067007	0.907492164	-1.10193789

239	-5.076520451	0.00044510100	0.003404610	-0.123778016	0.907568527	-1.101845173
240	-7.555319063	0.00001690000	0.000399575	3.282336571	0.907571072	-1.101842083
241	-5.882100302	0.00014045600	0.001559082	1.077224081	0.907609436	-1.101795508
242	-5.923845607	0.00013263500	0.001500230	1.136919402	0.907653471	-1.101742055
243	-6.354108322	0.00007450000	0.001022368	1.737791878	0.907757331	-1.101616
244	-6.11708923	0.00010205000	0.001261051	1.410021654	0.908095203	-1.101206125
245	-7.545550183	0.00001700000	0.000402097	3.270523863	0.908155607	-1.101132881
246	-3.749454698	0.00362988500	0.015257888	-2.293205904	0.908261684	-1.101004278
247	-8.619846124	0.00000517000	0.000196113	4.502368539	0.90847317	-1.100747973
248	-5.075029024	0.00044609100	0.003407902	-0.126087743	0.908759659	-1.100400959
249	-4.018012402	0.00232944900	0.011026268	-1.837743779	0.908944737	-1.100176896
250	-6.968042831	0.00003410000	0.000615455	2.550875988	0.909073287	-1.100021323
251	-6.125083705	0.00010096000	0.001251488	1.421205788	0.909211294	-1.099854353
252	-5.70594319	0.00017934600	0.001836241	0.822571596	0.909582952	-1.09940495
253	-4.603251935	0.00091507100	0.005639667	-0.87223129	0.909763434	-1.099186847
254	-5.56320903	0.00021932100	0.002091340	0.612963373	0.909764028	-1.099186129
255	-3.79495011	0.00336509800	0.014441992	-2.215595065	0.909817572	-1.09912144
256	-5.224608881	0.00035758400	0.002919671	0.103988299	0.909834008	-1.099101584
257	-6.060210734	0.00011017700	0.001329805	1.330188615	0.910251362	-1.098597642
258	-5.625009378	0.00020095100	0.001974506	0.704078694	0.910288109	-1.098553294
259	-5.668113394	0.00018911800	0.001899617	0.767303424	0.910412516	-1.098403177

Table 1.e3

			Probe sequence
	LS	Loop detected	**60 mer**
200	-1	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAGGTGGCTTGGGTCTTAGTCTTCCAGGCA
201	-1	PD-L1 responder	CATCATCACAGTCTACGGCTGTTTCCTCTCGAAGGCCCCCGTCCTCCTGCGCCATGGAGA
202	-1	PD-L1 responder	AAGCTCATTTTAGAGTCAAAAAGCTGGATCGAGGCCGTGCTGCGTCGGCGCGGGCCCGCG
203	-1	PD-L1 responder	TATTTTATTTGTTACTAAAACAAGGAACTCGATTTCGCCAAGGGCCAGGCTCCCAAGGCA
204	-1	PD-L1 responder	GAGGCTTCTGAGTTGCTCTGAGGGTACATCGATGCGCGCCCGCCGGGGCCCGGTCGGAGC
205	-1	PD-L1 responder	GTGTGGGCCCCCCTGCTACCGCTGCGTATCGAACTTTACAGAGGGATCTAGAATGAGTGA
206	-1	PD-L1 responder	CGGACAAGGTGAGGACCACGTGGGCCAGTCGATGGGGACCTGAACCGGGGCCGCACAAGC
207	-1	PD-L1 responder	GGACCTTGTCATCCTGCCCCTTCTTGGCTCGAGGCCCTGAAACAGGACTCTATGTCTCCT
208	-1	PD-L1 responder	AGTGCTGGGTTCCACACCTCTCAGCTCTTCGACCTCCAGGTCCCCCGCCACTTCCACGGC
209	-1	PD-L1 responder	TCAATGCCATCACTAGACATGGAACTCTTCGAGCCATCCTCCCAGTGACACTCCGCAAAG
210	-1	PD-L1 responder	GACCCCCGGGAATTGGCTCCAGCACATCTCGAGGGCGGGCCCGGCGGCCCCGGAGCAAAC
211	-1	PD-L1 responder	GTGTCTCGGCCCCCTGGGGCCCCACCCTTCGATACTATTACGAATGGAATCACTGTCTTA
212	-1	PD-L1 responder	GGCACCTGTTAGCAATGAAGGATAACCATCGACCATCTTGGTTCCACCTGGCAGTTTCTT

213	-1	PD-L1 responder	CGTGGATCCAGACTGGGAGCCCCCAGCCTCGAACCACGCCAGGCTTCCAGGCGTCAGTGC
214	-1	PD-L1 responder	GCACTACCCCGGCCTGCCGGAGCCCCAGTCGATGATGGCTTCCTCCCCCAGAGCACCAGC
215	-1	PD-L1 responder	AACAAGGCAGGTAGTGTTCCTGCCCTCATCGATGTGGCAGCGGGCCCGGACGGGTCGGTG
216	-1	PD-L1 responder	ACGCCCGCCTCCATGAGATTCAGAGCCCTCGAGAATGTGGACTCTCCTTTCCCCCAGCAC
217	-1	PD-L1 responder	TGAGCTAATAAACTATTTCTGGTTTTGCTCGAGCCATCCTCCCAGTGACACTCCGCAAAG
218	-1	PD-L1 responder	GTCACCAGGGCTCCCTCCTCCTGCGGAATCGAGGCTGTAGATAGCTGTGATTGTACCACT
219	-1	PD-L1 responder	TCTTAGAGTTGAACTTTTCTAATCTTTTTCGAAGACCCCTTCCATTGGGCATTCATCTAA
220	-1	PD-L1 responder	CCAGAAATTCTGTGGTTGATGAATTTGGTCGAGCCATCCTCCCAGTGACACTCCGCAAAG
221	-1	PD-L1 responder	TGAGATGAAGCCTATATTTTCCCAATCCTCGATGTTTGGGGGCGGAGGGCTTTGATGAGA
222	-1	PD-L1 responder	CAGGCTATTGTAGTGCTCTTCCTGGCCCTCGACACCCCCTTCAAGGGTCTGTGTCCCATA
223	-1	PD-L1 responder	CACCGCGCGGTACACCCCCACGTCGCTGTCGACATTTTCTTACCAGCCTGGCTGATAAAC
224	-1	PD-L1 responder	GTAAGCCATGGAAATATGAATCCATTTCTCGATGCCAATCCACGTCATTAGATGAGGACC
225	-1	PD-L1 responder	TTAATGCTGATACAATTCTATTGGATAATCGACGTGCCTTGGGGCCTCCCCTTTCCCTAT
226	-1	PD-L1 responder	CCATCTGCAAGTCGCTTTTGACTAGCACTCGAGTTCTTTCTGACATCTCCTGGGTGGAGC
227	-1	PD-L1 responder	AAGTCTTTTGTTTGGTTATTGTGCTGTATCGACCTCCTGGACTCAAGCAATCCTCGGCCT
228	-1	PD-L1 responder	GCACTACCCCGGCCTGCCGGAGCCCCAGTCGACATGTTGCCCCAGCTGGTCTCAAACTCC
229	-1	PD-L1 responder	AGGAAGTATGTTTGATTTAGAATGTTATTCGAGCCGCCCTTGACATAACACCATCTTTTA
230	-1	PD-L1 responder	GTGGCCACCGCCCTTGCGCTTTATGACATCGATTTTGGCTCTGTAGGGAAAGGCTCTTAT
231	-1	PD-L1 responder	CGCGCACTGAAACCCTAGCCGCGGGGGATCGAAATCATATCACCAGTCATTCCACTCCTG
232	-1	PD-L1 responder	TTTGCTAAATTACCCAAAATTTTGCTTTTCGATGCTGGGAACACTTTCCTCCAGAGTTGA
233	-1	PD-L1 responder	GTCCCTGAAAATGTTTGTAAATGTGGGGTCGACCTGCTGGGCTCGGGCTATCCTTCCATC
234	-1	PD-L1 responder	CACTAATCTTTACTCTTTTTCCACTTATTCGAGACCAGTGAAACCTCGTCGCTACAAAAA
235	-1	PD-L1 responder	TGTTTTTTATTGTTTGATGTCCAATGTATCGAGTCACATGATCAAGCGCTCATTTCTGTT
236	-1	PD-L1 responder	CTTTTCCATTGCTTCCTCAGATCCTCTGTCGAGATTCACTGCGCTGCACACCAGGGCCTC
237	-1	PD-L1 responder	AGGACCTGAAATCCAGGAAGATCTGACTTCGAGACGATCCCGGCCAACATGGTGAAACCC
238	-1	PD-L1 responder	TATTTGTATCCTTTCCTCATTTATTTACTCGAATCTCTGGGGTAGGGCTCTGCAACCTTG

239	-1	PD-L1 responder	CCGCCTCCGTCTGCGCCTGGGCCAGGCCTCGAGAATTATTCTTTTCATATACAAAGAATA
240	-1	PD-L1 responder	AAGCTCATTTTAGAGTCAAAAAGCTGGATCGAGGCCGTGCTGCGTCGGCGCGGGCCCGCG
241	-1	PD-L1 responder	GTAATAAACATACAAACTTAAACGTAGTTCGAGGCTCCCGTGGAGGGCACCGCTGTCCCC
242	-1	PD-L1 responder	GCACTACCCCGGCCTGCCGGAGCCCCAGTCGAGTTGGTTTCTGGGTCCGCACCCCCTCCC
243	-1	PD-L1 responder	AGCGGGCAGATCACTTGAGGTCAGGAGTTCGAACTCCTGACCTCAGGTGATCTGCCTGCC
244	-1	PD-L1 responder	CTTTTCCATTGCTTCCTCAGATCCTCTGTCGAGAGCACGGCCTCTCTGGCGCCTTGCCAT
245	-1	PD-L1 responder	AAACTTCCTTTCTTTGCTTAGAACTAGCTCGATCCTGGAAGCCCCCTAAAGGCAGGAACT
246	-1	PD-L1 responder	TTGCACTCTCGGTCTGTTTTACTAATCATCGAGCTTCCTGGCCACTTTGTTTACCTACTC
247	-1	PD-L1 responder	GCCATTAAATTCCCCTAATGCCATTGCCTCGACTTCAGTGGCGTCCATTGTCTGCTGGAG
248	-1	PD-L1 responder	TAACAAAAGTAACACCTCTTTGGTATCATCGAAGAGTCCTTGTTCCCATTTTGGCCCAGT
249	-1	PD-L1 responder	GTGACAATTAAGAGTGTGACATTGCTTCTCGATCCCAGAGCCGTCCCAGGCCTGGACAGA
250	-1	PD-L1 responder	GAAGGCTAGGCTCCCGCACAACGCCTCCTCGAGCAAGTTAGTTGAACCCAAGGAGGGTCA
251	-1	PD-L1 responder	TTCCATAGATTACTTTTCAAATCATCCTTCGAAGCTGGCGGCTGAGGGCCCGGCGCCAAG
252	-1	PD-L1 responder	GTGGCAGGAGAAAAACGCGGCCCCACCCTCGAAAATACTAGAATTATGCCGCACAGTCAG
253	-1	PD-L1 responder	TTGCCAAGCACACATAGCTCCTCAATCCTCGAAGCTGGCGGCTGAGGGCCCGGCGCCAAG
254	-1	PD-L1 responder	GACAAGCTGCACATCCCGGCGCTGACCCTCGAGGAAGTGAGGCTTAATTCCACTCCCTAC
255	-1	PD-L1 responder	AATTTATGGATTGTATGTTACTACTGTATCGAGATCTTCCTACCTCACCGTCCCAAGTAG
256	-1	PD-L1 responder	GCACTACAGACAAAAGACTCTAACTGGATCGATTAGCTTCTCCTCTCTCTTCTAATCCTC
257	-1	PD-L1 responder	GCACTACCCCGGCCTGCCGGAGCCCCAGTCGATGCTATTGGATAGCCAGGAGAACCGGAA
258	-1	PD-L1 responder	CTCTCAAACTGGCTTGTACCAGGAGTGTTCGATTTCGCCAAGGGCCAGGCTCCCAAGGCA
259	-1	PD-L1 responder	CGTGGATCCAGACTGGGAGCCCCCAGCCTCGAGCAGTTGCACTCCAGCCTAGGCAACAAG

Table 1.e4

	Probe Location					**4 kb Sequence Location**	
	Chr	**Start1**	**End1**	**Start2**	**End2**	**Chr**	**Start1**
200	8	42231190	42231219	42271172	42271201	8	42231190
201	16	29613906	29613935	29687198	29687227	16	29613906
202	8	140771375	140771404	141001276	141001305	8	140767405
203	11	78304462	78304491	78382804	78382833	11	78304462
204	11	119714016	119714045	119729290	119729319	11	119710046
205	11	60933651	60933680	60977086	60977115	11	60929681

206	16	2500834	2500863	2603718	2603747	16	2500834
207	11	119677784	119677813	119700079	119700108	11	119673814
208	9	120888368	120888397	120913548	120913577	9	120888368
209	17	36075904	36075933	36100161	36100190	17	36075904
210	2	241535462	241535491	241559194	241559223	2	241535462
211	5	132477881	132477910	132521320	132521349	5	132473911
212	4	77534163	77534192	77583786	77583815	4	77534163
213	19	47240983	47241012	47256214	47256243	19	47237013
214	11	64269780	64269809	64288583	64288612	11	64265810
215	12	112418671	112418700	112482384	112482413	12	112418671
216	11	44515605	44515634	44564825	44564854	11	44515605
217	17	36027997	36028026	36075904	36075933	17	36024027
218	19	51190927	51190956	51254263	51254292	19	51186957
219	15	98652567	98652596	98874709	98874738	15	98652567
220	17	36057113	36057142	36075904	36075933	17	36053143
221	5	157231399	157231428	157266727	157266756	5	157227429
222	4	109879089	109879118	110011337	110011366	4	109875119
223	6	32626932	32626961	32664929	32664958	6	32626932
224	8	81053412	81053441	81095102	81095131	8	81053412
225	11	60983696	60983725	60996253	60996282	11	60979726
226	6	167112408	167112437	167154579	167154608	6	167108438
227	8	140725050	140725079	140893213	140893242	8	140721080
228	11	64269780	64269809	64301869	64301898	11	64265810
229	1	198627330	198627359	198652843	198652872	1	198623360
230	2	241872994	241873023	241891225	241891254	2	241872994
231	7	155810093	155810122	155829185	155829214	7	155806123
232	9	90767555	90767584	90856874	90856903	9	90767555
233	19	44600230	44600259	44664295	44664324	19	44596260
234	9	125518476	125518505	125635069	125635098	9	125518476
235	1	198595740	198595769	198775795	198775824	1	198591770
236	17	80643706	80643735	80661870	80661899	17	80639736
237	15	74772374	74772403	74803992	74804021	15	74772374
238	2	105716874	105716903	105886461	105886490	2	105712904
239	12	6773968	6773997	6813427	6813456	12	6769998
240	8	140771375	140771404	141001276	141001305	8	140767405
241	2	215366806	215366835	215435724	215435753	2	215362836
242	11	64269780	64269809	64296893	64296922	11	64265810
243	17	45280832	45280861	45297940	45297969	17	45280832
244	17	80643706	80643735	80796044	80796073	17	80639736
245	12	93759385	93759414	93797874	93797903	12	93755415
246	2	201225491	201225520	201291005	201291034	2	201221521
247	12	47732327	47732356	47745286	47745315	12	47728357
248	11	77430381	77430410	77519072	77519101	11	77430381
249	11	2113134	2113163	2170500	2170529	11	2113134
250	1	15523983	15524012	15542556	15542585	1	15520013
251	17	42254410	42254439	42312278	42312307	17	42250440
252	15	67098634	67098663	67199586	67199615	15	67098634
253	17	42312278	42312307	42409959	42409988	17	42312278
254	19	18110333	18110362	18179079	18179108	19	18106363
255	1	150570654	150570683	150615515	150615544	1	150570654
256	13	23617888	23617917	23632821	23632850	13	23613918

257	11	64269780	64269809	64317607	64317636	11	64265810
258	11	78204243	78204272	78304462	78304491	11	78204243
259	19	47214453	47214482	47240983	47241012	19	47214453

Table 1.e5

	4 kb Sequence Location		
	End1	**Start2**	**End2**
200	42235189	42267202	42271201
201	29617905	29683228	29687227
202	140771404	141001276	141005275
203	78308461	78378834	78382833
204	119714045	119729290	119733289
205	60933680	60977086	60981085
206	2504833	2599748	2603747
207	119677813	119700079	119704078
208	120892367	120913548	120917547
209	36079903	36096191	36100190
210	241539461	241559194	241563193
211	132477910	132517350	132521349
212	77538162	77579816	77583815
213	47241012	47256214	47260213
214	64269809	64288583	64292582
215	112422670	112478414	112482413
216	44519604	44560855	44564854
217	36028026	36075904	36079903
218	51190956	51254263	51258262
219	98656566	98874709	98878708
220	36057142	36075904	36079903
221	157231428	157266727	157270726
222	109879118	110007367	110011366
223	32630931	32660959	32664958
224	81057411	81095102	81099101
225	60983725	60996253	61000252
226	167112437	167150609	167154608
227	140725079	140889243	140893242
228	64269809	64301869	64305868
229	198627359	198648873	198652872
230	241876993	241891225	241895224
231	155810122	155829185	155833184
232	90771554	90856874	90860873
233	44600259	44664295	44668294
234	125522475	125631099	125635098
235	198595769	198771825	198775824
236	80643735	80661870	80665869
237	74776373	74800022	74804021
238	105716903	105886461	105890460
239	6773997	6813427	6817426
240	140771404	141001276	141005275
241	215366835	215435724	215439723
242	64269809	64292923	64296922
243	45284831	45297940	45301939
244	80643735	80792074	80796073

245	93759414	93793904	93797903
246	201225520	201287035	201291034
247	47732356	47745286	47749285
248	77434380	77515102	77519101
249	2117133	2170500	2174499
250	15524012	15542556	15546555
251	42254439	42312278	42316277
252	67102633	67199586	67203585
253	42316277	42405989	42409988
254	18110362	18179079	18183078
255	150574653	150615515	150619514
256	23617917	23628851	23632850
257	64269809	64317607	64321606
258	78208242	78304462	78308461
259	47218452	47237013	47241012

Table 1.e6

	probe	GeneLocus	Probe_Count _Total
260	ORF402_16_30112759_30117149_30162846_30165864_FF	MAPK3	44
261	ORF224_6_151760868_151764563_151928859_151937822_RR	ESR1	198
262	CDKN2A_9_21967881_21969374_22029989_22034039_RF	CDKN2A	44
263	CD6_11_60922069_60925026_60977084_60983727_RR	CD6	56
264	ORF300_21_44209217_44216751_44251677_44254768_RR	ICOSLG	40
265	ORF708_1_3611941_3615812_3638742_3642185_FF	TP73	32
266	ORF86_1_56902220_56908104_56927372_56932246_RF	C8A	166
267	ORF574_5_38976283_38980760_39037737_39046956_RF	RICTOR	114
268	LYN_8_55939615_55941582_55961822_55966587_RF	LYN	48
269	ORF456_11_119711187_119714047_119729288_119738834_FR	PVRL1	96
270	SIRPA_20_1849966_1853129_1924633_1930962_RR	SIRPA	56
271	ORF173_4_77503292_77510413_77524478_77530204_RR	CXCL13	108
272	MTOR_1_11153017_11157168_11226037_11228251_FF	MTOR	60
273	ORF318_12_68159448_68161660_68183648_68186563_RR	IL26	20
274	CD33_19_51200116_51202883_51233917_51238043_RF	CD33	32
275	PTPRA_20_2873115_2878192_2986126_2989451_RF	PTPRA	82
276	ITK_5_157249288_157254103_157266725_157271762_FR	ITK	26
277	ORF368_1_32254316_32257966_32281860_32285193_RR	LCK	46
278	ORF173_4_77571558_77583817_77593834_77598247_FF	CXCL13	108
279	CD4_12_6813425_6817229_6829192_6834733_RR	CD4	42
280	BLNK_10_96186298_96190208_96274838_96286475_RF	BLNK	66
281	ORF332_6_379279_387635_399013_400061_RF	IRF4	40
282	CXCL13_4_77524478_77530204_77571558_77583817_RF	CXCL13	108
283	ORF480_11_77430379_77437843_77488853_77494447_FF	PAK1	136
284	ORF127_3_108038610_108048605_108107363_108112891_RF	CD47	46
285	ARHGEF7_13_111147918_111152467_111170222_111182176_FF	ARHGEF7	122
286	BBC3_19_47236830_47241014_47275384_47276951_FR	BBC3	56
287	TP73_1_3605228_3610228_3716440_3718086_FF	TP73	32
288	CD79A_19_41852821_41857717_41894637_41898341_RF	CD79A	44
289	ORF143_9_21967881_21969374_22029989_22034039_RF	CDKN2A	44
290	UBC_12_124897705_124900704_124946470_124947649_RF	UBC	64
291	ORF723_19_10361427_10365738_10416039_10417435_FR	TYK2	75
292	ORF673_6_149229853_149231712_149361564_149369248_FF	TAB2	151

293	ORF305_15_98652565_98657862_98957432_98962130_RR	IGF1R	104
294	ORF463_4_102522760_102539034_102577393_102582880_FR	NFKB1	64
295	ORF73_10_96204016_96209130_96290525_96304713_FR	BLNK	66
296	ORF401_4_85995509_86001303_86120725_86131416_RF	MAPK10	186
297	CD6_11_60922069_60925026_60977084_60983727_FF	CD6	56
298	PDPK1_16_2543954_2548518_2569272_2571597_FR	PDPK1	60
299	SHH_7_155800574_155803187_155834849_155837762_FF	SHH	36
300	ORF502_19_18105164_18110364_18179077_18180271_FR	PIK3R2	116
301	ORF241_10_88957987_88964666_88985428_88990419_FF	FAS	50
302	ORF698_18_62296384_62304812_62350513_62353490_FF	TNFRSF11A	58
303	ORF524_10_70591312_70596315_70645615_70650323_RR	PRF1	28
304	ORF168_15_74750296_74755004_74772372_74779791_FR	CSK	48
305	ORF311_5_149367706_149370779_149412565_149416567_RF	IL17B	44
306	ORF479_8_80976747_80979473_81007411_81018107_RF	PAG1	144
307	HLA-DMB_6_32954633_32960310_32978237_32979648_RR	HLA-DMB	26
308	ORF70_22_17731946_17735544_17804446_17806939_FF	BID	42
309	ORF87_1_56920282_56923866_56991331_56998079_FR	C8B	151
310	CCR6_6_167100641_167107689_167149742_167154610_FR	CCR6	46
311	ORF124_12_6767426_6773999_6813425_6817229_FR	CD4	42
312	PRF1_10_70625039_70635552_70645615_70650323_FR	PRF1	28
313	ORF703_1_6481328_6484248_6494588_6498048_FR	TNFRSF25	68
314	ORF112_5_140643798_140647427_140673116_140675478_RR	CD14	62
315	ORF98_11_119243827_119245328_119294588_119299643_RF	CBL	55
316	SYK_9_90761728_90767553_90799858_90802263_FF	SYK	78
317	ORF338_5_157249288_157254103_157266725_157271762_FR	ITK	26
318	ORF480_11_77352593_77360453_77413948_77425707_FR	PAK1	136
319	ORF723_19_10345998_10347157_10361427_10365738_RF	TYK2	75

Table 1.f1

	Probe_Count_Sig	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr
260	4	0.466402982	0.99999793	9.09	-0.135367103	-0.135367103
261	4	0.999928673	0.99999793	2.02	-0.135314539	-0.135314539
262	4	0.466402982	0.99999793	9.09	-0.135272194	-0.135272194
263	14	9.03E-05	0.005970563	25	-0.134887567	-0.134887567
264	8	0.012066038	0.223463015	20	-0.134719018	-0.134719018
265	4	0.246707931	0.99999793	12.5	-0.134700098	-0.134700098
266	8	0.957766442	0.99999793	4.82	-0.134558534	-0.134558534
267	2	0.99915023	0.99999793	1.75	-0.134523968	-0.134523968
268	2	0.903339407	0.99999793	4.17	-0.133947883	-0.133947883
269	8	0.497039718	0.99999793	8.33	-0.133203879	-0.133203879
270	4	0.659150649	0.99999793	7.14	-0.133176015	-0.133176015
271	14	0.046569042	0.598929617	12.96	-0.13317108	-0.13317108
272	4	0.711822793	0.99999793	6.67	-0.133096756	-0.133096756
273	2	0.479107134	0.99999793	10	-0.133028046	-0.133028046
274	4	0.246707931	0.99999793	12.5	-0.132614212	-0.132614212
275	8	0.325435728	0.99999793	9.76	-0.13255617	-0.13255617
276	10	1.57E-05	0.002607465	38.46	-0.132455148	-0.132455148
277	4	0.501622356	0.99999793	8.7	-0.132015778	-0.132015778
278	14	0.046569042	0.598929617	12.96	-0.131874693	-0.131874693
279	6	0.112492545	0.789152247	14.29	-0.131485584	-0.131485584
280	4	0.779227696	0.99999793	6.06	-0.130818373	-0.130818373
281	2	0.837619347	0.99999793	5	-0.130756722	-0.130756722

282	14	0.046569042	0.598929617	12.96	-0.13064065	-0.13064065
283	6	0.963851563	0.99999793	4.41	-0.130320594	-0.130320594
284	2	0.889742685	0.99999793	4.35	-0.13011673	-0.13011673
285	6	0.928958915	0.99999793	4.92	-0.12916025	-0.12916025
286	8	0.073465475	0.710624303	14.29	-0.129003985	-0.129003985
287	4	0.246707931	0.99999793	12.5	-0.128934989	-0.128934989
288	2	0.874387211	0.99999793	4.55	-0.128929587	-0.128929587
289	4	0.466402982	0.99999793	9.09	-0.128681113	-0.128681113
290	2	0.967461559	0.99999793	3.12	-0.128570744	-0.128570744
291	4	0.856164977	0.99999793	5.33	-0.128545894	-0.128545894
292	4	0.998322979	0.99999793	2.65	-0.12793801	-0.12793801
293	16	0.007797893	0.171924974	15.38	-0.127837192	-0.127837192
294	6	0.398773743	0.99999793	9.38	-0.127131862	-0.127131862
295	4	0.779227696	0.99999793	6.06	-0.126872989	-0.126872989
296	10	0.931377207	0.99999793	5.38	-0.126502065	-0.126502065
297	14	9.03E-05	0.005970563	25	-0.126459458	-0.126459458
298	6	0.340695433	0.99999793	10	-0.126355782	-0.126355782
299	6	0.062022042	0.70039526	16.67	-0.125630545	-0.125630545
300	8	0.71102088	0.99999793	6.9	-0.125584908	-0.125584908
301	8	0.041957105	0.555032562	16	-0.125541145	-0.125541145
302	4	0.686266831	0.99999793	6.9	-0.125497235	-0.125497235
303	4	0.178427395	0.954389149	14.29	-0.125470372	-0.125470372
304	6	0.178303905	0.954389149	12.5	-0.124886899	-0.124886899
305	4	0.466402982	0.99999793	9.09	-0.124824226	-0.124824226
306	12	0.474481533	0.99999793	8.33	-0.124687296	-0.124687296
307	2	0.622797749	0.99999793	7.69	-0.124537792	-0.124537792
308	2	0.857080857	0.99999793	4.76	-0.124385789	-0.124385789
309	9	0.85591599	0.99999793	5.96	-0.124075137	-0.124075137
310	4	0.501622356	0.99999793	8.7	-0.123511821	-0.123511821
311	6	0.112492545	0.789152247	14.29	-0.123094724	-0.123094724
312	4	0.178427395	0.954389149	14.29	-0.12298462	-0.12298462
313	16	6.44E-05	0.004967399	23.53	-0.122075997	-0.122075997
314	6	0.369692981	0.99999793	9.68	-0.122003303	-0.122003303
315	2	0.939538153	0.99999793	3.64	-0.121481932	-0.121481932
316	6	0.592795697	0.99999793	7.69	-0.121037593	-0.121037593
317	10	1.57E-05	0.002607465	38.46	-0.120710117	-0.120710117
318	6	0.963851563	0.99999793	4.41	-0.12002146	-0.12002146
319	4	0.856164977	0.99999793	5.33	-0.119396577	-0.119396577

Table 1.f2

	t	P.Value	adj.P.Val	B	FC	FC_1
260	-3.149031853	0.01005514500	0.032628994	-3.328767115	0.910438137	-1.098372266
261	-5.0414432	0.00046900800	0.003533752	-0.178184397	0.910471309	-1.098332248
262	-5.610750575	0.00020503800	0.002000516	0.683105065	0.910498033	-1.098300011
263	-3.981542416	0.00247280800	0.011523827	-1.899195685	0.910740807	-1.09800724
264	-4.354892024	0.00135270800	0.007473785	-1.276944573	0.910847214	-1.097878968
265	-3.915446617	0.00275663900	0.012498582	-2.010902308	0.91085916	-1.09786457
266	-6.002981158	0.00011906100	0.001397518	1.249399806	0.910948542	-1.097756848
267	-5.011745141	0.00049031700	0.003651403	-0.22438317	0.910970368	-1.097730547
268	-7.272499177	0.00002350000	0.000488496	2.935549576	0.911334202	-1.097292297
269	-5.919580786	0.00013341200	0.001506976	1.130832175	0.911804302	-1.096726565
270	-5.32199774	0.00031016400	0.002644833	0.252069164	0.911821913	-1.096705383

271	-6.487267552	0.00006260000	0.000907643	1.918501156	0.911825031	-1.096701632
272	-4.700405212	0.00078717700	0.005039991	-0.716093761	0.911872007	-1.096645134
273	-6.078653164	0.00010746800	0.001309762	1.356124071	0.911915438	-1.096592906
274	-6.29211388	0.00008080000	0.001077771	1.652820413	0.912177056	-1.096278396
275	-7.017751886	0.00003210000	0.000590507	2.61450293	0.912213756	-1.096234291
276	-6.269560727	0.00008330000	0.001098005	1.621775349	0.912277634	-1.096157533
277	-4.505737936	0.00106576100	0.006305461	-1.03019695	0.912555508	-1.095823751
278	-3.592674384	0.00472075700	0.018547070	-2.561861516	0.912644754	-1.095716593
279	-6.054125084	0.00011108700	0.001336285	1.32161983	0.912890936	-1.095421107
280	-3.959369224	0.00256445500	0.011843660	-1.936622527	0.913313223	-1.094914619
281	-5.313027786	0.00031423700	0.002670279	0.238487116	0.913352254	-1.09486783
282	-5.318017005	0.00031196500	0.002656279	0.246043076	0.91342574	-1.094779746
283	-7.189479005	0.00002600000	0.000519646	2.831839416	0.913628402	-1.094536901
284	-7.294936947	0.00002290000	0.000481540	2.963428677	0.913757514	-1.094382245
285	-4.103081237	0.00202785500	0.009963814	-1.694937692	0.914363519	-1.09365693
286	-5.508465599	0.00023709600	0.002203392	0.531792745	0.914462564	-1.093538478
287	-3.811259412	0.00327514400	0.014160524	-2.187814845	0.914506298	-1.093486181
288	-5.352279339	0.00029682400	0.002574803	0.297835331	0.914509723	-1.093482087
289	-3.685689982	0.00403801000	0.016534854	-2.402257893	0.914667241	-1.093293774
290	-6.22305225	0.00008860000	0.001147264	1.557530293	0.914737218	-1.093210138
291	-5.633416165	0.00019858300	0.001960017	0.716430725	0.914752974	-1.093191308
292	-3.056473063	0.01179465000	0.036808385	-3.489189991	0.915138489	-1.092730785
293	-2.485374714	0.03172122800	0.077306468	-4.4686147	0.915202443	-1.092654426
294	-2.581209623	0.02687197300	0.068079912	-4.306547541	0.915649992	-1.092120361
295	-4.83847752	0.00063702100	0.004371365	-0.496382047	0.915814309	-1.091924412
296	-4.919218514	0.00056357200	0.004023477	-0.369112955	0.9160498	-1.091643708
297	-4.254485223	0.00158809000	0.008387378	-1.442733094	0.916076853	-1.091611469
298	-5.139970533	0.00040509200	0.003180979	-0.02580694	0.916142688	-1.091533026
299	-4.39945421	0.00126030000	0.007108949	-1.20375598	0.916603345	-1.090984455
300	-4.704109135	0.00078269300	0.005020534	-0.710166036	0.91663234	-1.090949944
301	-5.122385245	0.00041578200	0.003234453	-0.052902519	0.916660146	-1.090916851
302	-3.32132345	0.00748217300	0.026196088	-3.030208996	0.916688046	-1.090883648
303	-5.658379001	0.00019172400	0.001913238	0.753048456	0.916705114	-1.090863337
304	-5.128181214	0.00041222600	0.003218804	-0.043967178	0.917075935	-1.090422245
305	-4.051920293	0.00220395800	0.010583936	-1.780731029	0.917115775	-1.090374876
306	-4.032457988	0.00227509500	0.010841231	-1.813440415	0.917202825	-1.090271391
307	-5.626658694	0.00020048400	0.001971776	0.706502825	0.917297878	-1.090158414
308	-5.6137313	0.00020417700	0.001994223	0.68749191	0.91739453	-1.09004356
309	-3.320634296	0.00749099100	0.026219939	-3.031402175	0.917592092	-1.089808869
310	-5.273154933	0.00033304700	0.002781909	0.177973048	0.917950446	-1.089383424
311	-5.618781302	0.00020272600	0.001985854	0.694921264	0.918215873	-1.089068518
312	-4.83756529	0.00063790700	0.004375282	-0.497825111	0.918285952	-1.088985406
313	-3.56192511	0.00497193600	0.019283080	-2.614747846	0.918864479	-1.088299769
314	-4.421253446	0.00121754200	0.006935681	-1.168042507	0.91891078	-1.088244933
315	-3.162143862	0.00983080300	0.032085012	-3.30603666	0.919242922	-1.087851727
316	-2.933230541	0.01459586800	0.043165204	-3.70250795	0.919526085	-1.087516728
317	-5.631541557	0.00019910800	0.001961946	0.713677259	0.919734832	-1.087269902
318	-5.084264999	0.00044000000	0.003375661	-0.111789333	0.920173963	-1.086751027
319	-5.397839603	0.00027789500	0.002452456	0.366444576	0.92057261	-1.086280419

Table 1.f3

			Probe sequence
	LS	Loop detected	60 mer
260	-1	PD-L1 responder	GTTTATCCCACACCCACCCTCATGTCTCTCGAATATGCGACGACGCACCCTCCCCTTGTT
261	-1	PD-L1 responder	ATCTTTTAATAGATAAGTGAAACTTTAATCGATATTTTCCAGCTATCTTTCTGTTGATTT
262	-1	PD-L1 responder	TGCTTTTTAAAAAATCAAAGGTGTAACTTCGACAGCTTCCGGAGGCTGCGAGGCTCGCAA
263	-1	PD-L1 responder	CTGGCGTTCCAGCCCTCGCACCTTGGCCTCGAACTTTACAGAGGGATCTAGAATGAGTGA
264	-1	PD-L1 responder	TGCCCAGAATGACCCCAACTAGGAACAATCGAAGGGTCCCCACTCCTCCACCTGCAGGAC
265	-1	PD-L1 responder	GCTTCTCCCCTCTTTATCCCACCTGGCCTCGAGCTCCTAAACTCACGCAATCCTTCCTTC
266	-1	PD-L1 responder	ATAATTGCCTAGCTTAGACTTGAATACCTCGACCTTATGCTAAGCCTAAACTTGCCTTCC
267	-1	PD-L1 responder	TTACCCTTTAAGTCAATGCCTCAAAAGTTCGATTGTCCCTTTTTTCCTGTGCCACCTTTT
268	-1	PD-L1 responder	GGGTTTCACTGTTTTAGCCAGGCTGGTTTCGAGCGGCCCGGTGCGCTGTGGGTTGGCCGC
269	-1	PD-L1 responder	GAGGCTTCTGAGTTGCTCTGAGGGTACATCGATGCGCGCCCGCCGGGGCCCGGTCGGAGC
270	-1	PD-L1 responder	ACCCCCTCCCAGCCTCCTGGTCAGGAGTTCGAGACATCTAAGAAGGTCCAGCCAGATGTT
271	-1	PD-L1 responder	GTATTTTGATGATAAAAGCTGAACAACTTCGATCTCAGGCTGTTGCACTTTCTCCATGGG
272	-1	PD-L1 responder	CTAGGAAGCTCACCATTCCCCCAAGGCCTCGAGCCACCGTGCTTCAGCTTGGACGACAGA
273	-1	PD-L1 responder	CTTGTTTGTGGTTGAAAATGACTGAATATCGATCGCACGCCTGAACTCCAGTCTTGGCAA
274	-1	PD-L1 responder	ATGAGCAAAGATAGCTCACGGGCTCTGCTCGAGTGTGACCGACGCTGCCCCTCACTTTCA
275	-1	PD-L1 responder	ACTCCATCTCAAAAAAACAAGAGCTTCCTCGAGTTGCAGGCCGCCCTGGTGGCTAGACAT
276	-1	PD-L1 responder	CCGCAATACACAGATTCTTTATTCCTATTCGATGTTTGGGGGCGGAGGGCTTTGATGAGA
277	-1	PD-L1 responder	GGGATTCACCATGATGGCCAGGCTGGTTTCGAGACCAGCCTGACCAACATGGTGAAACCC
278	-1	PD-L1 responder	GGCACCTGTTAGCAATGAAGGATAACCATCGATTCTGAACCAACGGCTTCCGCAAATCTT
279	-1	PD-L1 responder	TATTCTTTGTATATGAAAAGAATAATTCTCGAAGATGGAGGGACAGGGCCGCCTCTTCCT
280	-1	PD-L1 responder	GGCAAATGCTACAAATCAGAGTTGTTTTTCGATCACACTGGGAGCTGCAGACCGGAGCTG
281	-1	PD-L1 responder	TGAAATGAAACCTGCCCCGAGAATCACCTCGAGGCTCCCTCCTCCTAGCATGTGGCTTAA
282	-1	PD-L1 responder	GGCACCTGTTAGCAATGAAGGATAACCATCGATCTCAGGCTGTTGCACTTTCTCCATGGG
283	-1	PD-L1 responder	AGACTTTATTAGATAGGTATAAATGTTTTCGATACCAGCCTGGGCAACAAGACTCTTTGT

284	-1	PD-L1 responder	GTCCTAGGCCACGCCTTTAGACAGATCTTCGAAGCTTCTGTGGCTGTCTTTCAAGGGCAA
285	-1	PD-L1 responder	TGCCATTCCACTGAAAAAATGTACAGTTTCGACACCGTGAAGATCAACGAGACTGCTGCG
286	-1	PD-L1 responder	CGTGGATCCAGACTGGGAGCCCCCAGCCTCGAGAGCTCTGTGCTCCACGCCGAGGATGCA
287	-1	PD-L1 responder	GAGCTTGGACCCCCTCCTCTTCACCAGCTCGACCTGGGCCAGTGGCGGAGGGAGGCCCAG
288	-1	PD-L1 responder	GTCTGCTGCACGGGCCACCCTGCGGGCATCGAAGGATCCATAAAAGGTTAAGAAACATTT
289	-1	PD-L1 responder	TGCTTTTTAAAAAATCAAAGGTGTAACTTCGACAGCTTCCGGAGGCTGCGAGGCTCGCAA
290	-1	PD-L1 responder	CACGGGCGGCAGCACCCTTCATACGGGATCGAAAACCTGCTGCTAAGTGAGAGAAGTCAG
291	-1	PD-L1 responder	CTCTGTGCCGAAGCGGGGTGCCAGCCGCTCGAGTTCTAACAGGCTCCCACAGGGTCAGAT
292	-1	PD-L1 responder	AAAACACCTAAAATTAAGCAAAGTATTTTCGAAGTTGAAAACTACCCACCTTATTTTTAT
293	-1	PD-L1 responder	TCTTAGAGTTGAACTTTTCTAATCTTTTTCGACCTGCTGATCCTTGGATCCTGAATCTGT
294	-1	PD-L1 responder	GAGGCTAGCAGATCACAAGGTCAGGAGTTCGAAAACCAATGCAGAAATCAAGACTTTGTC
295	-1	PD-L1 responder	ATTCAATAAGAAAGAATGACTGTCACTTTCGAAACCCAGTGGATGATTCTAACTTCCCGG
296	-1	PD-L1 responder	GAGGATTTAATAAAACCCAAACTGTATTTCGAAGTAGTCGTGCCACCAGTAGCAGTGACA
297	-1	PD-L1 responder	TTCTGCGAGGGACCCCTCAGCCCGGGCATCGATTATCCAATAGAATTGTATCAGCATTAA
298	-1	PD-L1 responder	ACATGACCGTGATACCTCTGTCACTCTGTCGATCATTTGCGCCCAGGAGTTTGAGACCAG
299	-1	PD-L1 responder	GAAGGCCCGGTGCGCCCAGCTGTGCTCCTCGAGAACAGCCAGGCTAACACGGAGAAACCC
300	-1	PD-L1 responder	GACAAGCTGCACATCCCGGCGCTGACCCTCGAGGAAGTGAGGCTTAATTCCACTCCCTAC
301	-1	PD-L1 responder	GGGCAGAGAGATTTTTTGTATCTACTTCTCGAGAGCCGGCCTCCTGCCCTTTCTAAAGGC
302	-1	PD-L1 responder	GTTGGTGAAAAAGAAAGAAGAAATGGACTCGATGCTCTGCCTTCTTGTTTCAGCTCACAG
303	-1	PD-L1 responder	CCACTGGCTGATGAGGTCCTTTCCAGCCTCGAAGTGACCTCCGACCCTTTTATGTTTGAA
304	-1	PD-L1 responder	GAGTTCAGCGTGCCGCCGGGCGTGAAAGTCGAGACGATCCCGGCCAACATGGTGAAACCC
305	-1	PD-L1 responder	ATAAGCTGTCCTCGTGTGGACCCCGGCATCGACCCAGCCTTTTTCTGTTGACCGATGAGG
306	-1	PD-L1 responder	TCAGATAAGTAACTTCCTGATAATTAACTCGAAGTCTTTAACAGTAGCATAGAGATCATT
307	-1	PD-L1 responder	TTGGGTGATCTTATTCATGGCCTCTGCTTCGAGGCCGAGCTGGGGCCGATGAAGATGACA
308	-1	PD-L1 responder	TGGAAGCAGCTATACAGCTGTGACCACATCGACGCCCCTGTCACGGGCCCTGTTATTCAA
309	-1	PD-L1 responder	TCACCTTAGTGAAGGGAAGTCCATCAAATCGACTCACCAGTGAAGATAGTGTGCTCCACT

310	-1	PD-L1 responder	AAGTAAATTATGGTGTTAAAAACCACCATCGAGAGCGGCACGACCTGTGGGGACTGATGG
311	-1	PD-L1 responder	CCGCCTCCGTCTGCGCCTGGGCCAGGCCTCGAGAATTATTCTTTTCATATACAAAGAATA
312	-1	PD-L1 responder	ACTCCTCGCCTCAAAGGATTCTCCTATCTCGAAGTGACCTCCGACCCTTTTATGTTTGAA
313	-1	PD-L1 responder	GCACCCCACCCTGGATCCCTTGAAAGCCTCGACAATGTTATTCTTTGTTTCTCTTACCAA
314	-1	PD-L1 responder	CTGCCTCAGTTAGCAGGTTGCTTAGACATCGACGGGGCGGGTGGACGTGGAGCCACAGTT
315	-1	PD-L1 responder	ACCGCCTCACCTCAGCTCTCCAGTGAGATCGAGCAATTCTCTTGCCTTAGCCTCCTGAGT
316	-1	PD-L1 responder	AGGCTTTTAAAAGAAATAGAATATGAAATCGACTTCCTCGCGCTGTGCCTGATCCCAATC
317	-1	PD-L1 responder	CCGCAATACACAGATTCTTTATTCCTATTCGATGTTTGGGGGCGGAGGGCTTTGATGAGA
318	-1	PD-L1 responder	AGGTCCTTTCCCTGTCAAAATATGTATTTCGACTTCCCACCCCATGCAGCATCCTCTTAT
319	-1	PD-L1 responder	CTCTGTGCCGAAGCGGGGTGCCAGCCGCTCGAGCAAATGCAATTGGGGACTTTGTTTGTA

Table 1.f4

	Probe Location					**4 kb Sequence Location**	
	Chr	**Start1**	**End1**	**Start2**	**End2**	**Chr**	**Start1**
260	16	30117118	30117147	30165833	30165862	16	30113148
261	6	151760870	151760899	151928861	151928890	6	151760870
262	9	21967883	21967912	22034008	22034037	9	21967883
263	11	60922071	60922100	60977086	60977115	11	60922071
264	21	44209219	44209248	44251679	44251708	21	44209219
265	1	3615781	3615810	3642154	3642183	1	3611811
266	1	56902222	56902251	56932215	56932244	1	56902222
267	5	38976285	38976314	39046925	39046954	5	38976285
268	8	55939617	55939646	55966556	55966585	8	55939617
269	11	119714016	119714045	119729290	119729319	11	119710046
270	20	1849968	1849997	1924635	1924664	20	1849968
271	4	77503294	77503323	77524480	77524509	4	77503294
272	1	11157137	11157166	11228220	11228249	1	11153167
273	12	68159450	68159479	68183650	68183679	12	68159450
274	19	51200118	51200147	51238012	51238041	19	51200118
275	20	2873117	2873146	2989420	2989449	20	2873117
276	5	157254072	157254101	157266727	157266756	5	157250102
277	1	32254318	32254347	32281862	32281891	1	32254318
278	4	77583786	77583815	77598216	77598245	4	77579816
279	12	6813427	6813456	6829194	6829223	12	6813427
280	10	96186300	96186329	96286444	96286473	10	96186300
281	6	379281	379310	400030	400059	6	379281
282	4	77524480	77524509	77583786	77583815	4	77524480
283	11	77437812	77437841	77494416	77494445	11	77433842
284	3	108038612	108038641	108112860	108112889	3	108038612
285	13	111152436	111152465	111182145	111182174	13	111148466
286	19	47240983	47241012	47275386	47275415	19	47237013
287	1	3610197	3610226	3718055	3718084	1	3606227

288	19	41852823	41852852	41898310	41898339	19	41852823
289	9	21967883	21967912	22034008	22034037	9	21967883
290	12	124897707	124897736	124947618	124947647	12	124897707
291	19	10365707	10365736	10416041	10416070	19	10361737
292	6	149231681	149231710	149369217	149369246	6	149227711
293	15	98652567	98652596	98957434	98957463	15	98652567
294	4	102539003	102539032	102577395	102577424	4	102535033
295	10	96209099	96209128	96290527	96290556	10	96205129
296	4	85995511	85995540	86131385	86131414	4	85995511
297	11	60924995	60925024	60983696	60983725	11	60921025
298	16	2548487	2548516	2569274	2569303	16	2544517
299	7	155803156	155803185	155837731	155837760	7	155799186
300	19	18110333	18110362	18179079	18179108	19	18106363
301	10	88964635	88964664	88990388	88990417	10	88960665
302	18	62304781	62304810	62353459	62353488	18	62300811
303	10	70591314	70591343	70645617	70645646	10	70591314
304	15	74754973	74755002	74772374	74772403	15	74751003
305	5	149367708	149367737	149416536	149416565	5	149367708
306	8	80976749	80976778	81018076	81018105	8	80976749
307	6	32954635	32954664	32978239	32978268	6	32954635
308	22	17735513	17735542	17806908	17806937	22	17731543
309	1	56923835	56923864	56991333	56991362	1	56919865
310	6	167107658	167107687	167149744	167149773	6	167103688
311	12	6773968	6773997	6813427	6813456	12	6769998
312	10	70635521	70635550	70645617	70645646	10	70631551
313	1	6484217	6484246	6494590	6494619	1	6480247
314	5	140643800	140643829	140673118	140673147	5	140643800
315	11	119243829	119243858	119299612	119299641	11	119243829
316	9	90767522	90767551	90802232	90802261	9	90763552
317	5	157254072	157254101	157266727	157266756	5	157250102
318	11	77360422	77360451	77413950	77413979	11	77356452
319	19	10346000	10346029	10365707	10365736	19	10346000

Table 1.f5

	4 kb Sequence Location		
	End1	Start2	End2
260	30117147	30161863	30165862
261	151764869	151928861	151932860
262	21971882	22030038	22034037
263	60926070	60977086	60981085
264	44213218	44251679	44255678
265	3615810	3638184	3642183
266	56906221	56928245	56932244
267	38980284	39042955	39046954
268	55943616	55962586	55966585
269	119714045	119729290	119733289
270	1853967	1924635	1928634
271	77507293	77524480	77528479
272	11157166	11224250	11228249
273	68163449	68183650	68187649
274	51204117	51234042	51238041
275	2877116	2985450	2989449

276	157254101	157266727	157270726
277	32258317	32281862	32285861
278	77583815	77594246	77598245
279	6817426	6829194	6833193
280	96190299	96282474	96286473
281	383280	396060	400059
282	77528479	77579816	77583815
283	77437841	77490446	77494445
284	108042611	108108890	108112889
285	111152465	111178175	111182174
286	47241012	47275386	47279385
287	3610226	3714085	3718084
288	41856822	41894340	41898339
289	21971882	22030038	22034037
290	124901706	124943648	124947647
291	10365736	10416041	10420040
292	149231710	149365247	149369246
293	98656566	98957434	98961433
294	102539032	102577395	102581394
295	96209128	96290527	96294526
296	85999510	86127415	86131414
297	60925024	60979726	60983725
298	2548516	2569274	2573273
299	155803185	155833761	155837760
300	18110362	18179079	18183078
301	88964664	88986418	88990417
302	62304810	62349489	62353488
303	70595313	70645617	70649616
304	74755002	74772374	74776373
305	149371707	149412566	149416565
306	80980748	81014106	81018105
307	32958634	32978239	32982238
308	17735542	17802938	17806937
309	56923864	56991333	56995332
310	167107687	167149744	167153743
311	6773997	6813427	6817426
312	70635550	70645617	70649616
313	6484246	6494590	6498589
314	140647799	140673118	140677117
315	119247828	119295642	119299641
316	90767551	90798262	90802261
317	157254101	157266727	157270726
318	77360451	77413950	77417949
319	10349999	10361737	10365736

Table 1.f6

	probe	GeneLocus	Probe_Count_Total
320	ORF501_5_68187850_68194388_68258878_68268897_FF	PIK3R1	148
321	ORF250_2_215347261_215350354_215361328_215366837_RF	FN1	42
322	TNFRSF19_13_23643081_23657941_23678002_23680230_RR	TNFRSF19	60
323	TNFRSF19_13_23612221_23617919_23678002_23680230_RR	TNFRSF19	60

324	ORF312_16_88606860_88608937_88633762_88637512_RR	IL17C	40
325	ORF366_16_28975508_28978445_28988508_28993162_RR	LAT	58
326	ORF73_10_96204016_96209130_96290525_96304713_FF	BLNK	66
327	ORF490_16_2543954_2548518_2569272_2571597_FR	PDPK1	60
328	TYROBP_19_35889288_35891587_35942103_35947317_FF	TYROBP	50
329	CCL18_17_36023309_36028028_36075902_36084513_FR	CCL18	42
330	ORF173_4_77571558_77583817_77605999_77607786_FF	CXCL13	108
331	ORF543_20_2873115_2878192_2940645_2944261_RR	PTPRA	82
332	ORF463_4_102577393_102582880_102627099_102634363_FR	NFKB1	64
333	ARHGEF7_13_111255999_111262146_111317973_111320769_RR	ARHGEF7	122
334	BAD_11_64267793_64269811_64288581_64290103_FR	BAD	70
335	ORF112_5_140643798_140647427_140680993_140683629_FF	CD14	62
336	ORF658_17_42251917_42254441_42312276_42316438_FR	STAT5A	99
337	ORF133_17_63937911_63939713_63953850_63955210_FR	CD79B	20
338	ORF701_13_23612221_23617919_23627958_23632852_FR	TNFRSF19	60
339	ORF402_16_30100267_30104814_30117766_30120768_RR	MAPK3	44
340	PTPRA_20_2816709_2821045_2986126_2989451_RF	PTPRA	82
341	ORF401_4_86050968_86053502_86086215_86098061_FF	MAPK10	186
342	ORF168_15_74750296_74755004_74782868_74787702_FF	CSK	48
343	ORF705_9_114882931_114894596_114920994_114929419_RR	TNFSF8	50
344	BAD_11_64267793_64269811_64301867_64303120_FR	BAD	70
345	ORF587_17_80636056_80643737_80939071_80942385_FF	RPTOR	86
346	ORF173_4_77571558_77583817_77602626_77605431_FR	CXCL13	108
347	ORF542_12_6934234_6935639_6946597_6948368_RR	PTPN6	46
348	ORF143_9_22005915_22007157_22029989_22034039_RR	CDKN2A	44
349	ORF113_5_67178844_67182260_67231162_67233989_FR	CD180	38
350	IRF1_5_132472660_132477912_132527799_132529394_FR	IRF1	42
351	ORF58_19_47205563_47207855_47236830_47241014_RF	BBC3	56
352	ORF104_17_36075902_36084513_36106111_36108394_RF	CCL18	42
353	AKT1_14_104800011_104801022_104839372_104843321_RF	AKT1	60
354	ITK_5_157113872_157116385_157266725_157271762_FR	ITK	26
355	ORF531_22_44658236_44661757_44696835_44701888_RF	PRR5	64
356	ORF305_15_98642083_98644969_98874707_98883774_FR	IGF1R	104
357	IGF2_11_2141386_2143749_2170498_2173159_FR	IGF2	32
358	ORF703_1_6461604_6466207_6514024_6515315_RR	TNFRSF25	68
359	ORF401_4_86086215_86098061_86316594_86322797_FR	MAPK10	186
360	ORF401_4_86098061_86104840_86327055_86336679_FF	MAPK10	186

Table 1.g1

	Probe_Count_Sig	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr
320	12	0.513477047	0.99999793	8.11	-0.11882825	-0.11882825
321	4	0.430324418	0.99999793	9.52	-0.118808326	-0.118808326
322	8	0.100733588	0.781478358	13.33	-0.118340655	-0.118340655
323	8	0.100733588	0.781478358	13.33	-0.118259243	-0.118259243
324	2	0.837619347	0.99999793	5	-0.117868499	-0.117868499
325	4	0.686266831	0.99999793	6.9	-0.117762431	-0.117762431
326	4	0.779227696	0.99999793	6.06	-0.117391959	-0.117391959
327	6	0.340695433	0.99999793	10	-0.117182824	-0.117182824
328	2	0.915356314	0.99999793	4	-0.117179185	-0.117179185
329	8	0.016095432	0.256971894	19.05	-0.117094871	-0.117094871
330	14	0.046569042	0.598929617	12.96	-0.117077567	-0.117077567
331	8	0.325435728	0.99999793	9.76	-0.11662568	-0.11662568

332	6	0.398773743	0.99999793	9.38	-0.116513518	-0.116513518
333	6	0.928958915	0.99999793	4.92	-0.116248719	-0.116248719
334	8	0.18964104	0.954389149	11.43	-0.116128982	-0.116128982
335	6	0.369692981	0.99999793	9.68	-0.116023993	-0.116023993
336	3	0.987493488	0.99999793	3.03	-0.11591907	-0.11591907
337	2	0.479107134	0.99999793	10	-0.115917608	-0.115917608
338	8	0.100733588	0.781478358	13.33	-0.11572367	-0.11572367
339	4	0.466402982	0.99999793	9.09	-0.115670925	-0.115670925
340	8	0.325435728	0.99999793	9.76	-0.115508213	-0.115508213
341	10	0.931377207	0.99999793	5.38	-0.115273143	-0.115273143
342	6	0.178303905	0.954389149	12.5	-0.11493711	-0.11493711
343	4	0.568728839	0.99999793	8	-0.114816222	-0.114816222
344	8	0.18964104	0.954389149	11.43	-0.11476243	-0.11476243
345	6	0.687444338	0.99999793	6.98	-0.114623135	-0.114623135
346	14	0.046569042	0.598929617	12.96	-0.114256917	-0.114256917
347	4	0.501622356	0.99999793	8.7	-0.113829612	-0.113829612
348	4	0.466402982	0.99999793	9.09	-0.113818103	-0.113818103
349	4	0.356577228	0.99999793	10.53	-0.113814422	-0.113814422
350	8	0.016095432	0.256971894	19.05	-0.113325615	-0.113325615
351	8	0.073465475	0.710624303	14.29	-0.113310708	-0.113310708
352	8	0.016095432	0.256971894	19.05	-0.113014974	-0.113014974
353	4	0.711822793	0.99999793	6.67	-0.112838336	-0.112838336
354	10	1.57E-05	0.002607465	38.46	-0.112451827	-0.112451827
355	4	0.7582782	0.99999793	6.25	-0.112451732	-0.112451732
356	16	0.007797893	0.171924974	15.38	-0.11237057	-0.11237057
357	6	0.037675475	0.528598335	18.75	-0.111918978	-0.111918978
358	16	6.44E-05	0.004967399	23.53	-0.111885742	-0.111885742
359	10	0.931377207	0.99999793	5.38	-0.111716151	-0.111716151
360	10	0.931377207	0.99999793	5.38	-0.111190729	-0.111190729

Table 1.g2

	t	P.Value	adj.P.Val	B	FC	FC_1
320	-3.28569851	0.00795229900	0.027348446	-3.091904234	0.920935326	-1.08585258
321	-5.515807304	0.00023462500	0.002190731	0.542703708	0.920948045	-1.085837584
322	-5.826586351	0.00015163300	0.001635661	0.997453523	0.921246632	-1.085485651
323	-5.468019963	0.00025121700	0.002297775	0.471544728	0.92129862	-1.085424398
324	-4.149900419	0.00187961300	0.009459704	-1.616672944	0.921548181	-1.085130459
325	-5.560189598	0.00022026300	0.002097026	0.608497575	0.921615937	-1.085050681
326	-2.849923133	0.01686220500	0.048027440	-3.846341043	0.92185263	-1.084772085
327	-4.624546759	0.00088526700	0.005497061	-0.837900587	0.921986273	-1.084614847
328	-4.850787441	0.00062519600	0.004318657	-0.476920106	0.921988599	-1.084612111
329	-5.670796723	0.00018840600	0.001897248	0.771230471	0.922042483	-1.084548726
330	-4.321578858	0.00142644200	0.007770947	-1.331816291	0.922053542	-1.084535718
331	-5.531878455	0.00022931200	0.002158503	0.566560929	0.922342397	-1.084196068
332	-3.011085086	0.01275662000	0.038978718	-3.567805275	0.922414107	-1.084111781
333	-2.85057896	0.01684304500	0.047979425	-3.845210285	0.922583427	-1.083912816
334	-4.025458886	0.00230126300	0.010935916	-1.825213078	0.92266	-1.08382286
335	-3.603776786	0.00463332800	0.018277657	-2.542780708	0.922727147	-1.08374399
336	-5.245214347	0.00034694100	0.002861465	0.135432481	0.922794256	-1.083665176
337	-3.614904266	0.00454738300	0.018046224	-2.523664746	0.922795192	-1.083664077
338	-6.491621867	0.00006230000	0.000903821	1.924369043	0.922919249	-1.083518413
339	-4.570910561	0.00096238300	0.005851655	-0.924484832	0.922952992	-1.0834788

340	-4.368296497	0.00132418300	0.007358200	-1.254903515	0.923057091	-1.083356609
341	-2.392253605	0.03725465400	0.087236543	-4.624664393	0.923207505	-1.083180103
342	-3.586023328	0.00477395000	0.018706685	-2.57329588	0.923422564	-1.082927837
343	-4.50464524	0.00106759100	0.006313971	-1.031974008	0.923499943	-1.082837099
344	-4.136140891	0.00192196100	0.009605427	-1.639648926	0.923534378	-1.082796725
345	-3.091482075	0.01110326500	0.035177499	-3.428523652	0.923623551	-1.082692184
346	-3.936906064	0.00266092900	0.012188053	-1.974587934	0.923858036	-1.082417386
347	-5.350503047	0.00029759000	0.002579295	0.295154367	0.924131709	-1.082096837
348	-3.781820935	0.00343937900	0.014676164	-2.237974722	0.924139082	-1.082088205
349	-6.848194152	0.00003960000	0.000673517	2.396134025	0.92414144	-1.082085444
350	-6.471854762	0.00006390000	0.000919240	1.897709884	0.924454606	-1.081718879
351	-5.120964583	0.00041665800	0.003238646	-0.055093408	0.924464158	-1.081707702
352	-3.992024269	0.00243068300	0.011377126	-1.881520038	0.924653681	-1.081485988
353	-2.287328866	0.04462249800	0.099984429	-4.798481305	0.924766899	-1.081353584
354	-4.745750173	0.00073410000	0.004795176	-0.643651395	0.925014684	-1.081063919
355	-3.502877434	0.00549380500	0.020792455	-2.716459446	0.925014745	-1.081063848
356	-5.696914179	0.00018162800	0.001849178	0.809399196	0.925066785	-1.081003032
357	-3.235990306	0.00865942800	0.029201748	-3.178032026	0.925356395	-1.08066471
358	-5.236400527	0.00035145200	0.002884770	0.121989924	0.925377713	-1.080639815
359	-3.160153052	0.00986453300	0.032155286	-3.309487854	0.925486499	-1.080512791
360	-2.563478976	0.02771024400	0.069657481	-4.336632301	0.925823617	-1.080119346

Table 1.g3

			Probe sequence
	LS	Loop detected	**60 mer**
320	-1	PD-L1 responder	CTGAGTCTTCATTACCAAAAAAAAAAGTTCGACAGTCCTTGGGCACCAGCGGTGTGTGGG
321	-1	PD-L1 responder	GTAATAAACATACAAACTTAAACGTAGTTCGAGGTGCCTGCCACCACGTCATGCATGGTG
322	-1	PD-L1 responder	TTTGGTACTGACAGAACATTACTCTGGATCGAGCACAGCGCCGGCTGGGGTACCTGGCAC
323	-1	PD-L1 responder	AAAGAGGGAAAACAGCTGAAAGGGAAGCTCGAGCACAGCGCCGGCTGGGGTACCTGGCAC
324	-1	PD-L1 responder	CTCCAGCGATGGGTGGCTACGAACACCCTCGATGGGCGTCCACGCCCTCCAGGGACGTCC
325	-1	PD-L1 responder	GCTACTGTCCCCGATGTTGAAGAACTGCTCGAGACTGACCTGGCCAACATGGCGAAACCC
326	-1	PD-L1 responder	ATTCAATAAGAAAGAATGACTGTCACTTTCGATGCTGTCCTACCTGAGCTCATTTTCAAC
327	-1	PD-L1 responder	ACATGACCGTGATACCTCTGTCACTCTGTCGATCATTTGCGCCCAGGAGTTTGAGACCAG
328	-1	PD-L1 responder	ATACTGAGGTTTAAAAAGTTCTTTTTTTTCGAAACACTATGCCCCTGCTCCTAGGCCCCT
329	-1	PD-L1 responder	TGAGCTAATAAACTATTTCTGGTTTTGCTCGAGCCATCCTCCCAGTGACACTCCGCAAAG
330	-1	PD-L1 responder	GGCACCTGTTAGCAATGAAGGATAACCATCGATCAATGAAGCGTCTAGGGATAAAGACTG
331	-1	PD-L1 responder	ATGTCTAGCCACCAGGGCGGCCTGCAACTCGACCTCCCAGGCTCATGGGATCCTCCTGTC
332	-1	PD-L1 responder	TGTGATTGTTTGCAGATGACATCCAGATTCGATATTTTACATGGAATCTTTCCCTTTTTA

333	-1	PD-L1 responder	CTATTTTAGGAAAAAAATAATTAAAATATCGATTACATCGGCAAAGACCCTATTTCCAAA
334	-1	PD-L1 responder	GCACTACCCCGGCCTGCCGGAGCCCCAGTCGATGATGGCTTCCTCCCCCAGAGCACCAGC
335	-1	PD-L1 responder	GCGGGGGCTTCCCTCAACTTCAGGGAGGTCGAACCCCTGACCTCAGGCAATCCATCTGCC
336	-1	PD-L1 responder	TTCCATAGATTACTTTTCAAATCATCCTTCGAAGCTGGCGGCTGAGGGCCCGGCGCCAAG
337	-1	PD-L1 responder	TGGGCCTTCCCTGCTGCACGCCCCAGGGTCGAACCAGGATTCTAGTCATTGTATAACTTT
338	-1	PD-L1 responder	GCACTACAGACAAAAGACTCTAACTGGATCGATCCTCATTTTTATAATAGGTAAACATTC
339	-1	PD-L1 responder	TCCTGAAATGAACAGGTCATCTGCCTATTCGATGGACTTGGTATAGCCCTGGGGGAGAGG
340	-1	PD-L1 responder	ACTCCATCTCAAAAAAACAAGAGCTTCCTCGAACTGGCGGCAACCGCTGCAGCGCCTGCT
341	-1	PD-L1 responder	TTCCCCAATTTTGTAGCCTCTACTTATCTCGACACTAAATCAAGTCTTTAACAGGTCAAT
342	-1	PD-L1 responder	GAGTTCAGCGTGCCGCCGGGCGTGAAAGTCGACTCTGGGCCCAGACCACAGAAGGAGGGG
343	-1	PD-L1 responder	GGGGCCTGGCCCAGGCCTAGCCCTGAGCTCGAGTAATACTGACACTCCTGGCCCACAGAA
344	-1	PD-L1 responder	GCACTACCCCGGCCTGCCGGAGCCCCAGTCGACATGTTGCCCCAGCTGGTCTCAAACTCC
345	-1	PD-L1 responder	CTTTTCCATTGCTTCCTCAGATCCTCTGTCGAATGCCGGCTCTGTTTCGCACCCTGCTCA
346	-1	PD-L1 responder	GGCACCTGTTAGCAATGAAGGATAACCATCGATTCCAAAGTGAAGCAAAAAAAAAACTTC
347	-1	PD-L1 responder	CTGACCCCTCCAGGGGAGGCCCGGCCCCTCGAGGAGGAAGTGGCTGATTACTGAGCGGTT
348	-1	PD-L1 responder	CCCAATTTCCCACCCCCACCCACCTAATTCGATTTTAAGTCTATTTTGTTAGATCTAAAG
349	-1	PD-L1 responder	GACCTAAGGATTAAGAAGATTAATGGAGTCGAACTAATCTTGCATTCCTAGGATGATACC
350	-1	PD-L1 responder	GTGTCTCGGCCCCCTGGGGCCCCACCCTTCGAACATTACAACCTAATCTGTGCCCACACA
351	-1	PD-L1 responder	CGTGGATCCAGACTGGGAGCCCCCAGCCTCGAGCAGGATTCTGAGGCTCCCTGTAGACAA
352	-1	PD-L1 responder	AGCAATTACAAACAGCAGAATGGAATCCTCGAGCCATCCTCCCAGTGACACTCCGCAAAG
353	-1	PD-L1 responder	TAGGCCTGGGGGCCGAAAGGAAGAAGCTTCGACATCCTGCTTGAATGTTTGGAAGAGGGT
354	-1	PD-L1 responder	TGCTCCTGCCTGAGTAACTAAATGTCTTTCGATGTTTGGGGGCGGAGGGCTTTGATGAGA
355	-1	PD-L1 responder	CTGTGGAGGGAGACCTCCGGGGCCGGGGTCGATCATCCATGTAGAAGACGCTAAGGAATC
356	-1	PD-L1 responder	TGTCTTTTGATTTTTGTCTTAAATTGCATCGAAGACCCCTTCCATTGGGCATTCATCTAA
357	-1	PD-L1 responder	TAACGTCCAAGAAAATTATTGTGACCCGTCGATCCCAGAGCCGTCCCAGGCCTGGACAGA
358	-1	PD-L1 responder	CGCACGCTGGGGCTGCGCGAGGCAGAGATCGAGAAGCATAAAGCAGGGACAGGTATGGAG

359	-1	PD-L1 responder	ATTGACCTGTTAAAGACTTGATTTAGTGTCGAAATAAGACATAAAAGCAAAGCATTTTGC
360	-1	PD-L1 responder	ATGACCTTGTTTTATTACTTTTTACTCTTCGAGGAGAATGTTGAGCAGAAATATGGAATA

Table 1.g4

	Probe Location					**4 kb Sequence Location**	
	Chr	**Start1**	**End1**	**Start2**	**End2**	**Chr**	**Start1**
320	5	68194357	68194386	68268866	68268895	5	68190387
321	2	215347263	215347292	215366806	215366835	2	215347263
322	13	23643083	23643112	23678004	23678033	13	23643083
323	13	23612223	23612252	23678004	23678033	13	23612223
324	16	88606862	88606891	88633764	88633793	16	88606862
325	16	28975510	28975539	28988510	28988539	16	28975510
326	10	96209099	96209128	96304682	96304711	10	96205129
327	16	2548487	2548516	2569274	2569303	16	2544517
328	19	35891556	35891585	35947286	35947315	19	35887586
329	17	36027997	36028026	36075904	36075933	17	36024027
330	4	77583786	77583815	77607755	77607784	4	77579816
331	20	2873117	2873146	2940647	2940676	20	2873117
332	4	102582849	102582878	102627101	102627130	4	102578879
333	13	111256001	111256030	111317975	111318004	13	111256001
334	11	64269780	64269809	64288583	64288612	11	64265810
335	5	140647396	140647425	140683598	140683627	5	140643426
336	17	42254410	42254439	42312278	42312307	17	42250440
337	17	63939682	63939711	63953852	63953881	17	63935712
338	13	23617888	23617917	23627960	23627989	13	23613918
339	16	30100269	30100298	30117768	30117797	16	30100269
340	20	2816711	2816740	2989420	2989449	20	2816711
341	4	86053471	86053500	86098030	86098059	4	86049501
342	15	74754973	74755002	74787671	74787700	15	74751003
343	9	114882933	114882962	114920996	114921025	9	114882933
344	11	64269780	64269809	64301869	64301898	11	64265810
345	17	80643706	80643735	80942354	80942383	17	80639736
346	4	77583786	77583815	77602628	77602657	4	77579816
347	12	6934236	6934265	6946599	6946628	12	6934236
348	9	22005917	22005946	22029991	22030020	9	22005917
349	5	67182229	67182258	67231164	67231193	5	67178259
350	5	132477881	132477910	132527801	132527830	5	132473911
351	19	47205565	47205594	47240983	47241012	19	47205565
352	17	36075904	36075933	36108363	36108392	17	36075904
353	14	104800013	104800042	104843290	104843319	14	104800013
354	5	157116354	157116383	157266727	157266756	5	157112384
355	22	44658238	44658267	44701857	44701886	22	44658238
356	15	98644938	98644967	98874709	98874738	15	98640968
357	11	2143718	2143747	2170500	2170529	11	2139748
358	1	6461606	6461635	6514026	6514055	1	6461606
359	4	86098030	86098059	86316596	86316625	4	86094060
360	4	86104809	86104838	86336648	86336677	4	86100839

Table 1.g5

	4 kb Sequence Location		
	End1	Start2	End2
320	68194386	68264896	68268895
321	215351262	215362836	215366835
322	23647082	23678004	23682003
323	23616222	23678004	23682003
324	88610861	88633764	88637763
325	28979509	28988510	28992509
326	96209128	96300712	96304711
327	2548516	2569274	2573273
328	35891585	35943316	35947315
329	36028026	36075904	36079903
330	77583815	77603785	77607784
331	2877116	2940647	2944646
332	102582878	102627101	102631100
333	111260000	111317975	111321974
334	64269809	64288583	64292582
335	140647425	140679628	140683627
336	42254439	42312278	42316277
337	63939711	63953852	63957851
338	23617917	23627960	23631959
339	30104268	30117768	30121767
340	2820710	2985450	2989449
341	86053500	86094060	86098059
342	74755002	74783701	74787700
343	114886932	114920996	114924995
344	64269809	64301869	64305868
345	80643735	80938384	80942383
346	77583815	77602628	77606627
347	6938235	6946599	6950598
348	22009916	22029991	22033990
349	67182258	67231164	67235163
350	132477910	132527801	132531800
351	47209564	47237013	47241012
352	36079903	36104393	36108392
353	104804012	104839320	104843319
354	157116383	157266727	157270726
355	44662237	44697887	44701886
356	98644967	98874709	98878708
357	2143747	2170500	2174499
358	6465605	6514026	6518025
359	86098059	86316596	86320595
360	86104838	86332678	86336677

Table 1.g6

	GeneLocus	Probe_Count_Total	Probe_Count_Sig	HyperG_Stats	FDR_HyperG	Percent_Sig
1	PLEKHG5	61	16	0.0000150989812546337	0.00260746509581861	26.23
2	TNFRSF25	68	16	0.0000643723460057543	0.00496739936677737	23.53
3	IGF1R	104	16	0.0077978929721586500	0.1719249736242600	15.38
4	CD6	56	14	0.0000902676865389941	0.00597056269536490	25

5	CXCL13	108	14	0.0465690415089977000	0.59892961718516500	12.96
6	ESPN	74	13	0.0051548594302418800	0.12817437438629700	17.57
7	IKBKB	46	12	0.0001836303678197500	0.01062760753756800	26.09
8	PAG1	144	12	0.4744815327484530000	0.99999793037206300	8.33
9	PIK3R1	148	12	0.5134770470327030000	0.99999793037206300	8.11
10	PTK2	248	12	0.9797792860301600000	0.99999793037206300	4.84
11	SLC15A3	34	11	0.0000393466912660957	0.00364350361124046	32.35
12	NOL9	41	11	0.0002590590457356080	0.01209080667757340	26.83
13	ITK	26	10	0.0000157274410598937	0.00260746509581861	38.46
14	TMEM132A	28	10	0.0000335363454334773	0.00364350361124046	35.71
15	BOK	44	10	0.0019694080241128800	0.07598632626368880	22.73
16	MAPK10	186	10	0.9313772067444170000	0.99999793037206300	5.38
17	PTPRC	214	10	0.9784912428998600000	0.99999793037206300	4.67
18	THAP4	38	9	0.0024177875111874500	0.08611043212921460	23.68

Table 2.a

	GeneLocus	Probe_ Count_ Total	Probe_ Count_ Sig	HyperG_Stats	FDR_HyperG	Percent_ Sig
19	C8B	151	9	0.855915990410304000	0.9999979303720630	5.96
20	TMEM239	24	8	0.000359183930018026	0.0151183781453042	33.33
21	STAMBPL1	35	8	0.005252298370397750	0.1281743743862970	22.86
22	CCDC9	37	8	0.007481143494126220	0.1719249736242600	21.62
23	CYFIP2	40	8	0.012066037542322000	0.2234630152838030	20
24	ICOSLG	40	8	0.012066037542322000	0.2234630152838030	20
25	ITGAX	41	8	0.013975308160204600	0.2396506547472120	19.51
26	CCL18	42	8	0.016095431795565600	0.2569718938395470	19.05
27	IRF1	42	8	0.016095431795565600	0.2569718938395470	19.05
28	ACTA2	48	8	0.033871482209146300	0.5058869762204760	16.67
29	FAS	50	8	0.041957105143561900	0.5550325623276900	16
30	ITGAM	50	8	0.041957105143561900	0.5550325623276900	16
31	BBC3	56	8	0.073465474806733000	0.7106243027906220	14.29
32	PRDX5	57	8	0.079810936814497600	0.7106243027906220	14.04
33	TRMT112	57	8	0.079810936814497600	0.7106243027906220	14.04
34	PLCB3	58	8	0.086471735887070700	0.7554040323719570	13.79
35	TNFRSF19	60	8	0.100733588397967000	0.7814783579039930	13.33
36	ESRRA	64	8	0.132924777221067000	0.8316779980182970	12.5
37	BAD	70	8	0.189641040334946000	0.9543891486421730	11.43
38	GPR137	70	8	0.189641040334946000	0.95438914864217300	11.43
39	KCNK4	70	8	0.189641040334946000	0.95438914864217300	11.43
40	TEX40	70	8	0.189641040334946000	0.95438914864217300	11.43
41	C8A	166	8	0.957766442168891000	0.99999793037206300	4.82
42	PIK3R2	116	8	0.711020879711135000	0.99999793037206300	6.9
43	PTPRA	82	8	0.325435728472061000	0.99999793037206300	9.76
44	PVRL1	96	8	0.497039718077448000	0.99999793037206300	8.33
45	STK25	28	7	0.005259855536370700	0.12817437438629700	25
46	CCL4	32	7	0.011323324912557700	0.22346301528380300	21.88
47	CCL3	33	7	0.013410837025657200	0.23881605934151000	21.21
48	SAE1	53	7	0.124484434023389000	0.83167799801829700	13.21
49	PRPF19	9	6	0.000016895022219127	0.00260746509581861	66.67
50	TMEM109	13	6	0.000261140532992945	0.01209080667757340	46.15
51	C5AR1	20	6	0.003637021795314110	0.10524631820190200	30

52	INAFM1	20	6	0.003637021795314110	0.10524631820190200	30
53	TH	20	6	0.003637021795314110	0.10524631820190200	30
54	INS	24	6	0.009607292033915510	0.20218982780467700	25
55	IGF2	32	6	0.037675475247509100	0.52859833453323400	18.75
56	INS-IGF2	32	6	0.037675475247509100	0.52859833453323400	18.75
57	C5orf56	36	6	0.062022042427259000	0.70039525960538800	16.67
58	HARS2	36	6	0.062022042427259000	0.70039525960538800	16.67
59	SHH	36	6	0.062022042427259000	0.70039525960538800	16.67
60	CYP1A2	38	6	0.077003035039102400	0.71062430279062200	15.79
61	GPR162	41	6	0.102947013034154000	0.78147835790399300	14.63
62	CD4	42	6	0.112492544866268000	0.78915224656185100	14.29
63	PHF19	42	6	0.1124925448662680	0.789152246561851	14.29
64	TRAF1	42	6	0.1124925448662680	0.789152246561851	14.29
65	DND1	43	6	0.1224692325513000	0.831677998018297	13.95

Table 2.b

	GeneLocus	Probe_Count_Total	Probe_Count_Sig	HyperG_Stats	FDR_HyperG	Percent_Sig
66	FKBP2	44	6	0.1328638379525590	0.831677998018297	13.64
67	HARS	43	6	0.1224692325513000	0.831677998018297	13.95
68	PPP1R14B	44	6	0.1328638379525590	0.831677998018297	13.64
69	CSK	48	6	0.1783039053731780	0.954389148642173	12.5
70	WDR55	47	6	0.1663997350749940	0.954389148642173	12.77
71	CD82	50	6	0.2030836877588850	0.988148591681669	12
72	ARHGEF7	122	6	0.9289589150111290	0.999997930372063	4.92
73	CD14	62	6	0.3696929812329760	0.999997930372063	9.68
74	IK	54	6	0.2559285532533580	0.999997930372063	11.11
75	MAPKAP1	52	6	0.2290176352787400	0.999997930372063	11.54
76	NDUFA2	62	6	0.3696929812329760	0.999997930372063	9.68
77	NFKB1	64	6	0.3987737426208590	0.999997930372063	9.38
78	PAK1	136	6	0.9638515628459290	0.999997930372063	4.41
79	PDPK1	60	6	0.3406954325448980	0.999997930372063	10
80	PTPN11	56	6	0.2836340134590460	0.999997930372063	10.71
81	RPTOR	86	6	0.6874443375772050	0.999997930372063	6.98
82	SYK	78	6	0.5927956968440460	0.999997930372063	7.69
83	TMCO6	62	6	0.3696929812329760	0.999997930372063	9.68
84	LAG3	29	5	0.0755533118617940	0.710624302790622	17.24
85	MLF2	29	5	0.0755533118617940	0.710624302790622	17.24
86	PTMS	29	5	0.0755533118617940	0.710624302790622	17.24
87	VEGFB	28	5	0.0666925244865456	0.710624302790622	17.86
88	AMDHD2	47	5	0.3164628013515880	0.999997930372063	10.64
89	ATP6V0C	47	5	0.3164628013515880	0.999997930372063	10.64
90	CEMP1	47	5	0.3164628013515880	0.999997930372063	10.64
91	HES2	44	5	0.2689995823620770	0.999997930372063	11.36
92	RP11-20I23.1	47	5	0.3164628013515880	0.999997930372063	10.64
93	RP11-20I23.3	47	5	0.3164628013515880	0.999997930372063	10.64
94	IL5	20	4	0.0689391987008704	0.710624302790622	20
95	DNAJC4	23	4	0.1046472099137100	0.781478357903993	17.39
96	FERMT3	23	4	0.1046472099137100	0.781478357903993	17.39
97	HLA-DQB1	22	4	0.0919452518195525	0.781478357903993	18.18
98	NUDT22	23	4	0.1046472099137100	0.781478357903993	17.39

99	TRPT1	23	4	0.1046472099137100	0.781478357903993	17.39
100	CDCA3	26	4	0.1470546899826340	0.876931603559146	15.38
101	GNB3	26	4	0.1470546899826340	0.876931603559146	15.38
102	CYP1A1	27	4	0.1624652709870240	0.952169879329012	14.81
103	HLA-DQA1	28	4	0.1784273954037700	0.954389148642173	14.29
104	ITGAD	28	4	0.1784273954037700	0.954389148642173	14.29
105	PCED1A	28	4	0.1784273954037700	0.954389148642173	14.29
106	PRF1	28	4	0.1784273954037700	0.954389148642173	14.29
107	CPLX3	29	4	0.1948872487704860	0.970245120222958	13.79
108	AARS2	30	4	0.2117903328050300	0.988148591681669	13.33
109	P3H3	30	4	0.2117903328050300	0.988148591681669	13.33
110	RBM33	30	4	0.2117903328050300	0.988148591681669	13.33
111	AC009133.22	56	4	0.6591506486986940	0.999997930372063	7.14
112	AKT1	60	4	0.7118227932872120	0.999997930372063	6.67
113	ATN1	46	4	0.501622355732139	0.999997930372063	8.7

Table 2.c

	GeneLocus	Probe_Count_Total	Probe_Count_Sig	HyperG_Stats	FDR_HyperG	Percent_Sig
114	BLNK	66	4	0.779227696215700	0.999997930372063	6.06
115	C12orf57	46	4	0.501622355732139	0.999997930372063	8.7
116	C5	41	4	0.412035428682661	0.999997930372063	9.76
117	CASP8	41	4	0.412035428682661	0.999997930372063	9.76
118	CCR6	46	4	0.501622355732139	0.999997930372063	8.7
119	CD180	38	4	0.356577228215362	0.999997930372063	10.53
120	CD19	56	4	0.659150648698694	0.999997930372063	7.14
121	CD33	32	4	0.246707930589528	0.999997930372063	12.5
122	CDC37	43	4	0.448457218409109	0.999997930372063	9.3
123	CDKN2A	44	4	0.466402982013812	0.999997930372063	9.09
124	CDKN2B	32	4	0.246707930589528	0.999997930372063	12.5
125	CRADD	231	4	0.999992974704591	0.999997930372063	1.73
126	DAB1	60	4	0.711822793287212	0.999997930372063	6.67
127	DNMT3L	32	4	0.246707930589528	0.999997930372063	12.5
128	EMG1	40	4	0.393623595746639	0.999997930372063	10
129	ENO2	40	4	0.393623595746639	0.999997930372063	10
130	ESR1	198	4	0.999928673478001	0.999997930372063	2.02
131	FAM167B	33	4	0.264614551688586	0.999997930372063	12.12
132	FN1	42	4	0.430324417757699	0.999997930372063	9.52
133	GAB2	132	4	0.994374946176707	0.999997930372063	3.03
134	GDPD3	44	4	0.466402982013812	0.999997930372063	9.09
135	GPR31	44	4	0.466402982013812	0.999997930372063	9.09
136	HDAC1	33	4	0.264614551688586	0.999997930372063	12.12
137	IL17B	44	4	0.466402982013812	0.999997930372063	9.09
138	KIAA1468	48	4	0.535784564968372	0.999997930372063	8.33
139	LAT	58	4	0.686266830720114	0.999997930372063	6.9
140	LCK	46	4	0.501622355732139	0.999997930372063	8.7
141	LMAN1L	33	4	0.264614551688586	0.999997930372063	12.12
142	LPCAT3	37	4	0.338021739919006	0.999997930372063	10.81
143	LRRC23	43	4	0.448457218409109	0.999997930372063	9.3
144	MANBA	33	4	0.264614551688586	0.999997930372063	12.12
145	MAPK3	44	4	0.466402982013812	0.999997930372063	9.09

146	MFRP	84	4	0.909003420730453	0.999997930372063	4.76
147	MTOR	60	4	0.711822793287212	0.999997930372063	6.67
148	MYC	42	4	0.430324417757699	0.999997930372063	9.52
149	NCK2	66	4	0.779227696215700	0.999997930372063	6.06
150	NFATC2IP	54	4	0.630491543675306	0.999997930372063	7.41
151	NFKBIE	44	4	0.466402982013812	0.999997930372063	9.09
152	PHB2	40	4	0.393623595746639	0.999997930372063	10
153	PRR5	64	4	0.758278200178880	0.999997930372063	6.25
154	PRR5-ARHGAP8	62	4	0.735820497241091	0.999997930372063	6.45
155	PTPN6	46	4	0.501622355732139	0.999997930372063	8.7
156	RP11-145E5.5	44	4	0.466402982013812	0.999997930372063	9.09
157	RP11-444E17.6	39	4	0.375124758475278	0.999997930372063	10.26
158	RP3-461F17.3	40	4	0.393623595746639	0.999997930372063	10
159	SIRPA	56	4	0.659150648698694	0.999997930372063	7.14
160	SLC35B2	44	4	0.466402982013812	0.999997930372063	9.09
161	SPN	56	4	0.659150648698694	0.999997930372063	7.14

Table 2.d

	GeneLocus	Probe_ Count_ Total	Probe_ Count_ Sig	HyperG_Stats	FDR_HyperG	Percent_ Sig
162	SPNS1	58	4	0.686266830720114	0.999997930372063	6.9
163	TAB2	151	4	0.998322979214390	0.999997930372063	2.65
164	TBC1D24	41	4	0.412035428682661	0.999997930372063	9.76
165	TCP10L2	46	4	0.501622355732139	0.999997930372063	8.7
166	TCTE1	39	4	0.375124758475278	0.999997930372063	10.26
167	TMEM151B	39	4	0.375124758475278	0.999997930372063	10.26
168	TNFRSF11A	58	4	0.686266830720114	0.999997930372063	6.9
169	TNFSF8	50	4	0.568728838576346	0.999997930372063	8
170	TP73	32	4	0.246707930589528	0.999997930372063	12.5
171	TYK2	75	4	0.856164977014928	0.999997930372063	5.33
172	VPS16	33	4	0.264614551688586	0.999997930372063	12.12
173	ZBTB42	58	4	0.6862668307201140	0.999997930372063	6.9
174	ADAMTS14	11	3	0.0508678018832711	0.619784007156698	27.27
175	TAS1R1	11	3	0.0508678018832711	0.619784007156698	27.27
176	MIPEP	12	3	0.0639334616325914	0.704790303235472	25
177	PGPEP1L	13	3	0.0783691103023943	0.710624302790622	23.08
178	POLB	15	3	0.1109490178464970	0.789152246561851	20
179	FARP2	16	3	0.1288732831899840	0.831677998018297	18.75
180	RAD50	16	3	0.1288732831899840	0.831677998018297	18.75
181	AIRE	17	3	0.1477336178782150	0.876931603559146	17.65
182	ATIC	17	3	0.1477336178782150	0.876931603559146	17.65
183	MEGF6	20	3	0.2087722402131870	0.988148591681669	15
184	TPRG1L	20	3	0.2087722402131870	0.988148591681669	15
185	AC105009.1	54	3	0.8132350734881700	0.999997930372063	5.56
186	ALDOA	26	3	0.3412775623453530	0.999997930372063	11.54
187	ALS2CR12	21	3	0.2302291415790290	0.999997930372063	14.29
188	ANGPTL7	38	3	0.5901926157849590	0.999997930372063	7.89
189	CCDC88B	42	3	0.6586694353499270	0.999997930372063	7.14
190	CTD-2369P2.10	66	3	0.9040238254594840	0.999997930372063	4.55
191	CTD-2369P2.12	60	3	0.8652252087613920	0.999997930372063	5
192	FDX1L	60	3	0.8652252087613920	0.999997930372063	5

193	HECTD4	59	3	0.8575550879876830	0.999997930372063	5.08
194	ICAM3	70	3	0.9239561433116700	0.999997930372063	4.29
195	PCYOX1L	39	3	0.6081149372274330	0.999997930372063	7.69
196	PPP4C	29	3	0.4078878479067430	0.999997930372063	10.34
197	RABEP2	50	3	0.7698155828032130	0.999997930372063	6
198	RAVER1	61	3	0.8725291522297110	0.999997930372063	4.92
199	RPL6	36	3	0.5527984128114050	0.999997930372063	8.33
200	SIGLECL1	29	3	0.4078878479067430	0.999997930372063	10.34
201	SPSB2	30	3	0.4296764606958220	0.999997930372063	10
202	STAT3	100	3	0.9882826466279560	0.999997930372063	3
203	STAT5A	99	3	0.9874934884705020	0.999997930372063	3.03
204	STAT5B	106	3	0.9921011727563130	0.999997930372063	2.83
205	TBX6	29	3	0.4078878479067430	0.999997930372063	10.34
206	TPI1	25	3	0.3188672309188860	0.999997930372063	12
207	USP5	31	3	0.4511687243316760	0.999997930372063	9.68
208	WRAP73	25	3	0.3188672309188860	0.999997930372063	12
209	YPEL3	29	3	0.4078878479067430	0.999997930372063	10.34

Table 2.e

	GeneLocus	Probe_ Count_ Total	Probe_ Count_ Sig	HyperG_Stats	FDR_HyperG	Percent_ Sig
210	ZMAT2	23	3	0.2741758744693630	0.999997930372063	13.04
211	ZP1	3	2	0.0178992933709331	0.276245761024734	66.67
212	SIGLEC7	7	2	0.1012229245865700	0.781478357903993	28.57
213	UBIAD1	7	2	0.1012229245865700	0.781478357903993	28.57
214	HAVCR2	10	2	0.1856137157633120	0.954389148642173	20
215	IFNG	10	2	0.1856137157633120	0.954389148642173	20
216	MED7	10	2	0.1856137157633120	0.954389148642173	20
217	ATG4B	11	2	0.2155572521810980	0.988148591681669	18.18
218	HLA-DOA	11	2	0.2155572521810980	0.988148591681669	18.18
219	ABCD3	31	2	0.7175015183076030	0.999997930372063	6.45
220	ADM5	30	2	0.7003187574059310	0.999997930372063	6.67
221	AFAP1L1	36	2	0.7913651829204500	0.999997930372063	5.56
222	AGMAT	18	2	0.4242550801595520	0.999997930372063	11.11
223	AP000866.1	23	2	0.5550530577755810	0.999997930372063	8.7
224	ARHGAP24	14	2	0.3067159393788740	0.999997930372063	14.29
225	ARHGEF1	44	2	0.8743872112910340	0.999997930372063	4.55
226	BAX	52	2	0.9259587031948710	0.999997930372063	3.85
227	BCL2L12	30	2	0.7003187574059310	0.999997930372063	6.67
228	BCL2L2	86	2	0.9932337395965280	0.999997930372063	2.33
229	BCL2L2-PABPN1	93	2	0.9959456131341410	0.999997930372063	2.15
230	BID	42	2	0.8570808572073380	0.999997930372063	4.76
231	BRD2	15	2	0.3368339273069320	0.999997930372063	13.33
232	C16orf59	17	2	0.3957171204687430	0.999997930372063	11.76
233	C1orf137	16	2	0.366542590752210	0.999997930372063	12.5
234	C1S	29	2	0.682275937625257	0.999997930372063	6.9
235	C20orf141	12	2	0.245882010290800	0.999997930372063	16.67
236	C8G	35	2	0.778111473469947	0.999997930372063	5.71
237	CASP10	53	2	0.930777371745053	0.999997930372063	3.77
238	CASP6	28	2	0.663352621092945	0.999997930372063	7.14
239	CASP9	46	2	0.889742684761849	0.999997930372063	4.35

240	CBL	55	2	0.939538153185284	0.999997930372063	3.64
241	CBLB	182	2	0.999995464473068	0.999997930372063	1.1
242	CCDC109B	20	2	0.479107133771006	0.999997930372063	10
243	CCDC28B	22	2	0.530628954879388	0.999997930372063	9.09
244	CCL15	12	2	0.245882010290800	0.999997930372063	16.67
245	CCL23	16	2	0.366542590752210	0.999997930372063	12.5
246	CCNF	16	2	0.366542590752210	0.999997930372063	12.5
247	CD2	34	2	0.764125503160783	0.999997930372063	5.88
248	CD47	46	2	0.889742684761849	0.999997930372063	4.35
249	CD79A	44	2	0.874387211291034	0.999997930372063	4.55
250	CD79B	20	2	0.479107133771006	0.999997930372063	10
251	CD86	46	2	0.889742684761849	0.999997930372063	4.35
252	CEP170B	24	2	0.578560340672839	0.999997930372063	8.33
253	CFI	16	2	0.366542590752210	0.999997930372063	12.5
254	CLNS1A	28	2	0.663352621092945	0.999997930372063	7.14
255	CMTM5	74	2	0.983929844323545	0.999997930372063	2.7
256	COPS7A	16	2	0.366542590752210	0.999997930372063	12.5
257	COX6A2	12	2	0.245882010290800	0.999997930372063	16.67

Table 2.f

	GeneLocus	Probe_ Count_ Total	Probe_ Count_ Sig	HyperG_Stats	FDR_HyperG	Percent_ Sig
258	CPT1C	30	2	0.700318757405931	0.999997930372063	6.67
259	CPXM1	12	2	0.245882010290800	0.999997930372063	16.67
260	CSF2	36	2	0.791365182920450	0.999997930372063	5.56
261	CSHL1	20	2	0.479107133771006	0.999997930372063	10
262	CYBA	40	2	0.837619347075832	0.999997930372063	5
263	DCDC2B	22	2	0.530628954879388	0.999997930372063	9.09
264	DHDH	48	2	0.903339406944514	0.999997930372063	4.17
265	DHX37	24	2	0.578560340672839	0.999997930372063	8.33
266	DMRTC2	39	2	0.827013686075902	0.999997930372063	5.13
267	DNAJC16	31	2	0.717501518307603	0.999997930372063	6.45
268	DNMT1	25	2	0.601142350216661	0.999997930372063	8
269	DNTT	32	2	0.733846963466398	0.999997930372063	6.25
270	DUSP22	48	2	0.903339406944514	0.999997930372063	4.17
271	EFS	78	2	0.987931057370678	0.999997930372063	2.56
272	EGF	48	2	0.903339406944514	0.999997930372063	4.17
273	EIF3I	22	2	0.530628954879388	0.999997930372063	9.09
274	ENDOU	26	2	0.622797749205937	0.999997930372063	7.69
275	ENSA	88	2	0.994151783490876	0.999997930372063	2.27
276	ESAM	32	2	0.733846963466398	0.999997930372063	6.25
277	F3	36	2	0.791365182920450	0.999997930372063	5.56
278	FAM220A	52	2	0.925958703194871	0.999997930372063	3.85
279	FAM71B	12	2	0.245882010290800	0.999997930372063	16.67
280	FBXW5	35	2	0.778111473469947	0.999997930372063	5.71
281	FTL	52	2	0.925958703194871	0.999997930372063	3.85
282	GH1	20	2	0.479107133771006	0.999997930372063	10
283	GRPEL2	36	2	0.791365182920450	0.999997930372063	5.56
284	GYS1	46	2	0.889742684761849	0.999997930372063	4.35
285	HCST	50	2	0.915356314014006	0.999997930372063	4
286	HLA-DMA	16	2	0.366542590752210	0.999997930372063	12.5

287	HLA-DMB	26	2	0.622797749205937	0.999997930372063	7.69
288	HLA-DRB1	13	2	0.276338901197783	0.999997930372063	15.38
289	HSP90AB1	36	2	0.791365182920450	0.999997930372063	5.56
290	ICAM1	63	2	0.965115210029707	0.999997930372063	3.17
291	ICAM5	57	2	0.947238725405958	0.999997930372063	3.51
292	IGSF23	48	2	0.903339406944514	0.999997930372063	4.17
293	IL17C	40	2	0.837619347075832	0.999997930372063	5
294	IL25	74	2	0.983929844323545	0.999997930372063	2.7
295	IL26	20	2	0.479107133771006	0.999997930372063	10
296	IL3	42	2	0.857080857207338	0.999997930372063	4.76
297	IQCC	22	2	0.530628954879388	0.999997930372063	9.09
298	IRF2	38	2	0.815788109211877	0.999997930372063	5.26
299	IRF3	30	2	0.700318757405931	0.999997930372063	6.67
300	IRF4	40	2	0.837619347075832	0.999997930372063	5
301	LCN12	35	2	0.778111473469947	0.999997930372063	5.71
302	LRFN3	41	2	0.847632694261747	0.999997930372063	4.88
303	LTBR	33	2	0.749379646925559	0.999997930372063	6.06
304	LYN	48	2	0.903339406944514	0.999997930372063	4.17
305	LYPD4	35	2	0.778111473469947	0.999997930372063	5.71

Table 2.g

	GeneLocus	Probe_ Count_ Total	Probe_ Count_ Sig	HyperG_Stats	FDR_HyperG	Percent_ Sig
306	MAP3K11	41	2	0.847632694261747	0.999997930372063	4.88
307	MAP3K14	44	2	0.874387211291034	0.999997930372063	4.55
308	MARCKSL1	24	2	0.578560340672839	0.999997930372063	8.33
309	MAST3	62	2	0.962606551119358	0.999997930372063	3.23
310	MAST4	25	2	0.601142350216661	0.999997930372063	8
311	MCL1	77	2	0.987032863322398	0.999997930372063	2.6
312	MRPL4	40	2	0.837619347075832	0.999997930372063	5
313	MSANTD2	30	2	0.700318757405931	0.999997930372063	6.67
314	MVD	36	2	0.791365182920450	0.999997930372063	5.56
315	NFKBID	50	2	0.915356314014006	0.999997930372063	4
316	NRGN	30	2	0.700318757405931	0.999997930372063	6.67
317	NTN3	17	2	0.395717120468743	0.999997930372063	11.76
318	NUCB1	44	2	0.874387211291034	0.999997930372063	4.55
319	PABPN1	90	2	0.994947395103974	0.999997930372063	2.22
320	PCNXL3	48	2	0.903339406944514	0.999997930372063	4.17
321	PDCD1	36	2	0.791365182920450	0.999997930372063	5.56
322	PDYN	32	2	0.733846963466398	0.999997930372063	6.25
323	PFKL	14	2	0.306715939378874	0.999997930372063	14.29
324	PLA2G12A	23	2	0.555053057775581	0.999997930372063	8.7
325	PLAT	14	2	0.306715939378874	0.999997930372063	14.29
326	PRKCQ	106	2	0.998452565953663	0.999997930372063	1.89
327	PRMT1	30	2	0.700318757405931	0.999997930372063	6.67
328	PRR5L	192	2	0.999997930372063	0.999997930372063	1.04
329	PSMD5	14	2	0.306715939378874	0.999997930372063	14.29
330	PVR	65	2	0.969655535986940	0.999997930372063	3.08
331	QPRT	47	2	0.896749389307423	0.999997930372063	4.26
332	RABL6	46	2	0.889742684761849	0.999997930372063	4.35
333	RAC1	64	2	0.967461558699041	0.999997930372063	3.12

334	RAG1	51	2	0.920824527564584	0.999997930372063	3.92
335	RAPGEF3	25	2	0.601142350216661	0.999997930372063	8
336	RELA	56	2	0.943513219685347	0.999997930372063	3.57
337	RICTOR	114	2	0.999150230460213	0.999997930372063	1.75
338	RPAP3	25	2	0.601142350216661	0.999997930372063	8
339	RPS19	44	2	0.874387211291034	0.999997930372063	4.55
340	RTP5	30	2	0.700318757405931	0.999997930372063	6.67
341	RUVBL2	29	2	0.682275937625257	0.999997930372063	6.9
342	S1PR2	25	2	0.601142350216661	0.999997930372063	8
343	SCAF1	26	2	0.622797749205937	0.999997930372063	7.69
344	SCN4A	23	2	0.555053057775581	0.999997930372063	8.7
345	SCNN1A	39	2	0.827013686075902	0.999997930372063	5.13
346	SIPA1	69	2	0.977087651131023	0.999997930372063	2.9
347	SIVA1	36	2	0.791365182920450	0.999997930372063	5.56
348	SLC22A17	87	2	0.993709149379117	0.999997930372063	2.3
349	SLC29A1	29	2	0.682275937625257	0.999997930372063	6.9
350	SLC48A1	18	2	0.424255080159552	0.999997930372063	11.11
351	SMAD3	34	2	0.764125503160783	0.999997930372063	5.88
352	SPATA32	24	2	0.578560340672839	0.999997930372063	8.33
353	SPATS1	15	2	0.336833927306932	0.999997930372063	13.33

Table 2.h

	GeneLocus	Probe_Count_Total	Probe_Count_Sig	HyperG_Stats	FDR_HyperG	Percent_Sig
354	STAT4	58	2	0.950729209348889	0.999997930372063	3.45
355	SUMO4	87	2	0.993709149379117	0.999997930372063	2.3
356	TEX29	29	2	0.682275937625257	0.999997930372063	6.9
357	TMEM234	22	2	0.530628954879388	0.999997930372063	9.09
358	TNFRSF1A	46	2	0.889742684761849	0.999997930372063	4.35
359	TRAF2	46	2	0.889742684761849	0.999997930372063	4.35
360	TRAF6	60	2	0.957059623937612	0.999997930372063	3.33
361	TRIM72	16	2	0.366542590752210	0.999997930372063	12.5
362	TYROBP	50	2	0.915356314014006	0.999997930372063	4
363	UBC	64	2	0.967461558699041	0.999997930372063	3.12
364	ULK3	20	2	0.479107133771006	0.999997930372063	10
365	VSIG2	30	2	0.700318757405931	0.999997930372063	6.67
366	XXbac-BPG181M17.5	26	2	0.622797749205937	0.999997930372063	7.69
367	ZC3H18	35	2	0.778111473469947	0.999997930372063	5.71
368	ZNF518A	34	2	0.764125503160783	0.999997930372063	5.88
369	ZNF843	12	2	0.245882010290800	0.999997930372063	16.67
370	AAGAB	18	1	0.774551015160648	0.999997930372063	5.56
371	AC138028.1	29	1	0.909346620735280	0.999997930372063	3.45
372	ACSL6	22	1	0.838118527757470	0.999997930372063	4.55
373	ADAMTSL4	48	1	0.981231994372307	0.999997930372063	2.08
374	ADSSL1	21	1	0.824141728990284	0.999997930372063	4.76
375	APLP1	42	1	0.969133876315432	0.999997930372063	2.38
376	ATP6V0A1	17	1	0.755090129882809	0.999997930372063	5.88
377	BCL2L13	30	1	0.916554478091464	0.999997930372063	3.33
378	BOLA2B	15	1	0.710987544197401	0.999997930372063	6.67
379	BRI3BP	13	1	0.658949110426667	0.999997930372063	7.69

380	C1orf168	55	1	0.989498382048305	0.999997930372063	1.82
381	C1QTNF5	35	1	0.944859652291972	0.999997930372063	2.86
382	CCDC153	27	1	0.893010740890946	0.999997930372063	3.7
383	CCDC27	10	1	0.562821502082175	0.999997930372063	10
384	CCL14	9	1	0.525100723450289	0.999997930372063	11.11
385	CCL15-CCL14	10	1	0.562821502082175	0.999997930372063	10
386	CCL16	9	1	0.525100723450289	0.999997930372063	11.11
387	CEACAM16	48	1	0.981231994372307	0.999997930372063	2.08
388	CEACAM19	53	1	0.987603129345602	0.999997930372063	1.89
389	CEACAM3	19	1	0.792466424646505	0.999997930372063	5.26
390	CELA2A	30	1	0.916554478091464	0.999997930372063	3.33
391	CELA2B	38	1	0.956998223828945	0.999997930372063	2.63
392	CFLAR	58	1	0.991812373295601	0.999997930372063	1.72
393	CGB	15	1	0.710987544197401	0.999997930372063	6.67
394	CHMP6	7	1	0.439621833115841	0.999997930372063	14.29
395	CORO1A	17	1	0.755090129882809	0.999997930372063	5.88
396	CSH1	12	1	0.629517555870599	0.999997930372063	8.33
397	CTB-60B18.6	15	1	0.710987544197401	0.999997930372063	6.67
398	DAGLB	74	1	0.997830586254369	0.999997930372063	1.35
399	DKK4	7	1	0.439621833115841	0.999997930372063	14.29
400	EDF1	21	1	0.824141728990284	0.999997930372063	4.76

Table 2.i

	GeneLocus	Probe_Count_Total	Probe_Count_Sig	HyperG_Stats	FDR_HyperG	Percent_Sig
401	EHBP1L1	43	1	0.971589673511865	0.999997930372063	2.33
402	ELOVL6	12	1	0.629517555870599	0.999997930372063	8.33
403	FAM57B	18	1	0.774551015160648	0.999997930372063	5.56
404	FGFR1OP	32	1	0.929297402985911	0.999997930372063	3.12
405	FMNL1	14	1	0.686043969738036	0.999997930372063	7.14
406	FUS	6	1	0.391279131897374	0.999997930372063	16.67
407	GOLPH3L	53	1	0.987603129345602	0.999997930372063	1.89
408	HDAC7	8	1	0.484127577317580	0.999997930372063	12.5
409	HOMEZ	74	1	0.997830586254369	0.999997930372063	1.35
410	ICAM2	24	1	0.862829696523136	0.999997930372063	4.17
411	ICAM4	53	1	0.987603129345602	0.999997930372063	1.89
412	IFI30	40	1	0.963567575263993	0.999997930372063	2.5
413	IFT57	16	1	0.733950541093747	0.999997930372063	6.25
414	IGLON5	13	1	0.658949110426667	0.999997930372063	7.69
415	IGSF3	54	1	0.988590014250795	0.999997930372063	1.85
416	IL12RB1	51	1	0.985366094431372	0.999997930372063	1.96
417	ILDR1	23	1	0.850985140029373	0.999997930372063	4.35
418	INF2	21	1	0.824141728990284	0.999997930372063	4.76
419	KCNK7	38	1	0.956998223828945	0.999997930372063	2.63
420	KCTD21	19	1	0.792466424646505	0.999997930372063	5.26
421	KDELR2	49	1	0.982725688322447	0.999997930372063	2.04
422	KIRREL2	31	1	0.923189576750926	0.999997930372063	3.23
423	LCNL1	21	1	0.824141728990284	0.999997930372063	4.76
424	LHB	18	1	0.774551015160648	0.999997930372063	5.56
425	LRIT3	23	1	0.850985140029373	0.999997930372063	4.35
426	MAMDC4	19	1	0.792466424646505	0.999997930372063	5.26

427	MCAM	33	1	0.934919832862797	0.999997930372063	3.03
428	MICAL3	24	1	0.862829696523136	0.999997930372063	4.17
429	MPV17L2	37	1	0.953282168181128	0.999997930372063	2.7
430	MTAP	26	1	0.883770759422438	0.999997930372063	3.85
431	MYH6	59	1	0.992464337028886	0.999997930372063	1.69
432	NPHS1	31	1	0.923189576750926	0.999997930372063	3.23
433	OPALIN	13	1	0.658949110426667	0.999997930372063	7.69
434	OSMR	53	1	0.987603129345602	0.999997930372063	1.89
435	PALD1	17	1	0.755090129882809	0.999997930372063	5.88
436	PDE4A	22	1	0.838118527757470	0.999997930372063	4.55
437	PDE4C	37	1	0.953282168181128	0.999997930372063	2.7
438	PLEKHG6	44	1	0.973850195889094	0.999997930372063	2.27
439	PPP1R3E	82	1	0.998883779596881	0.999997930372063	1.22
440	PRR12	9	1	0.525100723450289	0.999997930372063	11.11
441	PRR29	19	1	0.792466424646505	0.999997930372063	5.26
442	PTGDS	21	1	0.824141728990284	0.999997930372063	4.76
443	PTRF	46	1	0.977846256754934	0.999997930372063	2.17
444	PYCARD	6	1	0.391279131897374	0.999997930372063	16.67
445	PYDC1	10	1	0.562821502082175	0.999997930372063	10
446	RAB3A	37	1	0.953282168181128	0.999997930372063	2.7
447	RNF26	32	1	0.929297402985911	0.999997930372063	3.12
448	RP11-347C12.3	13	1	0.658949110426667	0.999997930372063	7.69

Table 2.j

	GeneLocus	Probe_ Count_ Total	Probe_ Count_ Sig	HyperG_Stats	FDR_HyperG	Percen t_Sig
449	RPS6KA4	20	1	0.808959018903111	0.999997930372063	5
450	RRAS	13	1	0.658949110426667	0.999997930372063	7.69
451	RRH	10	1	0.562821502082175	0.999997930372063	10
452	SCAMP2	17	1	0.755090129882809	0.999997930372063	5.88
453	SCARB1	78	1	0.998443813773922	0.999997930372063	1.28
454	SDHAF1	6	1	0.391279131897374	0.999997930372063	16.67
455	SLX1A	15	1	0.710987544197401	0.999997930372063	6.67
456	SLX1A-SULT1A3	15	1	0.710987544197401	0.999997930372063	6.67
457	SNAI3	29	1	0.909346620735280	0.999997930372063	3.45
458	SPA17	17	1	0.755090129882809	0.999997930372063	5.88
459	SULT1A3	14	1	0.686043969738036	0.999997930372063	7.14
460	TSKS	17	1	0.755090129882809	0.999997930372063	5.88
461	TSSK3	15	1	0.710987544197401	0.999997930372063	6.67
462	USP35	31	1	0.923189576750926	0.999997930372063	3.23
463	ZGLP1	57	1	0.991104042882726	0.999997930372063	1.75

Table 2.k

	gene	Probe_Count_Total	Probe_Count_Sig	HyperG_Stats	FDR_HyperG	Percent_Sig
1	IGF1R	104	16	0.007797893	0.171924974	15.38
2	CD6	56	14	0.000090300	0.005970563	25
3	CXCL13	108	14	0.046569042	0.598929617	12.96
4	IKBKB	46	12	0.000183630	0.010627608	26.09
5	PIK3R1	148	12	0.513477047	0.99999793	8.11
6	ITK	26	10	0.000015700	0.002607465	38.46
7	PTPRC	214	10	0.978491243	0.99999793	4.67

8	C8B	151	9	0.855915990	0.99999793	5.96
9	C8A	166	8	0.957766442	0.99999793	4.82
10	CCL18	42	8	0.016095432	0.256971894	19.05
11	CYFIP2	40	8	0.012066038	0.223463015	20
12	FAS	50	8	0.041957105	0.555032562	16
13	ICOSLG	40	8	0.012066038	0.223463015	20
14	IRF1	42	8	0.016095432	0.256971894	19.05
15	ITGAM	50	8	0.041957105	0.555032562	16
16	ITGAX	41	8	0.013975308	0.239650655	19.51
17	CCL3	33	7	0.013410837	0.238816059	21.21
18	CCL4	32	7	0.011323325	0.223463015	21.88
19	CD14	62	6	0.369692981	0.99999793	9.68
20	CD4	42	6	0.112492545	0.789152247	14.29
21	NFKB1	64	6	0.398773743	0.99999793	9.38
22	SYK	78	6	0.592795697	0.99999793	7.69
23	LAG3	29	5	0.075553312	0.710624303	17.24
24	AKT1	60	4	0.711822793	0.99999793	6.67
25	BLNK	66	4	0.779227696	0.99999793	6.06
26	C5	41	4	0.412035429	0.99999793	9.76
27	CASP8	41	4	0.412035429	0.99999793	9.76
28	CCR6	46	4	0.501622356	0.99999793	8.7
29	CD180	38	4	0.356577228	0.99999793	10.53
30	CD19	56	4	0.659150649	0.99999793	7.14

Table 3.a

	gene	Probe_Count_Total	Probe_Count_Sig	HyperG_Stats	FDR_HyperG	Percent_Sig
31	CD33	32	4	0.246707931	0.99999793	12.5
32	FN1	42	4	0.430324418	0.99999793	9.52
33	HLA-DQA1	28	4	0.178427395	0.954389149	14.29
34	HLA-DQB1	22	4	0.091945252	0.781478358	18.18
35	IL17B	44	4	0.466402982	0.99999793	9.09
36	IL5	20	4	0.068939199	0.710624303	20
37	LCK	46	4	0.501622356	0.99999793	8.7
38	MAPK3	44	4	0.466402982	0.99999793	9.09
39	MTOR	60	4	0.711822793	0.99999793	6.67
40	PRF1	28	4	0.178427395	0.954389149	14.29
41	SPN	56	4	0.659150649	0.99999793	7.14
42	TNFRSF11A	58	4	0.686266831	0.99999793	6.9
43	TNFSF8	50	4	0.568728839	0.99999793	8
44	TYK2	75	4	0.856164977	0.99999793	5.33
45	AIRE	17	3	0.147733618	0.876931604	17.65
46	ICAM3	70	3	0.923956143	0.99999793	4.29
47	STAT3	100	3	0.988282647	0.99999793	3
48	STAT5B	106	3	0.992101173	0.99999793	2.83
49	BAX	52	2	0.925958703	0.99999793	3.85
50	BID	42	2	0.857080857	0.99999793	4.76
51	C1S	29	2	0.682275938	0.99999793	6.9
52	C8G	35	2	0.778111473	0.99999793	5.71
53	CASP10	53	2	0.930777372	0.99999793	3.77
54	CCL15	12	2	0.245882010	0.99999793	16.67
55	CCL23	16	2	0.366542591	0.99999793	12.5

56	CD2	34	2	0.764125503	0.99999793	5.88
57	CD47	46	2	0.889742685	0.99999793	4.35
58	CD79A	44	2	0.874387211	0.99999793	4.55
59	CD79B	20	2	0.479107134	0.99999793	10
60	CD86	46	2	0.889742685	0.99999793	4.35
61	CFI	16	2	0.366542591	0.99999793	12.5
62	CSF2	36	2	0.791365183	0.99999793	5.56

Table 3.b

	gene	Probe_Count _Total	Probe_Count_Sig	HyperG_Stats	FDR_HyperG	Percent_Sig
63	HAVCR2	10	2	0.185613716	0.954389149	20
64	HLA-DMA	16	2	0.366542591	0.99999793	12.5
65	HLA-DMB	26	2	0.622797749	0.99999793	7.69
66	ICAM1	63	2	0.965115210	0.99999793	3.17
67	IFNG	10	2	0.185613716	0.954389149	20
68	IL25	74	2	0.983929844	0.99999793	2.7
69	IL26	20	2	0.479107134	0.99999793	10
70	IL3	42	2	0.857080857	0.99999793	4.76
71	IRF2	38	2	0.815788109	0.99999793	5.26
72	IRF3	30	2	0.700318757	0.99999793	6.67
73	IRF4	40	2	0.837619347	0.99999793	5
74	LTBR	33	2	0.749379647	0.99999793	6.06
75	LYN	48	2	0.903339407	0.99999793	4.17
76	PDCD1	36	2	0.791365183	0.99999793	5.56
77	PVR	65	2	0.969655536	0.99999793	3.08
78	RAC1	64	2	0.967461559	0.99999793	3.12
79	RAG1	51	2	0.920824528	0.99999793	3.92
80	RELA	56	2	0.943513220	0.99999793	3.57
81	SMAD3	34	2	0.764125503	0.99999793	5.88
82	STAT4	58	2	0.950729209	0.99999793	3.45
83	TNFRSF1A	46	2	0.889742685	0.99999793	4.35
84	TRAF2	46	2	0.889742685	0.99999793	4.35
85	TRAF6	60	2	0.957059624	0.99999793	3.33
86	UBC	64	2	0.967461559	0.99999793	3.12
87	CCL14	9	1	0.525100723	0.99999793	11.11
88	CCL16	9	1	0.525100723	0.99999793	11.11
89	ICAM2	24	1	0.862829697	0.99999793	4.17
90	ICAM4	53	1	0.987603129	0.99999793	1.89
91	IL12RB1	51	1	0.985366094	0.99999793	1.96
92	MCAM	33	1	0.934919833	0.99999793	3.03
93	PYCARD	6	1	0.391279132	0.99999793	16.67
94	SPA17	17	1	0.755090130	0.99999793	5.88

Table 3.c

probe	GeneLocus	Probe_Count_Total
STAT5A_STAT5B_17_40403935_40406459_40464294_40468456_FR	STAT5A-STAT5B	20
IRF1_5_131808352_131813604_131831068_131832754_FF	IRF1	19
ITK_5_156605330_156608059_156693735_156698772_FR	ITK	63
CD14_5_140023383_140027012_140050153_140052313_RF	CD14	22
PDCD1LG2_9_5495992_5498009_5563479_5572986_RR	CD274-PDCD1LG2	8

Table 4.a

HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr
0.001866853	0.066190912	60	0.847262651666667	0.847262651666666
0.000987668	0.046843683	63.16	0.575333619	0.575333619
0.653537516	1	25.4	0.929375192333334	0.929375192333333
0.218923992	0.865271017	36.36	0.720976047333333	0.720976047333333
0.918612302	1	12.5	-0.351310575666667	-0.351310575666667

Table 4.b

t	P.Value	adj.P.Val	B
7.35944594338825	0.000150927923435752	0.0102743339719173	1.64393419184962
5.64430691077999	0.000700956470870541	0.0155534374671815	-0.0160747735782962
8.2961135309084	0.0000610123228131512	0.00959185677856724	2.42787963605984
7.76177819268656	0.0000944498918420986	0.0097813496834544	2.00179581849286
-6.21225357321395	0.000390149640704813	0.0122622958225811	0.582455106574847

Table 4.c

FC	FC_1	LS	Loop detected
1.79931599399832	1.79931599399832	1	R
1.49002198650363	1.49002198650363	1	R
1.90445103081467	1.90445103081467	1	R
1.64829680346345	1.64829680346345	1	R
0.783871688209362	-1.27571899207682	-1	NR

Table 4.d

Probe sequence	**Probe Location**
60 mer	**Chr**
TTCCATAGATTACTTTTCAAATCATCCTTCGAAGCTGGCGGCTGAGGGCCCGGCGCCAAG	17
GTGTCTCGGCCCCCTGGGGCCCCACCCTTCGATTTCCCTGTTGCCGCCGCGTTTGCAAGA	5
ATCCCAACAAAAGAGAAGAACTTCTCCCTCGATGTTTGGGGGCGGAGGGCTTTGATGAGA	5
GTGGCGATGGCGGCCTGCGCGCCGCGCCTCGATGTCTAAGCAACCTGCTAACTGAGGCAG	5
ACAGTTATTAGAAAAATAAAACATTTGGTCGAACAGCAAAGAGAAGATATTCAACTGCGA	9

Table 4.e

Probe Location				**4 kb Sequence Location**			
Start1	**End1**	**Start2**	**End2**	**Chr**	**Start1**	**End1**	**Start2**
40406428	40406457	40464296	40464325	17	40402458	40406457	40464296
131813573	131813602	131832723	131832752	5	131809603	131813602	131828753
156608028	156608057	156693737	156693766	5	156604058	156608057	156693737
140023385	140023414	140052282	140052311	5	140023385	140027384	140048312
5495994	5496023	5563481	5563510	9	5495994	5499993	5563481

Table 4.f

4 kb Sequence Location
End2
40468295
131832752
156697736
140052311
5567480

Table 4.g

	Inner_primers
probe	**PCR-Primer1_ID**
STAT5A_STAT5B_17_40403935_40406459_40464294_40468456_FR	OBD117-009
IRF1_5_131808352_131813604_131831068_131832754_FF	OBD117-045
ITK_5_156605330_156608059_156693735_156698772_FR	OBD117-089
CD14_5_140023383_140027012_140050153_140052313_RF	OBD117-105
PDCD1LG2_9_5495992_5498009_5563479_5572986_RR	OBD117-029

Table 4.h

Inner_primers			
PCR_Primer1	**PCR-Primer2_ID**	**PCR_Primer2**	GLMNET
TCTACAGCCCAAGATCCTGCTTT	OBD117-011	CCCCGAGGGTTGAGAAGCAT	0.251515381
GGACCCAACAGAGGGTCTGG	OBD117-047	ACTTGGGATAGACCTGCGGC	0
TTGTGCTAAGAGGTGATGCCCA	OBD117-090	TGTGGTTTCGGCCTTTGACATC	-0.332188811
CAGCGGATGGTTGTGCAGC	OBD117-107	CCTGGGCAGATTATGGTGCG	0.070125046
CTCACTGCCCAACAGGCTAGAA	OBD117-031	TCTTGACTCAGAGCCCACAACAA	-0.1009401

Table 4.i

Gene	Marker	GLMNET
STAT5A-STAT5B	OBD117-009/011	0.1947148
IRF1	OBD117-045/047	0.1946348
ITK	OBD117-089/090	0.1938877
CD14	OBD117-105/107	0.193081
CD274-PDCD1LG2	OBD117-029/030	-0.1922868

Table 4.j

Gene Locus	Probes	Chr	Start1	End1	Start2
PVRL1	AGAAAATATAGTATTGATTGCTTTCAAGTCGATGCGCGCCCGCCGGGGCCCGGTCGGAGC	11	119577280	119577309	119599999
HLA-DQB1	TACTGTAGTAAGTTCTCTGAGGAGGATATCGATTTTTTATTGTATCCTATATTTTTTCTA	6	32607973	32608002	32669133
HLA-DQB1	TACTGTAGTAAGTTCTCTGAGGAGGATATCGAAGTCTTGGATTAAGGTTCATTCAACAAA	6	32607973	32608002	32630139
BOK	CACTTCCCCAACATAAGCCTCGGTCTCTTCGAGGGCGGGCCCGGCGGCCCCGGAGCAAAC	2	242498608	242498637	242532080
CSK	GAGTTCAGCGTGCCGCCGGGCGTGAAAGTCGAGGCATATTTGAGTTTAGGGAGGTGTTGC	15	75047316	75047345	75083505
CSK	GAGTTCAGCGTGCCGCCGGGCGTGAAAGTCGACTCTGGGCCCAGACCACAGAAGGAGGGG	15	75047316	75047345	75080014
CSK	GAGTTCAGCGTGCCGCCGGGCGTGAAAGTCGATTTGTTTATGGTTTTATCCCCAGTGCCT	15	75047316	75047345	75072258
HLA-DQB1	TTTGTTGAATGAACCTTAATCCAAGACTTCGATTTTTTATTGTATCCTATATTTTTTCTA	6	32630139	32630168	32669133
STAT5B	TTCCATAGATTACTTTTCAAATCATCCTTCGAAGCTGGCGGCTGAGGGCCCGGCGCCAAG	17	40406430	40406459	40464295
BOK	GTTTGCTCCGGGGCCGCCGGGCCCGCCCTCGATTTTAACACCACCATGGTTTGAATGAAT	2	242498608	242498637	242517412
PTPRA	TCCATTGTCTTATTCCAGTCTAGGCTTGTCGAGTTGCAGGCCGCCCTGGTGGCTAGACAT	20	2853762	2853791	2948630
FCGR2B	AAAAAACAATTATGTAATTGAAAACCCATCGAGGGGCTTACTAATGCCTTTTAGCTCCCT	1	161569925	161569954	161615628
BOK	GACCCCCGGGAATTGGCTCCAGCACATCTCGAGGGCGGGCCCGGCGGCCCCGGAGCAAAC	2	242454061	242454090	242498608
FCGR2B	AAAAAACAATTATGTAATTGAAAACCCATCGAAGCTCTTTGGTTCCACAGAGTGATTCTG	15	75047316	75047345	75075210
HLA-DQB1	AGGCATTCGTTCTTCAGCTCTTCTATAATCGATTTTTTATTGTATCCTATATTTTTTCTA	1	6526238	6526267	6554649
PTPRA	GCTCTTATAAATTATGTATTCAAAGAAATCGAGTTGCAGGCCGCCCTGGTGGCTAGACAT	7	155595852	155595881	155630427
AKT1	CCCGCGGCGGAGCTGCTACTGTTTACTTTCGAAGCTTCTTCCTTTCGGCCCCCAGGCCTA	20	2797356	2797385	2948630
PTPRA	GCTCTTATAAATTATGTATTCAAAGAAATCGAACTGGCGGCAACCGCTGCAGCGCCTGCT	1	6526238	6526267	6558079
FCGR2B	AAAAAACAATTATGTAATTGAAAACCCATCGAGGGGCTTACTAATGCCTTTTAGCTCCCT	2	242454061	242454090	242498608
BOK	TCTCCTGCCTACCACACTGTGAGAAAGCTCGAGGGCGGGCCCGGCGGCCCCGGAGCAAAC	15	75047316	75047345	75075210
CSK	GAGTTCAGCGTGCCGCCGGGCGTGAAAGTCGAATTCTCCCAGGAGCCACTGTCAGAACCC	1	6526238	6526267	6554649
TNFRSF25	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGACAATGTTATTCTTTGTTTCTCTTACCAA	7	155595852	155595881	155630427
SHH	GAAGGCCCGGTGCGCCCAGCTGTGCTCCTCGAGAACAGCCAGGCTAACACGGAGAAACCC	20	2797356	2797385	2948630
PTPRA	TCCATTGTCTTATTCCAGTCTAGGCTTGTCGAACTGGCGGCAACCGCTGCAGCGCCTGCT	1	6526238	6526267	6558079
TNFRSF25	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGATGTGTTGGAAGTCAGGGCGGCGGTGCCC	2	242454061	242454090	242498608
PIK3CA					
IL12B					
MYD88					
PVRL1					
PIK3R3					
CD6					
TREM1					

IL12A					
	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGAGGCTTTCAAGGGATCCAGGGTGGGGTGC	1	6526238	6526267	6544279
	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGACAATGTTATTCTTTGTTTCTCTTACCAA	1	6526238	6526267	6554649
	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGATGTGTTGGAAGTCAGGGCGGCGGTGCCC	1	6526238	6526267	6558079
	CACTTCCCCAACATAAGCCTCGGTCTCTTCGAGGGCGGGCCCGGCGGCCCCGGAGCAAAC	2	242498608	242498637	242532080
	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGAGAAGCATAAAGCAGGGACAGGTATGGAG	1	6526238	6526267	6574085
	GACCCCCGGGAATTGGCTCCAGCACATCTCGAGGGCGGGCCCGGCGGCCCCGGAGCAAAC	2	242474876	242474905	242498608
	GTTTGCTCCGGGGCCGCCGGGCCCGCCCTCGATTTTAACACCACCATGGTTTGAATGAAT	2	242498608	242498637	242517412
	GTGTCTCGGCCCCCTGGGGCCCCACCCTTCGATTTCCCTGTTGCCGCCGCGTTTGCAAGA	5	131813575	131813604	131832725
	TCTCCTGCCTACCACACTGTGAGAAAGCTCGAGGGCGGGCCCGGCGGCCCCGGAGCAAAC	2	242454061	242454090	242498608
	GAGTTCAGCGTGCCGCCGGGCGTGAAAGTCGAGGCATATTTGAGTTTAGGGAGGTGTTGC	15	75047316	75047345	75083505
	GGGCACCGCCGCCCTGACTTCCAACACATCGATCTCTGCCTCGCGCAGCCCCAGCGTGCG	1	6521665	6521694	6558079
	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGATTTCCAAAAGCTCACACATGGGTGCACA	8	42128692	42128721	42148498
	GGGCACCGCCGCCCTGACTTCCAACACATCGAAGAATGGGTGGGGCCTTGCACCTCATAC	1	6510664	6510693	6558079
	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGACCCCCTGACATGGGGCTGCCTGGAGCAG	8	42128692	42128721	42188563
	GGGCACCGCCGCCCTGACTTCCAACACATCGAGAAGCATAAAGCAGGGACAGGTATGGAG	1	6558079	6558108	6574085
	GAGTTCAGCGTGCCGCCGGGCGTGAAAGTCGACTCTGGGCCCAGACCACAGAAGGAGGGG	15	75047316	75047345	75080014
	AATTCTGTTGGAAGAATAATTTAAAATATCGATGTGGCGACCGGCTGTGGGGGTCACGGA	13	111748013	111748042	111954400
	TTCCATAGATTACTTTTCAAATCATCCTTCGAAGCTGGCGGCTGAGGGCCCGGCGCCAAG	17	40406430	40406459	40464295
	GAGTTCAGCGTGCCGCCGGGCGTGAAAGTCGATTTGTTTATGGTTTTATCCCCAGTGCCT	15	75047316	75047345	75072258
	CACCCTCCCTTCTTCCTGGGCCCTCAGATCGACCCCCCCCACCCCCACCGGGCTGGCTGC	19	50158040	50158069	50185426
	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAGGGCCTGGCAAGAAGACAGAAGCCGACT	8	42128692	42128721	42138741
	TATGAGTAATAATTACAATTTCCCCCTTTCGACCTCCAGGTCCCCCGCCACTTCCACGGC	9	123675825	123675854	123702717
	CAGAAACTGCTGGTTGGGCTCATACTTTTCGAGGGCCAGCTCCCCGCACCCCCACCAAGC	11	64023978	64024007	64060064
	TTCCCCTGTAAGATTCATTTCCTGTGATTCGAGTCACAGCTGTAGTGGGGTGGGGGGTGA	21	45665442	45665471	45687443
	TCTTTGTTACTGGAATATACGAATAAAATCGATGTGGCGACCGGCTGTGGGGGTCACGGA	13	111732623	111732652	111748013

Table 5a

Gene Locus	End2	Chr	Start1	End1	Start2	End2
PVRL1	119600028	11	119573310	119577309	119599999	119603998
HLA-DQB1	32669162	6	32607973	32611972	32669133	32673132

HLA-DQB1	32630168	6	32607973	32611972	32630139	32634138
BOK	242532109	2	242498608	242502607	242528110	242532109
CSK	75083534	15	75043346	75047345	75083505	75087504
CSK	75080043	15	75043346	75047345	75076044	75080043
CSK	75072287	15	75043346	75047345	75072258	75076257
HLA-DQB1	32669162	6	32630139	32634138	32669133	32673132
STAT5B	40464324	17	40402460	40406459	40464295	40468294
BOK	242517441	2	242498608	242502607	242517412	242521411
PTPRA	2948659	20	2853762	2857761	2944660	2948659
FCGR2B	161615657	1	161565955	161569954	161615628	161619627
BOK	242498637	2	242454061	242458060	242498608	242502607
FCGR2B	75075239	15	75043346	75047345	75075210	75079209
HLA-DQB1	6554678	1	6522268	6526267	6554649	6558648
PTPRA	155630456	7	155591882	155595881	155626457	155630456
AKT1	2948659	20	2797356	2801355	2944660	2948659
PTPRA	6558108	1	6522268	6526267	6554109	6558108
FCGR2B	242498637	2	242454061	242458060	242498608	242502607
BOK	75075239	15	75043346	75047345	75075210	75079209
CSK	6554678	1	6522268	6526267	6554649	6558648
TNFRSF25	155630456	7	155591882	155595881	155626457	155630456
SHH	2948659	20	2797356	2801355	2944660	2948659
PTPRA	6558108	1	6522268	6526267	6554109	6558108
TNFRSF25	242498637	2	242454061	242458060	242498608	242502607
	6544308	1	6522268	6526267	6540309	6544308
	6554678	1	6522268	6526267	6554649	6558648
	6558108	1	6522268	6526267	6554109	6558108
	242532109	2	242498608	242502607	242528110	242532109
	6574114	1	6522268	6526267	6574085	6578084
	242498637	2	242474876	242478875	242498608	242502607
	242517441	2	242498608	242502607	242517412	242521411
	131832754	5	131809605	131813604	131828755	131832754
	242498637	2	242454061	242458060	242498608	242502607

	75083534	15	75043346	75047345	75083505	75087504
	6558108	1	6521665	6525664	6554109	6558108
	42148527	8	42124722	42128721	42148498	42152497
	6558108	1	6510664	6514663	6554109	6558108
	42188592	8	42124722	42128721	42188563	42192562
	6574114	1	6554109	6558108	6574085	6578084
	75080043	15	75043346	75047345	75076044	75080043
	111954429	13	111748013	111752012	111950430	111954429
	40464324	17	40402460	40406459	40464295	40468294
	75072287	15	75043346	75047345	75072258	75076257
	50185455	19	50158040	50162039	50181456	50185455
	42138770	8	42124722	42128721	42138741	42142740
	123702746	9	123675825	123679824	123698747	123702746
	64060093	11	64023978	64027977	64060064	64064063
	45687472	21	45661472	45665471	45687443	45691442
	111748042	13	111728653	111732652	111748013	111752012

Table 5b

Gene Locus	Probe	Chr	Start1	End1	Start2
BAX	AAGGCAGGCAGATCAGGAGCTCAAGAGATCGAAAGAAAAAAAAAAAAGCATAAAAATCCA	19	49419941	49419970	49474800
BAX	AAGGCAGGCAGATCAGGAGCTCAAGAGATCGAACGCTAAGTGTAGTTTAACACCTACTAG	19	49419941	49419970	49438538
CASP1	ATAGTAAAATGTGAAAATGTTACAGTTATCGAAGTTCAGCGAGTATATTTTTACTGATAC	11	104941452	104941481	104994206
NCK2	AAGGCCCAAGAACCAGGAATCTAGGTATTCGAAAAGCCCTAAAGTTGGCTTAATAAACTT	2	106375591	106375620	106457773
JAM2	GGTGGGCAGATCACTTAAGGCCAGGAATTCGAATGCAAAACTCACTACCCACTGGTAAGA	21	26998354	26998383	27012523
JAM2	GGTGGGCAGATCACTTAAGGCCAGGAATTCGATTCTATCAACTCTAGAATTTTTTTAAAT	21	26998354	26998383	27073929
BAX	AAGGCAGGCAGATCAGGAGCTCAAGAGATCGAGGTAAATGTGGGGGTTCTAGAACCCAGT	19	49419941	49419970	49471564
JAM2	GGTGGGCAGATCACTTAAGGCCAGGAATTCGAAATTCTTTCCTAATGCCAAGTGTGTTAT	21	26998354	26998383	27076729
CXCL2	GGTCCCCTGATTTCCATCCTAGTGCTTCTCGAAACATGTGCTCTGGAGATAAAGCGCCAA	4	74949500	74949529	74968427
JAM2	GGTGGGCAGATCACTTAAGGCCAGGAATTCGATATTCAATAAAAGACCGGATGTGCAAAG	21	26998354	26998383	27056448
JAM2	GGTGGGCAGATCACTTAAGGCCAGGAATTCGAGAAATGGTTTATCCAATTCATCCAAAAT	21	26998354	26998383	27060381
JAM2	GGTGGGCAGATCACTTAAGGCCAGGAATTCGAGAGACTGTAAAGACATGTGTCTGCCTCT	21	26998354	26998383	27047036
JAM2	GGTGGGCAGATCACTTAAGGCCAGGAATTCGATCACTTCTTAAAGGCCCTACCTCTTAAT	21	26998354	26998383	27035796
IL2	GTTGGGTTGAAGATGAAATCATAGGAAGTCGAGCTGTAACCTCTGCTTGGTATTCTCCCT	4	123404410	123404439	123422745

JAM2	GGTGGGCAGATCACTTAAGGCCAGGAATTCGAAACACCAGCTCTCTTAAATCCTGTGCCT	21	26998354	26998383	27028108
JAM2	GGTGGGCAGATCACTTAAGGCCAGGAATTCGAGGAAAACCTCGGGGCAAAATAGGGAAAG	21	26998354	26998383	27050012
BAX	TGAGAATGGAATAGATCAAAGGGAGGGTTCGAGACAAGGTCTCACTTTATCACCCAACCT	19	49421752	49421781	49475137
JAM2	GGTGGGCAGATCACTTAAGGCCAGGAATTCGACTGTGTGCCCATGAAGAAAGAAGATGGG	21	26998354	26998383	27070794
IL4	AGTGATAGAAGAGGGACAAGGTGGCAGTTCGATTTTAAAACACGCTCTTCAATAAAAAGA	5	131972293	131972322	131985853
CBLB	AGCAGGGGGATCACATAAGGCCAGGAGTTCGATAAAATAAATTAGAGAAGATATAAATAA	3	105394496	105394525	105635546
JAM2	GGTGGGCAGATCACTTAAGGCCAGGAATTCGATTTCTCTGCTTCTCTCACAGCCCACATC	21	26998354	26998383	27083337
NCK2	TCTTTGCAGATGTTGTAAGATAAGGATGTCGAAAAGCCCTAAAGTTGGCTTAATAAACTT	2	106358253	106358282	106457773
CXCL2	GGTCCCCTGATTTCCATCCTAGTGCTTCTCGATGATATAATACTCTGCTGACTACATTTT	4	74949500	74949529	74983629
NCK2	AAGGCCCAAGAACCAGGAATCTAGGTATTCGACCACCTTAAAAGAAAAATCTCTTGGAAC	2	106375591	106375620	106435341
CBLB	AGCAGGGGGATCACATAAGGCCAGGAGTTCGATGAACGTTTACCCAATTATTTCTAAACA	3	105394496	105394525	105606665
MAP3K14	GATGCGGACTGTTTCCTGCTTTGATTTATCGACTTCTTATTTCTATTTTGTGACTTAGGA				
MAP3K14	GATGCGGACTGTTTCCTGCTTTGATTTATCGACACAGTGTGTCTGAAGTTTGGGGTGGTA				
MAP3K14	GATGCGGACTGTTTCCTGCTTTGATTTATCGATATCTCCCTCCTTTCGCTTCTTCCTTTC				
MAP3K14	GATGCGGACTGTTTCCTGCTTTGATTTATCGAGTCATTAAGAGACTCTCCGCCTGGGTGG				
PRKCQ	TTCCACCTGTAATACTGTGCCTGTATTCTCGACTCTTCTCGCCCTCTTCTCCAGCTCTCT				
SIRPA	TAAAGTACTGTGTCCCACATATAAGTACTCGACCAAGAAATTCATTCTTACCTCCTAAGA				
MAPK1	ACCCCACCAATCTATAATAAGATTGATTTCGACACAAGGGTTTGTAACAAAAAACAAAAA				
SIRPA	AGCGCTTTATTTGTCAGGACGATAGACCTCGACAATGTCCTATTCTTCCAGAAACTCATT				
CBLB	TTATTACTTTATTCTGACTGAATATCATTCGAAAGAAACCAAAAACACAAGTATACATCA				
CBLB	TATCCTTTGGTTTAGAAGTATTTCTTATTCGACAAAATTTTAACATGTTATGCAGTTACA				
PRKCQ	TTCAGCTATTCACTGGTTTTTCTTCAGATCGACTCCTGCTTCCCTCCCCTCATCTTTAAA				
CBLB	TCCAGTACAATAAACAATGTACCAAAGATCGACAAAATTTTAACATGTTATGCAGTTACA				
IGKC	TAAACTCTGACATTGCCTATTAGCATTCTCGAATGCATGGCTCACTGTAACCTCCAACTC				
CBLB	TATCCTTTGGTTTAGAAGTATTTCTTATTCGACAACTACTGGCTTAAAAAAGGCAAAACA				
PRKCQ	TACCTCCTTGGGAACATATTTGAGAGTTTCGACTCCTGCTTCCCTCCCCTCATCTTTAAA				
SIRPA	ACACTTGATTTTTGCTTTCCAAGCTGACTCGAGACATCTAAGAAGGTCCAGCCAGATGTT				
SIRPA	GCGCCCTATTTCCACCTTGTGCCTTCTGTCGACACACCAAGATGTCACGGAGGAGTCTGT				
NCK2	CCAGCTGAAGTTTCGCAGGTCCCCTGCTTCGAGTAGGCCAATCCCATTTTTGGCGAAAAC				
PRKCQ	TACCTCCTTGGGAACATATTTGAGAGTTTCGACTCCTGCTTCCCTCCCCTCATCTTTAAA				
SIRPA	ACACTTGATTTTTGCTTTCCAAGCTGACTCGAGACATCTAAGAAGGTCCAGCCAGATGTT				
SIRPA	GCGCCCTATTTCCACCTTGTGCCTTCTGTCGACACACCAAGATGTCACGGAGGAGTCTGT				
NCK2	CCAGCTGAAGTTTCGCAGGTCCCCTGCTTCGAGTAGGCCAATCCCATTTTTGGCGAAAAC				

PRKCQ	ACTTTGGCTCAAGAGTGAAGATATTCAGTCGACTCCTGCTTCCCTCCCCTCATCTTTAAA				
MAPK1	TTCCTTAGGCAAGTCATCCAATTCCATGTCGACACAAGGGTTTGTAACAAAAAACAAAAA				
SIRPA	TCTTAGGAGGTAAGAATGAATTTCTTGGTCGAACTCCTGACCAGGAGGCTGGGAGGGGGT				
CASP7	CATCATTTTAATAGGTGCAAGAGTTCCGTCGAACGCCCATACCTGTGGGAATCAAGCAAT				
NCK2	AAAAACAAAAAAGCCAATTCTGTACCCCTCGAACCAGCCCTGGCTCTGTCCCCAGACCTT				
SIRPA	GCGCCCTATTTCCACCTTGTGCCTTCTGTCGAGACATCTAAGAAGGTCCAGCCAGATGTT				
PRKCQ	TTGATTATTTCAGGTTGACAGCTGTAAATCGACTCCTGCTTCCCTCCCCTCATCTTTAAA				
		10	6474856	6474885	6548385
		3	105471109	105471138	105544694
		2	89164038	89164067	89179765
		3	105442256	105442285	105466913
		10	6474856	6474885	6595633
		20	1905280	1905309	1933305
		20	1872136	1872165	1900305
		2	106403394	106403423	106473848
		10	6474856	6474885	6605104
		22	22123553	22123582	22210842
		20	1830613	1830642	1877967
		10	115421381	115421410	115481392
		2	106383184	106383213	106439122
		20	1872136	1872165	1905280
		10	6474856	6474885	6515326

Table 6a

Gene Locus	End2	Chr	Start1	End1	Start2	End2
BAX	49474829	19	49415971	49419970	49470830	5E+07
BAX	49438567	19	49415971	49419970	49434568	5E+07
CASP1	104994235	11	104941452	104945451	104994206	1E+08
NCK2	106457802	2	106375591	106379590	106457773	1E+08
JAM2	27012552	21	26994384	26998383	27012523	3E+07
JAM2	27073958	21	26994384	26998383	27069959	3E+07
BAX	49471593	19	49415971	49419970	49471564	5E+07
JAM2	27076758	21	26994384	26998383	27072759	3E+07
CXCL2	74968456	4	74949500	74953499	74968427	7E+07
JAM2	27056477	21	26994384	26998383	27056448	3E+07
JAM2	27060410	21	26994384	26998383	27056411	3E+07
JAM2	27047065	21	26994384	26998383	27047036	3E+07
JAM2	27035825	21	26994384	26998383	27031826	3E+07
IL2	123422774	4	123400440	123404439	123418775	1E+08
JAM2	27028137	21	26994384	26998383	27028108	3E+07
JAM2	27050041	21	26994384	26998383	27046042	3E+07
BAX	49475166	19	49421752	49425751	49475137	5E+07
JAM2	27070823	21	26994384	26998383	27070794	3E+07
IL4	131985882	5	131968323	131972322	131985853	1E+08
CBLB	105635575	3	105390526	105394525	105631576	1E+08
JAM2	27083366	21	26994384	26998383	27079367	3E+07
NCK2	106457802	2	106354283	106358282	106457773	1E+08
CXCL2	74983658	4	74949500	74953499	74983629	7E+07
NCK2	106435370	2	106375591	106379590	106435341	1E+08
CBLB	105606694	3	105390526	105394525	105606665	1E+08
	6548414	10	6474856	6478855	6544415	7E+06
	105544723	3	105471109	105475108	105540724	1E+08
	89179794	2	89160068	89164067	89175795	9E+07
	105466942	3	105442256	105446255	105466913	1E+08
	6595662	10	6474856	6478855	6591663	7E+06
	1933334	20	1905280	1909279	1929335	2E+06
	1900334	20	1872136	1876135	1900305	2E+06

	106473877	2	106403394	106407393	106473848	1E+08
	6605133	10	6474856	6478855	6601134	7E+06
	22210871	22	22119583	22123582	22210842	2E+07
	1877996	20	1830613	1834612	1873997	2E+06
	115481421	10	115417411	115421410	115477422	1E+08
	106439151	2	106383184	106387183	106435152	1E+08
	1905309	20	1872136	1876135	1905280	2E+06
	6515355	10	6474856	6478855	6511356	7E+06

Table 6b

Gene Locus	**PCR Primer 1 Sequence**	**PCR Primer 2 Sequence**	**Probe**
IL15	TGAGTAACACAAAGCATCTG	AGTGACTGGCTATGTTCC	
MYD88	CTGGTGATTTGTGTGACTTTG	AGGGAAGATGTGGAGGAG	
HLA-DQB1	GTACGACTCCAGCCAAATG	GCTGTCTGTTACTAGATTGCAC	
IL12B	ACCTTGCAAGAAGCACAG	ATGATACTTCCCAACTGACAC	
PVRL1	AGGAGCATCCATATCAAGTG	CTGCCATGTCTGACTATCC	
PIK3R3	CAGTGAAGAAGCCATCATCG	CTTAGAGAAATACACCAGCAG	
CD6	ATGGGCAGCATTTCTCAC	AGGGACGATTTATATGACTTGC	
STAT5B	GTGCTGGTATGTACCTGTAATC	GAGGGTTGAGAAGCATCTTG	
IL15			TGTAAACTGTAATATCAAAAATTCAAAATCGAAGAGTTGATTTACTTATTAACATTAGAA
MYD88			ACTTTTATAGTGAAAAGTGCCATTTGAGTCGACTGTGATTGAATGTAAAAGGTTTTAAAT
HLA-DQB1			TACTGTAGTAAGTTCTCTGAGGAGGATATCGAAGTCTTGGATTAAGGTTCATTCAACAAA
IL12B			TCCATTTGAAGGATGAGAAAACTGAGGCTCGAGGCTTAGAAAGTTTCATTTGGTTGCTCA
PVRL1			TTTTAAACCCAGGTGCACACACAAGAGCTCGAAGCAGGAATCCTGGTTCTGTTCCCAGGC
PIK3R3			CCACTCCCCCAGGCTTACCTGCGAGCCATCGAGGTGGGCCTGGGTTCTCGTGGAGGGAGA
CD6			TCACTCATTCTAGATCCCTCTGTAAAGTTCGAACTCTGGACCTTGTGATCCACCCACCTT
STAT5B			TTCCATAGATTACTTTTCAAATCATCCTTCGAAGCTGGCGGCTGAGGGCCCGGCGCCAAG

Table 7a

Gene Locus	**Chr**	**Start1**	**End1**	**Start2**	**End2**	**Chr**	**Start1**	**End1**	**Start2**	**End2**
IL15	4	142530357	142530386	142659035	142659066	4	142530357	142534356	142655067	142659066

Table 7b

Stimulatory checkpoint molecules	Inhibitory checkpoint molecules
CD27	A2AR
CD28	B7-H3
CD40	B7-H4
CD122	CTLA-4
CD137	IDO
OX40	KIR
GITR	LAG3
ICOS	PD-1
	TIM-3
	VISTA

Table 8

Drug	Targets	Preferred Cancer
Alemtuzumab (monoclonal antibody).	CD52	Fludarabine-refractory Chronic lymphocytic leukemia Cutaneous T-cell lymphoma Peripheral T-cell lymphoma T-cell prolymphocytic leukemia
Ofatumumab (Second generation human IgG1 antibody).	CD20	Chronic lymphocytic leukemia Follicular lymphoma Diffuse large B cell lymphoma
Pegylated liposomal doxorubicin (PLD) plus motolimod (VTX2337).		
Sipuleucel-T (Approved Cancer Vaccine).		Prostate cancer
Rituximab (monoclonal antibody).	CD20	B-cell malignancies

		Aggressive and indolent lymphomas such as diffuse large B-cell lymphoma and follicular lymphoma and leukaemias such as B-cell chronic lymphocytic leukaemia
Interferon gamma		
Combinatorial ablation and immunotherapy.		Curative metastatic cancer treatment
Polysaccharide-K		Stimulate the immune systems of patients undergoing chemotherapy.
Adoptive cell therapy		
Anti-CD47 antibodies.	CD47	
Polypurine reverse Hoogsteen oligonucleotides (PPRHs).		Breast cancer
Anti-GD2 antibodies.	GD2	
BGB-A317 (monoclonal antibody).	PD-1 inhibitor	
Affimer biotherapeutic.	PD-L1 inhibitor	
Polysaccharides		
Neoantigens		

Table 9

Drug	**targets**	**Preferred Disease**
Ipilimumab &Nivolumab	PD-1 and CTLA-4	metastatic melanoma
Paclitaxel, ipilimumab & carboplatin	CTLA4	non-small-cell lung cancer
Ipilimumab & GVAX	CTLA-4	pancreatic cancer
Pidilizumab & rituximab	PD-1	hematologic malignancies
L19-IL2 & L19-TNF	STAT	melanoma
MEDI0680 & Durvalumab	PD1/PDL1	Advanced solid malignancies

Table 10. Combinations in cancer immunotherapy (biologics, immunocytokines (L19-IL2 and L19-TNF), cytotoxics (Paxlitaxel)

Drug	targets	Disease
CA-170 (small molecule)	PD1-PDL1 and VISTA	Advanced solid tumour and lymphoma
Ruxolitinib (small molecule)	JAK	myelofibrosis and multiple myeloma
Tofacitinib (small molecule)	JAK	autoimmune disease
Galiellelactone (small molecule)	STAT3	prostate cancer
Ipilimumab (monoclonal antibody)	CTLA4	melanoma, prostate
L19-IL2 (immunocytokine)	STAT	melanoma, pancreatic cancer, RCC
L19-TNF (immunocytokine)	STAT	melanoma
Tremelimumab (monoclonal antibody)	CTLA4	mesothelioma
Nivolumab (ditto)	PD1	melanoma, non–small-cell lung cancer, renal cell carcinoma, and other solid tumors
Pembrolizumab	PD1	melanoma, non–small-cell lung cancer, renal cell carcinoma, and other solid tumors
Pidilizumab	PD1	hematologic malignancies
BMS935559	PD-L1	variety of solid tumors

GVAXMPDL3280A	PD-L1	bladder cancer, head and neck cancer, and GI malignancies
MEDI4736	PD-L1	bladder cancer, head and neck cancer, and GI malignancies
MSB0010718C	PD-L1	bladder cancer, head and neck cancer, and GI malignancies
MDX-1105/BMS-936559	PD-L1	cancer
AMP-224	PD1	colorectal cancer
MEDI0680	PD1	advanced solid tumors
Durvalumab	PDL1	non-small –cell lung cancer
Atezolizumab	PDL1	advanced or metastatic urothelial carcinoma
Avelumab	PDL1	metastatic Merkel cell carcinoma

Table 11. Other single molecules, immunocytokines and biologics for cancer therapy

Gene	Name	Function
AAGAB	Alpha- And Gamma-Adaptin Binding Protein	Protein Coding gene, interacts with gamma and alpha-adaptin subunits of complexes associated with clathrin-coated vesicle trafficking, associated with Punctate Palmoplantar Keratoderma
AARS2	Alanyl-TRNA Synthetase 2, Mitochondrial	Protein Coding gene, encodes a class-II aminoacyl-tRNA synthetase that aminoacylates alanyl-tRNA, associated with Combined Oxidative Phosphorylation Deficiency 8 and Leukoencephalopathy
ABCD3	ATP Binding Cassette Subfamily D Member 3	Protein Coding gene, member of ALD sub family of ATP-binding cassette (ABC) transporters, associated with Congenital Bile Acid Synthesis Defect 5 and Zellweger Syndrome
AC009133.22	ENSG00000277669	Protein Coding gene, associated with carboxylating and transferase activity
AC105009.1	ENSG00000281855	Predicted intracellular Protein Coding gene
AC138028.1	ENSG00000280603	Predicted intracellular Protein Coding gene, breast cancer
ACSL6	Acyl-CoA Synthetase Long-Chain Family Member 6	Protein Coding gene, catalyzes formation of acyl-CoA from fatty acids, associated with myelodysplastic syndromes and Chronic Intestinal Vascular Insufficiency

ACTA2	Actin, Alpha 2, Smooth Muscle, Aorta	Protein Coding gene, alpha actin found in skeletal muscle, associated with type 6 familial thoracic aortic aneurysms, multisystemic smooth muscle dysfunction syndrome and moyamoya disease
ADAMTS14	ADAM Metallopeptidase With Thrombospondin Type 1 Motif 14	Protein Coding gene, preproprotein processed into enzyme that cleaves amino-terminal propeptides from type I procollagen, may be associated with osteoarthritis
ADAMTSL4	ADAMTS Like 4	Protein Coding gene, protein with 7 thrombospondin type 1 repeats, associated with Ectopia Lentis Et Pupillae and Autosomal Recessive Isolated Ectopia Lentis
ADM5	Adrenomedullin 5 (Putative)	Protein Coding gene, associated with phlebotomus fever
ADSSL1	Adenylosuccinate Synthase Like 1	Protein Coding gene, functions in the purine nucleotide cycle during conversion of IMP to AMP, associated with adolescent distal myopathy, ADSS is an important paralog
AFAP1L1	Actin Filament Associated Protein 1 Like 1	Protein Coding gene, may have role in invadosome and podosome formation, AFAP1 is a paralog, associated with spindle cell sarcomas possibly prognostic
AGMAT	Agmatinase	Protein Coding gene, Involved in synthesising putrescine from agmatine, ARG2 is a paralog
AIRE	Autoimmune Regulator	Protein Coding gene, transcriptional regulator, regulates expression of autoantigens and role in the thymus selecting negatively against autoreactive T-Cells, associated with autoimmune polyendocrinopathy syndromes, APECED
ALDOA	Aldolase, Fructose-Bisphosphate A	Protein Coding gene, encodes Aldolase A, an enzyme that serves as a catalyst in conversion of fructose-1,6-bisphosphate to glyceraldehyde 3-phosphate and dihydroxyacetone phosphate (glycolysis and glucogenesis), associated with myopathy, hemolytic anaemia, potential oncogene in pancreatic cancer and marker in osteosarcoma
ALS2CR12	Amyotrophic Lateral Sclerosis 2 Chromosome Region 12	Protein coding gene, associated with ALS2 and lateral sclerosis, potential implication in breast cancer risk
AMDHD2	Amidohydrolase Domain Containing 2	Protein Coding gene, functions in Neu5Gc pathway by hydrolysing N-glycolyl group from N-glycolylglucosamine 6-phosphate (GlcNGc-6-P), ENSG00000259784 is a paralog
ANGPTL7	Angiopoietin Like 7	Protein Coding gene, a paralog is ANGPT4, may be associated with glaucoma
APLP1	Amyloid Beta Precursor Like Protein 1	Protein Coding gene, may act as trascriptional activator and function during maturation of synapses, associated with Alzheimer disease and Subendocardial Myocardial Infarction, APLP2 is a paralog
ARHGAP24	Rho GTPase Activating Protein 24	Protein coding gene, is an antagonist of Rac, regulating cell polarity, associated with Atypical Autism and Familial Idiopathic Steroid-Resistant Nephrotic Syndrome With Focal Segmental Hyalinosis
ARHGEF1	Rho Guanine Nucleotide Exchange Factor 1	Protein coding gene, may trigger signals dependent on Rho by forming complexes with G proteins, associated diseases are Skin Lipoma and Third Cranial Nerve Disease, ARHGEF2 is a paralog

ATG4B	Autophagy Related 4B Cysteine Peptidase	Protein Coding gene, needed for autophagy and Cvt, exposes glycine at C-terminus of ATG8 proteins this step is needed so ATG8 proteins can conjugate to phosphatidylethanolamine and insert in to membranes which is need for autophagy
ATIC	5-Aminoimidazole-4-Carboxamide Ribonucleotide Formyltransferase/IMP Cyclohydrolase	Protein Coding gene, is a catalyst for the final 2 steps in the de novo purine biosynthetic pathway, associated with AICA-ribosiduria and Mental retardation epilepsy
ATN1	Atrophin 1	Protein coding gene, transcriptional corepressor, promotes VSMC migration, corepressor of MTG8, associated with Dentatorubral pallidoluysian atrophy and Spinocerebellar Ataxia
ATP6V0A1	ATPase H+ Transporting V0 Subunit A1	Protein Coding gene, part of vacuolar ATPase, needed for sorting proteins, receptor-mediated endocytosis, synaptic vesicle proton gradient generation and zymogen activation, associated with Inferior Myocardial infarction and potentially CRC
ATP6V0C	ATPase H+ Transporting V0 Subunit C	Protein Coding gene, part of vacuolar ATPase, needed for sorting proteins, receptor-mediated endocytosis, synaptic vesicle proton gradient generation and zymogen activation, associated with Dravet syndrome
BCL2L12	BCL2 Like 12	Protein Coding gene, encodes anti-apoptotic inhibitor of Caspases 3 and 7, interacts with p53 protein, over expressed in different cancers, associated with breast cancer and AML
BCL2L13	BCL2 Like 13	Protein Coding gene, may have role activating caspase-3 and influencing apoptosis, overexpression causes apoptosis, associated with cat-eye syndrome, ALL and glioblastoma
BCL2L2	BCL2 Like 2	Protein coding gene, cell survival promoter, stops apoptosis by dexamethasone, and inhibits BAX activity on Sertoli cells, associated with small intestinal adenocarcinoma, BCL2L1 is a paralog
BCL2L2-PABPN1	BCL2L2-PABPN1 Readthrough	Protein Coding gene, fusion protein shares sequence from the two neighbouring genes, cell survival promoter, stops apoptosis by dexamethasone, inhibits BAX activity on Sertoli cells, PABPN1 is a paralog
BOLA2B	BolA Family Member 2B	Protein Coding Gene, may be associated with iron maturation, BOLA2 is a paralog
BRD2	Bromodomain Containing 2	Protein Coding gene, transcriptional regulator, potentially through chromatin remodelling through binding hyperacetylated chromatin, transcription regulator of CCND1, may have roles in folliculogenesis, spermatogenesis and, assembly of nucleosomes, associated with junior myoclonic epilepsy, BRD3 is a paralog.
BRI3BP	BRI3 Binding Protein	Protein Coding gene, has role in tumourigenesis, may stabilise p53/TP53, possible association to cervical cancer
C12orf57	Chromosome 12 Open Reading Frame 57	Protein Coding gene, functions in the development of corpus callosum, associated with Temtamy Syndrome and Colobomatous Microphthalmia

C16orf59	Chromosome 16 Open Reading Frame 59	Protein Coding gene, protein not characterised
C1orf137	Chromosome 1 Open Reading Frame 137	Protein Coding gene, protein not characterised
C1orf168	Chromosome 1 Open Reading Frame 168	Protein Coding gene, adapter protein that has function TCR activated signalling pathways, need for activating T-Cells and their response to TCR stimulaltion and integrin control adhesion
C1QTNF5	C1q And TNF Related 5	Protein Coding gene, may have function in cell adhesion, family member of proteins that have roles in basement membranes, associated with Retinal degradation and macular degeneration, C1QTNF9 is a paralog
C20orf141	Chromosome 20 Open Reading Frame 141	Protein Coding gene, protein not characterised, ENSG00000241690 is a paralog
C5AR1	Complement C5a Receptor 1	Protein Coding gene, receptor for C5a, activated can stimulate chemotaxis, granule enzyme release, superoxide anion production and role in the relase of intracellular calcium, associated with Listeria Meningitis and Malaria, C5AR2 is important paralog
C5orf56	Chromosome 5 Open Reading Frame 56	RNA gene associated to ncRNA family
NDUFA2	NADH:Ubiquinone Oxidoreductase Subunit A2	Protein coding gene, forms a subunit of the NADH:Ubiquinone oxidoreductase complex1, enzyme in electron transport chain
NFATC2IP	Nuclear Factor Of Activated T-Cells 2 Interacting Protein	Protein coding gene, promotes cytokine expression in T helper 2 cells through the magnitude regulation of NFAT- driven transcription
NFKB1	Nuclear Factor Kappa B Subunit 1	Protein coding gene, Rel ptorein-specific transcription inhibitor and as part of the DNA binding subunit of NF-kappa-B protein complex- transcritpion regulator controled by a large number of intra and extra cellular signals
NFKBID	NFKB Inhibitor Delta	Protein coding gene, regulates IL-2, IL-6 and others through its regualtion of NF-kappa-B activity
NFKBIE	NFKB Inhibitor Epsilon	Protein coding gene, binds to NF-kappa-B preventing cellular translocation from the cytoplasm to nucleus
NOL9	Nucleolar Protein 9	Protein coding gene, polynucleotide 5-kinase processes rRNA in the nucleos and cytosol, required for processing of 5.8s and 28S rRNA
NPHS1	Nephrin	Immunoglobulin family of cell adhesion member involved in the filtration barrier of the kidneys, primarily expressed in renal tissue, mutations can cause Finnish-type congential nephrosis 1
NRGN	Neurogranin	Encodes a protein kinase substrate, exon 1 and 2 encode protein, exons 3+4 contain UTR, protein binds calmodulin in the absence of calcium

NTN3	Netrin 3	Protein encoding gene, involved in Axon guidence of central nervous system and peripheral motor neurons
NUCB1	Nucleobindin 1	Protein coding gene, involved in Golgi calcium homoestasis and calcium regulated signal transduction
NUDT22	Nudix Hydrolase 22	Protein coding gene, protein with hydrolyase activity
OPALIN	Oligodendrocytic Myelin Paranodal And Inner Loop Protein	Protein coding gene, expression mostly found in brain tissues
OSMR	Oncostatin M Receptor	Protein coding gene, type I cytokine receptor, heteodimerizes with IL-6 signal transducer to form type II oncostatin M receptor and also IL-31 receptor A to form IL 31 receptor, mutations assoocated with familial primary localized cutaneous amyloidosis
P3H3	Prolyl 3-Hydroxylase 3	Protein coding, proteoglycan of the leprecan family, reuqired for collagen biosynthesis, folding and assrmbly. Found in the endoplasmic reticulum.Assoicated with breast and other cancers through epigenetics inactivation.
PABPN1	Poly(A) Binding Protein Nuclear 1	Protein coding gene, binds to nacent poly(A) tails with high affinity, required to enlarge poly(A) tail to apporx. 250 nt., expansion of GCG trinucleotide repeat of the 5' coding region associated with OPMD - oculopharyngeal muscular dystrophy
PAG1	Phosphoprotein Membrane Anchor With Glycosphingolipid Microdomains 1	Protein coding, type III transmembrane adaptor protein, involved in the regualtion of T cell activation through the binding of csk protein
PAK1	P21 (RAC1) Activated Kinase 1	Protein coding, encodes a emember of the PAK proteins (serine/threonine p21-activating kinases), link RhoGTPase to cytoskeletal reorganization and nuclear signaling, regaultes cell motility and morphology
PALD1	Phosphatase Domain Containing, Paladin 1	Protein coding
PCED1A	PC-Esterase Domain Containing 1A	Protein coding, a member of the GDSL/SGNH superfamily, Hydrolytic enzyme wither esterase activity
PCNXL3	Pecanex-like 3 (Drosophila)	Protein coding, paralog of PCNX1
PCYOX1L	Prenylcysteine Oxidase 1 Like	Protein coding, paralog of PCYOX1, involved in Resposne to elevated platelet cytosolic Ca2+
PDCD1	Programmed Cell Death 1	Protein coding, expressed in pro-B-cells and involved in their differentiaiton, important in T cell function and contribution to prevention of autoimmune disease
PDE4A	Phosphodiesterase 4A	Protein coding, cyclic nucleotide phoshodiesterase (PDE) family and PDE4 subfamily, hydrolyzes cAMP, through regulation of cAMP the protein can regulate a number of cellular responses to extracellular symbols

PDE4C	Phosphodiesterase 4C	Protein coding, cyclic nucleotide phoshodiesterase (PDE) family and PDE4 subfamily, hydrolyzes cAMP, through regulation of cAMP the protein can regulate a number of cellular responses to extracellular symbols
PDPK1	3-Phosphoinositide Dependent Protein Kinase 1	Protein coding, master serine/threonine kinase, phosphorylates and activates subgroup of AGC protein family, regulates pathways including insulin signal transduction, TGF-beta signaling and a mulitiude of others
PDYN	Prodynorphin	Protein coding, a preproprotein, after proteolytic processing forms sectreted opiod peptides beta-neoendorphin, dynorphin, leuenkephalin, rimorphon and leumorphin, each is a ligan for kappa-type opioid receptor
PFKL	Phosphofructokinase, Liver Type	Protein coding, involved in te citrate cycle (TCA cycle) and innate immune system, forms a subunit of the enzyme theat catalyzes production of D-fructose 1,6-bisphosphate from D-fructose 6-phosphate
PGPEP1L	Pyroglutamyl-Peptidase I-Like	Protein coding, paralog of PGPEP1, cycteine-type peptidae activity
PHB2	Prohibitin 2	Protein coding, related to MAPK signalling Mitogen stimulation pathway and GPCR pathway, is an estrogen receptor selective coregulator and competes with NCOA1, modulating ER transcriptional activity
PHF19	PHD Finger Protein 19	Protein coding, specifically binds H3K36me3, recruiting PRC2 complex and changing active state loci in embryonic stem cells to a repressed state loci, paralog of MTF2
PIK3R1	Phosphoinositide-3-Kinase Regulatory Subunit 1	Protein coding, the enzyme phosphorylates the inositol ring of phosphatidylinositol, the enzyme is importatnt in the metabolism of insulin, mutation of the gene is associated with insulin resistance
AKT1	AKT Serine/Threonine Kinase 1	Protein Coding gene, regulator of mediator of growth factor-induced neuronal survival, apoptosis suppressor, associated with Proteus syndrome
ARHGEF7	Rho Guanine Nucleotide Exchange Factor 7	Protein Coding gene, associated with Syndromic X-Linked Intellectual Disability and Non-Syndromic X-Linked Intellectual Disability
BAD	Protein Coding gene, BCL2 Associated Agonist Of Cell Death	Mediator of programmed cell death
BAX	BCL2 Associated X, Apoptosis Regulator	Protein Coding gene, anti or pro apoptotic mediator, regulated by tumor suppressor P53, associated with Colorectal Cancer and Leukemia
BBC3	BCL2 Binding Component 3	Initiates mitochondrial outer membrane permeabilization, apoptosis, mitochondrila dysfunction, caspase activation, potential drug target for cancer therapy
BID	BH3 Interacting Domain Death Agonist	Protein Coding gene, cell death and mitocondrial damage mediator
BLNK	B-Cell Linker	Involved in B-cell development, associated with pre-B acute lymphoblastic leukemia

BOK	BCL2 family apoptosis regulator	Protein coding gene, proapoptotic regulator involved in a wide variety of cellular processes
C8A	Complement C8 alpha chain	Encodes the alpha subunit of the C8 component of the complement system, which participates in formation of membrane attack complex
CASP6	Caspase 6	Encodes a caspase enzyme involved in the activation cascade responsible for the execution of cell apoptosis, associated with dystrophinopathies
CASP8	Caspase 8	Encodes a caspase enzyme involved in the activation cascade responsible for the execution of cell apoptosis, associated with hepatocellular carcinoma and autoimmune lymphopropiferative syndrome (ALPS). Also implicated in Huntington's disease/neurodegenertaive diseases.
CASP9	Caspase 9	Encodes a cysteine-aspartic acid protease thought to play a central role in apoptosis through activation of the caspase cascade and to be a tumour supressor
CBL	cbl proto-oncogene	Proto-oncogene encoding a RING finger E3 ubiquitin ligase, required for targeting substrates for proteasome degradation, found to be mutated/translocated in many cancers, associated with a range of acute myeloid leukemias and Noonan-like disorders
CBLB	cbl proto-oncogene B	Protein coding gene, E3 ubiquitin-protein ligase generally promoting degradation by the proteasome, negatively regulates T-cell receptor and B-cell receptor signal transduction pathways
CCL18	C-C motif chemokine receptor 18	Antimicrobial gene- a Cys-Cys cytokine gene on the q arm of chromosome 17, displays chemotactic activity for naive T cells, CD4+ and CD8+ T cells and nonactivated lymphocytes, attracts naive T lymphocytes towards dendritiv cells and activated macrophages in lymph nodes
CCR6	C-C motif chemokine receptor 6	Encodes a member of the beta chemokine receptor family, the gene is preferentially expressed by immature dendritic cells and memory T-cells, the receptor is important in B-lineage maturation and antigen driven B-cell differentiation, It may also regulate migration and recruitment of dendritic and T-cells during inflammatory and immunlogical responses
CD14	CD14 molecule	Protein coding gene, encodes a surface antigen that is preferentially expressed on monocytes/macrophages, it works with other proteins to mediate the innate immune response to bacterial lipopolysaccharide, acts via MyD88, TIRAP and TRAF6 to activate NF-kappaB, secrete cytokines and induce the inflamatory response
CD180	CD180 molecule	Cell surface molecule consisting of extracellular leucine-rich repeats(LRR) and a short cytoplasmic tail, belongs to the TLR family of pathogen receptors, the LRR associates with a molecule called MD-1 to form a cell surface receptor complex, RP105/MD-1, which controls B-cell recognition and signalling of lipopolysaccharide via interaction with TLR4

CD19	CD19 molecule	Protein coding gene- encodes a cell surface molecule which assembles with the antigen receptor of B lymphocytes to decease the threshold for antigen receptor-dependent stimulation, associated with immunodeficiency
CD33	CD33 molecule	Generally thought to be an adhesion molecule of myelomonocytic-derived cells that mediates sialic-acid dependent binding to cells, also seen to induce apoptosis in acute myeloid leukemoia in vitro
CD4	CD4 molecule	Protein coding gene, encodes a membrane glycoprotein of T-lymphocytes, interacts with MHCII antigens and is a receptor for HIV, expressed in B cells, macrophages, granulocytes and specific regions of the brain, functions to initate or augment early phase T-cell activation
CD47	CD47 molecule	Protein coding gene, encodes a membrane protein involved in increasing calcium concentration when cell binds to extracellular matrix, may also play a role in membrane transport and signal transduction, associated with neonatal meningitis
CD6	CD6 molecule	Protein coding gene, endcodes a protein found on the outer membrane of T-lymphocytes and other immune cells, responsible for cell adhesion, mediating cell-cell contact and regulating T-cell responses via interactions with ALCAM/CD166, associated with bronchus cancer and lower lip cancer
CD79A	CD79a molecule	Encodes the Ig-alpha protein which non-convalently associates with Ig-beta and surface Ig to cause the expression and function of B-cell antigen receptors, associated with agammaglobulinemia
CD79B	CD79b molecule	Encodes the Ig-beta protein which non-convalently associates with Ig-alpha and surface Ig to cause the expression and function of B-cell antigen receptors, associated with agammaglobulinemia
CD82	CD82 molecule	Metastasis suppressor gene encoding a membrane glycoprotein, gene expression shown to be down regulated in tumour progression of human cancers, expression is strongly correlated with p53 and loss of both proteins is associated with poor survival in prostate cancer, also associated with bladder cancer
CD86	CD86 molecule	Encodes a type I membrane protein of the immunoglobulin superfamily, the protein is expressed by antigen-presenting cells and is the ligand for 2 cell surface proteins on T-cells, binding with CD28 antigen caused a costimulatory signal for T-cell activation, associated with gallbladder squamous cell carcinoma and myocarditis
CDKN2A	Cyclin dependent kinase inhibitor 2A	Encodes at least 3 alternatively spliced varients, each encoding distinct proteins, 2 of which function as CDK4 kinase inhobitors. Known to be an important tumour suppressor gene. Frequently mutated or deleted in a wide variey of tumours including pancreatic cancer, melanoma and neural system tumours.
CRADD	CASP2 and RIPK1 domain containing adaptor with death domain	Promotes apoptosis by recruting caspase2/ICH1 to the cell death signal transduction complex, mutations of this gene assoicated with cognitive/intellectual disability
CSF2	Colony stimulating factor 2	Controls the production, differentiation and function of granulocytes and macrophages, associated with deletions in acute myeloid leukemia

CSK	C-terminal Src kinase	Protein coding gene, roles in the regulation of cell growth, differentiation, migration and immune response, associated with colorectal cancer and breast cancer
CXCL13	C-X-C motif chemokine ligand 13	Protein coding gene, chemoattractant of B-lymphocytes, strongly expressed in the follicles of the spleen, lymph nodes and Peyer's patches, asssociated with T-cell lymphoma and Burkitt lymphoma
EGF	Epidermal growth factor	Protein coding gene, encodes a preproprotein that acts as an important mitogenic factor in the growth, proliferation and differentiation of numerous cell types Dysregulation of gene associated with growth and progression of certain cancers.
ENDOU	Endonuclease Poly (U) specific	Protein coding gene- protease activity and expressed in the placenta. Associated with non-gestational choriocarcinoma.
ESAM	Endothelial cell adhesion molecule	Protein coding gene, related to the blood-brain barrier transmigration signalling pathway, may also mediate aggregation
ESR1	Estrogen receptor 1	Protein coding gene, encodes an estrogen receptor which localizes to the nucleus and is important for hormone binding, DNA binding and activation of transcription Associated with breast cancer, endometrial cancer and osteoporosis.
F3	Coagulation factor III, Tissue factor	Protein coding gene, encodes a cell surface glycoprotein which enables cells to initiate the blood coagulation cascade and is a receptor for coagulation factor VII Associated with carotid artery thrombosis and disseminated intravascular coagulation.
FAS	Fas cell surface death receptor	Protein coding gene, encodes a TNF-receptor containing a death domain, plays central roles in the regulation of programmed cell death, forms a death-inducing signalling complex with its ligand and has also been shown to activate NF-kappaB, associated with autoimmune lymphoproliferative syndrome
FN1	Fibronectin 1	Involved in cell adhesion and migration processes including embryogenesis, wound healing, blood coagulation, host defense, and metastasis
GAB2	GRB2 Associated Binding Protein 2	Activates phosphatidylinositol-3 kinase, involves in trasmitting various signals
HLA-DMB	Major Histocompatibility Complex, Class II, DM Beta	Protein Coding gene, involves in peptide loading
HLA-DQA1	Major Histocompatibility Complex, Class II, DQ Alpha 1	Protein Coding gene,involed in the immune system
ICAM1	Intercellular Adhesion Molecule 1	Encodes a cell surface glycoprotein, cell-cell adhesion, cell to extracellular binding, cell proliferation, differentiation, motility, apoptosis, trafiking tissue architecture, associated with MaLaria and Leukostasis
ICOSLG	Inducible T-Cell Costimulator Ligand	Associated with Inclusion Body Myositis and Diffuse Cutaneous Systemic Sclerosis, signaling for T-cell proliferation and cytokine secretion, involved in B-cell proliferation and differentiation to plasma cells

IGF1R	Insulin Like Growth Factor 1 Receptor	Involved in transformation events, cell growth, survival control, anti apoptosis, tumor transformation and malignant cell survival
IGF2	Insulin Like Growth Factor 2	Growth-promoting activity, fetal development
IKBKB	Inhibitor Of Nuclear Factor Kappa B Kinase Subunit Beta	Protein Coding gene, activation of NF-kappa-B
IL17B	Interleukin 17B	Protein Coding gene, associated with Leiomyoma, induces the secretion of TNF alpha and IL1 beta from a monocytic cell line
IL17C	Interleukin 17C	Protein Coding gene, induces the secretion of tumor necrosis factor alpha and interleukin 1 beta from a monocytic cell line
IL25	Interleukin 25	Stimulates NF-kappaB activation and interleukin 8 production
IL26	Interleukin 26	Protein Coding gene, initiates STAT1, STAT3 MPK1/3 (ERK1/2) and AKT, reduces proliferation of intestinal epithelial cells
IRF1	Interferon Regulatory Factor 1	Initiates the trascription of interferons alpha nad beta, regulates apoptosis and tumor suppression
IRF2	Interferon Regulatory Factor 2	Inhibits the transcription of interferons gamma and beta, activates the transcription of histone H4, associated with interferon gamma signaling
IRF3	Interferon Regulatory Factor 3	Initiates the transcription of interferons alpha, beta and other interferon-regulated genes
IRF4	Interferon Regulatory Factor 4	Mediates interferons in reponse to infection by virus, mediates interferon-induced genes, associated with multiple myeloma, mediates Toll-like-receptor signaling which activates immune system
ITGAM	Integrin Subunit Alpha M	Involved in the adhesion of neutrophils and monocytes to stimulated endothelium
ITGAX	Integrin Subunit Alpha X	Involved in the adhesion of neutrophils and monocytes to stimulated endothelium
ITK	IL2 Inducible T-Cell Kinase	T-cell proliferation and differentiation
LAT	Linker For Activation Of T-Cells	Protein Coding gene, associated with CTLA4 signaling
LCK	LCK Proto-Oncogene, Src Family Tyrosine Kinase	Involved in developing T-cell, mediates protein-protein interactions with phosphotyrosine-containing and protein-rich motifs
LYN	LYN Proto-Oncogene, Src Family Tyrosine Kinase	Regulates mast cell degranulation and erythroid differentiation, associated with Sacoma and Hantavirus Pulmonary Syndrome
MAP3K14	Mitogen-Activated Protein Kinase Kinase Kinase 14	Initiates the activity of NF-kappa B
MAPK10	Mitogen-Activated Protein Kinase 10	Involved in variouse cellular processes including proliferation, differentiation, trascription and development
MAPK3	Mitogen-Activated Protein Kinase 3	Involved in variety of cell processes including proliferation, differentiation and cell cycle progression

MAPKAP1	Mitogen-Activated Protein Kinase Associated Protein 1	Protein Coding gene, associated with Nephrogenic Systemic Fibrosis and Scleral Disease, related to Constitutive Signaling by AKT1 E17K in Cancer and Regulation of TP53 Activity pathways
MCL1	MCL1, BCL2 Family Apoptosis Regulator	Protein Coding gene, associated with Myeloid Leukemia and leukemia, cell survival, apoptosis, death-inducing
MTOR	Mechanistic Target Of Rapamycin	Protein Coding gene, DNA damage, nutrient deprivation, target for cell cycle arrest and immunosuppressive effects
MYC	MYC Proto-Oncogene, BHLH Transcription Factor	Protein Coding gene, associated with Burkitt Lymphoma and Precursor T-Cell Acute Lymphoblastic Leukemia
NCK2	NCK Adaptor Protein 2	Protein Coding gene, cytoskeletal restructure
PIK3R2	Phosphoinositide-3-Kinase Regulatory Subunit 2	Encods regulatory component of PI3K, related to growth signaling pathway
PRKCQ	Protein Kinase C Theta	Involved in variety of cellular signaling pathways, activates transcriptional facrors NF-kappa B and AP-1
PRR5	Proline Rich 5	Tumor suppressor gene, involved in breaset and colorectal tumorigenesis
PTK2	Protein Tyrosine Kinase 2	Involved in cell growth and intracellular signal transduction pathways
PTPN11	Protein Tyrosine Phosphatase, Non-Receptor Type 11	Regulates various cell processes such as ell growth, differentiation, mitotic cycle, and oncogenic transformation
PTPN6	Protein Tyrosine Phosphatase, Non-Receptor Type 6	Involved in variouse cell processes such as cell growth, differentiation, mitotic cycle, and oncogenic transformation
PTPRA	Protein Tyrosine Phosphatase, Receptor Type A	Involved in variouse cell processes such as cell growth, differentiation, mitotic cycle, oncogenic transformation, cell adhesion and proliferation
PVRL1	HGNC symbole for (NECTIN1) Nectin Cell Adhesion Molecule 1	adshesion of junctions and tight junctions in epithelial and endothelial cells
RELA	RELA Proto-Oncogene, NF-KB Subunit	Activates the transcription of specefic genes
RICTOR	RPTOR Independent Companion Of MTOR Complex 2	Cell growth
RPTOR	Regulatory Associated Protein Of MTOR Complex 1	Cell growth, negatively mediates the mTOR kinase,
SHH	Sonic Hedgehog	Induces patterning of the ventral neural tube, the anterior-posterior limb axis, and the ventral somites, associated with VACTERL syndrome

SIRPA	Signal Regulatory Protein Alpha	Negatively regulates receptor tyrosine kinase-coupled signaling processes,involved in transcuctional signals mediated by growth facror receptors
TAB2	TGF-Beta Activated Kinase 1/MAP3K7 Binding Protein 2	MAP3K7/TAK1 activator, involved in transduction signals, mediates the development and function of osteoclasts
TNFRSF19	TNF Receptor Superfamily Member 19	Activates JNK signaling pathway, initiates apoptosis, involved in embryonic development
TNFRSF25	TNF Receptor Superfamily Member 25	Regulates lymphocyte homeostasis and apoptosis, activates NF-kappa B function, regulates lymphocyte proliferation
TP73	Tumor Protein P73	Involved in cellular responses to stress and development, potential candidate gene for neuroblastoma
TRAF1	TNF Receptor Associated Factor 1	Mediates signal transduction from various receptors, mediates activation of MAPK8/JNK and NF-kappa B, regulates anti apoptotic signals,
TYROBP	TYRO Protein Tyrosine Kinase Binding Protein	Signal transduction activator, bone modeling, brain myelination and inflammation
C1S	Complement C1s	Protein Coding gene, lack of C1S, associated with Ehlers-Danlos Syndrome, Periodontal Type 2 and C1s Deficiency
C5	Complement C5	Inflammation, host homeostasis, host defense against pathogens, associated with Immunodeficiency disase
C8B	Complement C8 Beta Chain	Cell lysis, induces membrane penetration, associated with meningococcal infections
C8G	Complement C8 Gamma Chain	Membrane attack complex, associated with immunodeficiency and acute salpingo-Oophoritis, involved in Complement and Innate Immune System pathways
CASP10	Caspase 10	Apoptosis, associated with type IIA autoimmune lymphoproliferative syndrome, non-Hodgkin lymphoma and gastric cancer
CCL14	C-C Motif Chemokine Ligand 14	Protein Coding gene, related to PEDF Induced Signaling and TGF-Beta Pathway
CCL15	C-C Motif Chemokine Ligand 15	Protein Coding gene, related to PEDF Induced Signaling and TGF-Beta Pathway, associated with Hepatocellular Carcinoma and Spherocytosis
CCL16	C-C Motif Chemokine Ligand 16	Immunoregulatory process, inflammation, proliferation
CCL23	C-C Motif Chemokine Ligand 23	Protein Coding gene, immunoregulatory process, inflammation
CCL3	C-C Motif Chemokine Ligand 3	Protein Coding gene, inflammatory responses
CCL4	C-C Motif Chemokine Ligand 4	Chemokinetic and inflammatory processes

CCR6	C-C Motif Chemokine Receptor 6	B-lineage maturation, antigen-driven B-cell differentiation, migration and recruitment of dentritic and T cells during inflammatory and immunological responses, associated with Diffuse Cutaneous Systemic Sclerosis and Limited Scleroderma
CFI	Complement Factor I	Complement cascade regulator, associated with diseases including microangiopathic hemolytic anemia, thrombocytopenia and glomerulonephritis
CYFIP2	Cytoplasmic FMR1 Interacting Protein 2	Protein Coding gene, associated with Fragile X Syndrome and Amyotrophic Lateral Sclerosis 1, related to innate immune system and RET signaling pathways
FAS	Fas Cell Surface Death Receptor	Programmed cell death regulator, associated with malignant and immune diseases,
FN1	Fibronectin 1	Cell adhesion and migration processes such as embryogenesis, wound healing, blood coagulation, host defense, and metastasis
HAVCR2	Hepatitis A Virus Cellular Receptor 2	Protein Coding gene, innate and adaptive immune responses,
HLA-DMA	Major Histocompatibility Complex, Class II, DM Alpha	Membrane structure, associated with rheumatoid arthritis and systemic lupus erythematosus
HLA-DMB	Major Histocompatibility Complex, Class II, DM Beta	Protein Coding gene, peptide loading, related to CTLA4 signaling
HLA-DQA1	Major Histocompatibility Complex, Class II, DQ Alpha 1	Protein Coding gene, immune system, related to CRLA4 signaling
HLA-DQB1	Major Histocompatibility Complex, Class II, DQ Beta 1	Protein Coding gene, immune system, related to CRLA4 signaling
ICAM1	Intercellular Adhesion Molecule 1	Protein Coding gene, Immune system, associated with malaria and leukostasis
ICAM2	Intercellular Adhesion Molecule 2	Cell adhesion, regulator of adhesive process for antigen-specific immune response, assocoated with colon carcinoma
ICAM3	Intercellular Adhesion Molecule 3	Protein Coding gene,cell adhesion, signaling pathways, associated with Marburg Hemorrhagic Fever and Trichosporonosis
ICAM4	Intercellular Adhesion Molecule 4	Protein Coding gene, related to innate and immune system pathways
ICOSLG	Inducible T-Cell Costimulator Ligand	Protein Coding gene, related to immune system and CD28-co-stimulation, associated with Inclusion Body Myositis and Diffuse Cutaneous Systemic Sclerosis
IFNG	Interferon Gamma	Protein Coding gene, released by cells of innate and adaptive immune system, related to autoimmune diseases

IGF1R	Insulin Like Growth Factor 1 Receptor	Protein Coding gene, transformation processes, apoptosis suppressor, cell survival inhancer
IKBKB	Inhibitor Of Nuclear Factor Kappa B Kinase Subunit Beta	Protein Coding gene, NF-kappa-B activation, related to ICos-ICosL pathway in T-helper cell and development IGF-1 receptor signaling
IL12RB1	Interleukin 12 Receptor Subunit Beta 1	Protein Coding gene, IL12 receptor complex formation, related to immune response IL-23 signaling pathway and innate immune system
IL17B	Interleukin 17B	Protein Coding gene, initiates the secretion of TNF alpha and IL1 beta, associated with Leiomyoma
IL25	Interleukin 25	Protein Coding gene, activates NF-kappaB, initiates interleukin 8 production, related to Th2 differentiation pathway and IL-17 family signaling pathways
IL26	Interleukin 26	T cell phenotype transformation, related to PEDF induced signaling and TGF-Beta pathways
IL3	Interleukin 3	Hematopoietic cell types proliferation, cell growth, differentiationa nd apoptosis, possesses neurotrophic activity, associated with neurologic disorders
IL5	Interleukin 5	Differentiation and growth for B cell and eosinophils, regulate eosinophil formation, maturation recruitmen and survival
IRF1	Interferon Regulatory Factor 1	Activates interferons alpha and beta transcription, regulates apoptosis and tumor-suppressoion
IRF2	Interferon Regulatory Factor 2	Transcriptional inhibitor of interferons alpha and beta, transcriptional activator of histone H4, H4 and IL7 genes activator, regulates cell cycle
IRF3	Interferon Regulatory Factor 3	Transcriptional activator of interferons alpha and beta and other interferon mediated genes
IRF4	Interferon Regulatory Factor 4	Regulates interferons in response to infection, regulates interferon-innduced genes, negatively mediates Toll-like -receptor signaling, associated with myeloma
ITGAM	Integrin Subunit Alpha M	Adherence of neutrophils and monocytes to stimulated endothelium phagocytosis of complement coated particles
ITGAX	Integrin Subunit Alpha X	Adherence of neutrophils and monocytes to stimulated endothelium phagocytosis of complement coated particles
ITK	IL2 Inducible T-Cell Kinase	Protein Coding gene, T-cell proliferationa nd differentiation
LAG3	Lymphocyte Activating 3	Protein coding gene, related to innate immune system and NF-kappaB signaling pathways
LCK	LCK Proto-Oncogene, Src Family Tyrosine Kinase	Selection and maturation of developing T-cells, regulated protein-protein interactions
LTBR	Lymphotoxin Beta Receptor	Involved in signalling during the lymphoid and other organs development, lipid metabolism, immune response and programmed cell death
LYN	LYN Proto-Oncogene, Src Family Tyrosine Kinase	Regulates mast cell degranulation and erythroid differentiation, associated with Sarcoma and d Hantavirus Pulmonary Syndrome

MCAM	Melanoma Cell Adhesion Molecule	Cell adhesion, cohesion of the endothelial monolayer at intercellular junctions in vascular tissue, enhances hematogeneous tumor spread, adhesion agent in neural crest cells, associated with melanoma and skin melanoma
NFKB1	Nuclear Factor Kappa B Subunit 1	Induces the expression of genes involved in various biological processes, associated with inflammatory diseases
PRF1	Perforin 1	Generates transmembrane tubules, lyses non-specifically a variety of target cells, affects molecule for T-cell and natural killer-cell-regulated cytolysis, associated with lethal autosomal recessive disorder
PTPRC	Protein Tyrosine Phosphatase, Receptor Type C	Mediates a wide veriaty of cellular events such as cell growth, differentiation and mitosis and oncogenic transformation, inhibits JAK kinases and regulates cytokin receptor signaling
PVR	Poliovirus Receptor	Cell adhesion, poliovirus receptor
PYCARD	PYD And CARD Domain Containing	Inflammation, apoptosis
RAC1	Ras-Related C3 Botulinum Toxin Substrate 1	Regulates cell growth, cytoskeletal restructure and the activation of protein kinases
RELA	RELA Proto-Oncogene, NF-KB Subunit	Protein Coding gene, initiates the transcription of specific genes
SMAD3	SMAD Family Member 3	Regulated multiple signaling pathways, carsinogenesis regulator
SPA17	Sperm Autoantigenic Protein 17	Cell-cell adhesion, immune cell migration and metastasis
SPN	Sialophorin	Y-cell activation, negatively regulates adaptive immune responses
STAT3	Signal Transducer And Activator Of Transcription 3	Cell gwoth, apoptosis, mediates various genes in response to cell stimuli, associated with autoimmune diseases
STAT4	Signal Transducer And Activator Of Transcription 4	Transcriptional inducers, regulates T helper differentiation, regulates responses to IL12, associated with systemic lupus erythematosus and rheumatoid arthritis
STAT5B	Signal Transducer And Activator Of Transcription 5B	Transcriptional activator mediates the signal trasduction initiated by cell ligands and growth hormones, involved in TDR signaling, apoptosis, gland development
SYK	Spleen Associated Tyrosine Kinase	Proliferation, differentiation, phagocytosis, epithelial cell growth, tumor suppressor in breast carcinomas
TNFRSF11A	TNF Receptor Superfamily Member 11a	NF-kappa B and MAPK8/JNK activator,Tcell and dendritic cell interactions regulator, osteoclast and lymph node development
TNFRSF1A	TNF Receptor Superfamily Member 1A	Cell survival, apoptosis and inflammation
TNFSF8	TNF Superfamily Member 8	Ig class switch inhibitor, enhance cell proliferation and cell death

TRAF2	TNF Receptor Associated Factor 2	Activates MAPK8/JNK and NF-kappa B, apoptosis
TRAF6	TNF Receptor Associated Factor 6	Signal transducer in the NF-kappaB pathway, Smad activation
TYK2	Tyrosine Kinase 2	Encods component of type I and III interferon signaling pathways, associated with Immunodeficiency 35 and Primary Cutaneous Anaplastic Large Cell Lymphoma
UBC	Ubiquitin C	Protein degradation, DNA repair, cell cycel mediation, kinase modification endocytosis and other cell signaling pathway regulation
CD247	CD247 Molecule	Involved in coupling recognition to multiple intracellular signal transduction pathways
PDCD1LG2	Programmed Cell Death 1 Ligand 2	Protein Coding gene, related to innate immune system and CD28 co-stimulation, associated with Cysticercosis and Mediastinal Malignant Lymphoma
STAT5A	Signal Transducer And Activator Of Transcription 5A	Transcription inducer, regulates the responses of many cell ligands, crusial for tumorogenesis

Table 12

	Probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig
1	AKT1_14_104800011_104801022_104839372_104843321_FF	AKT1	60	4
2	BAD_11_64267793_64269811_64292591_64296924_FF	BAD	70	8
3	BAX_19_48955700_48958764_48973070_48975293_RR	BAX	52	2
4	BBC3_19_47236830_47241014_47256212_47257706_FR	BBC3	56	8
5	BID_22_17731946_17735544_17804446_17806939_FF	BID	42	2
6	BOK_2_241559192_241566423_241577996_241581000_RR	BOK	44	10
7	C8A_1_56824227_56829583_56902220_56908104_FR	C8A	166	8
8	C8A_1_56841210_56844685_56902220_56908104_RF	C8A	4	1
9	C8B_1_56959632_56962729_56991331_56998079_FF	C8B	151	9
10	CASP6_4_109703339_109705583_109735036_109741090_RF	CASP6	28	2
11	CASP9_1_15520953_15524014_15542554_15547367_FR	CASP9	46	2
12	CBLB_3_105723411_105731672_105883590_105884656_RF	CBLB	5	2
13	CD14_5_140643798_140647427_140670568_140672728_FF	CD14	62	6
14	CD2_1_116707374_116708774_116735758_116740399_FR	CD2	34	2
15	CD4_12_6767426_6773999_6813425_6817229_FR	CD4	42	6
16	CD6_11_60922069_60925026_61017867_61025585_RR	CD6	56	14
17	CD6_11_60932387_60933682_60977084_60983727_FR	CD6	56	14
18	CD6_11_60932387_60933682_61017867_61025585_FR	CD6	56	14
19	CD6_11_60938640_60941215_60977084_60983727_RF	CD6	56	14
20	CD6_11_60938640_60941215_61017867_61025585_RF	CD6	56	14
21	CD6_11_60977084_60983727_60996251_60998956_FR	CD6	56	14
22	CD82_11_44515603_44522167_44561823_44564856_RF	CD82	50	6
23	CD82_11_44526701_44529279_44592038_44600902_RF	CD82	50	6
24	CD82_11_44561823_44564856_44624533_44629606_FF	CD82	50	6
25	CFP_X_47636868_47644403_47672279_47679605_RR	CFP	1	1
26	CRADD_12_93830263_93837995_93848656_93851009_FR	CRADD	231	4
27	EGF_4_109875299_109879120_110005130_110011368_FF	EGF	48	2
28	ELK1_X_47636868_47644403_47672279_47679605_RR	ELK1	2	1
29	FAS_10_88940885_88944343_88985428_88990419_FF	FAS	50	8
30	FAS_10_88953662_88956472_88985428_88990419_FF	FAS	50	8
31	FCGR2B_1_161620964_161624310_161645837_161653201_RR	FCGR2B	1	1
32	HLA-DQA1_6_32634077_32639503_32662361_32664960_FF	HLA-DQA1	28	4
33	ICOSLG_21_44243731_44245588_44267559_44270033_RR	ICOSLG	40	8
34	IGF1R_15_98731539_98737034_98785670_98790114_FF	IGF1R	104	16
35	IGF2_11_2113132_2119465_2180328_2182624_RR	IGF2	32	6
36	IKBKB_8_42241866_42245619_42264241_42271203_RF	IKBKB	46	12
37	IKBKB_8_42264241_42271203_42281222_42285075_FR	IKBKB	46	12
38	IKBKB_8_42264241_42271203_42290979_42292124_FF	IKBKB	46	12
39	IKBKB_8_42264241_42271203_42290979_42292124_FR	IKBKB	46	12
40	IKBKB_8_42264241_42271203_42302441_42304680_FF	IKBKB	46	12
41	IKBKB_8_42264241_42271203_42331044_42332799_FR	IKBKB	46	12
42	IL17D_13_20664875_20671757_20688261_20691044_FF	IL17D	2	1
43	IL17RA_22_17061373_17065953_17132107_17134862_RR	IL17RA	3	1
44	IRF1_5_132472660_132477912_132495376_132497062_FF	IRF1	42	8
45	IRF1_5_132472660_132477912_132517598_132521351_FF	IRF1	42	8
46	IRF1_5_132472660_132477912_132536450_132537922_FR	IRF1	42	8
47	IRF2_4_184439815_184446749_184518370_184519514_RF	IRF2	38	2
48	IRF3_19_49654782_49660360_49691432_49693107_RR	IRF3	30	2
49	ITGAM_16_31214801_31216194_31318595_31324659_RF	ITGAM	50	8
50	ITGAM_16_31278026_31284381_31331188_31333058_RR	ITGAM	50	8
51	ITGAM_16_31331188_31333058_31344274_31352361_RF	ITGAM	50	8
52	ITGAX_16_31331188_31333058_31344274_31352361_RF	ITGAX	41	8

Table 13.a1

	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr	t
1	0.711822793	0.99999793	6.67	-0.219972658	-0.219972658	-4.996552469
2	0.18964104	0.954389149	11.43	-0.139786492	-0.139786492	-5.923845607
3	0.925958703	0.99999793	3.85	-0.15962933	-0.15962933	-6.204852631
4	0.073465475	0.710624303	14.29	-0.166543413	-0.166543413	-6.557217188
5	0.857080857	0.99999793	4.76	-0.1760267	-0.1760267	-8.001384234
6	0.001969408	0.075986326	22.73	-0.362483584	-0.362483584	-10.9324899
7	0.957766442	0.99999793	4.82	-0.374033997	-0.374033997	-10.68867959
8	0.229343441	1	25	0.338570638	0.338570638	3.416892289
9	0.85591599	0.99999793	5.96	-0.161358241	-0.161358241	-2.947668664
10	0.663352621	0.99999793	7.14	-0.339412631	-0.339412631	-13.55417084
11	0.889742685	0.99999793	4.35	-0.137531489	-0.137531489	-6.968042831
12	0.034964245	0.465381017	40	0.464289848	0.464289848	8.34149661
13	0.369692981	0.99999793	9.68	-0.178209877	-0.178209877	-7.696109127
14	0.764125503	0.99999793	5.88	-0.18498091	-0.18498091	-9.04469975
15	0.112492545	0.789152247	14.29	-0.139921516	-0.139921516	-5.076520451
16	9.03E-05	0.005970563	25	-0.21998431	-0.21998431	-6.891261434
17	9.03E-05	0.005970563	25	-0.149724624	-0.149724624	-8.117825922
18	9.03E-05	0.005970563	25	-0.159211463	-0.159211463	-8.406010145
19	9.03E-05	0.005970563	25	-0.321565937	-0.321565937	-13.11065547
20	9.03E-05	0.005970563	25	-0.207569599	-0.207569599	-8.105335573
21	9.03E-05	0.005970563	25	-0.169304269	-0.169304269	-9.223976152
22	0.203083688	0.988148592	12	-0.145793053	-0.145793053	-5.45369143
23	0.203083688	0.988148592	12	-0.348220668	-0.348220668	-12.64682486
24	0.203083688	0.988148592	12	-0.162924558	-0.162924558	-4.377302648
25	0.06993762	0.594154735	100	-0.191997367	-0.191997367	-3.324047424
26	0.999992975	0.99999793	1.73	-0.249667458	-0.249667458	-9.588148198
27	0.903339407	0.99999793	4.17	-0.144833276	-0.144833276	-7.422808069
28	0.13498553	0.877871412	50	-0.18736422	-0.18736422	-3.275422717
29	0.041957105	0.555032562	16	-0.193599779	-0.193599779	-5.573764843
30	0.041957105	0.555032562	16	-0.194159165	-0.194159165	-8.590649368
31	0.066362764	0.687693257	100	0.187306985	0.187306985	3.719020117
32	0.178427395	0.954389149	14.29	-0.211239457	-0.211239457	-3.939059704
33	0.012066038	0.223463015	20	-0.156295949	-0.156295949	-6.247769863
34	0.007797893	0.171924974	15.38	-0.178097117	-0.178097117	-7.086728608
35	0.037675475	0.528598335	18.75	-0.180180699	-0.180180699	-8.22189382
36	0.00018363	0.010627608	26.09	-0.304258892	-0.304258892	-11.89187759
37	0.00018363	0.010627608	26.09	-0.265642352	-0.265642352	-11.56467535
38	0.00018363	0.010627608	26.09	-0.325741973	-0.325741973	-15.03154881
39	0.00018363	0.010627608	26.09	-0.307578042	-0.307578042	-13.22491838
40	0.00018363	0.010627608	26.09	-0.393553534	-0.393553534	-17.46788221
41	0.00018363	0.010627608	26.09	-0.363126662	-0.363126662	-16.40706083
42	0.122126697	0.904598768	50	0.19255788	0.19255788	6.703121045
43	0.195485486	0.98238612	33.33	-0.261366196	-0.261366196	-5.18175145
44	0.016095432	0.256971894	19.05	-0.25495765	-0.25495765	-13.36737718
45	0.016095432	0.256971894	19.05	-0.147678268	-0.147678268	-6.626064358
46	0.016095432	0.256971894	19.05	-0.165001138	-0.165001138	-9.029584345
47	0.815788109	0.99999793	5.26	-0.204963087	-0.204963087	-3.763496869
48	0.700318757	0.99999793	6.67	-0.175351435	-0.175351435	-7.320634642
49	0.041957105	0.555032562	16	-0.266411523	-0.266411523	-9.608582862
50	0.041957105	0.555032562	16	-0.179650611	-0.179650611	-8.796652754
51	0.041957105	0.555032562	16	-0.215030115	-0.215030115	-9.152973735
52	0.013975308	0.239650655	19.51	-0.212953478	-0.212953478	-9.692570589

Table 13.a2

	P.Value	adj.P.Val	B	FC	FC_1	LS
1	0.000501614	0.003704426	-0.24806514	0.858581708	-1.164711512	-1
2	0.000132635	0.00150023	1.136919402	0.907653471	-1.101742055	-1
3	0.0000907	0.001165246	1.532307434	0.895255058	-1.117000111	-1
4	0.0000572	0.000856101	2.012450668	0.890974834	-1.122366157	-1
5	0.0000101	0.000288637	3.809465717	0.885137383	-1.129768123	-1
6	0.000000565	0.000062	6.755470255	0.77782441	-1.285637205	-1
7	0.0000007	0.0000689	6.540229405	0.771621904	-1.295971504	-1
8	0.006357009	0.023175587	-2.864888701	1.264503156	1.264503156	1
9	0.01423557	0.042361163	-3.677544832	0.894182836	-1.118339516	-1
10	0.0000000712	0.0000221	8.801357166	0.790363029	-1.265241367	-1
11	0.0000341	0.000615455	2.550875988	0.909073287	-1.100021323	-1
12	0.00000696	0.000231622	4.19579057	1.379638073	1.379638073	1
13	0.0000143	0.000359185	3.451288223	0.883798951	-1.131479053	-1
14	0.00000333	0.00015367	4.954405786	0.879660716	-1.13680193	-1
15	0.000445101	0.00340461	-0.123778016	0.907568527	-1.101845173	-1
16	0.0000375	0.000650749	2.451958669	0.858574774	-1.164720919	-1
17	0.0000089	0.000266511	3.943211829	0.901422506	-1.109357702	-1
18	0.0000065	0.000223939	4.267601817	0.8955144	-1.116676627	-1
19	0.0000000984	0.0000263	8.486465281	0.800200848	-1.249686254	-1
20	0.00000902	0.000268394	3.928939971	0.86599488	-1.154741238	-1
21	0.00000278	0.000140257	5.139609489	0.889271424	-1.124516063	-1
22	0.000256432	0.002326445	0.450144339	0.903882374	-1.106338644	-1
23	0.00000014	0.0000332	8.144494866	0.785552353	-1.272989631	-1
24	0.001305374	0.007284682	-1.240107008	0.89321256	-1.119554343	-1
25	0.007447421	0.026094146	-3.025492926	0.875392927	-1.142344162	-1
26	0.00000194	0.000115278	5.506120648	0.841090265	-1.188933034	-1
27	0.0000197	0.000439652	3.121097762	0.904483898	-1.105602877	-1
28	0.00809346	0.027703335	-3.109705135	0.878208729	-1.138681462	-1
29	0.00021606	0.002072157	0.628565303	0.874421161	-1.143613677	-1
30	0.00000533	0.000200984	4.470605821	0.874082182	-1.144057184	-1
31	0.003819047	0.015841136	-2.345217043	1.138636289	1.138636289	1
32	0.002651517	0.012158182	-1.970945908	0.863794804	-1.157682352	-1
33	0.0000857	0.001121376	1.591712007	0.897325957	-1.114422236	-1
34	0.0000295	0.000560642	2.702258066	0.88386803	-1.131390622	-1
35	0.00000793	0.000252813	4.061431872	0.882592444	-1.133025789	-1
36	0.000000253	0.0000427	7.5583041	0.809858131	-1.234784169	-1
37	0.00000033	0.0000483	7.292110963	0.831828285	-1.202171191	-1
38	0.0000000258	0.0000141	9.772437866	0.79788793	-1.253308845	-1
39	0.0000000905	0.0000252	8.56869633	0.807997065	-1.237628258	-1
40	0.0000000059	0.0000101	11.15054812	0.761252236	-1.313625041	-1
41	0.0000000109	0.0000107	10.58128991	0.777477774	-1.286210402	-1
42	0.0000475	0.000761747	2.20626716	1.142788069	1.142788069	1
43	0.000380851	0.003058531	0.038392966	0.834297487	-1.198613224	-1
44	0.0000000815	0.000024	8.670136499	0.838011734	-1.193300714	-1
45	0.0000524	0.000805791	2.104266413	0.902702014	-1.107785276	-1
46	0.00000338	0.000154851	4.938642975	0.891927816	-1.121166963	-1
47	0.003545919	0.015017871	-2.269233273	0.867560884	-1.152656855	-1
48	0.0000222	0.000473074	2.995279965	0.885551776	-1.12923945	-1
49	0.0000019	0.000114103	5.526310904	0.831384915	-1.202812298	-1
50	0.0000043	0.000176706	4.692775469	0.882916793	-1.132609559	-1
51	0.00000298	0.000144884	5.066643761	0.861528176	-1.160728143	-1
52	0.00000175	0.000109375	5.608883602	0.862769165	-1.159058576	-1

Table 13.a3

		Probe sequence
	Loop detected	**60 mer**
1	PD-L1 responder	CCCGCGGCGGAGCTGCTACTGTTTACTTTCGAAGCTTCTTCCTTTCGGCCCCCAGGCCTA
2	PD-L1 responder	GCACTACCCCGGCCTGCCGGAGCCCCAGTCGAGTTGGTTTCTGGGTCCGCACCCCCTCCC
3	PD-L1 responder	CGGGTGCCTCCCCCCCCATTCGCCCTGCTCGAGGGAGGGAAATGATTGGATTACGGGGT
4	PD-L1 responder	CGTGGATCCAGACTGGGAGCCCCCAGCCTCGAACCACGCCAGGCTTCCAGGCGTCAGTGC
5	PD-L1 responder	TGGAAGCAGCTATACAGCTGTGACCACATCGACGCCCCTGTCACGGGCCCTGTTATTCAA
6	PD-L1 responder	GTTTGCTCCGGGGCCGCCGGGCCCGCCCTCGATTTTAACACCACCATGGTTTGAATGAAT
7	PD-L1 responder	GGTGACTGCTCAGAAGAGCAGTACTCATTCGACCTTATGCTAAGCCTAAACTTGCCTTCC
8	PD-L1 Non-responder	AGGTCATTAAAGTATAATCCTGTTGTTATCGAGAGATCAAGACCATCCTGGCCAACATGG
9	PD-L1 responder	ATTTTGACATCTGCATTTTACAGCAGCCTCGATGCGAGCTCGTGGTGGGTGCTCAAGACT
10	PD-L1 responder	GGGGCCTCCAGAGTCCCCTTTACAGGCATCGACGCCCCCTGCCTACCTGCCGGGTGCCCC
11	PD-L1 responder	GAAGGCTAGGCTCCCGCACAACGCCTCCTCGAGCAAGTTAGTTGAACCCAAGGAGGGTCA
12	PD-L1 Non-responder	CCTAATATTTCATTATGATAAGAAAGATTCGAATAAGAAATACTTCTAAACCAAAGGATA
13	PD-L1 responder	GCGGGGGCTTCCCTCAACTTCAGGGAGGTCGAGGCGCGGCGCGCAGGCCGCCATCGCCAC
14	PD-L1 responder	ATTTGACAACGCTGGCACGGAGGCAAGATCGACCTCCCTGTCCCTCCTGGGCCTCTCCGG
15	PD-L1 responder	CCGCCTCCGTCTGCGCCTGGGCCAGGCCTCGAGAATTATTCTTTTCATATACAAAGAATA
16	PD-L1 responder	CTGGCGTTCCAGCCCTCGCACCTTGGCCTCGAGCACCTCTTCAGGGGAGGATTACTGCAA
17	PD-L1 responder	GTGTGGGCCCCCCTGCTACCGCTGCGTATCGAACTTTACAGAGGGATCTAGAATGAGTGA
18	PD-L1 responder	GTGTGGGCCCCCCTGCTACCGCTGCGTATCGAGCACCTCTTCAGGGGAGGATTACTGCAA
19	PD-L1 responder	TTAATGCTGATACAATTCTATTGGATAATCGACACTTCGGCTCCCTGCACCTCCCATGCC
20	PD-L1 responder	CAATATGACGGTGACATTAATGATAGCTTCGACACTTCGGCTCCCTGCACCTCCCATGCC
21	PD-L1 responder	TTAATGCTGATACAATTCTATTGGATAATCGACGTGCCTTGGGGCCTCCCCTTTCCCTAT
22	PD-L1 responder	ACGCCCGCCTCCATGAGATTCAGAGCCCTCGAGAATGTGGACTCTCCTTTCCCCCAGCAC
23	PD-L1 responder	CACAGCTTCTAAATGGTAGGTGTGGGACTCGACCCGCTTTCCTCCCCGCCCCCTCATCCG
24	PD-L1 responder	ACGCCCGCCTCCATGAGATTCAGAGCCCTCGACTCCTTTCCCAGACACATTCAGCACGTG
25	PD-L1 responder	CATCCCTTCTATCAGCGTGGATGGCCTCTCGAGGCCCAAGGGCTTGTCAGTCAGCTTGTG
26	PD-L1 responder	ACAGTTTTATTGTTGACCTTCCATGGACTCGAGATGCGCCACGCCCTGTTCCTCCTTCAT
27	PD-L1 responder	CAGGCTATTGTAGTGCTCTTCCTGGCCCTCGACACCCCCTTCAAGGGTCTGTGTCCCATA
28	PD-L1 responder	CATCCCTTCTATCAGCGTGGATGGCCTCTCGAGGCCCAAGGGCTTGTCAGTCAGCTTGTG
29	PD-L1 responder	GTCTTTGTGTAAATAAATAAGGTAACCCTCGAGAGCCGGCCTCCTGCCCTTTCTAAAGGC
30	PD-L1 responder	CGTGAATATATTGGGCTCTAATGGATAATCGAGAGCCGGCCTCCTGCCCTTTCTAAAGGC
31	PD-L1 Non-responder	AGGACAGAGACCCCTAATTCCACCACCATCGAGGGGCTTACTAATGCCTTTTAGCTCCCT
32	PD-L1 responder	CCCGTCTTCCCCAAAATCTATGTGGTCCTCGACAGCGACGTGGGGGTGTACCGCGCGGTG
33	PD-L1 responder	AGGTGGAGATCAGAAGACCCCCACGCCCTCGAGTCACAGCTGTAGTGGGGTGGGGGGTGA
34	PD-L1 responder	CGTAGAACTAAGATGTATTCAAAGTCAGTCGAAATCACCTGTCCCGGCCTCTTTCCAAAC
35	PD-L1 responder	GTGACAATTAAGAGTGTGACATTGCTTCTCGAGGACTCACTGGGCCTGCAGGGGGGCAGC
36	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAACTAATATTAGAGGAGAGAGGTCAGTTA
37	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAGGGCCTGGCAAGAAGACAGAAGCCGACT
38	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAAGTGCTGTTGAGTTCCCCCATCTCTCAT
39	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGATTTCCAAAAGCTCACACATGGGTGCACA
40	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGACAGTCCCAAGAGGTCAGAACTGGCTTCC
41	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGACCCCCTGACATGGGGCTGCCTGGAGCAG
42	PD-L1 Non-responder	TTAAAGAAGCTAATTTTAAAAATAAATGTCGAAGAGATTGTCACGTTAGAGTTATGTAAA
43	PD-L1 responder	TATTATCCTGCACCCTGAAAAGGTGTTATCGATGCACTCAGTCTTTTTTTTTTATTCACT
44	PD-L1 responder	GTGTCTCGGCCCCCTGGGGCCCCACCCTTCGATTTCCCTGTTGCCGCCGCGTTTGCAAGA
45	PD-L1 responder	GTGTCTCGGCCCCCTGGGGCCCCACCCTTCGATACTATTACGAATGGAATCACTGTCTTA
46	PD-L1 responder	GTGTCTCGGCCCCCTGGGGCCCCACCCTTCGAGTGCATCCTGCAGCTGTTTGTCCAGAAG
47	PD-L1 responder	TTATGATATTGTAAATTATTTTTAATATTCGAGCAAACTGACTTGGGGCCCCTATGTGTG
48	PD-L1 responder	GCAGCCAGCCCGGTGGGGGTGGGGGGGGTCGACGCTCGCCTCCGCTCACAGCCTCAGCAT
49	PD-L1 responder	CAAATCCCGGCTATCTCTTAGAATTGCATCGACGCGCCCGTGACAGCCGAGTGCGGCCAC

50	PD-L1 responder	ACATCGCTACCAGGCCGATGTGCTGATATCGAGGTCCCCAACCCCCTGCCGCTCATCGTG
51	PD-L1 responder	AGTGGTCTCACCATGGCTTTCTTCCAATTCGAGGTCCCCAACCCCCTGCCGCTCATCGTG
52	PD-L1 responder	AGTGGTCTCACCATGGCTTTCTTCCAATTCGAGGTCCCCAACCCCCTGCCGCTCATCGTG

Table 13.a4

	Probe Location					4 kb Sequence Location		
	Chr	**Start1**	**End1**	**Start2**	**End2**	**Chr**	**Start1**	**End1**
1	14	104800993	104801022	104843292	104843321	14	104797023	104801022
2	11	64269782	64269811	64296895	64296924	11	64265812	64269811
3	19	48955700	48955729	48973070	48973099	19	48955700	48959699
4	19	47240985	47241014	47256212	47256241	19	47237015	47241014
5	22	17735515	17735544	17806910	17806939	22	17731545	17735544
6	2	241559192	241559221	241577996	241578025	2	241559192	241563191
7	1	56829554	56829583	56902220	56902249	1	56825584	56829583
8	1	56841210	56841239	56908075	56908104	1	56841210	56845209
9	1	56962700	56962729	56998050	56998079	1	56958730	56962729
10	4	109703339	109703368	109741061	109741090	4	109703339	109707338
11	1	15523985	15524014	15542554	15542583	1	15520015	15524014
12	3	105723411	105723440	105884627	105884656	3	105723411	105727410
13	5	140647398	140647427	140672699	140672728	5	140643428	140647427
14	1	116708745	116708774	116735758	116735787	1	116704775	116708774
15	12	6773970	6773999	6813425	6813454	12	6770000	6773999
16	11	60922069	60922098	61017867	61017896	11	60922069	60926068
17	11	60933653	60933682	60977084	60977113	11	60929683	60933682
18	11	60933653	60933682	61017867	61017896	11	60929683	60933682
19	11	60938640	60938669	60983698	60983727	11	60938640	60942639
20	11	60938640	60938669	61025556	61025585	11	60938640	60942639
21	11	60983698	60983727	60996251	60996280	11	60979728	60983727
22	11	44515603	44515632	44564827	44564856	11	44515603	44519602
23	11	44526701	44526730	44600873	44600902	11	44526701	44530700
24	11	44564827	44564856	44629577	44629606	11	44560857	44564856
25	X	47636868	47636897	47672279	47672308	X	47636868	47640867
26	12	93837966	93837995	93848656	93848685	12	93833996	93837995
27	4	109879091	109879120	110011339	110011368	4	109875121	109879120
28	X	47636868	47636897	47672279	47672308	X	47636868	47640867
29	10	88944314	88944343	88990390	88990419	10	88940344	88944343
30	10	88956443	88956472	88990390	88990419	10	88952473	88956472
31	1	161620964	161620993	161645837	161645866	1	161620964	161624963
32	6	32639474	32639503	32664931	32664960	6	32635504	32639503
33	21	44243731	44243760	44267559	44267588	21	44243731	44247730
34	15	98737005	98737034	98790085	98790114	15	98733035	98737034
35	11	2113132	2113161	2180328	2180357	11	2113132	2117131
36	8	42241866	42241895	42271174	42271203	8	42241866	42245865
37	8	42271174	42271203	42281222	42281251	8	42267204	42271203
38	8	42271174	42271203	42292095	42292124	8	42267204	42271203
39	8	42271174	42271203	42290979	42291008	8	42267204	42271203
40	8	42271174	42271203	42304651	42304680	8	42267204	42271203
41	8	42271174	42271203	42331044	42331073	8	42267204	42271203
42	13	20671728	20671757	20691015	20691044	13	20667758	20671757
43	22	17061373	17061402	17132107	17132136	22	17061373	17065372
44	5	132477883	132477912	132497033	132497062	5	132473913	132477912
45	5	132477883	132477912	132521322	132521351	5	132473913	132477912
46	5	132477883	132477912	132536450	132536479	5	132473913	132477912
47	4	184439815	184439844	184519485	184519514	4	184439815	184443814
48	19	49654782	49654811	49691432	49691461	19	49654782	49658781

49	16	31214801	31214830	31324630	31324659	16	31214801	31218800
50	16	31278026	31278055	31331188	31331217	16	31278026	31282025
51	16	31331188	31331217	31352332	31352361	16	31331188	31335187
52	16	31331188	31331217	31352332	31352361	16	31331188	31335187

Table 13.a5

	4 kb Sequence Location		Inner_primers		
	Start2	End2	PCR-Primer1_ID	PCR_Primer1	PCR-Primer2_ID
1	104839322	104843321	OBD117.1.833	GGGAGTGAAGTTCAGGAGCG	OBD117.1.835
2	64292925	64296924	OBD117.1.265	TGTCGCTGGATGTCAGGCAGAGC	OBD117.1.267
3	48973070	48977069	OBD117.1.781	ACACTCGCTCAGCTTCTTGG	OBD117.1.783
4	47256212	47260211	OBD117.1.405	AGGAGGGAGTAGTGGAGAGGTTG	OBD117.1.407
5	17802940	17806939	OBD117.1.277	GTGGAAATAAAGGCACCGTGTGTAGA	OBD117.1.279
6	241577996	241581995	OBD117.1.737	GCGCCACCTTCTTTCAGAG	OBD117.1.739
7	56902220	56906219	OBD117.1.817	GAAACATTACAGGGGCTTGG	OBD117.1.819
8	56904105	56908104	OBD117.1.1573	CTTGGCACAGAACAGGAGCACCA	OBD117.1.1575
9	56994080	56998079	OBD117.1.321	CCTGGGACTAACGAGGAGCCACA	OBD117.1.323
10	109737091	109741090	OBD117.1.821	CAGACTAAGGGGCCTCCAGA	OBD117.1.823
11	15542554	15546553	OBD117.1.121	GGATTCTTTGGCTCCGCTGAGGG	OBD117.1.123
12	105880657	105884656	OBD117.1.1453	CCTATTGCCTGGAGCATAAAGGGAAA	OBD117.1.1455
13	140668729	140672728	OBD117.1.797	GGAGCATTCGCGGATTAGGA	OBD117.1.799
14	116735758	116739757	OBD117.1.009	GGCAGGAGCCAGCAGACACAAAG	OBD117.1.011
15	6813425	6817424	OBD117.1.769	CGGGGACTTCTCGCTATGG	OBD117.1.771
16	61017867	61021866	OBD117.1.345	GCTCTTTGGTATGACACTGGCGG	OBD117.1.347
17	60977084	60981083	OBD117.1.373	TGTTCGTGGCTGGCAAGGAGAGC	OBD117.1.375
18	61017867	61021866	OBD117.1.337	TGTTCGTGGCTGGCAAGGAGAGC	OBD117.1.339
19	60979728	60983727	OBD117.1.329	TGTCCCTTTCTCCTAAATACCCCAAC	OBD117.1.331
20	61021586	61025585	OBD117.1.085	CCAACACAGCAGCCTCCAGCCAT	OBD117.1.087
21	60996251	61000250	OBD117.1.293	GTCCCTTTCTCCTAAATACCCCAACG	OBD117.1.295
22	44560857	44564856	OBD117.1.393	TGGTTGTTCTGGGCTACTTCCCC	OBD117.1.395
23	44596903	44600902	OBD117.1.741	GCTGATGAGGCACCTGCTAT	OBD117.1.743
24	44625607	44629606	OBD117.1.025	TGGTTGTTCTGGGCTACTTCCCC	OBD117.1.027
25	47672279	47676278	OBD117.1.941	CCAGTTTCCATCCAGTGGCAG CG	OBD117.1.943
26	93848656	93852655	OBD117.1.109	GTGTCCACCCTACCACCCACCTT	OBD117.1.111
27	110007369	110011368	OBD117.1.117	CCAGGAGACACCCTCTAAAGGAG	OBD117.1.119
28	47672279	47676278	OBD117.1.429	CCAGTTTCCATCCAGTGGCAGCG	OBD117.1.431
29	88986420	88990419	OBD117.1.133	GTGAGGCAGGATGGTATGGCAGT	OBD117.1.135
30	88986420	88990419	OBD117.1.409	TAATCCTCCTGTCTCCCTCTTAGAAG	OBD117.1.411
31	161645837	161649836	OBD117.1.713	ATTAGTCTTCAACCCACGCTGTTTTG	OBD117.1.715
32	32660961	32664960	OBD117.1.385	TGGTTCTGCTACCTGTGTGCCTG	OBD117.1.387
33	44267559	44271558	OBD117.1.353	TGTGCCAGACCCCAAAAGGACCC	OBD117.1.355
34	98786115	98790114	OBD117.1.777	AATTCACCACACCCCAACAT	OBD117.1.779
35	2180328	2184327	OBD117.1.801	AGGATTGTACACACAGCCCC	OBD117.1.803
36	42267204	42271203	OBD117.1.825	GGTGTAACGGGGGTCATTTC	OBD117.1.827
37	42281222	42285221	OBD117.1.201	GCACGGTCTGTCTACTTTCCCTC	OBD117.1.203
38	42288125	42292124	OBD117.1.417	GCACGGTCTGTCTACTTTCCCTC	OBD117.1.419
39	42290979	42294978	OBD117.1.753	GGTGTAACGGGGGTCATTTC	OBD117.1.755
40	42300681	42304680	OBD117.1.077	GCACGGTCTGTCTACTTTCCCTC	OBD117.1.079
41	42331044	42335043	OBD117.1.261	CGGTGAGCACGGTCTGTCTACTT	OBD117.1.263
42	20687045	20691044	OBD117.1.645	TCTCTACTTCAGGCAGGCAGTGTAAG	OBD117.1.647
43	17132107	17136106	OBD117.1.537	CACTCCAGTCCACCCACACTTTACTC	OBD117.1.539
44	132493063	132497062	OBD117.1.805	CACTGAGGCCAAGTTACAAGC	OBD117.1.807
45	132517352	132521351	OBD117.1.785	CTGAGTCTCACAGCCATCCA	OBD117.1.787
46	132536450	132540449	OBD117.1.837	CATCTGTGCATGGTCCTGAG	OBD117.1.839
47	184515515	184519514	OBD117.1.1077	GCTGGCATTTGGATTGAGA	OBD117.1.1079

48	49691432	49695431	OBD117.1.197	GCTGCCCTCTCTCTTGTCAGACG	OBD117.1.199
49	31320660	31324659	OBD117.1.789	TCTTCCAAGCATGGAGTGGG	OBD117.1.791
50	31331188	31335187	OBD117.1.309	CTGGGTGCCCTTGACATTAGCGT	OBD117.1.311
51	31348362	31352361	OBD117.1.937	CCTGTCTTCCTCTTTGCTGAG CC	OBD117.1.939
52	31348362	31352361	OBD117.1.369	CCTGTCTTCCTCTTTGCTGAGCC	OBD117.1.371

Table 13.a6

	Inner_primers	
	PCR_Primer2	GLMNET
1	TGGCAGATGAGGTACCAGGA	0.000126471
2	TCTGCTGTAAGGGACTGCCTCCT	0
3	GGTGCAGGAAAAACGAACAT	-0.0000963
4	TTTCCGCCTCCAGCCCCTCATTC	-0.012797314
5	GGCAAAACCCTAACGCCAATCTTCAG	-0.001049357
6	CCCTGAGAACCCATTAGTCC	0.000120571
7	ATTTGTGTGGTTGCAAGGGC	-0.003603391
8	TCCTGCCTCAGCCTCCCAAGTAG	0
9	GCCTGTCGTGATGCTGATGTCCA	-0.002344366
10	CGCAATCAGAACCAACTGGC	-0.015124118
11	CCAGAAGTCCCAGGTTGTGTCCT	0.003583466
12	GTGGAGAATGTAGTATTATGAAGGTT	0
13	TCAACGCTCAGCTCACACTT	0.000119448
14	CCAAAGGAGGAGACCAGCATTGC	0.007257883
15	TGCAGCCGTAAGAGAGGAAT	-0.007336559
16	GCTTTATGCCTCCTCCAGCCAGG	0.013413486
17	CCCCAGGGAGAAGTCTGATTCCT	-0.020821569
18	CTTACCTGAAAAGGCTGGCTGGG	0.017522073
19	TAGGAGGAGCGGTCTTACAGGCAGA	0.000137163
20	TAGGAGGAGCGGTCTTACAGGCA	-0.009581325
21	TGTGATGCTTCCCACTGCTCTGATAG	-0.003930475
22	GTGAGGCTCTGGGTGAAGGTGCT	-0.013038403
23	CTCCCCTTATTGCTCCCCAC	-0.009743329
24	CGGTGTCCTGAGTCCCTGGCAAT	-0.015977346
25	GAAGGAAGAGACTCAGGACTGGC	0
26	TGTGCCCAGCAAAACCAGTGAGC	-0.00783453
27	GTCCCCAGGTAATGGAGCGAAGC	0.01716512
28	GAAGGAAGAGACTCAGGACTGGC	0
29	CAAGACCTCCCCAACTTCCCAGG	-0.016360123
30	CCCAGGTTGAACTACAGCAGAAGCCT	-0.006985618
31	GGTTCTAAGGAGAGTTGTAAAGAGAG	-0.00011137
32	CGCCACCTCGTAGTTGTGTCTGC	0.001576194
33	CAGCGGCACTTTGTCTTCAGGAG	-0.010502797
34	CTCCGGAGGATTTCTGTGAA	-0.008978891
35	CAGGGGCTCTTCTTTCAGC	0.00011913
36	CCAGGCCAGCTTCAAACTC	0.000123838
37	TGGAGATGCTGCTCTGCCCACCT	-0.003994085
38	CACAGCCCTTGGCATCACCCACA	-0.023515041
39	TGTGGGAACCATACCTGTGC	0.01434467
40	CGTTGCCTCCTCACAGCAGAAGC	-0.001425541
41	GTCCTGGGTCCTGGGTGAAAGTC	0.01710902
42	GGGAGACCATTTCTGTTCACTCTGAG	-0.0134076
43	CTAAACCCTGGAACCAAAACTCATCC	0
44	TGTAAATTGCCGCAGGGGAA	0.006327654
45	GGCACTCACACACGAGAAAA	0.000121603
46	ATCAGGATCAGGCTTCAAGG	0.000116599

47	GGCTTGATCTCTGGACGAAG	0
48	GTCCACCCCATTGCCGCTTTTCA	0.018616515
49	CTGCAGGTTGGTGCTGAGT	-0.01814247
50	GCCACCCTCCCTAAGAGACTGAG	-0.010425
51	GCCACCCTCCCTAAGAGACTGAG	0
52	GCCACCCTCCCTAAGAGACTGAG	0.00590703

Table 13.a7

	Probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig
53	ITK_5_157178319_157181048_157266725_157271762_FR	ITK	26	10
54	ITK_5_157178319_157181048_157266725_157271762_RR	ITK	26	10
55	ITK_5_157225228_157231430_157263646_157266576_RF	ITK	26	10
56	ITK_5_157225228_157231430_157266725_157271762_FR	ITK	26	10
57	ITK_5_157249288_157254103_157266725_157271762_RR	ITK	26	10
58	LYN_8_55939615_55941582_55961822_55966587_RR	LYN	48	2
59	MAPKAP1_9_125549822_125553339_125631239_125635100_RF	MAPKAP1	52	6
60	MTOR_1_11162452_11169997_11281372_11283081_FR	MTOR	60	4
61	MYC_8_127691489_127694045_127732337_127733526_FF	MYC	42	4
62	MYC_8_127691489_127694045_127738939_127740424_FR	MYC	42	4
63	NCK2_2_105715815_105716905_105886459_105893355_FR	NCK2	66	4
64	NFKBIE_6_44253666_44257911_44307667_44312139_RF	NFKBIE	44	4
65	NFKBIE_6_44270723_44274914_44307667_44312139_RF	NFKBIE	44	4
66	ORF102_17_34316073_34325822_34367538_34373948_RF	ORF102	11	1
67	ORF104_17_36075902_36084513_36095759_36100192_FR	CCL18	42	8
68	ORF107_6_41947755_41951350_42050648_42055406_RF	ORF107	6	1
69	ORF108_6_167109295_167112439_167149742_167154610_FF	CCR6	46	4
70	ORF110_3_46429853_46436496_46457806_46461162_RR	ORF110	23	0
71	ORF113_5_67178844_67182260_67233989_67237362_FR	CD180	38	4
72	ORF114_16_28959098_28963335_28975508_28978445_RF	CD19	56	4
73	ORF116_3_112306429_112316088_112398394_112403968_RR	ORF116	58	3
74	ORF117_19_35294083_35295665_35307063_35310549_FF	ORF117	27	1
75	ORF118_18_69825656_69827597_69936161_69945341_RR	ORF118	86	5
76	ORF120_9_5422951_5431331_5460319_5468105_RR	ORF120	29	2
77	ORF120_9_5422951_5431331_5512277_5514690_FR	ORF120	29	2
78	ORF128_11_61068642_61071684_61139962_61143879_RR	ORF128	27	1
79	ORF130_11_60938640_60941215_60977084_60983727_RF	CD6	56	14
80	ORF130_11_60938640_60941215_61017867_61025585_RF	CD6	56	14
81	ORF130_11_60977084_60983727_60996251_60998956_FR	CD6	56	14
82	ORF136_6_14070076_14075830_14126334_14131467_FF	ORF136	28	9
83	ORF136_6_14083566_14087253_14136228_14137347_FR	ORF136	28	9
84	ORF138_3_122014664_122021863_122097537_122100802_RF	CD86	46	2
85	ORF139_5_131244508_131249689_131303538_131314316_FR	ORF139	69	2
86	ORF140_7_90713266_90719769_90855907_90868783_FF	ORF140	174	48
87	ORF140_7_90855907_90868783_90936378_90943000_FF	ORF140	174	48
88	ORF140_7_90855907_90868783_90994572_90999177_FR	ORF140	174	48
89	ORF140_7_90855907_90868783_91103050_91110422_FF	ORF140	174	48
90	ORF140_7_90936378_90943000_91140859_91158297_RF	ORF140	174	48
91	ORF142_6_36654202_36659227_36691067_36693657_RF	ORF142	31	3
92	ORF142_6_36684519_36687230_36719341_36723631_RR	ORF142	31	3
93	ORF142_6_36691067_36693657_36719341_36723631_FR	ORF142	31	3
94	ORF145_6_4826110_4834568_4928803_4930806_RF	ORF145	38	4
95	ORF146_10_11274452_11277542_11303118_11312162_RR	ORF146	188	11
96	ORF147_2_168472568_168475902_168685690_168692951_RF	ORF147	182	25
97	ORF149_X_47581313_47587657_47613512_47618008_FF	ORF149	23	15

98	ORF149_X_47581313_47587657_47636868_47644403_FR	ORF149	23	15
99	ORF149_X_47581313_47587657_47636868_47644403_RR	ORF149	23	15
100	ORF149_X_47581313_47587657_47652990_47657846_FF	ORF149	23	15
101	ORF149_X_47581313_47587657_47652990_47657846_RR	ORF149	23	15
102	ORF149_X_47581313_47587657_47672279_47679605_FR	ORF149	23	15
103	ORF149_X_47599663_47605051_47636868_47644403_FR	ORF149	23	0
104	ORF149_X_47613512_47618008_47636868_47644403_FF	ORF149	23	15

Table 13.b1

	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr	t
53	1.57E-05	0.002607465	38.46	-0.17535973	-0.17535973	-7.936893754
54	1.57E-05	0.002607465	38.46	-0.204619133	-0.204619133	-9.041273175
55	1.57E-05	0.002607465	38.46	-0.226854713	-0.226854713	-7.188770374
56	1.57E-05	0.002607465	38.46	-0.144955613	-0.144955613	-8.636856152
57	1.57E-05	0.002607465	38.46	-0.191450511	-0.191450511	-6.961093779
58	0.903339407	0.99999793	4.17	-0.237388831	-0.237388831	-9.072038739
59	0.229017635	0.99999793	11.54	-0.208545117	-0.208545117	-7.711401904
60	0.711822793	0.99999793	6.67	-0.206498971	-0.206498971	-2.697141397
61	0.430324418	0.99999793	9.52	-0.204707302	-0.204707302	-8.414783357
62	0.430324418	0.99999793	9.52	-0.186601169	-0.186601169	-8.01397424
63	0.779227696	0.99999793	6.06	-0.14004291	-0.14004291	-6.51116257
64	0.466402982	0.99999793	9.09	-0.195945166	-0.195945166	-9.511762166
65	0.466402982	0.99999793	9.09	-0.293579626	-0.293579626	-14.68901883
66	0.511527165	1	9.09	0.2840641	0.2840641	6.643829188
67	0.016095432	0.256971894	19.05	-0.291933406	-0.291933406	-10.89682004
68	0.352766908	1	16.67	-0.242419598	-0.242419598	-10.57460987
69	0.501622356	0.99999793	8.7	-0.14391148	-0.14391148	-7.030078326
70	1	1	0	-0.362268923	-0.362268923	-16.68456661
71	0.356577228	0.99999793	10.53	-0.176986579	-0.176986579	-9.75949409
72	0.659150649	0.99999793	7.14	-0.295598703	-0.295598703	-10.15502575
73	0.716692043	1	5.17	0.602056594	0.602056594	15.84030024
74	0.858892218	1	3.7	-0.186844857	-0.186844857	-7.153732488
75	0.637873022	1	5.81	0.289045633	0.289045633	7.422638917
76	0.582184628	1	6.9	0.184678337	0.184678337	10.5440004
77	0.582184628	1	6.9	0.167067809	0.167067809	6.795574962
78	0.843487021	1	3.7	0.147449655	0.147449655	5.62371066
79	9.03E-05	0.005970563	25	-0.262767321	-0.262767321	-9.763551812
80	9.03E-05	0.005970563	25	-0.24505568	-0.24505568	-9.532818868
81	9.03E-05	0.005970563	25	-0.143973167	-0.143973167	-8.04914211
82	3.57E-05	0.00197047	32.14	0.304730566	0.304730566	7.972556939
83	3.57E-05	0.00197047	32.14	0.45046821	0.45046821	8.040999966
84	0.889742685	0.99999793	4.35	-0.17550915	-0.17550915	-7.944299089
85	0.937060046	1	2.9	0.337466811	0.337466811	7.122034666
86	1.33E-18	6.25E-16	27.59	0.299560844	0.299560844	7.349855302
87	1.33E-18	6.25E-16	27.59	0.376066641	0.376066641	11.18729546
88	1.33E-18	6.25E-16	27.59	0.328115734	0.328115734	8.388709848
89	1.33E-18	6.25E-16	27.59	0.426278456	0.426278456	9.130196924
90	1.33E-18	6.25E-16	27.59	0.290736601	0.290736601	14.83391512
91	0.370280429	1	9.68	-0.157021793	-0.157021793	-5.367709243
92	0.370280429	1	9.68	-0.155240529	-0.155240529	-6.981397089
93	0.370280429	1	9.68	-0.165320069	-0.165320069	-6.491602168
94	0.216095329	1	10.53	0.357099569	0.357099569	3.100523963
95	0.644185758	1	5.85	0.350492829	0.350492829	2.971293917
96	0.000206728	0.007220151	13.74	0.313589664	0.313589664	9.144161779
97	1.30E-12	6.11E-10	65.22	-0.325788697	-0.325788697	-3.268992003

98	1.30E-12	6.11E-10	65.22	-0.184978686	-0.184978686	-3.038398575
99	1.30E-12	6.11E-10	65.22	-0.140733478	-0.140733478	-2.92069017
100	1.30E-12	6.11E-10	65.22	-0.317936544	-0.317936544	-3.193281824
101	1.30E-12	6.11E-10	65.22	-0.392260745	-0.392260745	-3.656585798
102	1.30E-12	6.11E-10	65.22	-0.213145814	-0.213145814	-3.009155124
103	1	1	0	-0.146041724	-0.146041724	-4.02292989
104	1.30E-12	6.11E-10	65.22	-0.222139537	-0.222139537	-5.68201205

Table 13.b2

	P.Value	adj.P.Val	B	FC	FC_1	LS
53	0.0000109	0.000300885	3.734715272	0.885546684	-1.129245942	-1
54	0.00000334	0.000153695	4.950834477	0.867767745	-1.152382081	-1
55	0.000026	0.000519842	2.830950394	0.854495789	-1.170280782	-1
56	0.00000508	0.000194036	4.520831371	0.904407203	-1.105696634	-1
57	0.0000344	0.000618186	2.541955486	0.87572481	-1.141911236	-1
58	0.00000324	0.000150461	4.982857006	0.848279245	-1.178857087	-1
59	0.0000141	0.000355136	3.469495184	0.865409512	-1.155522312	-1
60	0.02197855	0.058573399	-4.108873892	0.866637776	-1.153884619	-1
61	0.00000643	0.000223311	4.277331934	0.867714714	-1.15245251	-1
62	0.00000998	0.000286168	3.824002229	0.878673343	-1.138079365	-1
63	0.0000607	0.0008901	1.95067007	0.907492164	-1.10193789	-1
64	0.00000209	0.000119285	5.430299258	0.873000772	-1.14547436	-1
65	0.0000000324	0.0000158	9.557329978	0.815875189	-1.225677668	-1
66	0.0000512	0.000797045	2.127853229	1.217620117	1.217620117	1
67	0.000000583	0.0000632	6.724276277	0.816806693	-1.224279879	-1
68	0.000000774	0.0000716	6.437875016	0.845326394	-1.18297501	-1
69	0.0000316	0.000584325	2.630230616	0.905061993	-1.104896689	-1
70	0.0000000092	0.0000107	10.73453386	0.777940153	-1.285445926	-1
71	0.00000165	0.000106067	5.674210448	0.884548664	-1.13052005	-1
72	0.00000113	0.0000855	6.052012506	0.814734156	-1.227394227	-1
73	0.0000000154	0.0000115	10.25824114	1.517878795	1.517878795	1
74	0.0000272	0.00053455	2.786912756	0.878524937	-1.138271616	-1
75	0.0000197	0.000439652	3.120890546	1.221831748	1.221831748	1
76	0.000000796	0.0000726	6.410227046	1.136563537	1.136563537	1
77	0.0000423	0.00070501	2.327593259	1.122774193	1.122774193	1
78	0.00020132	0.001977662	0.70216959	1.107609748	1.107609748	1
79	0.00000164	0.000106067	5.678158075	0.833487622	-1.199777866	-1
80	0.00000205	0.000117891	5.451255469	0.84378323	-1.18513851	-1
81	0.0000096	0.000278481	3.864510034	0.905023296	-1.104943933	-1
82	0.0000105	0.000294144	3.776112142	1.235187935	1.235187935	1
83	0.00000969	0.000280237	3.855144299	1.366483661	1.366483661	1
84	0.0000108	0.000298984	3.743323414	0.885454973	-1.129362905	-1
85	0.0000282	0.00054663	2.746937043	1.263536036	1.263536036	1
86	0.0000215	0.000464107	3.031396559	1.230769711	1.230769711	1
87	0.000000454	0.0000563	6.975413589	1.297798713	1.297798713	1
88	0.00000662	0.000226164	4.248389692	1.255372694	1.255372694	1
89	0.00000305	0.000145428	5.043130801	1.343762761	1.343762761	1
90	0.0000000294	0.0000153	9.64902897	1.223264684	1.223264684	1
91	0.000290264	0.002534245	0.32110467	0.896874612	-1.114983061	-1
92	0.0000335	0.000609191	2.568001061	0.897982647	-1.113607265	-1
93	0.0000623	0.000903821	1.924342502	0.891730663	-1.121414842	-1
94	0.010931496	0.034736273	-3.41285233	1.280848257	1.280848257	1
95	0.013665308	0.041030377	-3.636678978	1.274996095	1.274996095	1
96	0.00000301	0.000144884	5.057553149	1.242796139	1.242796139	1
97	0.008183105	0.027939057	-3.120846211	0.797862089	-1.253349437	-1

98	0.012168576	0.037672866	-3.520502123	0.879662072	-1.136800178	-1
99	0.014916282	0.043846027	-3.724182352	0.907057882	-1.102465476	-1
100	0.009318298	0.030820985	-3.252058133	0.80221645	-1.246546365	-1
101	0.004239872	0.0171443	-2.452133159	0.761934695	-1.312448438	-1
102	0.012799247	0.039057427	-3.571146947	0.862654151	-1.159213108	-1
103	0.002310795	0.010964378	-1.829468152	0.90372659	-1.106529354	-1
104	0.000185463	0.001878108	0.787632865	0.857293116	-1.166462184	-1

Table 13.b3

		Probe sequence
	Loop detected	**60 mer**
53	PD-L1 responder	ATCCCAACAAAAGAGAAGAACTTCTCCCTCGATGTTTGGGGGCGGAGGGCTTTGATGAGA
54	PD-L1 responder	CAAAATCAAACACAAATCTAATCAAACTTCGATGTTTGGGGGCGGAGGGCTTTGATGAGA
55	PD-L1 responder	GGCCGCGAGCCCGGCAGCGGCGACATCCTCGAGAAATTCTCCCGCTTTAGCCTCCCAAAG
56	PD-L1 responder	TGAGATGAAGCCTATATTTTCCCAATCCTCGATGTTTGGGGGCGGAGGGCTTTGATGAGA
57	PD-L1 responder	TACAGACTTTTTTTCTCTTCTCAGAAAATCGATGTTTGGGGGCGGAGGGCTTTGATGAGA
58	PD-L1 responder	GCGGCCAACCCACAGCGCACCGGGCCGCTCGACCTCTGAGAGGAAACTTGCTAGCCCCAG
59	PD-L1 responder	CACTAATCTTTACTCTTTTTCCACTTATTCGACCCTCCCCTTCCAGCTGGGCACAGGTGG
60	PD-L1 responder	ATTCCCAATGTTTCCTGAGTAGAACTGTTCGACTGCGAGCTCCCTCCCTGCAGTCAGGGA
61	PD-L1 responder	AGGGAGAACAAAAGAAGTTCCATCCATCTCGATCCCCCCGGGCTCAAAGCAAACCTCCTA
62	PD-L1 responder	AGGGAGAACAAAAGAAGTTCCATCCATCTCGACGGAGTCCTCCCCGCAGGGCAGCCCCGA
63	PD-L1 responder	TATTTGTATCCTTTCCTCATTTATTTACTCGAATCTCTGGGGTAGGGCTCTGCAACCTTG
64	PD-L1 responder	TTTCAAAGAAGGTATGATGGGAAAGGTCTCGAGTGCCCCTGTCCCACCTGGCTCCCCCTG
65	PD-L1 responder	TTTCAAAGAAGGTATGATGGGAAAGGTCTCGACGCGCCCCCTCTACGCCATGTCCCCCCC
66	PD-L1 Non-responder	ATATAAATCTACTTTATAAATAAGGAAATCGAAGTATAATTCAATATACTGTCCAGTAAA
67	PD-L1 responder	TCCAGCCTTGCCTGGAGCTAGGGCCACCTCGATCTTGGCTCACCGCAACCTTGGCCTCCC
68	PD-L1 responder	CTGTGAACATTGGTGTACTAGTAGCTTTTCGATTTCCACTTCTACCCCCCGGTCCGAGTT
69	PD-L1 responder	CCATCTGCAAGTCGCTTTTGACTAGCACTCGAGTTCTTTCTGACATCTCCTGGGTGGAGC
70	PD-L1 responder	GTGGATTACATCCTTCTATAGGTGTGGCTCGAGCGGAGTCACCCAGGCTGGAGTGCAGTG
71	PD-L1 responder	GACCTAAGGATTAAGAAGATTAATGGAGTCGAGCATCCTCTACCTCTATCTCCAACCCCT
72	PD-L1 responder	CCTGCACTTCCTCACGCCTGCTCACCCCTCGAGTGAGTGGGAGAGATGGCTCTCCACGCC
73	PD-L1 Non-responder	TATATAATTTCCACTTTGTTTTTAATAATCGAAATTAAAAATTATTTTATCTCACATAGA
74	PD-L1 responder	GCCTGGATGCCCTCGTCCATCTCGGCCTTCGATCTGAGGACAGAAAAGACCCAGGCGCCC
75	PD-L1 Non-responder	TTAAATCTTGAATAGAAGTTATGATTGATCGATTATTGAATTCAATTGTGTATATAAATT
76	PD-L1 Non-responder	TATTAAGAAAATAAGTCAGCCAGGTGTTTCGAGTACTACTACAATTAGCACTTGCTTATT
77	PD-L1 Non-responder	GGCCAGTAGATCATTTGAGGCCAGGAGTTCGATAACCTTCAAATCAACTCACAGAATTCC
78	PD-L1 Non-responder	TGGGAGGTGGCCAGAGTCTGACTACATCTCGAACTACTGGGCTCAAACAATTCTCCTGCC
79	PD-L1 responder	TTAATGCTGATACAATTCTATTGGATAATCGACACTTCGGCTCCCTGCACCTCCCATGCC
80	PD-L1 responder	CAATATGACGGTGACATTAATGATAGCTTCGACACTTCGGCTCCCTGCACCTCCCATGCC
81	PD-L1 responder	TTAATGCTGATACAATTCTATTGGATAATCGACGTGCCTTGGGGCCTCCCCTTTCCCTAT
82	PD-L1 Non-responder	AATAAAAATAGAAAACAATCCTTCAAAATCGACACCAATGTTTCCATTTTGTTTTCAGAA
83	PD-L1 Non-responder	AATGATTAAATGTGTACCTTAATGAGTTTCGAAACTCCATTGAGTCATTATCCTTGCTAT
84	PD-L1 responder	CATCATAGCAACCCATTGTAACTAGACTTCGAATAGATACTTCAGGAAAGAAATGTATAT
85	PD-L1 Non-responder	AGACAATATTAAAATTGAGAACTTTTGTTCGATTTTATTTTTAACTTATAAGAAGATCTG
86	PD-L1 Non-responder	TGTGATGATTTCTTCTTTTTATATGTTTTCGATAAAATACTTCATAAAAATAACATGCTA

87	PD-L1 Non-responder	TAGCATGTTATTTTTATGAAGTATTTTATCGACAGTTTTTTTTAAAAAAAAACCTTGACA
88	PD-L1 Non-responder	TAGCATGTTATTTTTATGAAGTATTTTATCGAGCTGATAAACAGCTTTGTAGGGAAAAAC
89	PD-L1 Non-responder	TAGCATGTTATTTTTATGAAGTATTTTATCGAAGAATTATAAACACTTATAGTTGTATCT
90	PD-L1 Non-responder	AGTGGTGCAATCTTGACTCACTGCAGTCTCGAAATCTAGTAACATCATATTCTAACATGA
91	PD-L1 responder	GGCCTCGGCACTCACCGTTCCCTCCCCCTCGATTTCCATGAGCCCCTCTGAATCCTTCCA
92	PD-L1 responder	CACCTGTCATGCTGGTCTGCCGCCGTTTTCGAGGCAGGCCCCTCCTGCCAAGTGAAGAGA
93	PD-L1 responder	GGCCTCGGCACTCACCGTTCCCTCCCCCTCGAGGCAGGCCCCTCCTGCCAAGTGAAGAGA
94	PD-L1 Non-responder	GAGATACTAAAATAGGTTTCTTTCCTAGTCGACTAGGATCAGTTGTTTGTAGGATTATAA
95	PD-L1 Non-responder	AACTCACAACTATCTGGTGCTATGTACATCGAACTAAAATCTGCCTCTGAACAGCTTCCA
96	PD-L1 Non-responder	ATCTTTAGCATATATGTTAAATTGATAATCGAATTTAATAAAGAAATTACTGAAAAAGGA
97	PD-L1 responder	CCCCTCACCCAAACTAGGGTCTCTAGACTCGAGCTCCCATAGATCAACTTTCTGCACTCC
98	PD-L1 responder	CCCCTCACCCAAACTAGGGTCTCTAGACTCGAGAGGCCATCCACGCTGATAGAAGGGATG
99	PD-L1 responder	CCCTGGGGTTCTGATTAACATCCTTAATTCGAGAGGCCATCCACGCTGATAGAAGGGATG
100	PD-L1 responder	CCCCTCACCCAAACTAGGGTCTCTAGACTCGAGACAAGGTATATGAGCAGCTGGCCAAAT
101	PD-L1 responder	CCCTGGGGTTCTGATTAACATCCTTAATTCGAAGAATGCCTAATGGTTAAGCAGTAGGAA
102	PD-L1 responder	CCCCTCACCCAAACTAGGGTCTCTAGACTCGAGGCCCAAGGGCTTGTCAGTCAGCTTGTG
103	PD-L1 responder	ATTCTTCTGTCCCCAGTTTCTTATGCAGTCGAGAGGCCATCCACGCTGATAGAAGGGATG
104	PD-L1 responder	GGAGTGCAGAAAGTTGATCTATGGGAGCTCGACTGTATCCGCAGCACCTGGCCCACAGTA

Table 13.b4

	Probe Location					4 kb Sequence Location		
	Chr	**Start1**	**End1**	**Start2**	**End2**	**Chr**	**Start1**	**End1**
53	5	157181019	157181048	157266725	157266754	5	157177049	157181048
54	5	157178319	157178348	157266725	157266754	5	157178319	157182318
55	5	157225228	157225257	157266547	157266576	5	157225228	157229227
56	5	157231401	157231430	157266725	157266754	5	157227431	157231430
57	5	157249288	157249317	157266725	157266754	5	157249288	157253287
58	8	55939615	55939644	55961822	55961851	8	55939615	55943614
59	9	125549822	125549851	125635071	125635100	9	125549822	125553821
60	1	11169968	11169997	11281372	11281401	1	11165998	11169997
61	8	127694016	127694045	127733497	127733526	8	127690046	127694045
62	8	127694016	127694045	127738939	127738968	8	127690046	127694045
63	2	105716876	105716905	105886459	105886488	2	105712906	105716905
64	6	44253666	44253695	44312110	44312139	6	44253666	44257665
65	6	44270723	44270752	44312110	44312139	6	44270723	44274722
66	17	34316073	34316102	34373919	34373948	17	34316073	34320072
67	17	36084484	36084513	36095759	36095788	17	36080514	36084513
68	6	41947755	41947784	42055377	42055406	6	41947755	41951754
69	6	167112410	167112439	167154581	167154610	6	167108440	167112439
70	3	46429853	46429882	46457806	46457835	3	46429853	46433852
71	5	67182231	67182260	67233989	67234018	5	67178261	67182260
72	16	28959098	28959127	28978416	28978445	16	28959098	28963097
73	3	112306429	112306458	112398394	112398423	3	112306429	112310428
74	19	35295636	35295665	35310520	35310549	19	35291666	35295665
75	18	69825656	69825685	69936161	69936190	18	69825656	69829655
76	9	5422951	5422980	5460319	5460348	9	5422951	5426950
77	9	5431302	5431331	5512277	5512306	9	5427332	5431331
78	11	61068642	61068671	61139962	61139991	11	61068642	61072641

79	11	60938640	60938669	60983698	60983727	11	60938640	60942639
80	11	60938640	60938669	61025556	61025585	11	60938640	60942639
81	11	60983698	60983727	60996251	60996280	11	60979728	60983727
82	6	14075801	14075830	14131438	14131467	6	14071831	14075830
83	6	14087224	14087253	14136228	14136257	6	14083254	14087253
84	3	122014664	122014693	122100773	122100802	3	122014664	122018663
85	5	131249660	131249689	131303538	131303567	5	131245690	131249689
86	7	90719740	90719769	90868754	90868783	7	90715770	90719769
87	7	90868754	90868783	90942971	90943000	7	90864784	90868783
88	7	90868754	90868783	90994572	90994601	7	90864784	90868783
89	7	90868754	90868783	91110393	91110422	7	90864784	90868783
90	7	90936378	90936407	91158268	91158297	7	90936378	90940377
91	6	36654202	36654231	36693628	36693657	6	36654202	36658201
92	6	36684519	36684548	36719341	36719370	6	36684519	36688518
93	6	36693628	36693657	36719341	36719370	6	36689658	36693657
94	6	4826110	4826139	4930777	4930806	6	4826110	4830109
95	10	11274452	11274481	11303118	11303147	10	11274452	11278451
96	2	168472568	168472597	168692922	168692951	2	168472568	168476567
97	X	47587628	47587657	47617979	47618008	X	47583658	47587657
98	X	47587628	47587657	47636868	47636897	X	47583658	47587657
99	X	47581313	47581342	47636868	47636897	X	47581313	47585312
100	X	47587628	47587657	47657817	47657846	X	47583658	47587657
101	X	47581313	47581342	47652990	47653019	X	47581313	47585312
102	X	47587628	47587657	47672279	47672308	X	47583658	47587657
103	X	47605022	47605051	47636868	47636897	X	47601052	47605051
104	X	47617979	47618008	47644374	47644403	X	47614009	47618008

Table 13.b5

	4 kb Sequence Location		**Inner_primers**		
	Start2	**End2**	**PCR-Primer1_ID**	**PCR_Primer1**	**PCR-Primer2_ID**
53	157266725	157270724	OBD117.1.269	CTAAGAGGTGATGCCCAAGGTGC	OBD117.1.271
54	157266725	157270724	OBD117.1.397	GTCTCCTGAGGTGAAGCAAGAGG	OBD117.1.399
55	157262577	157266576	OBD117.1.773	GGTGCTAATCTCAGGGACCG	OBD117.1.775
56	157266725	157270724	OBD117.1.001	CTCTCTTGCTGGCATTCCCTTCCC	OBD117.1.003
57	157266725	157270724	OBD117.1.041	GTAAATGAGCCACCTGGGCGGGT	OBD117.1.043
58	55961822	55965821	OBD117.1.809	GGCAAATACGTTAATAGCAGCAC	OBD117.1.811
59	125631101	125635100	OBD117.1.257	GTCATCTCCTCTCCAGTTAGTCAACA	OBD117.1.259
60	11281372	11285371	OBD117.1.793	TTCAGAGGGTTCTTCGGGGA	OBD117.1.795
61	127729527	127733526	OBD117.1.377	GCCCCTAAGCAACCACCTTGGAC	OBD117.1.379
62	127738939	127742938	OBD117.1.045	CCCTAAGCAACCACCTTGGACTG	OBD117.1.047
63	105886459	105890458	OBD117.1.813	AATGTTGGCATGGTGTTTTC	OBD117.1.815
64	44308140	44312139	OBD117.1.049	CACTTTGCCTCCACATCTGGTATGAG	OBD117.1.051
65	44308140	44312139	OBD117.1.1069	TAGCACTTTGCCTCCACATC	OBD117.1.1071
66	34369949	34373948	OBD117.1.893	ACTTGTGGCTTCCTTAGCCC	OBD117.1.895
67	36095759	36099758	OBD117.1.389	CAGAAAGAGAAGCAAAGAGGACTCAT	OBD117.1.391
68	42051407	42055406	OBD117.1.1045	GGCTGCTGTGAATCATGCTG	OBD117.1.1047
69	167150611	167154610	OBD117.1.185	GGCGGTAAAGTCACACAGCCAGA	OBD117.1.187
70	46457806	46461805	OBD117.1.953	AGTGTCGCTGTACATGACCAG	OBD117.1.955
71	67233989	67237988	OBD117.1.313	CTGCCTGGTTTCTGAACTGAGTGAGG	OBD117.1.315
72	28974446	28978445	OBD117.1.125	GAGCGTGGTGCCAGTGTGGGTAA	OBD117.1.127
73	112398394	112402393	OBD117.1.1293	GCACCTTACTCGGAGGAGGACCA	OBD117.1.1295
74	35306550	35310549	OBD117.1.433	AGGTAACGGCTGACAGGTGCTGG	OBD117.1.435
75	69936161	69940160	OBD117.1.1221	TCAAAAGAGCACAGCATAATCTGAAT	OBD117.1.1223
76	5460319	5464318	OBD117.1.577	CTAAGTGCCAGCAGACTATGGAGCCA	OBD117.1.579

77	5512277	5516276	OBD117.1.625	GTTTCCGTGCCTTTTCCAGCCTC	OBD117.1.627
78	61139962	61143961	OBD117.1.913	CAGGGAGAACACCCGGAAGG	OBD117.1.915
79	60979728	60983727	OBD117.1.089	TGTCCCTTTCTCCTAAATACCCCAAC	OBD117.1.091
80	61021586	61025585	OBD117.1.237	CCAACACAGCAGCCTCCAGCCAT	OBD117.1.239
81	60996251	61000250	OBD117.1.153	GTCCCTTTCTCCTAAATACCCCAACG	OBD117.1.155
82	14127468	14131467	OBD117.1.1865	CTTTGGACTTATGTAAATGTTTT	OBD117.1.1867
83	14136228	14140227	OBD117.1.1501	TAAATACCAGCCTTGGAATCAGGGC	OBD117.1.1503
84	122096803	122100802	OBD117.1.253	CTGGATTCTTGAGCGACTTGTTCCTG	OBD117.1.255
85	131303538	131307537	OBD117.1.1305	GAAGAAACTGGATTCCTACCTGGCAC	OBD117.1.1307
86	90864784	90868783	OBD117.1.1193	GCTGTGCTCTTTCAAATCCACTGCTG	OBD117.1.1195
87	90939001	90943000	OBD117.1.1117	TTATTTTATTAGATGCCACCCTCAGC	OBD117.1.1119
88	90994572	90998571	OBD117.1.1517	TTATTTTATTAGATGCCACCCTCAGC	OBD117.1.1519
89	91106423	91110422	OBD117.1.1533	TTATTTTATTAGATGCCACCCTCAGC	OBD117.1.1535
90	91154298	91158297	OBD117.1.1393	GGGATGCCACTGTATTTCTCAAAGCC	OBD117.1.1395
91	36689658	36693657	OBD117.1.957	CCATATGGTCTCCGGGTCCT	OBD117.1.959
92	36719341	36723340	OBD117.1.501	TGGTCCCTTACAAAGTCCTTCCGTGC	OBD117.1.503
93	36719341	36723340	OBD117.1.473	TTTCCTCTGTCTCCATCTCCGCCCAT	OBD117.1.475
94	4926807	4930806	OBD117.1.1597	GGTGGGAAGAGGGTGTCACAAGTCAT	OBD117.1.1599
95	11303118	11307117	OBD117.1.1641	GGTTCACTGACTCTGGTGCCAAC	OBD117.1.1643
96	168688952	168692951	OBD117.1.1633	GCTGATTTCTTTGTGTGTGGGTGGG	OBD117.1.1635
97	47614009	47618008	OBD117.1.481	ACACACCTCCCTCAACCCAACTGTC	OBD117.1.483
98	47636868	47640867	OBD117.1.453	CACACCTCCCTCAACCCAACTGT	OBD117.1.455
99	47636868	47640867	OBD117.1.493	AACTAATCCCCACCCCATCCTGC	OBD117.1.495
100	47653847	47657846	OBD117.1.509	CCACACACCTCCCTCAACCCAAC	OBD117.1.511
101	47652990	47656989	OBD117.1.529	ACTAATCCCCACCCCATCCTGCC	OBD117.1.531
102	47672279	47676278	OBD117.1.973	CTCCCTCAACCCAACTGTCC	OBD117.1.975
103	47636868	47640867	OBD117.1.441	CTCCTGCCCACTCTATTTTCCCC	OBD117.1.443
104	47640404	47644403	OBD117.1.469	AGAAGACACTCCATAAATGCTCAGGG	OBD117.1.471

Table 13.b6

	Inner_primers	
	PCR_Primer2	GLMNET
53	GACGCCACAACAGACAGGCAAGC	0.013514368
54	AGTCAGCCCACTCATCCCCTTCC	-0.009002897
55	TTTGGCAAGCTTTGTGAGG	0.000108207
56	GTAGACGCCACAACAGACAGGCA	-0.006474726
57	GGCAAGCATCTTCCTGGTTCTTCAG	-0.021298663
58	CAGGAAGGTCGGAATAGCTG	-0.024082323
59	GGTTGGAAGTAGCCCACGGTGTGTTT	0.017680421
60	ATGACGGGGTGTGGGTTAT	0.01727269
61	CCAGCAGTTTCAGAGGCAAAGGC	-0.006220015
62	GCTTCGCTTACCAGAGTCGCTGC	-0.010058174
63	TCAAGTGCATACTCCACAACG	0.000127348
64	GGCTTGACACCCTTAGTTTACTGCCT	-0.009744914
65	CCTAGACTCTCACCTCCTCTCG	0
66	TCCTTTGCAGGTATGGACATC	0.008460581
67	GTTGGATGCTGTGTGGTGGGATAGAT	-0.011403512
68	TGAGACTAGACTGGAGGGCC	0
69	ACACCTGTGAGCAGAGTGGAGGG	0.005137905
70	GCCCGGCCTTGAGTTATTCT	-0.007948899
71	AGAAACTGATGGAAGAAGGAAACTCC	0.000116162
72	GGGAGGGAAGTTGAACGATGGGT	-0.011725271
73	CAGCCTTCTCTCCAAAGCAGGGA	0
74	TCACCACCACCCATAGCCCTAAG	0
75	AATCAACCCTCAGGCTTTCAGGCAAA	0
76	GACACACTCAGATTTCAGACACAACA	0.001022887

77	GGGCAGTTCATCATAGGGAGCCG	-0.005572532
78	GCTATGGAGCTGGACATGG	0.000119295
79	TAGGAGGAGCGGTCTTACAGGCAGA	0
80	TAGGAGGAGCGGTCTTACAGGCA	0.00011596
81	TGTGATGCTTCCCACTGCTCTGATAG	-0.014829951
82	ACAAACATAAGTTGAGGCTGGAT	0
83	CACCCTCTCATCCCCAAAACACCATC	0
84	GGGACTGTCACTGGCTATTTATGGGA	-0.001718735
85	GGAATGTCCTGCCTTAGGGTATCTGT	0
86	TTATTTTATTAGATGCCACCCTCAGC	0
87	CAGAACAGTGGGTAGGGACTTGCTTT	0
88	TGCTAAGAAGTGTCACCACCTCCTCA	0
89	GACAAAGGCTCTGATGTTGAAAATGC	0
90	GGTAAAAGGAAGCAAAGGACTGATTC	0
91	ACCCAGAGGTTCCTTTGTCA	0.009388509
92	GGGTGAAGGAATAAATGATTGGAGGG	0
93	GGGTGAAGGAATAAATGATTGGAGGG	0
94	GGATACTAAACCACCTGCTCATAAGG	0
95	GTCCCGAGAAGGGTGACCAGACA	0
96	CATTCTGACATCCTCTTCCCATTCCT	0
97	AGAAGACACTCCATAAATGCTCAGGG	0
98	CCAGTTTCCATCCAGTGGCAGCG	0
99	CCAGTTTCCATCCAGTGGCAGCG	0
100	CCTCCCTTGCCCACACATACCAA	0
101	GCCACTTTCCCTCCCCACTCAAT	0
102	CTGGCAGCATTCACCACAAG	0
103	CCAGTTTCCATCCAGTGGCAGCG	-0.017184561
104	CCCACTTGACCCCTCATAAGAGTTCT	0.001327318

Table 13.b7

	Probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig
105	ORF149_X_47613512_47618008_47636868_47644403_FR	ORF149	23	15
106	ORF149_X_47613512_47618008_47636868_47644403_RR	ORF149	23	15
107	ORF149_X_47613512_47618008_47672279_47679605_RR	ORF149	23	15
108	ORF157_9_121063123_121064862_121152751_121162678_RF	ORF157	64	5
109	ORF159_8_120045608_120049042_120170620_120179901_FR	ORF159	171	15
110	ORF159_8_120058539_120067601_120170620_120179901_FR	ORF159	171	15
111	ORF159_8_120324759_120327604_120388396_120396997_RR	ORF159	171	15
112	ORF159_8_120368738_120373426_120388396_120396997_RR	ORF159	171	15
113	ORF16_10_74576267_74586651_74616954_74620476_RF	ORF16	115	7
114	ORF160_5_178219671_178228100_178451151_178455914_FR	ORF160	34	11
115	ORF160_5_178219671_178228100_178475905_178480029_FF	ORF160	34	11
116	ORF160_5_178254981_178259471_178436965_178443271_FR	ORF160	34	11
117	ORF163_12_93752886_93759416_93791200_93797905_FF	CRADD	231	4
118	ORF167_5_132051982_132053273_132068115_132074991_FF	CSF2	36	2
119	ORF171_1_112368886_112372835_112478496_112485740_FF	ORF171	37	7
120	ORF171_1_112478496_112485740_112502466_112507019_FR	ORF171	37	7
121	ORF175_4_74083782_74086942_74117911_74125141_RR	ORF175	38	1
122	ORF179_2_157461901_157469311_157533412_157536043_RF	ORF179	33	1
123	ORF185_12_122194669_122198199_122226656_122228976_RR	ORF185	20	1
124	ORF188_1_231816751_231823980_231852208_231857319_FF	ORF188	173	14
125	ORF189_13_50726484_50732327_50881905_50885725_RR	ORF189	107	10
126	ORF190_18_4001462_4005154_4185416_4194441_RF	ORF190	182	15
127	ORF190_18_4185416_4194441_4248756_4252697_FR	ORF190	182	15

128	ORF190_18_4185416_4194441_4410806_4417824_FR	ORF190	182	15
129	ORF193_2_224946941_224952242_224984447_224994669_RF	ORF193	190	29
130	ORF195_7_111887117_111893545_112094382_112105308_FF	ORF195	158	7
131	ORF195_7_112094382_112105308_112160919_112168008_FF	ORF195	158	7
132	ORF197_8_26561792_26565691_26638318_26644530_FR	ORF197	31	9
133	ORF197_8_26561792_26565691_26638318_26644530_RR	ORF197	31	9
134	ORF20_5_281198_284937_355623_362397_FR	ORF20	33	6
135	ORF20_5_281198_284937_467048_471770_FF	ORF20	33	6
136	ORF202_8_29312029_29317185_29361816_29366925_FF	ORF202	22	1
137	ORF205_3_5223126_5230817_5254657_5258841_FF	ORF205	30	5
138	ORF206_12_92776962_92786640_92823177_92825247_RR	ORF206	46	7
139	ORF209_4_109875299_109879120_110005130_110011368_FF	EGF	48	2
140	ORF211_11_34573815_34582810_34673477_34682282_RF	ORF211	99	7
141	ORF211_11_34659116_34661654_34673477_34682282_RF	ORF211	99	7
142	ORF212_X_47636868_47644403_47688049_47692767_RR	ORF212	2	1
143	ORF213_7_36990112_36997961_37106040_37113398_RR	ORF213	171	10
144	ORF214_2_42145559_42150768_42194745_42201093_FF	ORF214	114	14
145	ORF214_2_42237154_42240281_42363233_42373092_FR	ORF214	114	14
146	ORF215_12_47728716_47732358_47745284_47751054_FR	ENDOU	26	2
147	ORF224_6_151870936_151873891_151928859_151937822_FR	ORF224	158	22
148	ORF226_1_94522204_94526809_94565070_94571537_RR	F3	36	2
149	ORF229_8_58019132_58028120_58156560_58160085_FR	ORF229	173	12
150	ORF229_8_58019132_58028120_58192936_58197384_FR	ORF229	173	12
151	ORF229_8_58207979_58216653_58245172_58252090_FR	ORF229	173	12
152	ORF233_12_61732349_61741819_61763501_61778266_RR	ORF233	196	4
153	ORF240_12_29277865_29278935_29307954_29317490_FR	ORF240	136	11
154	ORF241_10_88946200_88948398_88998943_89014190_FF	FAS	50	8
155	ORF243_1_161620964_161624310_161643724_161645551_RR	ORF243	17	6
156	ORF243_1_161620964_161624310_161645837_161653201_RR	ORF243	17	6

Table 13.c1

	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr	t
105	1.30E-12	6.11E-10	65.22	-0.191402284	-0.191402284	-3.367194119
106	1.30E-12	6.11E-10	65.22	-0.18368985	-0.18368985	-3.875425412
107	1.30E-12	6.11E-10	65.22	-0.178892791	-0.178892791	-2.633426192
108	0.378198431	1	7.81	0.311603864	0.311603864	10.97706382
109	0.122880445	0.904598768	8.77	0.281827736	0.281827736	4.843986126
110	0.122880445	0.904598768	8.77	0.315358869	0.315358869	8.713690406
111	0.122880445	0.904598768	8.77	0.362400462	0.362400462	7.04193327
112	0.122880445	0.904598768	8.77	0.323044543	0.323044543	11.51888935
113	0.593052688	1	6.09	0.335907499	0.335907499	6.250465094
114	7.38E-06	0.000580328	32.35	0.236876295	0.236876295	4.314666444
115	4.52E-06	0.000387515	32.35	0.246788348	0.246788348	4.478260313
116	7.38E-06	0.000580328	32.35	0.140271069	0.140271069	6.960305101
117	0.999992975	0.99999793	1.73	-0.138988579	-0.138988579	-7.545550183
118	0.791365183	0.99999793	5.56	-0.158073637	-0.158073637	-5.410812733
119	0.00759753	0.152435545	18.92	0.293285512	0.293285512	16.18229062
120	0.00759753	0.152435545	18.92	0.352425494	0.352425494	11.00394191
121	0.926506445	1	2.63	0.141461092	0.141461092	3.611237851
122	0.883515927	1	3.03	0.298609963	0.298609963	7.099629688
123	0.746824008	1	5	0.154427751	0.154427751	9.022897646
124	0.203516369	1	8.09	0.280940922	0.280940922	5.410547977
125	0.137504735	0.956987014	9.35	0.281307391	0.281307391	3.125990032
126	0.175422864	1	8.24	0.379009191	0.379009191	8.972595592
127	0.175422864	1	8.24	0.306592709	0.306592709	5.979272377

128	0.175422864	1	8.24	0.5021624	0.5021624	7.058516782
129	9.14E-06	0.000663127	15.26	0.282386591	0.282386591	6.179848359
130	0.876059487	1	4.43	0.319388984	0.319388984	7.281636739
131	0.876059487	1	4.43	0.475565551	0.475565551	9.654875537
132	8.78E-05	0.003599994	29.03	0.283654606	0.283654606	8.975747403
133	8.78E-05	0.003599994	29.03	0.329174321	0.329174321	10.11190446
134	0.015893505	0.26293992	18.18	0.367007322	0.367007322	3.722842716
135	0.015893505	0.26293992	18.18	0.37888586	0.37888586	4.011231915
136	0.797192199	1	4.55	-0.159809632	-0.159809632	-4.427546783
137	0.037848586	0.469621268	16.67	0.300529644	0.300529644	2.711336791
138	0.02419036	0.362087451	15.22	0.397149182	0.397149182	10.0125645
139	0.903339407	0.99999793	4.17	-0.210308957	-0.210308957	-10.40736882
140	0.433763829	1	7.07	0.342396305	0.342396305	7.282974678
141	0.433763829	1	7.07	0.311736862	0.311736862	14.33468227
142	0.13498553	0.877871412	50	-0.137915679	-0.137915679	-2.573853727
143	0.642310571	1	5.85	0.837580169	0.837580169	2.690859837
144	0.012609648	0.224347261	12.28	0.331373318	0.331373318	9.145897755
145	0.012609648	0.224347261	12.28	0.392170538	0.392170538	8.386917517
146	0.622797749	0.99999793	7.69	-0.138484187	-0.138484187	-8.619846124
147	0.000398298	0.012833299	13.92	0.519014068	0.519014068	14.44253214
148	0.791365183	0.99999793	5.56	-0.436454288	-0.436454288	-6.068793285
149	0.409269399	1	6.94	0.281775997	0.281775997	9.229228715
150	0.409269399	1	6.94	0.304197038	0.304197038	6.706923479
151	0.409269399	1	6.94	0.442742286	0.442742286	8.01968993
152	0.998659439	1	2.04	0.337166653	0.337166653	7.064012738
153	0.239371673	1	8.09	0.359322711	0.359322711	5.631130929
154	0.041957105	0.555032562	16	-0.625760222	-0.625760222	-6.24344027
155	0.000555352	0.016365522	35.29	0.151463789	0.151463789	3.447879011
156	0.000421879	0.012833299	35.29	0.152480082	0.152480082	3.157950885

Table 13.c2

	P.Value	adj.P.Val	B	FC	FC_1	LS
105	0.006918565	0.024672545	-2.950820981	0.875754084	-1.141873065	-1
106	0.002944867	0.013082931	-2.078743148	0.880448272	-1.135785068	-1
107	0.024546577	0.063658901	-4.217709989	0.883380694	-1.132014777	-1
108	0.000000543	0.0000607	6.79431013	1.241086666	1.241086666	1
109	0.0006317	0.004343505	-0.487670379	1.21573411	1.21573411	1
110	0.00000468	0.000184004	4.603843587	1.244321138	1.244321138	1
111	0.0000311	0.000577835	2.645338013	1.285563133	1.285563133	1
112	0.000000343	0.0000498	7.254248938	1.250967703	1.250967703	1
113	0.0000854	0.001117726	1.595434033	1.262171103	1.262171103	1
114	0.001442265	0.007834621	-1.343218857	1.178438357	1.178438357	1
115	0.001112805	0.006508715	-1.074930345	1.186562709	1.186562709	1
116	0.0000344	0.000618386	2.54094266	1.102112173	1.102112173	1
117	0.000017	0.000402097	3.270523863	0.908155607	-1.101132881	-1
118	0.000272744	0.002422901	0.3859262	0.896220954	-1.115796272	-1
119	0.0000000125	0.0000107	10.45481919	1.225427822	1.225427822	1
120	0.000000531	0.0000601	6.817655292	1.276705252	1.276705252	1
121	0.004575517	0.018119918	-2.529962413	1.103021638	1.103021638	1
122	0.000029	0.00055581	2.718602774	1.229958777	1.229958777	1
123	0.0000034	0.000155397	4.931662488	1.112980064	1.112980064	1
124	0.000272848	0.00242331	0.385528861	1.214987037	1.214987037	1
125	0.010462121	0.033595661	-3.368710433	1.215295704	1.215295704	1
126	0.00000358	0.000160081	4.879004534	1.300448431	1.300448431	1
127	0.000122964	0.001428447	1.215794625	1.23678327	1.23678327	1

128	0.0000305	0.000571478	2.66644057	1.416334861	1.416334861	1
129	0.0000938	0.001195013	1.497578085	1.216205139	1.216205139	1
130	0.0000233	0.000485595	2.946910771	1.247801963	1.247801963	1
131	0.00000182	0.000112168	5.571905072	1.390463188	1.390463188	1
132	0.00000357	0.000159919	4.882311538	1.217274557	1.217274557	1
133	0.00000118	0.0000874	6.011500362	1.25629417	1.25629417	1
134	0.003794736	0.015760102	-2.338680459	1.289674796	1.289674796	1
135	0.002355428	0.011122308	-1.849158701	1.300337265	1.300337265	1
136	0.001205485	0.006894159	-1.157743215	0.89514318	-1.117139718	-1
137	0.02144394	0.057515838	-4.084567148	1.231596475	1.231596475	1
138	0.00000129	0.0000932	5.917548476	1.316903089	1.316903089	1
139	0.0000009	0.000077	6.285863051	0.864352108	-1.156935918	-1
140	0.0000233	0.000485546	2.948573409	1.267860752	1.267860752	1
141	0.0000000412	0.0000172	9.328618853	1.241201084	1.241201084	1
142	0.027216654	0.068727574	-4.319033972	0.908831233	-1.100314297	-1
143	0.022219346	0.059045237	-4.119623299	1.787050209	1.787050209	1
144	0.000003	0.000144884	5.059344635	1.258210509	1.258210509	1
145	0.00000663	0.000226164	4.246397404	1.312366378	1.312366378	1
146	0.00000517	0.000196113	4.502368539	0.90847317	-1.100747973	-1
147	0.0000000383	0.000017	9.398912888	1.432975624	1.432975624	1
148	0.000108908	0.001320738	1.342264192	0.738948493	-1.353274294	-1
149	0.00000276	0.000139969	5.144987441	1.215690512	1.215690512	1
150	0.0000473	0.000761013	2.211279703	1.23473123	1.23473123	1
151	0.00000992	0.000285195	3.830595539	1.359185424	1.359185424	1
152	0.0000303	0.00056988	2.673426296	1.263273181	1.263273181	1
153	0.000199224	0.001962619	0.713074052	1.282823521	1.282823521	1
154	0.0000862	0.001125209	1.58573085	0.648078185	-1.543023701	-1
155	0.006030852	0.022309044	-2.811359709	1.110695836	1.110695836	1
156	0.009901982	0.032241793	-3.313305449	1.111478531	1.111478531	1

Table 13.c3

		Probe sequence
	Loop detected	**60 mer**
105	PD-L1 responder	GGAGTGCAGAAAGTTGATCTATGGGAGCTCGAGAGGCCATCCACGCTGATAGAAGGGATG
106	PD-L1 responder	ACTCAAATATGGAATATTCCAGTCAAAATCGAGAGGCCATCCACGCTGATAGAAGGGATG
107	PD-L1 responder	ACTCAAATATGGAATATTCCAGTCAAAATCGAGGCCCAAGGGCTTGTCAGTCAGCTTGTG
108	PD-L1 Non-responder	CTGGTTCTAAAATTATATGAACCTAGAATCGATGGTATACCAAAGGTCTGTCTTTATGTA
109	PD-L1 Non-responder	TGGACTTAATATCATGTTTAAGTTTACATCGATGGTATTAGTCCATTTCTATTTGTAACT
110	PD-L1 Non-responder	ATTAAATGCACATTGTTGAATATATTTTTCGATGGTATTAGTCCATTTCTATTTGTAACT
111	PD-L1 Non-responder	ATTATACTATTCTTCATTCATATCTTCTTCGATCTTTTGAAATAGTTTCAGTAGGATTGG
112	PD-L1 Non-responder	TGGAGGGGACCAATGACAAGTTTGACATTCGATCTTTTGAAATAGTTTCAGTAGGATTGG
113	PD-L1 Non-responder	TTCATTCTTCTTTATAGATAAGTAGTATTCGATGAAGTCTCATTTTTCATGTATTAAATT
114	PD-L1 Non-responder	GTCAGATGTCACAGGGGCAGTTAGAACCTCGAACAATTATTTACATTTTAAGAACTGGTA
115	Non-Responder	GTCAGATGTCACAGGGGCAGTTAGAACCTCGATACACACATACCTACCGTTTTATCTCAG
116	PD-L1 Non-responder	CCCTGAAGTGGGCAGGAATTTCATGTGTTCGAATTGCTTGTTTCCTGGTGATCCCCCTCC
117	PD-L1 responder	AAACTTCCTTTCTTTGCTTAGAACTAGCTCGATCCTGGAAGCCCCCTAAAGGCAGGAACT
118	PD-L1 responder	TAACAAGGAGTGGAGTATTCCTGGGATATCGACCCCACCCCCTAGATTAAGACATTCCTG

119	PD-L1 Non-responder	AGGTGGGAGGATCATCTGAACCCGGAGGTCGAAAATATATCTTCAGTTAATTTTTGTATA
120	PD-L1 Non-responder	TATACAAAAATTAACTGAAGATATATTTTCGAAAATAAGGTAATGATTTGGCAGAGGGAA
121	PD-L1 Non-responder	GGTCCCCTGATTTCCATCCTAGTGCTTCTCGATGATATAATACTCTGCTGACTACATTTT
122	PD-L1 Non-responder	TCAGAAATAAATAAATAAAGTAGAAAACTCGACAGGACAAATTTTCTAAAGACTGAATGA
123	PD-L1 Non-responder	CAGGAGTTCAAGACCAACCTGGTCAACATCGAAACAGCAAACGAAGGCCAGGAAGCCCAC
124	PD-L1 Non-responder	TTTTAAGAAACATTAAGATATTAAACTGTCGAAATGTGTGAAAAAGTAAGAGTAGTACTT
125	PD-L1 Non-responder	TACCCTTAATTTAAACCCTTGTGTATTTTCGATGATTTCATTACTGTAATTACCTCATAT
126	PD-L1 Non-responder	TTAGCTTTATTACAGATAAAATATTATATCGATGGCCATTTTTTTCTTTATTAATGTTTA
127	PD-L1 Non-responder	TTAGCTTTATTACAGATAAAATATTATATCGAATCACGTTACTCCTTTCTTAAAAACCTA
128	PD-L1 Non-responder	TTAGCTTTATTACAGATAAAATATTATATCGATGGATCTCACAATTATAACCAACAAAAG
129	PD-L1 Non-responder	GAAAGAGGTCACTGGTACACATCCAGTGTCGAAAACTCATCGTATTGCTATAATTTGAGT
130	PD-L1 Non-responder	ACATTTATATGAAGTACCATTTATGTTTTCGATTTTTAAATTTCTTTCCCTAAACATATT
131	PD-L1 Non-responder	AATATGTTTAGGGAAAGAAATTTAAAAATCGATACAGTTTCAAATTTTAATTTAGATGTA
132	PD-L1 Non-responder	ATAAATAGACTCCACTATGTATAATGACTCGAAATTTTGCTATAAATGTGAGCTTTGAAA
133	PD-L1 Non-responder	CAGCCAGCCAGTAGATCTTCATAGGAGCTCGAAATTTTGCTATAAATGTGAGCTTTGAAA
134	PD-L1 Non-responder	GCTGGAGACCCGGGGAGGAATATCAAACTCGATTCTGGTGTTTCCAGCAAGTTTGGACAC
135	PD-L1 Non-responder	GCTGGAGACCCGGGGAGGAATATCAAACTCGACCCTAACTGCAGTCACTGTTACTTGGAT
136	PD-L1 responder	CTATCTAGTCCTTATCAGAAGGGAACCTTCGAAGTCTCTCTTGAGATGGGTTCTTACTTT
137	PD-L1 Non-responder	AATAAAGTGCACTATAGATGTTATGTGCTCGAAATTTCTTTTGAGCTCTGCATTGTTTGA
138	PD-L1 Non-responder	TCTTTAAAATGTTGAATACTATAATATATCGACAAGAATATTCTATTTAAAAAGCAAATC
139	PD-L1 responder	CAGGCTATTGTAGTGCTCTTCCTGGCCCTCGACACCCCCTTCAAGGGTCTGTGTCCCATA
140	PD-L1 Non-responder	AAAAAAATAAATATAAAATAGAAAAATATCGATATTTTCATTTGTCTTTCCTAGGAACTC
141	PD-L1 Non-responder	AAAAAAATAAATATAAAATAGAAAAATATCGAAGTATGTCCTATATGGGGAAAAAACGTA
142	PD-L1 responder	CATCCCTTCTATCAGCGTGGATGGCCTCTCGATGTTAACCTTGATCCTTTGGTTAAAGTA
143	PD-L1 Non-responder	CCCATGCAAAAATTCTTTGGAAGTTTCCTCGATTAACAAAAAAGAGTTAATACATATTAG
144	PD-L1 Non-responder	CAAATAATGTTACTAAAATCAATTCAAGTCGACTTGATTGATGGAAATTAGAATACAGGT
145	PD-L1 Non-responder	AAATTAATACACATTTTTATTGTGAAATTCGACTACCTCAAAAGAAAATGATCCATTGAC
146	PD-L1 responder	GCCATTAAATTCCCCTAATGCCATTGCCTCGACTTCAGTGGCGTCCATTGTCTGCTGGAG
147	PD-L1 Non-responder	TAAACCATAGTTAATTTTATGTAAATATTCGATATTTTCCAGCTATCTTTCTGTTGATTT
148	PD-L1 responder	TTAGCATCACTTGAAAGCTAGTTAAAAATCGATTGCAAATGATATGACAGAATTGCTTTG
149	PD-L1 Non-responder	ATCCTTATAAACACTTTATATTTTCTTTTCGAGGATTTCTAGGCATACATAATCTTTTCC

150	PD-L1 Non-responder	ATCCTTATAAACACTTTATATTTTCTTTTCGAAATAACTATAGAAGCTAGGAGCTGATAA
151	PD-L1 Non-responder	TGAAAAAGAAAAAAAGAAATCTACTTTTTCGAATATAAGCTTTCTTCAATATTATCAAAT
152	PD-L1 Non-responder	TTCATTGAATAATTCATTGAGTTATTCATCGATGTTAAGAAAGGTGTATCTAAAGGAATA
153	PD-L1 Non-responder	ATTTTTATTTTTTGGATTTAAGATACTATCGAATATGAACCCATTATACTAGGGCAAAAT
154	PD-L1 responder	GTAATATTATGTAAAATTGCATTTGGTATCGAACAAAGCCTTTAACTTGACTTAGTGTCA
155	PD-L1 Non-responder	AGGACAGAGACCCCTAATTCCACCACCATCGAACAACTGCAAACTCCACTCAACATCTTT
156	Non-Responder	AGGACAGAGACCCCTAATTCCACCACCATCGAGGGGCTTACTAATGCCTTTTAGCTCCCT

Table 13.c4

	Probe Location					**4 kb Sequence Location**		
	Chr	**Start1**	**End1**	**Start2**	**End2**	**Chr**	**Start1**	**End1**
105	X	47617979	47618008	47636868	47636897	X	47614009	47618008
106	X	47613512	47613541	47636868	47636897	X	47613512	47617511
107	X	47613512	47613541	47672279	47672308	X	47613512	47617511
108	9	121063123	121063152	121162649	121162678	9	121063123	121067122
109	8	120049013	120049042	120170620	120170649	8	120045043	120049042
110	8	120067572	120067601	120170620	120170649	8	120063602	120067601
111	8	120324759	120324788	120388396	120388425	8	120324759	120328758
112	8	120368738	120368767	120388396	120388425	8	120368738	120372737
113	10	74576267	74576296	74620447	74620476	10	74576267	74580266
114	5	178228071	178228100	178451151	178451180	5	178224101	178228100
115	5	178228071	178228100	178480000	178480029	5	178224101	178228100
116	5	178259442	178259471	178436965	178436994	5	178255472	178259471
117	12	93759387	93759416	93797876	93797905	12	93755417	93759416
118	5	132053244	132053273	132074962	132074991	5	132049274	132053273
119	1	112372806	112372835	112485711	112485740	1	112368836	112372835
120	1	112485711	112485740	112502466	112502495	1	112481741	112485740
121	4	74083782	74083811	74117911	74117940	4	74083782	74087781
122	2	157461901	157461930	157536014	157536043	2	157461901	157465900
123	12	122194669	122194698	122226656	122226685	12	122194669	122198668
124	1	231823951	231823980	231857290	231857319	1	231819981	231823980
125	13	50726484	50726513	50881905	50881934	13	50726484	50730483
126	18	4001462	4001491	4194412	4194441	18	4001462	4005461
127	18	4194412	4194441	4248756	4248785	18	4190442	4194441
128	18	4194412	4194441	4410806	4410835	18	4190442	4194441
129	2	224946941	224946970	224994640	224994669	2	224946941	224950940
130	7	111893516	111893545	112105279	112105308	7	111889546	111893545
131	7	112105279	112105308	112167979	112168008	7	112101309	112105308
132	8	26565662	26565691	26638318	26638347	8	26561692	26565691
133	8	26561792	26561821	26638318	26638347	8	26561792	26565791
134	5	284908	284937	355623	355652	5	280938	284937
135	5	284908	284937	471741	471770	5	280938	284937
136	8	29317156	29317185	29366896	29366925	8	29313186	29317185
137	3	5230788	5230817	5258812	5258841	3	5226818	5230817
138	12	92776962	92776991	92823177	92823206	12	92776962	92780961
139	4	109879091	109879120	110011339	110011368	4	109875121	109879120
140	11	34573815	34573844	34682253	34682282	11	34573815	34577814
141	11	34659116	34659145	34682253	34682282	11	34659116	34663115
142	X	47636868	47636897	47688049	47688078	X	47636868	47640867
143	7	36990112	36990141	37106040	37106069	7	36990112	36994111

144	2	42150739	42150768	42201064	42201093	2	42146769	42150768
145	2	42240252	42240281	42363233	42363262	2	42236282	42240281
146	12	47732329	47732358	47745284	47745313	12	47728359	47732358
147	6	151873862	151873891	151928859	151928888	6	151869892	151873891
148	1	94522204	94522233	94565070	94565099	1	94522204	94526203
149	8	58028091	58028120	58156560	58156589	8	58024121	58028120
150	8	58028091	58028120	58192936	58192965	8	58024121	58028120
151	8	58216624	58216653	58245172	58245201	8	58212654	58216653
152	12	61732349	61732378	61763501	61763530	12	61732349	61736348
153	12	29278906	29278935	29307954	29307983	12	29274936	29278935
154	10	88948369	88948398	89014161	89014190	10	88944399	88948398
155	1	161620964	161620993	161643724	161643753	1	161620964	161624963
156	1	161620964	161620993	161645837	161645866	1	161620964	161624963

Table 13.c5

	4 kb Sequence Location		Inner_primers		
	Start2	End2	PCR-Primer1_ID	PCR_Primer1	PCR-Primer2_ID
105	47636868	47640867	OBD117.1.437	AGAAGACACTCCATAAATGCTCAGGG	OBD117.1.439
106	47636868	47640867	OBD117.1.513	CGGGTGGCGTGGTGTGTAATACC	OBD117.1.515
107	47672279	47676278	OBD117.1.489	CGGGTGGCGTGGTGTGTAATACC	OBD117.1.491
108	121158679	121162678	OBD117.1.1521	AAATCTCAATAGCCTTTCCTTGTGGA	OBD117.1.1523
109	120170620	120174619	OBD117.1.1549	CCTCATCTTTTCCACAGTGACAGAGC	OBD117.1.1551
110	120170620	120174619	OBD117.1.1169	ATGACTATGAAGAGTGGAAATGTCC	OBD117.1.1171
111	120388396	120392395	OBD117.1.1253	CTGTAGCCAGCGGAAATACTGCTTAG	OBD117.1.1255
112	120388396	120392395	OBD117.1.1329	CAACCTCATCAACAGTTAGAATAGCC	OBD117.1.1331
113	74616477	74620476	OBD117.1.1309	TTCTTACCCTTCCCAGCCTCTAATA	OBD117.1.1311
114	178451151	178455150	OBD117.1.1025	GGTGAGTGGGGATAGCCTTC	OBD117.1.1027
115	178476030	178480029	OBD117.1.609	CTTGGGCAGGTGAGGGAGAACAG	OBD117.1.611
116	178436965	178440964	OBD117.1.701	GGGCTGGTCAAACAAACTCTGGC	OBD117.1.703
117	93793906	93797905	OBD117.1.213	TGCCTTGGAGGTAGCGATGGGTG	OBD117.1.215
118	132070992	132074991	OBD117.1.225	CCCCAAGATGAAAACTGAGCGGC	OBD117.1.227
119	112481741	112485740	OBD117.1.1209	GCCTGGACAAGATGGTGAAACCCTGT	OBD117.1.1211
120	112502466	112506465	OBD117.1.1121	GCCTGGGCGACAAAGTGAGACTC	OBD117.1.1123
121	74117911	74121910	OBD117.1.605	GGCTCTGGGCAATAGTTGTAGTGTGG	OBD117.1.607
122	157532044	157536043	OBD117.1.1673	TATCCCTATGGACTGAGCCAGGC	OBD117.1.1675
123	122226656	122230655	OBD117.1.909	GTGCCCCACATCTGTAATTG	OBD117.1.911
124	231853320	231857319	OBD117.1.1241	CTTCAAAGCAGGAGGGACTGTGC	OBD117.1.1243
125	50881905	50885904	OBD117.1.1409	CCAGTGGGCTCTTAGAACGATGACAC	OBD117.1.1411
126	4190442	4194441	OBD117.1.1805	TAAGATACACATTTATTGTCCAA	OBD117.1.1807
127	4248756	4252755	OBD117.1.1781	TAAGATACACATTTATTGTCCAA	OBD117.1.1783
128	4410806	4414805	OBD117.1.1769	TAAGATACACATTTATTGTCCAA	OBD117.1.1771
129	224990670	224994669	OBD117.1.1413	CTCTACTTCTGCTTTCTCTCACAGGC	OBD117.1.1415
130	112101309	112105308	OBD117.1.1817	TTATCTCAGCCTTATCTTTTCTG	OBD117.1.1819
131	112164009	112168008	OBD117.1.1097	CTGCCTTTATTTTCCATCTTTCTCTT	OBD117.1.1099
132	26638318	26642317	OBD117.1.661	GATGCTGCTGGTGAGAGTAGTCC	OBD117.1.663
133	26638318	26642317	OBD117.1.613	GCAAGTGAGCCAGCATTACCGCC	OBD117.1.615
134	355623	359622	OBD117.1.1593	TGATGTTCCAGTCTGAGGGTCTTGC	OBD117.1.1595
135	467771	471770	OBD117.1.1265	GCTGATGTTCCAGTCTGAGGGTC	OBD117.1.1267
136	29362926	29366925	OBD117.1.497	CTCTGTGCCTGTCATCACCCTCT	OBD117.1.499
137	5254842	5258841	OBD117.1.1373	TCTGTCACTGTCTCCCACCACCC	OBD117.1.1375
138	92823177	92827176	OBD117.1.1561	CTCTGGCAGCAAGTTAGAAATAATCT	OBD117.1.1563
139	110007369	110011368	OBD117.1.149	CCAGGAGACACCCTCTAAAGGAG	OBD117.1.151
140	34678283	34682282	OBD117.1.1425	GGGCTGGAATGAGAAGTGGTAGG	OBD117.1.1427
141	34678283	34682282	OBD117.1.1433	GGCTGGAATGAGAAGTGGTAGGATGG	OBD117.1.1435

142	47688049	47692048	OBD117.1.521	TTCCCCGTTTTGGACAGGGTGAGAGA	OBD117.1.523
143	37106040	37110039	OBD117.1.1669	CCATAACAAAACCGCTGGACAAGAT	OBD117.1.1671
144	42197094	42201093	OBD117.1.1145	GGAATCGGGAAAGTCTAAACCAGAAG	OBD117.1.1147
145	42363233	42367232	OBD117.1.1105	GGAACACTGTAACTGGAGGAAACTTG	OBD117.1.1107
146	47745284	47749283	OBD117.1.325	CCCCTGTAACATTCTCCCACCCT	OBD117.1.327
147	151928859	151932858	OBD117.1.1261	GTTCCTGGATGCTTCAAAATGTGATA	OBD117.1.1263
148	94565070	94569069	OBD117.1.113	CTGCTACTTCAACTGTGGTCTGGGAC	OBD117.1.115
149	58156560	58160559	OBD117.1.1553	TAAGGCTGCTGTGAACATTCTTGTGC	OBD117.1.1555
150	58192936	58196935	OBD117.1.1365	TAAGGCTGCTGTGAACATTCTTGTGC	OBD117.1.1367
151	58245172	58249171	OBD117.1.1629	GAAGAGAAGGAGTGGAGCAAGGGTTG	OBD117.1.1631
152	61763501	61767500	OBD117.1.1321	GTCTGCTTTTGCCTACGGTTTAGCCT	OBD117.1.1323
153	29307954	29311953	OBD117.1.1557	GGGTAGATGAGACTGATTGCTTACAG	OBD117.1.1559
154	89010191	89014190	OBD117.1.305	GGCATAAACATCAATCAGATAGCCTC	OBD117.1.307
155	161643724	161647723	OBD117.1.649	ATTAGTCTTCAACCCACGCTGTTTTG	OBD117.1.651
156	161645837	161649836	OBD117.1.717	ATTAGTCTTCAACCCACGCTGTTTTG	OBD117.1.719

Table 13.c6

	Inner_primers	
	PCR_Primer2	GLMNET
105	CCCCATCTGTGACCTCTCCCTCTTTT	0
106	CCCATCTGTGACCTCTCCCTCTT	0
107	GAAGGAAGAGACTCAGGACTGGC	0
108	TTGAGATTATCCAGTCTGAGGAGCAG	0
109	CTTGAACTTGAGACACAAAGAGAGTG	0
110	AGATAAAATAGTCCTTGAGGTGAATA	0
111	CCCAAACAGCCCAATAACAAGCAGAG	0
112	CCCAAACAGCCCAATAACAAGCAGAG	0
113	CTCCTATTACTTTTCATTTTGTGGTT	0
114	TTCTAGAGATCAGAGTGTTTGGG	0
115	CCACTGCTCCTGGCTACAAACCT	0.011827837
116	CACTGAGGTGGAGGGCAGGGTAT	0.00010841
117	GGCAAGTATGGCGTAGAAAGGGC	0.012057101
118	GCCAGCCACTACAAGCAGCACTG	0.002120736
119	AGAATGAAGAGTCCAGAAACAGTCTC	0
120	CCAGCCCTTCTCTGAGGTTTCCT	0
121	CAAGCACGGTTGTAGGAGTTGTAAGT	-0.005375017
122	CCCCATCCCACACAACTAAGCACC	0
123	ACGAGGGCAGTTTGGGTTGA	0.019526388
124	GACCCTCCAGAACTACAGGCTCC	0
125	GACCAGTCACAAAAGGGCAAATACTA	0
126	TACAAGAAAACTCATCTCACTTA	0
127	ACAAAGGAAGCCATTCGGTAGGT	0
128	GCTGGGAAAACGATTACCTCAGG	0
129	TTGTTCAGCCTGGTGACGCTTCAGAA	0
130	CTTTATTTTCCATCTTTCTCTTA	0
131	TTTTCTTCATACCTCTAAATAACAAT	0
132	CATTACTACTCCTCCCAGGGCAGG	0.027392782
133	ATTACTACTCCTCCCAGGGCAGG	0.0000923
134	GGGCAGGCAGCAGGATGGGAAGC	0
135	TCACTGACTGGGCAGGGCTTGCT	0
136	CTGCCCCAGTTGCCCTTTTCCTG	0
137	GTGAGTTCCAGGCAGCAGAGGTA	0
138	GGTGGTAGTGAGAAGTTTACTCCAGA	0
139	GTCCCCAGGTAATGGAGCGAAGC	-0.013629912
140	CACAGTGGAGGGCACACCAGCAA	0
141	GCACAAGGCTACAAATCCTGTTACTC	0

142	GGTGGAGAAACTGGCAGACATTACTT	0
143	CCTGCTTCAATGGCTTGTGAGGACC	0
144	TGGGCTGCCTGCTGTATTCTCCTAAG	0
145	GAAGTCAGTGGGATGGAGACAGTAGC	0
146	AGAGTAGGACCCCAGAGCAGGCA	0
147	GCACCAAGATAGACCACATTCTGGGT	0
148	TTCTGACAAACCTCATTGCCAGGATG	0.006221331
149	CTCACCTGGCTGCTGTTCTCCATCTA	0
150	CTGTCGTGGTATTGGTGGGTGTGTGA	0
151	GCTCTTTGTGGTCTTATGCCCTATCA	0
152	GGTTACCTGACTCCTGATACCAGACA	0
153	GTCAAGATAACTGCCAGAGGAGCCAC	0
154	CTCTTCATAGACCTTTAGGACTTAGC	0.011677917
155	CCATTTCTTCCTTTCCACACACCCTC	-0.003930014
156	GGTTCTAAGGAGAGTTGTAAAGAGAG	-0.023642297

Table 13.c7

	Probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig
157	ORF243_1_161620964_161624310_161718261_161721039_RF	ORF243	17	6
158	ORF243_1_161633494_161637462_161657362_161661864_RF	ORF243	17	6
159	ORF243_1_161643724_161645551_161657362_161661864_RF	ORF243	17	6
160	ORF243_1_161657362_161661864_161718261_161721039_FF	ORF243	17	6
161	ORF249_2_152472124_152479172_152576166_152584355_RR	ORF249	179	14
162	ORF249_2_152472124_152479172_152664286_152673031_RR	ORF249	179	14
163	ORF25_11_10273331_10278409_10371170_10376885_RR	ORF25	130	14
164	ORF25_11_10376885_10382511_10426676_10435291_FR	ORF25	130	14
165	ORF252_14_65046195_65050388_65076556_65085228_FF	ORF252	22	3
166	ORF257_10_13924860_13932958_14052225_14057587_FF	ORF257	118	11
167	ORF263_11_78304460_78312808_78374350_78382835_RF	GAB2	132	4
168	ORF263_11_78351934_78362957_78374350_78382835_FR	ORF263	87	13
169	ORF264_11_11305555_11318540_11360474_11364977_RR	ORF264	188	18
170	ORF264_11_11305555_11318540_11366643_11369350_RR	ORF264	188	18
171	ORF264_11_11305555_11318540_11464315_11471329_RR	ORF264	188	18
172	ORF264_11_11305555_11318540_11473385_11479393_RR	ORF264	188	18
173	ORF264_11_11305555_11318540_11483465_11487603_RR	ORF264	188	18
174	ORF264_11_11305555_11318540_11547650_11553187_RR	ORF264	188	18
175	ORF264_11_11305555_11318540_11553187_11562871_RR	ORF264	188	18
176	ORF264_11_11438569_11448713_11547650_11553187_RF	ORF264	188	18
177	ORF272_9_3998831_4010284_4158439_4161041_RR	ORF272	181	4
178	ORF276_X_133488174_133495210_133692164_133694868_FF	ORF276	144	74
179	ORF285_14_24595596_24607974_24651000_24656891_FR	ORF285	38	1
180	ORF290_6_11980949_11988889_12009862_12015635_RR	ORF290	58	8
181	ORF290_6_11980949_11988889_12060031_12070485_RR	ORF290	58	8
182	ORF293_6_32626930_32634077_32662361_32664960_RF	HLA-DQA1	28	4
183	ORF293_6_32626930_32634077_32662361_32664960_RR	HLA-DQA1	28	4
184	ORF293_6_32634077_32639503_32662361_32664960_FF	HLA-DQA1	28	4
185	ORF293_6_32634077_32639503_32662361_32664960_FR	HLA-DQA1	28	4
186	ORF30_3_15678757_15686176_15802964_15806181_RF	ORF30	123	8
187	ORF305_15_98779700_98784973_98893484_98899517_FR	IGF1R	104	16
188	ORF305_15_98886232_98891127_98957432_98962130_FR	IGF1R	104	16
189	ORF305_15_98893484_98899517_98957432_98962130_RR	IGF1R	104	16
190	ORF307_8_42241866_42245619_42264241_42271203_RF	IKBKB	46	12
191	ORF307_8_42264241_42271203_42281222_42285075_FR	IKBKB	46	12
192	ORF307_8_42264241_42271203_42302441_42304680_FF	IKBKB	46	12

193	ORF307_8_42264241_42271203_42331044_42332799_FR	IKBKB	46	12
194	ORF313_13_20664875_20671757_20688261_20691044_FF	ORF313	33	4
195	ORF313_13_20664875_20671757_20695143_20698635_FF	ORF313	33	4
196	ORF313_13_20664875_20671757_20728864_20730586_FR	ORF313	33	4
197	ORF313_13_20664875_20671757_20737979_20744490_FR	ORF313	33	4
198	ORF316_2_102199956_102206419_102218862_102223625_FF	ORF316	31	2
199	ORF316_2_102206419_102213233_102261221_102268036_RF	ORF316	31	2
200	ORF317_14_23324243_23329232_23356396_23359421_RF	IL25	74	2
201	ORF319_10_6057923_6061396_6103786_6110024_FF	ORF319	15	1
202	ORF325_5_76475531_76481400_76658102_76664388_FR	ORF325	148	12
203	ORF325_5_76540898_76542545_76717099_76725306_RF	ORF325	148	12
204	ORF325_5_76654480_76657126_76717099_76725306_RF	ORF325	148	13
205	ORF329_5_132472660_132477912_132495376_132497062_FF	IRF1	42	8
206	ORF331_19_49654782_49660360_49691432_49693107_RR	IRF3	30	2
207	ORF336_16_31318595_31324659_31385398_31389135_FF	ITGAX	41	8
208	ORF336_16_31344274_31352361_31385398_31389135_FF	ITGAX	41	8

Table 13.d1

	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr	t
157	0.000555352	0.016365522	35.29	0.190429167	0.190429167	2.868181541
158	0.000421879	0.012833299	35.29	0.218107645	0.218107645	8.463198869
159	0.000555352	0.016365522	35.29	0.272288899	0.272288899	13.97024262
160	0.000555352	0.016365522	35.29	0.240440097	0.240440097	10.87424514
161	0.23994375	1	7.82	0.329346898	0.329346898	5.487827099
162	0.23994375	1	7.82	0.440433009	0.440433009	7.855500481
163	0.035039292	0.465381017	10.77	0.35621009	0.35621009	4.725121222
164	0.035039292	0.465381017	10.77	0.318598485	0.318598485	10.52304142
165	0.158363507	1	13.64	0.296111136	0.296111136	6.243845297
166	0.125273656	0.904598768	9.32	0.28667877	0.28667877	16.14644629
167	0.994374946	0.99999793	3.03	-0.152150489	-0.152150489	-4.577281937
168	0.003092682	0.074779463	14.94	0.329695975	0.329695975	9.796649349
169	0.051180377	0.595840686	9.57	0.32375356	0.32375356	8.313452807
170	0.051180377	0.595840686	9.57	0.296855026	0.296855026	7.019357248
171	0.051180377	0.595840686	9.57	0.297470188	0.297470188	7.154103826
172	0.051180377	0.595840686	9.57	0.296912063	0.296912063	6.910476496
173	0.051180377	0.595840686	9.57	0.315806978	0.315806978	7.244128466
174	0.051180377	0.595840686	9.57	0.334773184	0.334773184	4.919067102
175	0.051180377	0.595840686	9.57	0.288731756	0.288731756	6.132980113
176	0.051180377	0.595840686	9.57	0.286221172	0.286221172	4.735145343
177	0.997131949	1	2.21	0.285774765	0.285774765	11.23232236
178	1.43E-46	1.35E-43	51.39	-0.694724463	-0.694724463	-7.136811388
179	0.926506445	1	2.63	0.159055003	0.159055003	6.118067037
180	0.028416181	0.407301886	13.79	0.310955216	0.310955216	6.317177296
181	0.028416181	0.407301886	13.79	0.423599949	0.423599949	10.84857261
182	0.178427395	0.954389149	14.29	-0.144695604	-0.144695604	-3.861408042
183	0.178427395	0.954389149	14.29	-0.491099473	-0.491099473	-3.580221478
184	0.178427395	0.954389149	14.29	-0.188169485	-0.188169485	-3.287365783
185	0.178427395	0.954389149	14.29	-0.64455528	-0.64455528	-2.980618242
186	0.516062575	1	6.5	0.30577162	0.30577162	8.841735547
187	0.007797893	0.171924974	15.38	-0.171537182	-0.171537182	-4.993189956
188	0.007797893	0.171924974	15.38	-0.193623643	-0.193623643	-4.845372443
189	0.007797893	0.171924974	15.38	-0.160584806	-0.160584806	-5.690028109
190	0.00018363	0.010627608	26.09	-0.291244548	-0.291244548	-11.89788921
191	0.00018363	0.010627608	26.09	-0.291439389	-0.291439389	-11.64817138
192	0.00018363	0.010627608	26.09	-0.346675126	-0.346675126	-16.03607714

193	0.00018363	0.010627608	26.09	-0.348439424	-0.348439424	-16.6498587
194	0.151869322	0.98090939	12.12	0.162592643	0.162592643	5.607585861
195	0.151869322	0.98090939	12.12	0.213925835	0.213925835	5.878475438
196	0.172978396	1	12.12	0.225971443	0.225971443	5.816491381
197	0.151869322	0.98090939	12.12	0.261432751	0.261432751	5.250369871
198	0.648170238	1	6.45	-0.143835834	-0.143835834	-5.364884245
199	0.648170238	1	6.45	-0.218690375	-0.218690375	-9.469982161
200	0.983929844	0.99999793	2.7	-0.159277184	-0.159277184	-5.699454074
201	0.643060444	1	6.67	0.158451923	0.158451923	6.957742989
202	0.224208567	1	8.11	0.302741837	0.302741837	4.645263853
203	0.224208567	1	8.11	0.362966909	0.362966909	15.17483554
204	0.184544386	1	8.78	0.196151577	0.196151577	3.614499961
205	0.016095432	0.256971894	19.05	-0.279967907	-0.279967907	-13.66679402
206	0.700318757	0.99999793	6.67	-0.160722895	-0.160722895	-7.035502311
207	0.013975308	0.239650655	19.51	-0.187127305	-0.187127305	-10.29247019
208	0.013975308	0.239650655	19.51	-0.204949768	-0.204949768	-11.39755162

Table 13.d2

	P.Value	adj.P.Val	B	FC	FC_1	LS
157	0.016336892	0.046928877	-3.814850432	1.141103116	1.141103116	1
158	0.00000611	0.000216321	4.330876071	1.16320683	1.16320683	1
159	0.000000053	0.0000198	9.086555803	1.207722413	1.207722413	1
160	0.000000594	0.0000638	6.704482072	1.181352981	1.181352981	1
161	0.000244192	0.002250317	0.501078985	1.256444458	1.256444458	1
162	0.0000119	0.000317452	3.639677292	1.357011558	1.357011558	1
163	0.00075776	0.004908191	-0.676573444	1.280058807	1.280058807	1
164	0.000000811	0.0000728	6.391251092	1.247118439	1.247118439	1
165	0.0000862	0.001125109	1.58629049	1.227830265	1.227830265	1
166	0.0000000128	0.0000107	10.43445283	1.219828873	1.219828873	1
167	0.000952862	0.005814117	-0.914179847	0.899908054	-1.111224636	-1
168	0.00000159	0.000104892	5.710301134	1.256748507	1.256748507	1
169	0.00000718	0.000235815	4.164430478	1.251582646	1.251582646	1
170	0.000032	0.000589865	2.616552385	1.228463528	1.228463528	1
171	0.0000272	0.00053455	2.787380302	1.228987454	1.228987454	1
172	0.0000366	0.000640507	2.476786347	1.228512097	1.228512097	1
173	0.0000244	0.000499696	2.900207241	1.244707692	1.244707692	1
174	0.000563701	0.004023477	-0.369350773	1.261179114	1.261179114	1
175	0.0000999	0.001241731	1.432243865	1.221565952	1.221565952	1
176	0.000746164	0.004854957	-0.660568608	1.219442026	1.219442026	1
177	0.000000437	0.0000553	7.013760547	1.219064757	1.219064757	1
178	0.0000277	0.000540415	2.765588821	0.617827304	-1.618575276	-1
179	0.000101916	0.001260517	1.411390075	1.11655553	1.11655553	1
180	0.0000782	0.001056594	1.687237591	1.240528789	1.240528789	1
181	0.000000608	0.0000645	6.681922607	1.341270247	1.341270247	1
182	0.003013925	0.013289266	-2.102539121	0.904570214	-1.105497379	-1
183	0.004820858	0.01883207	-2.583272553	0.711482673	-1.405515606	-1
184	0.007929635	0.027297251	-3.089016199	0.877718679	-1.139317214	-1
185	0.013446654	0.040517443	-3.620544416	0.639689949	-1.563257327	-1
186	0.0000041	0.000173496	4.74079963	1.236079573	1.236079573	1
187	0.000504152	0.003717896	-0.253310928	0.88789613	-1.126257866	-1
188	0.000630368	0.004341248	-0.485478626	0.874406698	-1.143632594	-1
189	0.00018339	0.001862995	0.799345244	0.89466234	-1.11774013	-1
190	0.000000252	0.0000426	7.56312403	0.817196796	-1.223695449	-1
191	0.000000308	0.0000464	7.360765169	0.817086438	-1.223860725	-1
192	0.0000000137	0.0000109	10.37139589	0.786394357	-1.271626622	-1

193	0.00000000942	0.0000107	10.71553998	0.785433249	-1.273182669	-1
194	0.000205957	0.002007604	0.678446037	1.119296801	1.119296801	1
195	0.000141158	0.001563544	1.07202881	1.159840029	1.159840029	1
196	0.000153765	0.001651404	0.982900151	1.169564513	1.169564513	1
197	0.000344332	0.002847073	0.143290367	1.19866852	1.19866852	1
198	0.000291453	0.002541967	0.316846942	0.90510945	-1.104838757	-1
199	0.00000218	0.000122482	5.388593691	0.859345164	-1.163676764	-1
200	0.000180983	0.001844393	0.813105827	0.895473607	-1.116727498	-1
201	0.0000345	0.000618944	2.537651809	1.116088881	1.116088881	1
202	0.000857256	0.0053651	-0.804558824	1.233486424	1.233486424	1
203	0.0000000235	0.0000135	9.86073016	1.286067985	1.286067985	1
204	0.004550477	0.018055062	-2.524359163	1.145638258	1.145638258	1
205	0.0000000657	0.0000214	8.879509786	0.823609338	-1.214167875	-1
206	0.0000314	0.000581633	2.637144966	0.894576711	-1.117847121	-1
207	0.000000999	0.0000814	6.180062011	0.878352958	-1.138494487	-1
208	0.00000038	0.0000516	7.153167186	0.867568894	-1.152646213	-1

Table 13.d3

		Probe sequence
	Loop detected	**60 mer**
157	PD-L1 Non-responder	GTTTTGGTGTACTAAGGTTTCTTCTGAATCGATGGTGGTGGAATTAGGGGTCTCTGTCCT
158	Non-Responder	AAAGCACGCGTCAGAGTGGGTGGGGCTGTCGATTGTCATCCTCTAGGACTTACAGTTTCT
159	PD-L1 Non-responder	AAAGCACGCGTCAGAGTGGGTGGGGCTGTCGAACAACTGCAAACTCCACTCAACATCTTT
160	PD-L1 Non-responder	AAAGCACGCGTCAGAGTGGGTGGGGCTGTCGATTCAGAAGAAACCTTAGTACACCAAAAC
161	PD-L1 Non-responder	CTATTATAATGTAGAAAGACTATATTAATCGAGGGTTGGTGTTAGAGTTCAAACCAACAC
162	PD-L1 Non-responder	CTATTATAATGTAGAAAGACTATATTAATCGAGTACATGAGAAATAAGCGTCTAACATGA
163	PD-L1 Non-responder	TTGAAGCAATTTTTTAAAAAACAGTAATTCGATGTACCATCCACAGTTCTTTAGGATACT
164	PD-L1 Non-responder	AGGGGCTGGTAGATTTGACTACATAAACTCGAGTATGTCAGCTTGATGATGAAAGAGACT
165	PD-L1 Non-responder	GCCGAGTTGGGCAGATCATTTTAGGAGTTCGAGTAGAACCAATTAAAAAGTTAAACAGGT
166	PD-L1 Non-responder	GGCGGGTGGATCACCTGAGCTGAGGATTTCGAAAAAAAAAAAAAGATTATAAATTCACAC
167	PD-L1 responder	TATTTTATTTGTTACTAAAACAAGGAACTCGATTTCGCCAAGGGCCAGGCTCCCAAGGCA
168	PD-L1 Non-responder	AAAAGTATGTGTACCTAGTAATATGGCCTCGAGCCATTTCTGAACTCATTATAAAACTAT
169	PD-L1 Non-responder	TCGTGGGTAGTGGGGGCAGAGACTTGAGTCGATTTTCTATAGACCAAATTAAAATATTTC
170	PD-L1 Non-responder	TCGTGGGTAGTGGGGGCAGAGACTTGAGTCGAAAATATAGATGAAAGGTACTGCCATTGT
171	PD-L1 Non-responder	TCGTGGGTAGTGGGGGCAGAGACTTGAGTCGAGGTCTCCTAGGCTCAGATCTAAGGAGGA
172	PD-L1 Non-responder	TCGTGGGTAGTGGGGGCAGAGACTTGAGTCGAAATGAAAGATTTGCCTTTCAATGGAGAA
173	PD-L1 Non-responder	TCGTGGGTAGTGGGGGCAGAGACTTGAGTCGAAGAGGAAAGGATGTCCACTGGACATTAT
174	PD-L1 Non-responder	TCGTGGGTAGTGGGGGCAGAGACTTGAGTCGAGACCCTGCTACCATGAATCTTAGGGTTC

175	PD-L1 Non-responder	TCGTGGGTAGTGGGGGCAGAGACTTGAGTCGAGAACCACTCTGAAGTTTGGCCTAGTTTT
176	PD-L1 Non-responder	TCCAGGTGACTCCGACCTACTCTCAAGTTCGAGATGGTAAGTTATCTTCCAGGGTTTAAA
177	PD-L1 Non-responder	TGATTGGAGAATACCTACTTAAATAGTTTCGAGATTAAGAAAGAAGAGCTTCATTTACCT
178	PD-L1 responder	AATCAGTCAATCCCTAATTTGAGTATTTTCGAACCTCATCTTGATCTTCTTCAAATTGTC
179	PD-L1 Non-responder	TTGCCTTCAGGAAATATCATGAAATTGCTCGAAAAGATATGTCATCCCAGGGATGTAGGG
180	PD-L1 Non-responder	AATATTCCTTCAACATTTCATATATACATCGAAATTGCATGTATGTTTTGTTAGAAAGTT
181	PD-L1 Non-responder	AATATTCCTTCAACATTTCATATATACATCGAATACATGTTTTGGAGAATATTAAACCCA
182	PD-L1 responder	CACCGCGCGGTACACCCCCACGTCGCTGTCGACATTTTCTTACCAGCCTGGCTGATAAAC
183	PD-L1 responder	GTTTATCAGCCAGGCTGGTAAGAAAATGTCGAAGTCTTGGATTAAGGTTCATTCAACAAA
184	PD-L1 responder	CCCGTCTTCCCCAAAATCTATGTGGTCCTCGACAGCGACGTGGGGGTGTACCGCGCGGTG
185	PD-L1 responder	CCCGTCTTCCCCAAAATCTATGTGGTCCTCGAAGTCTTGGATTAAGGTTCATTCAACAAA
186	PD-L1 Non-responder	TTTCTTTTATACATAAATTTTCACGCCTTCGAAAGAGAGGGAAAAATATTTACATGTTAA
187	PD-L1 responder	TGACTGTATTTACAACATGTCTAGATTTTCGAGTGTAAAAGGGCTTTTACTGGTGCACAC
188	PD-L1 responder	TCCTAGGAGAGACTGAACTTTAAAGATATCGACCTGCTGATCCTTGGATCCTGAATCTGT
189	PD-L1 responder	GTGTGCACCAGTAAAAGCCCTTTTACACTCGACCTGCTGATCCTTGGATCCTGAATCTGT
190	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAACTAATATTAGAGGAGAGAGGTCAGTTA
191	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAGGGCCTGGCAAGAAGACAGAAGCCGACT
192	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGACAGTCCCAAGAGGTCAGAACTGGCTTCC
193	PD-L1 responder	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGACCCCCTGACATGGGGCTGCCTGGAGCAG
194	Non-Responder	TTAAAGAAGCTAATTTTAAAAATAAATGTCGAAGAGATTGTCACGTTAGAGTTATGTAAA
195	Non-Responder	TTAAAGAAGCTAATTTTAAAAATAAATGTCGAGGAGCATCTGGATTTAATGATAGTTCAA
196	PD-L1 Non-responder	TTAAAGAAGCTAATTTTAAAAATAAATGTCGAATTCCATGGATTCAGGTTGGCAGAAGAC
197	Non-Responder	TTAAAGAAGCTAATTTTAAAAATAAATGTCGAAATTACTTTAAATTAATACAAGCCCCTA
198	PD-L1 responder	GGAAGGCCTTCCAAAGGATTTGAGTGTTTCGAGAGTACTGATGCCCTCTGCTCTGTAAAC
199	PD-L1 responder	CCACTCCACTTGACATTCACTCTGCTTGTCGATCAAAGCTGTATCTGCTTTAGGGGGCAC
200	PD-L1 responder	CTCCATCTCCCTGCCCTCTGGATCCCCCTCGATTCTACAGTGGTTTTAACAGCAGGCCCC
201	PD-L1 Non-responder	CAGAGACAGTGTCAAAAAAAAAAAATCTTCGAGGTCTTGAGTCCTCTTCATAAGGAAAT
202	PD-L1 Non-responder	CAATGTACAAAAAAAGTTTTTTTTTTTTTCGAGGTAACTTATGTTAACTTTCTTTCCCAG
203	PD-L1 Non-responder	ATTTAAACTATTTAATAATTTGCTGTATTCGAATGAGTGATAGTGCTTATTCCTGTATTG
204	PD-L1 Non-responder	ATTTAAACTATTTAATAATTTGCTGTATTCGATAGAAAATGGGTGAGGGGAAAACTGTGG
205	PD-L1 responder	GTGTCTCGGCCCCCTGGGGCCCCACCCTTCGATTTCCCTGTTGCCGCCGCGTTTGCAAGA
206	PD-L1 responder	GCAGCCAGCCCGGTGGGGGTGGGGGGGGTCGACGCTCGCCTCCGCTCACAGCCTCAGCAT
207	PD-L1 responder	CAAATCCCGGCTATCTCTTAGAATTGCATCGATTCACCCTCCTCAGCCTCCCAAAGTGCT
208	PD-L1 responder	AGTGGTCTCACCATGGCTTTCTTCCAATTCGATTCACCCTCCTCAGCCTCCCAAAGTGCT

Table 13.d4

	Probe Location					4 kb Sequence Location		
	Chr	Start1	End1	Start2	End2	Chr	Start1	End1
157	1	161620964	161620993	161721010	161721039	1	161620964	161624963
158	1	161633494	161633523	161661835	161661864	1	161633494	161637493
159	1	161643724	161643753	161661835	161661864	1	161643724	161647723
160	1	161661835	161661864	161721010	161721039	1	161657865	161661864
161	2	152472124	152472153	152576166	152576195	2	152472124	152476123

162	2	152472124	152472153	152664286	152664315	2	152472124	152476123
163	11	10273331	10273360	10371170	10371199	11	10273331	10277330
164	11	10382482	10382511	10426676	10426705	11	10378512	10382511
165	14	65050359	65050388	65085199	65085228	14	65046389	65050388
166	10	13932929	13932958	14057558	14057587	10	13928959	13932958
167	11	78304460	78304489	78382806	78382835	11	78304460	78308459
168	11	78362928	78362957	78374350	78374379	11	78358958	78362957
169	11	11305555	11305584	11360474	11360503	11	11305555	11309554
170	11	11305555	11305584	11366643	11366672	11	11305555	11309554
171	11	11305555	11305584	11464315	11464344	11	11305555	11309554
172	11	11305555	11305584	11473385	11473414	11	11305555	11309554
173	11	11305555	11305584	11483465	11483494	11	11305555	11309554
174	11	11305555	11305584	11547650	11547679	11	11305555	11309554
175	11	11305555	11305584	11553187	11553216	11	11305555	11309554
176	11	11438569	11438598	11553158	11553187	11	11438569	11442568
177	9	3998831	3998860	4158439	4158468	9	3998831	4002830
178	X	133495181	133495210	133694839	133694868	X	133491211	133495210
179	14	24607945	24607974	24651000	24651029	14	24603975	24607974
180	6	11980949	11980978	12009862	12009891	6	11980949	11984948
181	6	11980949	11980978	12060031	12060060	6	11980949	11984948
182	6	32626930	32626959	32664931	32664960	6	32626930	32630929
183	6	32626930	32626959	32662361	32662390	6	32626930	32630929
184	6	32639474	32639503	32664931	32664960	6	32635504	32639503
185	6	32639474	32639503	32662361	32662390	6	32635504	32639503
186	3	15678757	15678786	15806152	15806181	3	15678757	15682756
187	15	98784944	98784973	98893484	98893513	15	98780974	98784973
188	15	98891098	98891127	98957432	98957461	15	98887128	98891127
189	15	98893484	98893513	98957432	98957461	15	98893484	98897483
190	8	42241866	42241895	42271174	42271203	8	42241866	42245865
191	8	42271174	42271203	42281222	42281251	8	42267204	42271203
192	8	42271174	42271203	42304651	42304680	8	42267204	42271203
193	8	42271174	42271203	42331044	42331073	8	42267204	42271203
194	13	20671728	20671757	20691015	20691044	13	20667758	20671757
195	13	20671728	20671757	20698606	20698635	13	20667758	20671757
196	13	20671728	20671757	20728864	20728893	13	20667758	20671757
197	13	20671728	20671757	20737979	20738008	13	20667758	20671757
198	2	102206390	102206419	102223596	102223625	2	102202420	102206419
199	2	102206419	102206448	102268007	102268036	2	102206419	102210418
200	14	23324243	23324272	23359392	23359421	14	23324243	23328242
201	10	6061367	6061396	6109995	6110024	10	6057397	6061396
202	5	76481371	76481400	76658102	76658131	5	76477401	76481400
203	5	76540898	76540927	76725277	76725306	5	76540898	76544897
204	5	76654480	76654509	76725277	76725306	5	76654480	76658479
205	5	132477883	132477912	132497033	132497062	5	132473913	132477912
206	19	49654782	49654811	49691432	49691461	19	49654782	49658781
207	16	31324630	31324659	31389106	31389135	16	31320660	31324659
208	16	31352332	31352361	31389106	31389135	16	31348362	31352361

Table 13.d5

	4 kb Sequence Location		**Inner_primers**		
	Start2	**End2**	**PCR-Primer1_ID**	**PCR_Primer1**	**PCR-Primer2_ID**
157	161717040	161721039	OBD117.1.901	TGGATGGTTCCAGAGGTTTC	OBD117.1.903
158	161657865	161661864	OBD117.1.905	GCTGGAGATGGATCTGGGGG	OBD117.1.907
159	161657865	161661864	OBD117.1.573	GCCACCTGTCTCAGATACCCTTGGTT	OBD117.1.575

160	161717040	161721039	OBD117.1.897	GGGTAGAACGGGGGCAGTAG	OBD117.1.899
161	152576166	152580165	OBD117.1.1317	CCTTCAGGACACTGCTGGGAGGT	OBD117.1.1319
162	152664286	152668285	OBD117.1.1529	CTTCAGGACACTGCTGGGAGGTTTCT	OBD117.1.1531
163	10371170	10375169	OBD117.1.1445	CAGCAGTGTGGGAAGGGACATCT	OBD117.1.1447
164	10426676	10430675	OBD117.1.1165	GAGTGGGAAAGACCATTCTGAGATTC	OBD117.1.1167
165	65081229	65085228	OBD117.1.1201	GTGGTGGCTCACGCCTGTAATCCTA	OBD117.1.1203
166	14053588	14057587	OBD117.1.1401	TCTGAAAGGCTGGGTGCGGTAGC	OBD117.1.1403
167	78378836	78382835	OBD117.1.141	AGTCCCTGTAGATTTGAGAGCAGAAA	OBD117.1.143
168	78374350	78378349	OBD117.1.1325	CAAAGAGGGTCAGGCACTTCACAAAG	OBD117.1.1327
169	11360474	11364473	OBD117.1.1333	GGATGAATGGCTGTGTAAACTGTCTC	OBD117.1.1335
170	11366643	11370642	OBD117.1.1833	AATGGCTGTGTAAACTGTCTCTA	OBD117.1.1835
171	11464315	11468314	OBD117.1.1785	AATGGCTGTGTAAACTGTCTCTA	OBD117.1.1787
172	11473385	11477384	OBD117.1.1377	GGATGAATGGCTGTGTAAACTGTCTC	OBD117.1.1379
173	11483465	11487464	OBD117.1.1741	AATGGCTGTGTAAACTGTCTCTA	OBD117.1.1743
174	11547650	11551649	OBD117.1.1141	GGATGAATGGCTGTGTAAACTGTCTC	OBD117.1.1143
175	11553187	11557186	OBD117.1.1841	AATGGCTGTGTAAACTGTCTCTA	OBD117.1.1843
176	11549188	11553187	OBD117.1.1845	ATACCCACTGAAGCAGAAACTCT	OBD117.1.1847
177	4158439	4162438	OBD117.1.1225	CAGGATAGATAAGCCAGAAGGTAATA	OBD117.1.1227
178	133690869	133694868	OBD117.1.1061	TCTTCCTCCCCCTACCCTCT	OBD117.1.1063
179	24651000	24654999	OBD117.1.923	TTCCGGTTCAATATGAGATGG	OBD117.1.921
180	12009862	12013861	OBD117.1.1777	AAATAAAATCACCAACCCAGACG	OBD117.1.1779
181	12060031	12064030	OBD117.1.1101	CCTAAATAAAATCACCAACCCAGACG	OBD117.1.1103
182	32660961	32664960	OBD117.1.401	CGCCACCTCGTAGTTGTGTCTGC	OBD117.1.403
183	32662361	32666360	OBD117.1.721	AGTCAGCCACAAATCCTGGG	OBD117.1.723
184	32660961	32664960	OBD117.1.413	TGGTTCTGCTACCTGTGTGCCTG	OBD117.1.415
185	32662361	32666360	OBD117.1.425	TGGTTCTGCTACCTGTGTGCCTGC	OBD117.1.427
186	15802182	15806181	OBD117.1.1749	TGTAATGTGTCTCAGGTGTGGAG	OBD117.1.1751
187	98893484	98897483	OBD117.1.209	GATTTTGTATCCGTGGGAGTCCTGG	OBD117.1.211
188	98957432	98961431	OBD117.1.317	TTCCTGTAGGGCTTCCACTGGCT	OBD117.1.319
189	98957432	98961431	OBD117.1.101	CCCACTTTGCCACAACTCTGGTG	OBD117.1.103
190	42267204	42271203	OBD117.1.757	GGTGTAACGGGGGTCATTTC	OBD117.1.759
191	42281222	42285221	OBD117.1.281	GCACGGTCTGTCTACTTTCCCTC	OBD117.1.283
192	42300681	42304680	OBD117.1.037	GCACGGTCTGTCTACTTTCCCTC	OBD117.1.039
193	42331044	42335043	OBD117.1.073	CGGTGAGCACGGTCTGTCTACTT	OBD117.1.075
194	20687045	20691044	OBD117.1.693	TCTCTACTTCAGGCAGGCAGTGTAAG	OBD117.1.695
195	20694636	20698635	OBD117.1.929	AGTTTTCCACCCCTTCTTCC	OBD117.1.931
196	20728864	20732863	OBD117.1.665	TCTCTACTTCAGGCAGGCAGTGTAAG	OBD117.1.667
197	20737979	20741978	OBD117.1.581	TCTCTACTTCAGGCAGGCAGTGTAAG	OBD117.1.583
198	102219626	102223625	OBD117.1.1041	GAATTTCTTTGCGTTTCCTCAAC	OBD117.1.1043
199	102264037	102268036	OBD117.1.485	GCCTGGCATTGCTCCTCTTCAGC	OBD117.1.487
200	23355422	23359421	OBD117.1.289	TTGTGGTGTCCTGCTGGGTCATC	OBD117.1.291
201	6106025	6110024	OBD117.1.1017	TGGTTTGAGGTAGAAGTTGGTGGT	OBD117.1.1019
202	76658102	76662101	OBD117.1.1861	TTTAACCTAGTATATCCCAAAC	OBD117.1.1863
203	76721307	76725306	OBD117.1.1129	GAAGGGCAGAACTGTGAGTCAAAACC	OBD117.1.1131
204	76721307	76725306	OBD117.1.653	CCCGAAGGGCAGAACTGTGAGTCAAA	OBD117.1.655
205	132493063	132497062	OBD117.1.765	GCATGGTCCTGAGTCTCACA	OBD117.1.767
206	49691432	49695431	OBD117.1.285	GCTGCCCTCTCTCTTGTCAGACG	OBD117.1.287
207	31385136	31389135	OBD117.1.177	AAGAACAGCACACGCAGACAGACACA	OBD117.1.179
208	31385136	31389135	OBD117.1.173	CCTCTTTGCTGAGCCTGAGTTGTCTG	OBD117.1.175

Table 13.d6

	Inner_primers	
	PCR_Primer2	GLMNET
157	GTCTGAGGACAGAGACCCCT	0.007197773
158	TGTCACAGTCCCTCTAGCACT	-0.014372166
159	CTTCCTTTCCACACACCCTCAAATAC	-0.000142339

160	TCCAGAGGTTTCTAGGGACGAC	0.009781389
161	GTCTCCCCTCCCTGGAAAGTAAG	0
162	GGTTTGGGATAACATTGGTAGAAGAG	0
163	GTAGGCTCTCTCCCTGTGTGTCAC	0
164	TGGAGAGATGTGAGGCTTGTGGTCCT	0
165	GAGGCAGGTTTCTTTTCACATCCACT	0
166	GCCTCCCTTCCTATCTACTGTGTG	0
167	GGGACTACAGTTTCTCTGAGGGCTAA	-0.007419107
168	CCCCAAGTCTTTCCTTTGTTGTAGGG	0
169	CAGGAAAACTAAACTTGGTGGAAATC	0
170	CTGGCTTTGTCTGCTGCTTCTAT	0
171	TGGAGGAGGAACTTCAGGGCTGC	0
172	CCCAAAACGAGCCTTCTGGAATCCTC	0
173	TGACCTTTCCTGAACCCTCCTCA	0
174	CAGCGTAGAGGATGGGATAGAAGGGA	0
175	CGGTGGGATAAAGAAAGGAAAAC	0
176	GGAATCAAATGAGCCCAGGTTTA	0
177	GGAAAATGAGGAAAAGTCTGACAACT	0
178	CCCTACCTCCAAACCCCCTC	0
179	GGGGATGGGTCTTTTCACAG	0.000121346
180	GGATTCAGCATTACTACGAACTT	0
181	GGAACAAGATACTACTGGTGAACAAT	0
182	CCTTCCCTCCTTATTCCCACCCA	0.009992562
183	GCTGTCTGTTACTAGATTGCAC	0.00011425
184	CGCCACCTCGTAGTTGTGTCTGC	0.002234049
185	GGATGAGATGTGTAAAAGAGGCGGG	0.0000993
186	ACTACTGGCTGGTGTGAGAGAAT	0
187	ATTCCCACTTTGCCACAACTCTGGTG	0.012827643
188	GGGCAGCAAGGGCAGTTCTGAAG	-0.010330599
189	GGGCAGCAAGGGCAGTTCTGAAG	0.0000979
190	TGCAACCTCTGCCTTCTG	0.00012094
191	TGGAGATGCTGCTCTGCCCACCT	-0.00399849
192	CGTTGCCTCCTCACAGCAGAAGC	0.002891486
193	GTCCTGGGTCCTGGGTGAAAGTC	0.017565968
194	GGGAGACCATTTCTGTTCACTCTGAG	-0.022219432
195	GGGCTGTGTCCTGATAAACC	-0.015662127
196	TTATTGTTTCCTTAGGGAGGGCGTCC	0.000119444
197	GGTAATAGCCGTTGATACTCAGTGCC	-0.027382095
198	TACATCAACAGTGGGCTCCC	0
199	TGCCTGTGTCACTCCACCATCAG	0
200	GGAGCAGCCCATCTATCCTGACC	0.007589853
201	TCCAATAGTACCCCGAGATTTTCCT	0
202	GAGAGAGAGCTGATAAAAGGGATA	0.000113252
203	GGTAGGTGTCTGTCAAAAGGAGTGCT	0
204	TATTCAGGAAGAAATCCCTCCCAGG	0.003005705
205	CTGGGTTTCGGTTTCTTGC	-0.010031296
206	GTCCACCCCATTGCCGCTTTTCA	-0.025409945
207	CCCTCTGGACAAAGGTATTATCCCTG	0.006986068
208	CCTCTGGACAAAGGTATTATCCCTGA	0.004807037

Table 13.d7

	Probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig
209	ORF338_5_157249288_157254103_157266725_157271762_RR	ITK	26	10
210	ORF344_11_134020188_134023093_134179549_134189517_FR	ORF344	34	2

211	ORF344_11_134159769_134169350_134179549_134189517_FF	ORF344	34	2
212	ORF346_7_27813244_27816991_28040393_28050768_RR	ORF346	183	7
213	ORF346_7_28023391_28029625_28087716_28092793_FR	ORF346	183	7
214	ORF348_9_554821_562273_667141_671048_RR	ORF348	106	14
215	ORF348_9_554821_562273_787920_792102_RR	ORF348	106	14
216	ORF362_6_112077312_112085830_112110080_112119298_RR	ORF362	167	8
217	ORF362_6_112212817_112219150_112260826_112263612_FF	ORF362	167	8
218	ORF368_1_32214585_32217213_32237144_32241139_RF	ORF368	29	2
219	ORF369_13_46087370_46090583_46186579_46193039_RF	ORF369	31	1
220	ORF375_8_29646848_29651360_29765923_29776926_RF	ORF375	94	12
221	ORF38_13_111078224_111080305_111255999_111262146_RF	ORF38	86	4
222	ORF38_13_111170222_111182176_111317973_111320769_FF	ARHGEF7	122	6
223	ORF38_13_111255999_111262146_111299563_111302082_RF	ORF38	86	4
224	ORF38_13_111255999_111262146_111317973_111320769_FF	ARHGEF7	122	6
225	ORF380_4_150333761_150340859_150518099_150527260_RF	ORF380	167	15
226	ORF380_4_150518099_150527260_150647820_150652813_FR	ORF380	167	15
227	ORF382_1_89794704_89801882_89881274_89886132_RR	ORF382	44	2
228	ORF385_6_31567353_31572622_31588788_31590397_FR	ORF385	16	2
229	ORF385_6_31567353_31572622_31621846_31623705_FF	ORF385	16	2
230	ORF39_6_156816268_156822259_157042082_157049787_RF	ORF39	156	10
231	ORF39_6_156830748_156835572_157042082_157049787_RF	ORF39	156	10
232	ORF390_6_6365985_6370040_6413040_6420698_RR	ORF390	136	6
233	ORF393_1_235718481_235723036_235759465_235763923_RR	ORF393	32	5
234	ORF396_20_34509223_34513477_34530923_34534728_FR	ORF396	30	2
235	ORF396_20_34530923_34534728_34578621_34584178_RF	ORF396	30	2
236	ORF400_6_136518089_136523843_136551414_136554889_FR	ORF400	170	13
237	ORF401_4_86120725_86131416_86336679_86343485_FF	MAPK10	186	10
238	ORF403_9_125608173_125614421_125631239_125635100_RF	MAPKAP1	52	6
239	ORF404_3_192770374_192778803_192893705_192896438_FF	ORF404	95	5
240	ORF404_3_192893705_192896438_192941417_192949607_FF	ORF404	95	5
241	ORF408_11_86466088_86493462_86595548_86597707_RF	ORF408	141	26
242	ORF41_3_5096550_5098368_5223126_5230817_FR	ORF41	16	2
243	ORF41_3_5096550_5098368_5223126_5230817_RR	ORF41	16	2
244	ORF415_11_123335039_123337301_123352543_123361037_FR	ORF415	27	2
245	ORF415_11_123335039_123337301_123381608_123388566_FR	ORF415	27	2
246	ORF420_17_62595182_62602105_62650420_62653849_FR	ORF420	30	5
247	ORF430_17_32545190_32546373_32729890_32740232_FR	ORF430	168	28
248	ORF430_17_32585527_32592720_32673793_32677732_FR	ORF430	168	28
249	ORF430_17_32585527_32592720_32729890_32740232_FF	ORF430	168	28
250	ORF430_17_32585527_32592720_32729890_32740232_FR	ORF430	168	28
251	ORF430_17_32585527_32592720_32761107_32765317_FF	ORF430	168	28
252	ORF430_17_32585527_32592720_32797503_32800497_FR	ORF430	168	28
253	ORF430_17_32585527_32592720_32833313_32837843_FR	ORF430	168	28
254	ORF430_17_32585527_32592720_32856904_32867594_FR	ORF430	168	28
255	ORF430_17_32585527_32592720_32890505_32898320_FF	ORF430	168	28
256	ORF433_17_78250119_78253853_78298158_78301405_RF	ORF433	6	1
257	ORF439_4_153659613_153661830_153693586_153700349_RF	ORF439	31	4
258	ORF440_5_142382167_142389103_142659891_142662908_RF	ORF440	107	11
259	ORF440_5_142457784_142464671_142659891_142662908_RF	ORF440	107	11
260	ORF441_5_68187850_68194388_68215410_68221074_FR	PIK3R1	148	12

Table 13.e1

	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr	t
209	1.57E-05	0.002607465	38.46	-0.180610127	-0.180610127	-7.561434137
210	0.669241433	1	5.88	0.357950707	0.357950707	2.340298734

211	0.669241433	1	5.88	0.152342312	0.152342312	3.053183376
212	0.946917297	1	3.83	0.283333374	0.283333374	12.94789466
213	0.946917297	1	3.83	0.298409308	0.298409308	7.840334822
214	0.006786743	0.142219973	13.21	0.387341996	0.387341996	5.392692894
215	0.006786743	0.142219973	13.21	0.428239329	0.428239329	3.25451194
216	0.832957146	1	4.79	0.330158237	0.330158237	7.62185597
217	0.832957146	1	4.79	0.328841609	0.328841609	6.21961495
218	0.553587753	1	6.9	0.320236904	0.320236904	6.484888245
219	0.867297772	1	3.23	0.148960904	0.148960904	5.342674119
220	0.015049943	0.258038105	12.77	0.287047599	0.287047599	7.276689361
221	0.79882882	1	4.65	0.380176873	0.380176873	5.637761714
222	0.928958915	0.99999793	4.92	-0.390398405	-0.390398405	-17.0031469
223	0.79882882	1	4.65	0.376927136	0.376927136	11.41950058
224	0.928958915	0.99999793	4.92	-0.47329526	-0.47329526	-22.94378205
225	0.106360783	0.853264106	8.98	0.329280423	0.329280423	7.536413978
226	0.106360783	0.853264106	8.98	0.30661866	0.30661866	8.522452372
227	0.774574169	1	4.55	0.280706816	0.280706816	6.330999822
228	0.309387385	1	12.5	-0.206647528	-0.206647528	-10.52550054
229	0.309387385	1	12.5	-0.139665252	-0.139665252	-6.665441939
230	0.525030009	1	6.41	0.475425436	0.475425436	10.95020836
231	0.525030009	1	6.41	0.311742802	0.311742802	7.907001501
232	0.86474997	1	4.41	0.337386785	0.337386785	5.875969399
233	0.048263623	0.576108821	15.62	0.284781992	0.284781992	11.20881501
234	0.630241863	1	6.67	-0.161515168	-0.161515168	-9.011068418
235	0.630241863	1	6.67	-0.153338244	-0.153338244	-7.520061763
236	0.276096504	1	7.65	0.310767638	0.310767638	3.855741234
237	0.931377207	0.99999793	5.38	-0.18453906	-0.18453906	-3.956476668
238	0.229017635	0.99999793	11.54	-0.163709607	-0.163709607	-3.931754114
239	0.72257664	1	5.26	0.345706098	0.345706098	4.276857582
240	0.72257664	1	5.26	0.579695032	0.579695032	2.972500329
241	7.32E-07	0.000126288	18.44	0.292429157	0.292429157	8.470996679
242	0.267454675	1	12.5	0.310792224	0.310792224	9.410865337
243	0.267454675	1	12.5	0.304505394	0.304505394	7.908184476
244	0.514651704	1	7.41	0.285130311	0.285130311	10.6103307
245	0.514651704	1	7.41	0.292704671	0.292704671	6.331170439
246	0.037848586	0.469621268	16.67	0.333271938	0.333271938	10.68233567
247	2.30E-06	0.000217011	16.67	0.313678475	0.313678475	6.668777731
248	2.30E-06	0.000217011	16.67	0.718337876	0.718337876	3.390385035
249	2.30E-06	0.000217011	16.67	0.67380724	0.67380724	3.364859567
250	2.30E-06	0.000217011	16.67	0.922461761	0.922461761	3.446514196
251	2.30E-06	0.000217011	16.67	0.914009139	0.914009139	3.641671967
252	2.30E-06	0.000217011	16.67	0.942537109	0.942537109	3.821121196
253	2.30E-06	0.000217011	16.67	0.722069612	0.722069612	3.216502836
254	2.30E-06	0.000217011	16.67	0.476534879	0.476534879	3.333055657
255	2.30E-06	0.000217011	16.67	0.419624416	0.419624416	3.646251648
256	0.352766908	1	16.67	-0.195782617	-0.195782617	-5.226124183
257	0.128543197	0.904598768	12.9	0.29139179	0.29139179	8.633276617
258	0.074555092	0.72879893	10.28	0.330476001	0.330476001	11.06260353
259	0.074555092	0.72879893	10.28	0.364678783	0.364678783	12.7287492
260	0.513477047	0.99999793	8.11	-0.396269087	-0.396269087	-16.24057806

Table 13.e2

	P.Value	adj.P.Val	B	FC	FC_1	LS
209	0.0000167	0.000397765	3.289725067	0.882329773	-1.133363092	-1
210	0.040741366	0.093212255	-4.711020953	1.281604134	1.281604134	1

211	0.011861827	0.036959918	-3.494889529	1.111372396	1.111372396	1
212	0.000000111	0.0000279	8.36797508	1.217003548	1.217003548	1
213	0.0000121	0.000321152	3.621882899	1.229787722	1.229787722	1
214	0.000279967	0.002466566	0.358709102	1.307981373	1.307981373	1
215	0.008388704	0.028471537	-3.14593534	1.34559041	1.34559041	1
216	0.0000156	0.000381287	3.362483276	1.257151253	1.257151253	1
217	0.000089	0.001151446	1.5527701	1.256004479	1.256004479	1
218	0.0000628	0.000908877	1.915293694	1.248535553	1.248535553	1
219	0.000300988	0.002596993	0.283332726	1.108770596	1.108770596	1
220	0.0000234	0.000487262	2.940760759	1.220140766	1.220140766	1
221	0.00019737	0.001952202	0.722811617	1.301501408	1.301501408	1
222	0.00000000765	0.0000107	10.90661915	0.762918893	-1.310755324	-1
223	0.000000373	0.0000513	7.171532484	1.298573016	1.298573016	1
224	0.000000000382	0.00000159	13.50068753	0.72031744	-1.388276813	-1
225	0.0000172	0.000404351	3.259465584	1.256386566	1.256386566	1
226	0.00000573	0.000209476	4.396057544	1.236805517	1.236805517	1
227	0.0000768	0.001043977	1.70618126	1.214789898	1.214789898	1
228	0.000000809	0.0000728	6.393479433	0.866548541	-1.154003443	-1
229	0.0000498	0.000782222	2.156491332	0.907729751	-1.101649471	-1
230	0.000000556	0.0000617	6.770928087	1.390328153	1.390328153	1
231	0.0000113	0.000306728	3.699902454	1.241206194	1.241206194	1
232	0.000141646	0.001566448	1.068435975	1.26346595	1.26346595	1
233	0.000000445	0.0000562	6.993759854	1.218226162	1.218226162	1
234	0.00000345	0.000156596	4.919302407	0.894085578	-1.118461168	-1
235	0.0000176	0.000409391	3.239647539	0.899167475	-1.112139872	-1
236	0.003042322	0.013373385	-2.112164163	1.240367507	1.240367507	1
237	0.00257667	0.0118777	-1.941508536	0.879930168	-1.136453819	-1
238	0.002683585	0.012258029	-1.983302218	0.892726646	-1.120163719	-1
239	0.001532146	0.008180014	-1.405688605	1.270772784	1.270772784	1
240	0.013636816	0.040961218	-3.634591611	1.494533289	1.494533289	1
241	0.00000606	0.000215806	4.339475884	1.224700649	1.224700649	1
242	0.00000231	0.0001274	5.329296753	1.240388645	1.240388645	1
243	0.0000112	0.000306728	3.701282153	1.234995165	1.234995165	1
244	0.00000075	0.0000707	6.470042002	1.218520321	1.218520321	1
245	0.0000768	0.001043977	1.706414923	1.224934555	1.224934555	1
246	0.000000704	0.0000689	6.534564973	1.259867433	1.259867433	1
247	0.0000496	0.000780674	2.160905808	1.242872647	1.242872647	1
248	0.006650427	0.023946067	-2.910710578	1.645285415	1.645285415	1
249	0.006946167	0.024741342	-2.95485979	1.595277318	1.595277318	1
250	0.006044847	0.022344385	-2.813716523	1.895346684	1.895346684	1
251	0.004347344	0.017453856	-2.477713882	1.884274484	1.884274484	1
252	0.003221971	0.013975957	-2.171027926	1.921905112	1.921905112	1
253	0.008953939	0.029904578	-3.211807256	1.649546688	1.649546688	1
254	0.007333674	0.025784467	-3.009898236	1.391397737	1.391397737	1
255	0.004314044	0.017363236	-2.469857016	1.337579291	1.337579291	1
256	0.00035679	0.002914808	0.106302737	0.873099138	-1.145345306	-1
257	0.0000051	0.000194414	4.516948685	1.223820347	1.223820347	1
258	0.000000505	0.0000588	6.868410636	1.257428181	1.257428181	1
259	0.000000131	0.000032	8.205867689	1.287594914	1.287594914	1
260	0.000000012	0.0000107	10.48782055	0.759820695	-1.316099977	-1

Table 13.e3

		Probe sequence
	Loop detected	**60 mer**
209	PD-L1 responder	TACAGACTTTTTTTCTCTTCTCAGAAAATCGATGTTTGGGGGCGGAGGGCTTTGATGAGA

210	PD-L1 Non-responder	TGCCCATTTGCATTTCATATCCATCATCTCGATTAGCTCTGGTGAACACCTGTGTATCCT
211	PD-L1 Non-responder	CCAGCTGCAGTTCAAGTGGGGAAAGTAATCGAAGGTCAAAGACCAGTGAATTGGAAGATT
212	PD-L1 Non-responder	GGCAGGAGGATCACTTCAGCCCAAGAGGTCGAAGAGAGATGAGTACTATAAAGAAAATTA
213	PD-L1 Non-responder	TCTATAGAATTCTTAGGAAATAATGTTTTCGACATAAGGTTTTTCAAAATTCCTAATCAG
214	PD-L1 Non-responder	TTTTAAATTTTCACATCGTTCTAGTATATCGAGGTTTTCTCTTTCTTCGTGGTTCAATTT
215	PD-L1 Non-responder	TTTTAAATTTTCACATCGTTCTAGTATATCGAAGAAAGATGAAAAGGATTGAGAAAATCT
216	PD-L1 Non-responder	ATCAGAAAGTTATCTTTAATGAGATTCCTCGAATAAACTAAGATTCAATTTTTCTGAGCT
217	PD-L1 Non-responder	TATTTTTACTGAATCTTTCTTTGAAATTTCGATTATTAAATACTCAAGGAATAAGGGATG
218	PD-L1 Non-responder	AAGGGCTCGGGAGCTCCCTCGGCACACCTCGAGGAGTGCCAGGCATCTACTGCTCTGTCC
219	Non-Responder	AGGAGGGAGAAAAGTGATGAAGGCCATTTCGAGATGGGTGCCTGGGTGAGAATTTTAATA
220	PD-L1 Non-responder	GTGAATTCTGCAGGATATGATGGCCAATTCGAGATAATTTTAATTTGTCTACTGATGAGC
221	PD-L1 Non-responder	GTAAATGAATTTGAAATATTACAAAAGATCGATTACAGGCATTTTATAGCCACAAACTCA
222	PD-L1 responder	CGCAGCAGTCTCGTTGATCTTCACGGTGTCGACTCACCTGCGCCTCACATCCCAGGCGGG
223	PD-L1 Non-responder	AATTCTGTTGGAAGAATAATTTAAAATATCGATATTTTAATTATTTTTTTCCTAAAATAG
224	PD-L1 responder	GTAAATGAATTTGAAATATTACAAAAGATCGACTCACCTGCGCCTCACATCCCAGGCGGG
225	PD-L1 Non-responder	ATACTTTTCTTTCTAGATTATTTAAACATCGATATCAGTTAAGTTTAAAAACATATTAAT
226	PD-L1 Non-responder	ATACTTTTCTTTCTAGATTATTTAAACATCGAGATATTTATCTACATCTATTATTGTGGT
227	PD-L1 Non-responder	CCCCCAAAATAGGGTCTGATTTGGGGGTTCGATTGCATATTCTTTGGAAAATACAAAGTG
228	PD-L1 responder	CTCTGACTGCATCTTGTCCCCTTCTCTGTCGAGCCTCCGTTCAAATTGATCATCATCAAA
229	PD-L1 responder	CTCTGACTGCATCTTGTCCCCTTCTCTGTCGAAAATGCCTCATGTGGGAGATCTGATGGC
230	PD-L1 Non-responder	TATTCTAAAATTAATTTCAAACAAATTTTCGATTTTCATAATTTTATTACTTATACTTGA
231	PD-L1 Non-responder	TATTCTAAAATTAATTTCAAACAAATTTTCGAGACCCTAAAAAAAAAAGAAATAAAATAA
232	PD-L1 Non-responder	CTAATTAAATATAATCTAAATTTCCATCTCGACGTACATACGAGGAGAATGAGTAGGAAC
233	PD-L1 Non-responder	GGCAGGCAGATCACCTGACGTCAGGAGTTCGATACTACAACCCAAACTTCCAGTCAGTTT
234	PD-L1 responder	GTACTGCTACTTACCACAACACTGGGAGTCGAGCCATCTGCCACTGCCTTTTGACATCTC
235	PD-L1 responder	TGGGAAAATCATCCCACCTCTCTGAGCATCGAGCCATCTGCCACTGCCTTTTGACATCTC
236	PD-L1 Non-responder	CAAAAATTGCCAAAAATAAGTAGGTTTTTCGAGAACAGTATTGGATTTATTGTTAGGGTT
237	PD-L1 responder	GAGGATTTAATAAAACCCAAACTGTATTTCGAGAAAATAGTGTTTTGCTATTTAGATAAG
238	PD-L1 responder	CACTAATCTTTACTCTTTTTCCACTTATTCGAAGTTTCCAGAAAAGTCCTGAAGTTTTAA
239	PD-L1 Non-responder	TGTCCCCAGATGGATTGTAGACATAAATTCGAAGTTGCAGTGTACTATGACTGCACAACA
240	PD-L1 Non-responder	TGTTGTGCAGTCATAGTACACTGCAACTTCGAACTGACTTCTTCCACTCAGTATAATGTC
241	PD-L1 Non-responder	TTCTTTAAAATATTTGAAGAGATTTATTTCGAGTTTTGTAACCTATTTTTCCTTTTAACA
242	PD-L1 Non-responder	TTAGGGTGCACCCTAACCCAATAGGATGTCGAAGAAAATGACCTGATCATTTGAAAAGCT

243	PD-L1 Non-responder	CCTCCCTTACTGGGTATCATTATTAAGCTCGAAGAAAATGACCTGATCATTTGAAAAGCT
244	PD-L1 Non-responder	TAAATGTAAAACATAAAACTACAAAACTTCGATTATCACATTATATACTTATCGTGTGGC
245	PD-L1 Non-responder	TAAATGTAAAACATAAAACTACAAAACTTCGAGGTTCTAATATATAGGTTGAAGGTTCCT
246	PD-L1 Non-responder	AGAGATAAAAATTACAGATTTTGGTCTTTCGACTGGAAATCTACATTTTTATGTGTAATC
247	PD-L1 Non-responder	CCTCTGCGAGGAGCTCTGTCTGTCTTTGTCGAACTGATATAAACTTTCAGTTGTTCTATT
248	PD-L1 Non-responder	GAGAAAACAATCTAGCTGTTACAAATGTTCGATAGTTCTTAATTGTTTTGGGGTAACTGG
249	PD-L1 Non-responder	GAGAAAACAATCTAGCTGTTACAAATGTTCGAAATTTTCAAAGTACACAAAGTGCAATTT
250	PD-L1 Non-responder	GAGAAAACAATCTAGCTGTTACAAATGTTCGAACTGATATAAACTTTCAGTTGTTCTATT
251	PD-L1 Non-responder	GAGAAAACAATCTAGCTGTTACAAATGTTCGATTACATAAAAATGTAAAACTTTTATCTA
252	PD-L1 Non-responder	GAGAAAACAATCTAGCTGTTACAAATGTTCGAGAGAAACATCACATTCATATAACTTTTA
253	PD-L1 Non-responder	GAGAAAACAATCTAGCTGTTACAAATGTTCGAGAATCCATCTATCTTCAAAGTATAAACA
254	PD-L1 Non-responder	GAGAAAACAATCTAGCTGTTACAAATGTTCGATATTCTACACATACAGTCATCCCCTCCC
255	PD-L1 Non-responder	GAGAAAACAATCTAGCTGTTACAAATGTTCGACTCAAGTTGTCTCACCTTTCCAGACTGA
256	PD-L1 responder	GGATTCACCTTGATGCTATCTAAGTCCCTCGAGGGAGACGCCGCTGCTCCCATTTCACAG
257	PD-L1 Non-responder	TAAAACTATTTTAAATGTTTTTAAAGTATCGATGTGTACTTTGACATCTGTGATGATGAT
258	PD-L1 Non-responder	AGTGGCACAATCTCAGCTCATTATAGCCTCGAATCAGAATGTTTGGGGGTGAGCTTGGAA
259	PD-L1 Non-responder	AGTGGCACAATCTCAGCTCATTATAGCCTCGAATTGTAACTACCAGTGTTGGAGGAGGGG
260	PD-L1 responder	CTGAGTCTTCATTACCAAAAAAAAAAGTTCGACCTCCCCGAACCCCTCCGCCTCTGCGCT

Table 13.e4

	Probe Location					4 kb Sequence Location		
	Chr	**Start1**	**End1**	**Start2**	**End2**	**Chr**	**Start1**	**End1**
209	5	157249288	157249317	157266725	157266754	5	157249288	157253287
210	11	134023064	134023093	134179549	134179578	11	134019094	134023093
211	11	134169321	134169350	134189488	134189517	11	134165351	134169350
212	7	27813244	27813273	28040393	28040422	7	27813244	27817243
213	7	28029596	28029625	28087716	28087745	7	28025626	28029625
214	9	554821	554850	667141	667170	9	554821	558820
215	9	554821	554850	787920	787949	9	554821	558820
216	6	112077312	112077341	112110080	112110109	6	112077312	112081311
217	6	112219121	112219150	112263583	112263612	6	112215151	112219150
218	1	32214585	32214614	32241110	32241139	1	32214585	32218584
219	13	46087370	46087399	46193010	46193039	13	46087370	46091369
220	8	29646848	29646877	29776897	29776926	8	29646848	29650847
221	13	111078224	111078253	111262117	111262146	13	111078224	111082223
222	13	111182147	111182176	111320740	111320769	13	111178177	111182176
223	13	111255999	111256028	111302053	111302082	13	111255999	111259998
224	13	111262117	111262146	111320740	111320769	13	111258147	111262146
225	4	150333761	150333790	150527231	150527260	4	150333761	150337760

226	4	150527231	150527260	150647820	150647849	4	150523261	150527260
227	1	89794704	89794733	89881274	89881303	1	89794704	89798703
228	6	31572593	31572622	31588788	31588817	6	31568623	31572622
229	6	31572593	31572622	31623676	31623705	6	31568623	31572622
230	6	156816268	156816297	157049758	157049787	6	156816268	156820267
231	6	156830748	156830777	157049758	157049787	6	156830748	156834747
232	6	6365985	6366014	6413040	6413069	6	6365985	6369984
233	1	235718481	235718510	235759465	235759494	1	235718481	235722480
234	20	34513448	34513477	34530923	34530952	20	34509478	34513477
235	20	34530923	34530952	34584149	34584178	20	34530923	34534922
236	6	136523814	136523843	136551414	136551443	6	136519844	136523843
237	4	86131387	86131416	86343456	86343485	4	86127417	86131416
238	9	125608173	125608202	125635071	125635100	9	125608173	125612172
239	3	192778774	192778803	192896409	192896438	3	192774804	192778803
240	3	192896409	192896438	192949578	192949607	3	192892439	192896438
241	11	86466088	86466117	86597678	86597707	11	86466088	86470087
242	3	5098339	5098368	5223126	5223155	3	5094369	5098368
243	3	5096550	5096579	5223126	5223155	3	5096550	5100549
244	11	123337272	123337301	123352543	123352572	11	123333302	123337301
245	11	123337272	123337301	123381608	123381637	11	123333302	123337301
246	17	62602076	62602105	62650420	62650449	17	62598106	62602105
247	17	32546344	32546373	32729890	32729919	17	32542374	32546373
248	17	32592691	32592720	32673793	32673822	17	32588721	32592720
249	17	32592691	32592720	32740203	32740232	17	32588721	32592720
250	17	32592691	32592720	32729890	32729919	17	32588721	32592720
251	17	32592691	32592720	32765288	32765317	17	32588721	32592720
252	17	32592691	32592720	32797503	32797532	17	32588721	32592720
253	17	32592691	32592720	32833313	32833342	17	32588721	32592720
254	17	32592691	32592720	32856904	32856933	17	32588721	32592720
255	17	32592691	32592720	32898291	32898320	17	32588721	32592720
256	17	78250119	78250148	78301376	78301405	17	78250119	78254118
257	4	153659613	153659642	153700320	153700349	4	153659613	153663612
258	5	142382167	142382196	142662879	142662908	5	142382167	142386166
259	5	142457784	142457813	142662879	142662908	5	142457784	142461783
260	5	68194359	68194388	68215410	68215439	5	68190389	68194388

Table 13.e5

	4 kb Sequence Location		**Inner_primers**		
	Start2	**End2**	**PCR-Primer1_ID**	**PCR_Primer1**	**PCR-Primer2_ID**
209	157266725	157270724	OBD117.1.165	GTAAATGAGCCACCTGGGCGGGT	OBD117.1.167
210	134179549	134183548	OBD117.1.585	GAACACGAGAATGGAGAGGGAGCATC	OBD117.1.587
211	134185518	134189517	OBD117.1.593	GCTATTTGGTCTGTCCTTGCTCCACA	OBD117.1.595
212	28040393	28044392	OBD117.1.1717	AGCCTGGGTGACAGAGTAAGACC	OBD117.1.1719
213	28087716	28091715	OBD117.1.1617	CAAGCACAGGCAACAGAACAGACCAT	OBD117.1.1619
214	667141	671140	OBD117.1.1289	CTGTTTGCCCTGAGAATACTTGCCCA	OBD117.1.1291
215	787920	791919	OBD117.1.1605	GCCAACTTGACTGGGCAAACGGA	OBD117.1.1607
216	112110080	112114079	OBD117.1.1513	CATCGGATTAGAGGATTCCAGTTTTA	OBD117.1.1515
217	112259613	112263612	OBD117.1.1469	CGTCTGGTGTTGTGGAACTTTGGAGG	OBD117.1.1471
218	32237140	32241139	OBD117.1.1337	GCGGAGCCTCTTTGAACAGAAGC	OBD117.1.1339
219	46189040	46193039	OBD117.1.925	TGATGTATAGCTGGGCCTTG	OBD117.1.927
220	29772927	29776926	OBD117.1.1397	CTAAGAAGCAGATGCCACAGGCTGGT	OBD117.1.1399
221	111258147	111262146	OBD117.1.1113	GTGCTCCTGAATGACCAGTGGGT	OBD117.1.1115
222	111316770	111320769	OBD117.1.157	TGGGAGGGTTTTATTCACAAGAGTGG	OBD117.1.159
223	111298083	111302082	OBD117.1.1457	TGAGCCACAGAGCAAGACTCCGTC	OBD117.1.1459

224	111316770	111320769	OBD117.1.725	AAGTGATCGTGGAAACACAGC	OBD117.1.727
225	150523261	150527260	OBD117.1.1849	TTTCCAAGAACGGTTTTGCTTTC	OBD117.1.1851
226	150647820	150651819	OBD117.1.1829	TTTCCAAGAACGGTTTTGCTTTC	OBD117.1.1831
227	89881274	89885273	OBD117.1.1421	CAGCCTGGCAACAGAGTGAGACT	OBD117.1.1423
228	31588788	31592787	OBD117.1.977	CCGTGCTTCGTGCTTTGGAC	OBD117.1.979
229	31619706	31623705	OBD117.1.965	TTCGTGCTTTGGACTACCGC	OBD117.1.967
230	157045788	157049787	OBD117.1.1821	TATCACGGTAAAATCAATAAAAT	OBD117.1.1823
231	157045788	157049787	OBD117.1.1857	TATCACGGTAAAATCAATAAAAT	OBD117.1.1859
232	6413040	6417039	OBD117.1.1301	GGTGTGTCTGGGAGATTAGTAGATGG	OBD117.1.1303
233	235759465	235763464	OBD117.1.1229	GTGGCTCAAGTCTGTAATCCCAGCAC	OBD117.1.1231
234	34530923	34534922	OBD117.1.477	TCCAGGATGGTTTGACTCTAAAGCAT	OBD117.1.479
235	34580179	34584178	OBD117.1.553	CTCTTTCAGGTTCCCCAGACCATC	OBD117.1.555
236	136551414	136555413	OBD117.1.1177	AATACCTACCCTTGCCCTTCCCACCA	OBD117.1.1179
237	86339486	86343485	OBD117.1.221	TGGCAGATTGTAGGTGGTTGGAGAAT	OBD117.1.223
238	125631101	125635100	OBD117.1.033	GTCATCTCCTCTCCAGTTAGTCAACA	OBD117.1.035
239	192892439	192896438	OBD117.1.1133	GTGATACAACACTTTAGATACCTGGA	OBD117.1.1135
240	192945608	192949607	OBD117.1.1285	ACACAACCCAGCGTCCTTCGCCTTTT	OBD117.1.1287
241	86593708	86597707	OBD117.1.1693	CCACCTCTGTGAAGTATGCTCTCTGG	OBD117.1.1695
242	5223126	5227125	OBD117.1.1581	GAGTCCAAGCAAACGACAAGGAAGTC	OBD117.1.1583
243	5223126	5227125	OBD117.1.1637	TTGAGATGACAGGCTGGCACCCC	OBD117.1.1639
244	123352543	123356542	OBD117.1.1713	GCAGAAACTCAAAATGGATGGTAGGC	OBD117.1.1715
245	123381608	123385607	OBD117.1.1205	GCAGAAACTCAAAATGGATGGTAGGC	OBD117.1.1207
246	62650420	62654419	OBD117.1.1729	TATCTGCTATTACTTTGGGTTTT	OBD117.1.1731
247	32729890	32733889	OBD117.1.1429	GCCACTTTGAGGGCTGAACAGTAGC	OBD117.1.1431
248	32673793	32677792	OBD117.1.1089	GGATGCCAGAATAAGATGGAACTGTG	OBD117.1.1091
249	32736233	32740232	OBD117.1.1589	GGATGCCAGAATAAGATGGAACTGTG	OBD117.1.1591
250	32729890	32733889	OBD117.1.1493	GGATGCCAGAATAAGATGGAACTGTG	OBD117.1.1495
251	32761318	32765317	OBD117.1.1661	GGATGCCAGAATAAGATGGAACTGTG	OBD117.1.1663
252	32797503	32801502	OBD117.1.1081	GGATGCCAGAATAAGATGGAACTGTG	OBD117.1.1083
253	32833313	32837312	OBD117.1.1085	GGATGCCAGAATAAGATGGAACTGTG	OBD117.1.1087
254	32856904	32860903	OBD117.1.1509	GGATGCCAGAATAAGATGGAACTGTG	OBD117.1.1511
255	32894321	32898320	OBD117.1.1489	GGATGCCAGAATAAGATGGAACTGTG	OBD117.1.1491
256	78297406	78301405	OBD117.1.1053	TCACCCAGCTGCTGTATATGACT	OBD117.1.1055
257	153696350	153700349	OBD117.1.1697	AACGCTTTCCACCAGGTCCTACC	OBD117.1.1699
258	142658909	142662908	OBD117.1.1149	CATCTCACTCCCTCACCAGGCTG	OBD117.1.1151
259	142658909	142662908	OBD117.1.1505	CATCTCACTCCCTCACCAGGCTG	OBD117.1.1507
260	68215410	68219409	OBD117.1.829	GGGGAATGACTCAGGTTCAC	OBD117.1.831

Table 13.e6

	Inner_primers	
	PCR_Primer2	GLMNET
209	GGCAAGCATCTTCCTGGTTCTTCAG	-0.004038003
210	CTGAGGAAAGAGAGCAGTATCTAAGG	0.000108113
211	GCTCATCAGTTTTCAGTCCTTTTCCT	-0.012488304
212	GGCACCGTGTATCCCTCTCTCTG	0
213	ATAGACAAATGACCTCCTCCTTGC	0
214	GAAGACAAAGATACATTCCTGGACAT	0
215	CCCCTTTCTGTCCTGCTCTCTGC	0
216	GTGCCCACACAAAGACTAAGCGAGTT	0
217	GCCAAGCATAGACTCAGACTTTTAGG	0
218	GCCTCTTCCCACCAGCCTGACTT	0
219	ACCAAGGATGCACCAGAAAG	0.015771071
220	TCTGAGGGTGACCTTATTTTGTCCAC	0
221	CAGCCTGGGCGACAGAAACCTTG	0
222	ACAGTCCATAGTGAGCGGCAGACAGA	-0.008898153
223	GCTACAGCCTACTAATCAAGGAACTG	0

224	CCACAGTCCATAGTGAGCGG	0.00011344
225	ATTTACTTGCTATGGGTCCTTTT	0
226	ATTTACTTGCTATGGGTCCTTTT	0
227	GAAATCTCCTCCCCACCCTCAGC	0
228	GGTGGAAGGGTGAGCCATGT	0
229	CCCAGGATAGGAGGCCATCAGA	-0.006509693
230	AAGCCATCCTTTTCTAAACAATA	0
231	AGAGGAAAGACAACATTTTATTT	0
232	CCGTAGAGGATAAAAGGAAAGAAAGC	0
233	CCAGCATTCCCTACTTCTTCACTACT	0
234	TGTGGGTAGCAGCAGAGGATGGCA	0.011140328
235	TGGGTAGCAGCAGAGGATGGCAG	0
236	TCATCACAGACCACAGCAGAAGTGTT	0
237	GTCTGGCAGCCTTCCTCATTTATGGT	-0.009554407
238	CCCTTGCTATGATGGCTTGTTCACTG	-0.010767501
239	TTCTTCCCACTACACCACACAACCCA	0
240	CAGCAGCAAGAATGGAGTTCAAAGAC	0
241	CCAGCATCAAAGAGCAAGAATGGAGT	0
242	CGATGGCAACTGGCTCTTGTTCCTTT	0
243	CGATGGCAACTGGCTCTTGTTCC	0
244	CTATGTGGGTGTGTGGATGTGTATGG	0
245	TTTGTTCCCCAGGCAGCATTCAGTGC	0
246	TTCAGGATGTGTGAGAGAGATTA	0
247	AAAACAAAGAATCCTCCCTGCCCC	0
248	GAAACAGCCTCACTTTGGAGTTCAGG	0
249	CATCACCAGCAAGCAGTGCCAACTAC	0
250	AAAACAAAGAATCCTCCCTGCCCC	0
251	CCATTCTCAATAAGAGGCGTGTCACC	0
252	CTGTGAGGGATACACTCCAAGACATC	0
253	GCAGAGGTGGTGAGAAGTAGTCAGAC	0
254	GTGCTTGACATTTCTGCTACCCCTGC	0
255	TCCGTGACACAGTCTCAGGAGGTTCT	0
256	ACAAGCTCGTGTGAGTGCCC	0
257	GGAAAGTGGGCACCAGCCGCATT	0
258	GGCAGGAGAAGGGCTACTGAAAG	0
259	CAAACCACCTCCCATCAAACCCC	0
260	GCGGAGTGCTCTGGCTCTAC	0.000114527

Table 13.e7

	Probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig
261	ORF442_7_142753523_142755244_142766140_142771360_FR	ORF442	30	8
262	ORF442_7_142753523_142755244_142812001_142818261_FF	ORF442	30	8
263	ORF447_13_32504086_32509501_32577917_32582372_FF	ORF447	29	3
264	ORF447_13_32540613_32545777_32577917_32582372_FF	ORF447	29	3
265	ORF454_2_105728227_105741825_105841316_105844511_FF	NCK2	66	4
266	ORF456_11_119671081_119677815_119700077_119705149_FR	PVRL1	96	8
267	ORF457_1_198199892_198201903_198244755_198253085_FF	ORF457	130	22
268	ORF457_1_198199892_198201903_198346795_198354552_FR	ORF457	130	22
269	ORF457_1_198279876_198287932_198346795_198354552_RR	ORF457	130	22
270	ORF458_17_31150085_31156746_31224131_31234469_FR	ORF458	136	9
271	ORF458_17_31332261_31339438_31382125_31387511_FR	ORF458	136	9
272	ORF460_20_51355850_51362174_51482831_51487722_FR	ORF460	65	2
273	ORF462_1_60869920_60875614_60989414_60996659_RR	ORF462	165	19
274	ORF464_6_44253666_44257911_44307667_44312139_RF	NFKBIE	44	4

275	ORF464_6_44270723_44274914_44307667_44312139_RF	NFKBIE	44	4
276	ORF465_3_101806474_101809017_101822519_101827725_RR	ORF465	26	6
277	ORF472_16_27189621_27195287_27236516_27245702_FF	ORF472	16	1
278	ORF479_8_80968986_80975857_81095100_81099880_RR	PAG1	144	12
279	ORF479_8_81007411_81018107_81053410_81059648_FR	PAG1	144	12
280	ORF479_8_81007411_81018107_81077565_81079322_FR	PAG1	144	12
281	ORF479_8_81007411_81018107_81095100_81099880_FR	PAG1	144	12
282	ORF479_8_81053410_81059648_81095100_81099880_RR	PAG1	144	12
283	ORF48_1_212523302_212528520_212585744_212588822_RF	ORF48	30	11
284	ORF48_1_212572997_212579940_212643074_212645915_RF	ORF48	30	11
285	ORF480_11_77430379_77437843_77514783_77519103_RF	PAK1	136	6
286	ORF481_4_168689667_168697449_168861254_168870461_FF	ORF481	125	18
287	ORF482_5_168579937_168582137_168614429_168620163_RR	ORF482	25	5
288	ORF489_10_95194975_95203396_95282952_95289853_RR	ORF489	35	10
289	ORF494_3_170115709_170117792_170195523_170206472_FR	ORF494	23	1
290	ORF500_7_106905450_106908201_106938904_106944761_FF	ORF500	31	3
291	ORF501_5_68203536_68213336_68272048_68277769_FF	PIK3R1	148	12
292	ORF501_5_68215410_68221074_68272048_68277769_RF	PIK3R1	148	12
293	ORF505_17_67329565_67337138_67493397_67497612_FR	ORF505	61	8
294	ORF510_12_19116277_19126697_19175194_19181683_RR	ORF510	105	20
295	ORF510_12_19116277_19126697_19247123_19249380_RR	ORF510	105	20
296	ORF510_12_19116277_19126697_19321592_19322644_RF	ORF510	105	20
297	ORF510_12_19116277_19126697_19330800_19333489_RR	ORF510	105	20
298	ORF514_16_57264324_57265825_57311821_57315910_RF	ORF514	13	4
299	ORF518_12_62612835_62616434_62635972_62643837_FR	ORF518	98	7
300	ORF52_6_16559432_16569316_16745336_16747298_RR	ORF52	170	12
301	ORF520_4_100984121_100992210_101215421_101227213_RR	ORF520	151	14
302	ORF520_4_100993481_100996110_101215421_101227213_FR	ORF520	151	14
303	ORF527_16_23918616_23926918_24180817_24184913_FF	ORF527	167	6
304	ORF529_10_6432893_6439235_6460245_6464187_RF	PRKCQ	106	2
305	ORF531_22_44662780_44666500_44696835_44701888_FF	PRR5	64	4
306	ORF532_11_36295021_36302583_36442359_36447012_FF	ORF532	154	18
307	ORF532_11_36295021_36302583_36486258_36488847_FF	ORF532	154	18
308	ORF534_2_113175431_113181015_113215780_113218742_RR	ORF534	28	1
309	ORF538_8_140715391_140725081_140763162_140771406_FF	PTK2	248	12
310	ORF538_8_140715391_140725081_140877455_140883144_FR	PTK2	248	12
311	ORF538_8_140725196_140731179_140877455_140883144_RF	PTK2	248	12
312	ORF540_12_112418669_112423831_112478543_112482415_RR	PTPN11	56	6

Table 13.f1

	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr	t
261	0.000412702	0.012833299	26.67	0.282182665	0.282182665	8.633617733
262	0.000412702	0.012833299	26.67	0.296850132	0.296850132	10.04415773
263	0.302066279	1	10.34	0.254568442	0.254568442	5.844514895
264	0.275359272	1	10.34	0.257220838	0.257220838	4.875635995
265	0.779227696	0.99999793	6.06	-0.308568317	-0.308568317	-13.88505293
266	0.497039718	0.99999793	8.33	-0.149050171	-0.149050171	-6.891048765
267	2.09E-05	0.00123352	16.92	0.326119857	0.326119857	14.46240036
268	2.09E-05	0.00123352	16.92	0.364744284	0.364744284	4.767804449
269	2.09E-05	0.00123352	16.92	0.407405048	0.407405048	4.303224495
270	0.489837398	1	6.62	0.356227721	0.356227721	5.408044247
271	0.489837398	1	6.62	0.306778753	0.306778753	8.548684381
272	0.922199982	1	3.08	0.315145804	0.315145804	4.450181318
273	0.008195505	0.161007518	11.52	0.522735303	0.522735303	8.344744415
274	0.466402982	0.99999793	9.09	-0.239598775	-0.239598775	-11.49610245

275	0.466402982	0.99999793	9.09	-0.361055592	-0.361055592	-19.65763701
276	0.004811744	0.105522664	23.08	0.39419325	0.39419325	7.788511223
277	0.666756467	1	6.25	0.240506289	0.240506289	6.459645292
278	0.474481533	0.99999793	8.33	-0.226025291	-0.226025291	-8.99633921
279	0.474481533	0.99999793	8.33	-0.229747184	-0.229747184	-5.910931698
280	0.474481533	0.99999793	8.33	-0.154283407	-0.154283407	-3.020061123
281	0.474481533	0.99999793	8.33	-0.219792116	-0.219792116	-8.380946819
282	0.474481533	0.99999793	8.33	-0.143993345	-0.143993345	-4.923920109
283	1.09E-06	0.000147069	36.67	0.347208645	0.347208645	10.26020662
284	1.81E-06	0.000223432	36.67	0.247499169	0.247499169	10.06614725
285	0.963851563	0.99999793	4.41	-0.138029302	-0.138029302	-5.075029024
286	0.000866538	0.022698472	14.4	0.282685362	0.282685362	6.001930767
287	0.018277026	0.292122629	20	0.139860217	0.139860217	2.682542914
288	4.16E-05	0.002051839	28.57	0.345918136	0.345918136	5.148443654
289	0.776490089	1	4.35	0.349135569	0.349135569	13.52580262
290	0.310510231	1	9.68	0.305010185	0.305010185	6.196106538
291	0.513477047	0.99999793	8.11	-0.158345461	-0.158345461	-4.255312553
292	0.513477047	0.99999793	8.11	-0.384094729	-0.384094729	-16.16361934
293	0.047733938	0.555717324	13.11	0.145028051	0.145028051	5.238896186
294	8.08E-06	0.000635046	19.05	0.376644852	0.376644852	11.02917154
295	8.08E-06	0.000635046	19.05	0.326634321	0.326634321	7.908617509
296	8.08E-06	0.000635046	19.05	0.296253745	0.296253745	4.138933763
297	8.08E-06	0.000635046	19.05	0.351520286	0.351520286	15.21067568
298	0.008516834	0.15747793	30.77	0.227494853	0.227494853	8.573818628
299	0.423328583	1	7.14	0.299633874	0.299633874	7.710688541
300	0.385937569	1	7.06	0.333292833	0.333292833	6.455577776
301	0.095696301	0.807051655	9.27	0.37381143	0.37381143	15.1958863
302	0.095696301	0.807051655	9.27	0.327001567	0.327001567	6.995430928
303	0.955788004	1	3.59	0.315269518	0.315269518	8.479485602
304	0.998452566	0.99999793	1.89	-0.301937872	-0.301937872	-16.13705896
305	0.7582782	0.99999793	6.25	-0.38593493	-0.38593493	-15.39183699
306	0.008522642	0.164017369	11.69	0.327277188	0.327277188	15.01502481
307	0.008522642	0.164017369	11.69	0.285606598	0.285606598	13.61645345
308	0.853880387	1	3.57	0.146480654	0.146480654	4.980868538
309	0.979779286	0.99999793	4.84	-0.161243979	-0.161243979	-7.690183808
310	0.979779286	0.99999793	4.84	-0.179032383	-0.179032383	-4.998863428
311	0.979779286	0.99999793	4.84	-0.205518478	-0.205518478	-7.923787367
312	0.283634013	0.99999793	10.71	-0.281116435	-0.281116435	-10.51176015

Table 13.f2

	P.Value	adj.P.Val	B	FC	FC_1	LS
261	0.0000051	0.000194414	4.517318749	1.21603324	1.21603324	1
262	0.00000126	0.0000913	5.947522775	1.228459361	1.228459361	1
263	0.000147922	0.001608124	1.023264128	1.19297883	1.19297883	1
264	0.00060203	0.004200216	-0.437698362	1.19517414	1.19517414	1
265	0.0000000563	0.0000204	9.028942709	0.807442641	-1.238478065	-1
266	0.0000375	0.000650749	2.451683607	0.901844015	-1.108839204	-1
267	0.0000000378	0.000017	9.411796984	1.253637166	1.253637166	1
268	0.000709669	0.004690158	-0.608518471	1.287653374	1.287653374	1
269	0.001468864	0.007933618	-1.362105846	1.326298076	1.326298076	1
270	0.000273835	0.002430708	0.381770825	1.280074451	1.280074451	1
271	0.00000558	0.000205624	4.42479206	1.236942771	1.236942771	1
272	0.001163152	0.006712076	-1.120741967	1.244137384	1.244137384	1
273	0.00000694	0.000231622	4.199416787	1.43667656	1.43667656	1
274	0.00000035	0.0000501	7.235348626	0.846980832	-1.180664264	-1

275	0.00000000180	0.00000577	12.19684795	0.778594689	-1.284365299	-1
276	0.0000129	0.00033477	3.560870429	1.314207654	1.314207654	1
277	0.0000649	0.000929428	1.881216554	1.181407184	1.181407184	1
278	0.0000035	0.00015845	4.90389231	0.854987189	-1.169608168	-1
279	0.000135003	0.001520418	1.118479259	0.85278432	-1.172629441	-1
280	0.012560255	0.038539753	-3.552262166	0.89857859	-1.112868714	-1
281	0.00000667	0.000227068	4.239758043	0.85868916	-1.164565767	-1
282	0.000559582	0.004010305	-0.361729876	0.905010637	-1.104959388	-1
283	0.00000103	0.0000822	6.150150312	1.272096966	1.272096966	1
284	0.00000123	0.0000904	5.968333273	1.187147477	1.187147477	1
285	0.000446091	0.003407902	-0.126087743	0.908759659	-1.100400959	-1
286	0.000119231	0.001398727	1.247912659	1.216457032	1.216457032	1
287	0.022542218	0.05969012	-4.133849469	1.101798357	1.101798357	1
288	0.000400046	0.003156349	-0.012767176	1.270959568	1.270959568	1
289	0.0000000727	0.0000221	8.78155797	1.273797167	1.273797167	1
290	0.0000918	0.001174535	1.520169664	1.235427359	1.235427359	1
291	0.001585984	0.00838257	-1.441362142	0.896052109	-1.116006524	-1
292	0.0000000126	0.0000107	10.44421723	0.766259665	-1.305040636	-1
293	0.000350168	0.002877636	0.125797352	1.105752153	1.105752153	1
294	0.000000519	0.0000596	6.839517342	1.298318956	1.298318956	1
295	0.0000112	0.000306728	3.701787155	1.254084292	1.254084292	1
296	0.001913285	0.009573546	-1.634983629	1.22795164	1.22795164	1
297	0.000000023	0.0000135	9.882661566	1.275904444	1.275904444	1
298	0.00000543	0.000202914	4.452254274	1.170800164	1.170800164	1
299	0.0000141	0.000355212	3.468646509	1.230832014	1.230832014	1
300	0.0000653	0.000933916	1.875717331	1.259885681	1.259885681	1
301	0.0000000232	0.0000135	9.873618979	1.295771588	1.295771588	1
302	0.000033	0.000601894	2.585972415	1.254403567	1.254403567	1
303	0.000006	0.000215141	4.348830339	1.244244076	1.244244076	1
304	0.0000000128	0.0000107	10.42910997	0.811162087	-1.232799235	-1
305	0.0000000205	0.0000131	9.992593359	0.765282901	-1.306706316	-1
306	0.0000000261	0.0000141	9.762192491	1.254643239	1.254643239	1
307	0.0000000681	0.0000215	8.844665717	1.218922666	1.218922666	1
308	0.000513568	0.003768664	-0.272546891	1.10686606	1.10686606	1
309	0.0000144	0.000361067	3.444226195	0.894253659	-1.118250946	-1
310	0.000499878	0.003693568	-0.24446078	0.883295225	-1.132124314	-1
311	0.000011	0.000303945	3.719464345	0.867226966	-1.153100675	-1
312	0.000000819	0.0000729	6.381022079	0.822953925	-1.215134857	-1

Table 13.f3

		Probe sequence
	Loop detected	**60 mer**
261	PD-L1 Non-responder	TGAAAGTCTGCAGGGTGTGTGCTCAGGATCGAGGCTGGTACTGTTCACCTGTGGGTCCAG
262	PD-L1 Non-responder	TGAAAGTCTGCAGGGTGTGTGCTCAGGATCGACCAAGATCTAGTAATTATTCATACTGTA
263	PD-L1 Non-responder	TGTTTTAGGGAGAAGACTGTGCCTAATATCGAGTGGAGTGGAAGAATACCAAAATCATCT
264	Non-Responder	AAGACTGAGATAAAAATTCTCAAGATCATCGAGTGGAGTGGAAGAATACCAAAATCATCT
265	PD-L1 responder	TCTTTGCAGATGTTGTAAGATAAGGATGTCGACTTCATAATCCGCCCGCCTCAGCCTCCC
266	PD-L1 responder	GGACCTTGTCATCCTGCCCCTTCTTGGCTCGAGGCCCTGAAACAGGACTCTATGTCTCCT
267	PD-L1 Non-responder	CAAGCTTTATTTAAAAATATAGCATATATCGAAAGTTGGCTAATGTATTATAGCCCATAT
268	PD-L1 Non-responder	CAAGCTTTATTTAAAAATATAGCATATATCGAACAACCAGGGGAAATAACAATGGTTACA

269	PD-L1 Non-responder	AGGTACTGTTTTAGAAATATAGAAAAATTCGAACAACCAGGGGAAATAACAATGGTTACA
270	PD-L1 Non-responder	ATTTCTTTCTTCTTCCCATTTTCTAAAATCGATTCCTCCAATAAGGGTTTCACCTCTTGA
271	PD-L1 Non-responder	GTTTTTGTATTAATAAAATGAAAAAGATTCGAAAACTTCCTTATTAGGTAGTAAAACAAA
272	PD-L1 Non-responder	GTGGCTAAAACAAGATTCAATCTCAATCTCGAGTTTATGTACTGTCTCCATTGACTAAGA
273	PD-L1 Non-responder	TTAATATACTTACATATATTTATAATGGTCGATCTCACTATTGATAGCTCCATTTTACAG
274	PD-L1 responder	TTTCAAAGAAGGTATGATGGGAAAGGTCTCGAGTGCCCCTGTCCCACCTGGCTCCCCCTG
275	PD-L1 responder	TTTCAAAGAAGGTATGATGGGAAAGGTCTCGACGCGCCCCCTCTACGCCATGTCCCCCCC
276	PD-L1 Non-responder	AAATAAAATAAAATAAAACATATACTACTCGAGTTTTTTAGTGAATATTTACAATTTCCT
277	PD-L1 Non-responder	GCTGCCTATGGGGCAGTGTGCAGGGGTGTCGATGAATTTCTCAACATACAGAATTGACAG
278	PD-L1 responder	CTTTTTAAAAATTATCTTTTTATTTGCTTCGATGCCAATCCACGTCATTAGATGAGGACC
279	PD-L1 responder	TCAGATAAGTAACTTCCTGATAATTAACTCGAGAAATGGATTCATATTTCCATGGCTTAC
280	PD-L1 responder	TCAGATAAGTAACTTCCTGATAATTAACTCGAAAAAACATTAATTTCTTCAGGTGTAAAG
281	PD-L1 responder	TCAGATAAGTAACTTCCTGATAATTAACTCGATGCCAATCCACGTCATTAGATGAGGACC
282	PD-L1 responder	GTAAGCCATGGAAATATGAATCCATTTCTCGATGCCAATCCACGTCATTAGATGAGGACC
283	PD-L1 Non-responder	TATCTATTTCTTTCTTATTTTGGACATTTCGAGGGTGATAATGCTAAGGGGTCTGGATTG
284	PD-L1 Non-responder	GAGAGGAGAGTAAGGTTGGGGTGTAAGGTCGATTCTAATAATTCTTAGTTGAATTGTTCT
285	PD-L1 responder	TAACAAAAGTAACACCTCTTTGGTATCATCGAAGAGTCCTTGTTCCCATTTTGGCCCAGT
286	PD-L1 Non-responder	GGGCAAGTTCAGATTGAAGCCTCGTGTCTCGAGAGGCAGATAAAAACAATTCCATGGTAA
287	Non-Responder	GAATGGCCGAACAGCCATGACAGTCCTCTCGAGGCTACTGGAGTCATTGAAAAGAGGAAT
288	PD-L1 Non-responder	TTTTTATTGATTGTCTCATTTAATCTTCTCGAGTTCCTCAAAAGTTTCCAAACAAGCTCC
289	PD-L1 Non-responder	CAAGGTGGGTGGATCACCTGAGGAGAATTCGAATCCAACAGCACATCAAAAAAATACACC
290	PD-L1 Non-responder	TCCCATCATTCAAAAATTATTAAGAAATTCGAGGTATTAAAGTATGCTTTTATTGTGTAA
291	PD-L1 responder	CGTTGCAAATTGTACATCTTCTGCTATTTCGAGACCTCATATAACTCGGTGATTGACTGC
292	PD-L1 responder	GCAGTCAATCACCGAGTTATATGAGGTCTCGACCTCCCCGAACCCCTCCGCCTCTGCGCT
293	PD-L1 Non-responder	AGGAGGGGCAAAGTCCGTCAGCTGGCTTTCGAGACTCAGAAATAAATTTGCAGTCTTTTA
294	PD-L1 Non-responder	TTTTTTCTCTATAGTTCATTACTTATTTTCGAGTGTAAACTGTGAAAATAGTCAAATATA
295	PD-L1 Non-responder	TTTTTTCTCTATAGTTCATTACTTATTTTCGACTCTACGAAAAGTATCTTCCTTTAATTA
296	PD-L1 Non-responder	ATTTACAAAATGGACTGCTTAGTACGTGTCGAAAATAAGTAATGAACTATAGAGAAAAAA
297	PD-L1 Non-responder	TTTTTTCTCTATAGTTCATTACTTATTTTCGAAATATACCAGTAAAATTAATTTAAATAT
298	PD-L1 Non-responder	GATGGGCAGATTACTTGAAGTCAAGAGTTCGAGCTTGGAAGTCAAAAGCTGTGTGGCTGT
299	PD-L1 Non-responder	TTGGTTTTAATTTTTTTTTTTAAATAAATCGACTACATATAAGCTTTAGATTTGAAATAT
300	PD-L1 Non-responder	TTATTCTTTTTTAGTATCTAAATAGTATTCGAATGTCCAAAAATGATAGGAAACTTAAAA
301	PD-L1 Non-responder	TTTGTTGAATTTTTAATATTGAATTTATTCGATTTCTTCCCAATTCCTCATTTCTAATAT
302	PD-L1 Non-responder	ATTATCTAGATCTTGTAAGATGGAAAAATCGATTTCTTCCCAATTCCTCATTTCTAATAT

303	PD-L1 Non-responder	TTTTTAAAAGCAAGTTTTCTCAAAAGCTTCGAAGCACTAAGTAAGGTGTATTGTTATTAT
304	PD-L1 responder	TCACAACCTGGGAAAACTGTCGCCTTGCTCGACTCCTGCTTCCCTCCCCTCATCTTTAAA
305	PD-L1 responder	CCAAACTGGCAATCAACCCAGATAGTCTTCGACCCCGGCCCCGGAGGTCTCCCTCCACAG
306	PD-L1 Non-responder	GGCAGGCAGATCACCTGAGCTCAGGAGTTCGATCAGGTACAAACCAAACACAGAACATAA
307	PD-L1 Non-responder	GGCAGGCAGATCACCTGAGCTCAGGAGTTCGATTAAAAAGAACAAAATTGATTTCCTAAA
308	PD-L1 Non-responder	GGGTCTGAAGCACCGTGAGAGAAATGACTCGAATTGTCTTTCTTTCGCCCGATACATAAA
309	PD-L1 responder	AAGTCTTTTGTTTGGTTATTGTGCTGTATCGATCCAGCTTTTTGACTCTAAAATGAGCTT
310	PD-L1 responder	AAGTCTTTTGTTTGGTTATTGTGCTGTATCGAATCAAAGCTGTGTCACAAACTATGTAAC
311	PD-L1 responder	CTTTCAAACAAATGACCTTCACCACTGTTCGATCACGGCTCACTGCAGCCTTGGCCTCCT
312	PD-L1 responder	CACCGACCCGTCCGGGCCCGCTGCCACATCGAATAGCTTCTTTTGCTATGTCTCCAAGTT

Table 13.f4

	Probe Location					**4 kb Sequence Location**		
	Chr	**Start1**	**End1**	**Start2**	**End2**	**Chr**	**Start1**	**End1**
261	7	142755215	142755244	142766140	142766169	7	142751245	142755244
262	7	142755215	142755244	142818232	142818261	7	142751245	142755244
263	13	32509472	32509501	32582343	32582372	13	32505502	32509501
264	13	32545748	32545777	32582343	32582372	13	32541778	32545777
265	2	105741796	105741825	105844482	105844511	2	105737826	105741825
266	11	119677786	119677815	119700077	119700106	11	119673816	119677815
267	1	198201874	198201903	198253056	198253085	1	198197904	198201903
268	1	198201874	198201903	198346795	198346824	1	198197904	198201903
269	1	198279876	198279905	198346795	198346824	1	198279876	198283875
270	17	31156717	31156746	31224131	31224160	17	31152747	31156746
271	17	31339409	31339438	31382125	31382154	17	31335439	31339438
272	20	51362145	51362174	51482831	51482860	20	51358175	51362174
273	1	60869920	60869949	60989414	60989443	1	60869920	60873919
274	6	44253666	44253695	44312110	44312139	6	44253666	44257665
275	6	44270723	44270752	44312110	44312139	6	44270723	44274722
276	3	101806474	101806503	101822519	101822548	3	101806474	101810473
277	16	27195258	27195287	27245673	27245702	16	27191288	27195287
278	8	80968986	80969015	81095100	81095129	8	80968986	80972985
279	8	81018078	81018107	81053410	81053439	8	81014108	81018107
280	8	81018078	81018107	81077565	81077594	8	81014108	81018107
281	8	81018078	81018107	81095100	81095129	8	81014108	81018107
282	8	81053410	81053439	81095100	81095129	8	81053410	81057409
283	1	212523302	212523331	212588793	212588822	1	212523302	212527301
284	1	212572997	212573026	212645886	212645915	1	212572997	212576996
285	11	77430379	77430408	77519074	77519103	11	77430379	77434378
286	4	168697420	168697449	168870432	168870461	4	168693450	168697449
287	5	168579937	168579966	168614429	168614458	5	168579937	168583936
288	10	95194975	95195004	95282952	95282981	10	95194975	95198974
289	3	170117763	170117792	170195523	170195552	3	170113793	170117792
290	7	106908172	106908201	106944732	106944761	7	106904202	106908201
291	5	68213307	68213336	68277740	68277769	5	68209337	68213336
292	5	68215410	68215439	68277740	68277769	5	68215410	68219409
293	17	67337109	67337138	67493397	67493426	17	67333139	67337138
294	12	19116277	19116306	19175194	19175223	12	19116277	19120276
295	12	19116277	19116306	19247123	19247152	12	19116277	19120276
296	12	19116277	19116306	19322615	19322644	12	19116277	19120276
297	12	19116277	19116306	19330800	19330829	12	19116277	19120276

298	16	57264324	57264353	57315881	57315910	16	57264324	57268323
299	12	62616405	62616434	62635972	62636001	12	62612435	62616434
300	6	16559432	16559461	16745336	16745365	6	16559432	16563431
301	4	100984121	100984150	101215421	101215450	4	100984121	100988120
302	4	100996081	100996110	101215421	101215450	4	100992111	100996110
303	16	23926889	23926918	24184884	24184913	16	23922919	23926918
304	10	6432893	6432922	6464158	6464187	10	6432893	6436892
305	22	44666471	44666500	44701859	44701888	22	44662501	44666500
306	11	36302554	36302583	36446983	36447012	11	36298584	36302583
307	11	36302554	36302583	36488818	36488847	11	36298584	36302583
308	2	113175431	113175460	113215780	113215809	2	113175431	113179430
309	8	140725052	140725081	140771377	140771406	8	140721082	140725081
310	8	140725052	140725081	140877455	140877484	8	140721082	140725081
311	8	140725196	140725225	140883115	140883144	8	140725196	140729195
312	12	112418669	112418698	112478543	112478572	12	112418669	112422668

Table 13.f5

	4 kb Sequence Location		**Inner_primers**		
	Start2	**End2**	**PCR-Primer1_ID**	**PCR_Primer1**	**PCR-Primer2_ID**
261	142766140	142770139	OBD117.1.1417	AGGGTTGCCAGAAGAAACAGGGC	OBD117.1.1419
262	142814262	142818261	OBD117.1.1677	CCCCAGTGAGAAGGGTTGCCAGA	OBD117.1.1679
263	32578373	32582372	OBD117.1.1021	ACTGCCCTGTAACGTTGCTC	OBD117.1.1023
264	32578373	32582372	OBD117.1.885	TGTTGGGGATTTGTCTGGAT	OBD117.1.887
265	105840512	105844511	OBD117.1.751	ATCCTGGGTGGGATCTTG	OBD117.1.749
266	119700077	119704076	OBD117.1.057	GGATACCACACTGGGAGGCTTCC	OBD117.1.059
267	198249086	198253085	OBD117.1.1161	GGAGCCTCACCCTGTTGATAGTC	OBD117.1.1163
268	198346795	198350794	OBD117.1.1281	CGGAGCCTCACCCTGTTGATAGTC	OBD117.1.1283
269	198346795	198350794	OBD117.1.1665	GTGCTGGGCAAACTTATCCATTTCTT	OBD117.1.1667
270	31224131	31228130	OBD117.1.1657	CGGTTGTCCCAGCCCTAAGTAGATGA	OBD117.1.1659
271	31382125	31386124	OBD117.1.1809	CCACTGTTTTAGGATGGTCTGAC	OBD117.1.1811
272	51482831	51486830	OBD117.1.1341	AGCCTGGGTGACAGAGTGAGACT	OBD117.1.1343
273	60989414	60993413	OBD117.1.1269	ACCTATCCCATTCAGATTTTGCTTGC	OBD117.1.1271
274	44308140	44312139	OBD117.1.065	CACTTTGCCTCCACATCTGGTATGAG	OBD117.1.067
275	44308140	44312139	OBD117.1.1065	CCGGCTCAACTAGCACTTTG	OBD117.1.1067
276	101822519	101826518	OBD117.1.1249	CCAGGACTCTTTAGTGTCTGTTCCCC	OBD117.1.1251
277	27241703	27245702	OBD117.1.641	AAGCACTGGGACAAGCCTGGAGG	OBD117.1.643
278	81095100	81099099	OBD117.1.081	CCTATGTGCCACTACCCGCCCAT	OBD117.1.083
279	81053410	81057409	OBD117.1.145	AAAACCCAGCACTGAAATACTACAGC	OBD117.1.147
280	81077565	81081564	OBD117.1.129	AAAACCCAGCACTGAAATACTACAGC	OBD117.1.131
281	81095100	81099099	OBD117.1.105	GGACAGCCACTACTCAACCTTTTCCT	OBD117.1.107
282	81095100	81099099	OBD117.1.217	GCCTGATGTCTTCAAAAGGGCTGTTC	OBD117.1.219
283	212584823	212588822	OBD117.1.709	CCTGATTCCCACTCCCTGAAGGCAAT	OBD117.1.711
284	212641916	212645915	OBD117.1.705	GGGAAGAAGCCTGTTGTCTGGTAGG	OBD117.1.707
285	77515104	77519103	OBD117.1.297	CATAACCACACTGCTACCAACACACC	OBD117.1.299
286	168866462	168870461	OBD117.1.1545	AAGCAAGAGGCAAAGGGCATCCC	OBD117.1.1547
287	168614429	168618428	OBD117.1.669	CCGACCCTAACATTCAAGGTGTCTCT	OBD117.1.671
288	95282952	95286951	OBD117.1.1645	TGAGTGTTTTCAGGGTGTTGAGTCCT	OBD117.1.1647
289	170195523	170199522	OBD117.1.1277	CTGTAATGCCAGCACTTTGGGAGGTC	OBD117.1.1279
290	106940762	106944761	OBD117.1.1361	CATCCTGCTACTGGGAACTACCC	OBD117.1.1363
291	68273770	68277769	OBD117.1.069	TGACACCCCTGTATCACCCCTTTCGT	OBD117.1.071
292	68273770	68277769	OBD117.1.735	CTCTGGCTCTACACGTCCC	OBD117.1.733
293	67493397	67497396	OBD117.1.569	CCACCAACCCCAAATCGGGAGTT	OBD117.1.571
294	19175194	19179193	OBD117.1.1461	GAGTAGAGAAGAAGGATAGGTAATCT	OBD117.1.1463
295	19247123	19251122	OBD117.1.1525	CGGTAGGCTGAGGCAGGGAGAAT	OBD117.1.1527

296	19318645	19322644	OBD117.1.1381	CCCAGCAGCCATTCAGACAGTGG	OBD117.1.1383
297	19330800	19334799	OBD117.1.1137	TGGGTGACAAGAGCAAGACTCCGTC	OBD117.1.1139
298	57311911	57315910	OBD117.1.561	CCCCTAACTTCCTCTTCTCACCC	OBD117.1.563
299	62635972	62639971	OBD117.1.1853	AAGTAGTAAGCCTTCATTTCTTT	OBD117.1.1855
300	16745336	16749335	OBD117.1.1313	CACCTAACAGTGTGTCCTGGAAAACC	OBD117.1.1315
301	101215421	101219420	OBD117.1.1473	AAGTTTGCCCCTCACTGGTGCTAAT	OBD117.1.1475
302	101215421	101219420	OBD117.1.1157	AGGAATCGCATTGGGAACAGAGACTT	OBD117.1.1159
303	24180914	24184913	OBD117.1.1345	CTTTATCCAGTCATCCATTGATTGAT	OBD117.1.1347
304	6460188	6464187	OBD117.1.365	GCCTGATGAATCGGGATGGTTCCTTA	OBD117.1.367
305	44697889	44701888	OBD117.1.005	TTACACTCCTGGGCACTCTTCCC	OBD117.1.007
306	36443013	36447012	OBD117.1.1565	GGGCTCACACCTGTTATCCCAGC	OBD117.1.1567
307	36484848	36488847	OBD117.1.1217	GGCTCACACCTGTTATCCCAGCACTT	OBD117.1.1219
308	113215780	113219779	OBD117.1.673	CGCTCCCTCCTTTTACCCTGGAA	OBD117.1.675
309	140767407	140771406	OBD117.1.229	TAGGGATGGCATACCTGGAAGTAGC	OBD117.1.231
310	140877455	140881454	OBD117.1.233	GGGATGGCATACCTGGAAGTAGC	OBD117.1.235
311	140879145	140883144	OBD117.1.357	GCTTGGTTCCATTTAGCCACTTACCT	OBD117.1.359
312	112478543	112482542	OBD117.1.761	ACTTCCTGCTTCCCGTCAG	OBD117.1.763

Table 13.f6

	Inner_primers	
	PCR_Primer2	**GLMNET**
261	GCCGTGGCGGTGGACAGAGTTAT	0
262	CCATTGGGTGAAACTCCACAGGG	0
263	TCAAAGCAGCAGTCTAAATTCTCC	0
264	TGGATGATAATGCAAGCTACG	0.019910002
265	CCCATGTTAAGCCTTGCAGT	0.011140328
266	TGACCACAAGGGCAGATTCTCCC	0.002451894
267	CAGTGTGTAGGACAGTGCCTGGC	0
268	GGAGCCCAAAATGTCCAGGTGAC	0
269	TAAGGAGCCCAAAATGTCCAGGTGAC	0
270	CTTCTCTATCTTCCACAACCTCACCA	0
271	CAAAGCATAATCTGGACCTTCTA	0
272	GTCCGAACCCTGGGATGTGCCAT	0
273	GAGCATTGTCTGGGAATCAGGTGTTT	0
274	GGCTTGACACCCTTAGTTTACTGCCT	0.006729048
275	CCCTAGACTCTCACCTCCTCTC	0
276	CCCCTTCCAGTTCCAAAAGTAGTTAT	0
277	GCCAGCAAGAGCCAGAGACACAA	0.000955334
278	CAGATTGGACCTCACAGCCCCAT	0.0196745
279	TATGCCCAAGGTGTATCTCCCCT	0.012784814
280	GGTCAGTCTGTCCTTGTCTCTAACCA	0.000107394
281	AAATGCTGGGCTCCTCTTTTGTCCTC	0.011672595
282	AATGCTGGGCTCCTCTTTTGTCCTCT	0.006914365
283	TCTCGTCTTAGTTGAAATCCACCCAG	0.000126022
284	CACAAACACTGGAAGGGAGAAAATAG	-0.002734128
285	GGTTATTCGGACACTCATAGGACTGG	-0.020410863
286	ATAGCAGAACCACATCCAACTCTA	0
287	CCACTTCATTTCATCCCTACTGCCAC	0.022244309
288	TTAGGCTTTGGGTTATGGGTGGTAGC	0
289	GTGGTGAAAGTAGGCATCCTTGTCTT	0
290	GCACCACTCCCTCTTCCCACAGT	0
291	GGATACTACCTTCTCCCACTCATTTA	-0.007209703
292	CCTAGTGGGGCAAGTTTGG	0.000117929
293	TCCAAGGTCAAAGCCACCCTCCC	0.000114434
294	TGCTATTTTGTATGTGTTGGGTGTAT	0
295	CTGTTGTTTGCCTCCCTTTCCAGG	0

296	GGTGACAAGAGCAAGACTCCGTC	0
297	GAGGGAGAGGCAATAGATGTAGTGTA	0
298	CGGGCACTGTTGGGCACTGAAGA	0.010030034
299	GCCAAGTAGCACCAAAGCCAATA	0
300	CCCTTTGATTCCACCATTCCAGTCCA	0
301	GAACTTTCTTTCCCCTTCATTTAGT	0
302	GTTAGAAGGGACATTAGGATTAGAAT	0
303	TACAGAGGAGTAAAGACAGTTTT	0
304	GCTGAGCCCTGAAAGATAAGGCAGAA	0.007672168
305	AGCAAATCCTCCAGGCAGCCAGG	0.016924425
306	GGCAGATGGACTTCAGGAGGGAT	0
307	GTTAGGCTACAGCAACATACTCAAGC	0
308	GGGTCCCCTTTTCGGGCTCAGAA	0.006586768
309	GCATTACGGATTCATTTGCTCACTCA	-0.017032217
310	GGGACTCTGCCATCTGTATGCTGC	0.000119638
311	AATCTGGCTGCCTATGGTTGCTCTCC	-0.01499141
312	AGAGCGGATGACATATTGCAG	0.00011938

Table 13.f7

	Probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig
313	ORF541_7_77589308_77593066_77652906_77658625_RF	ORF541	23	4
314	ORF541_7_77628734_77632614_77645983_77651804_FF	ORF541	23	4
315	ORF544_1_198591683_198595771_198768850_198775826_FF	PTPRC	214	10
316	ORF544_1_198659753_198666156_198697386_198704777_FR	ORF544	187	30
317	ORF544_1_198659753_198666156_198735456_198749256_FF	ORF544	187	30
318	ORF544_1_198735456_198749256_198779053_198786841_RF	ORF544	187	30
319	ORF547_11_82936602_82938148_83048972_83059269_RR	ORF547	99	7
320	ORF547_11_82938763_82948488_82974616_82981008_FR	ORF547	99	7
321	ORF55_11_64267793_64269811_64288581_64290103_FR	BAD	70	8
322	ORF55_11_64267793_64269811_64292591_64296924_FF	BAD	70	8
323	ORF552_1_174835362_174838725_175007460_175017921_RF	ORF552	93	6
324	ORF553_7_6325447_6327369_6392091_6396545_RR	RAC1	64	2
325	ORF554_20_20425025_20439432_20458256_20459854_RF	ORF554	117	8
326	ORF556_13_97440604_97443754_97479189_97487608_FF	ORF556	66	5
327	ORF558_2_33390711_33398991_33442363_33444238_FR	ORF558	34	5
328	ORF56_14_75477136_75478350_75491596_75496634_FR	ORF56	18	2
329	ORF56_14_75491596_75496634_75573735_75577816_RF	ORF56	18	2
330	ORF560_21_14176916_14181369_14267912_14269012_RF	ORF560	37	3
331	ORF560_21_14210379_14215717_14236469_14248873_RR	ORF560	37	3
332	ORF564_21_34500925_34506011_34574861_34579728_FR	ORF564	67	7
333	ORF567_11_65634932_65641044_65653258_65654626_RF	RELA	56	2
334	ORF568_12_18259444_18261081_18350532_18364514_FF	ORF568	34	5
335	ORF569_3_16448043_16456162_16496760_16499694_FF	ORF569	139	10
336	ORF57_19_48914276_48916713_48932242_48935310_FF	ORF57	30	6
337	ORF57_19_48914276_48916713_48968306_48971572_FF	ORF57	30	6
338	ORF576_6_3027907_3030237_3146778_3149848_FR	ORF576	25	8
339	ORF576_6_3045545_3051391_3146778_3149848_FR	ORF576	25	8
340	ORF576_6_3114019_3116008_3146778_3149848_RR	ORF576	25	8
341	ORF586_6_166614982_166618999_166826698_166835940_RR	ORF586	176	12
342	ORF586_6_166614982_166618999_166877620_166884513_RR	ORF586	176	12
343	ORF589_21_35511164_35517830_35766255_35775694_FF	ORF589	197	5
344	ORF59_20_50749321_50753502_50888426_50893318_FR	ORF59	17	4
345	ORF596_1_243286011_243289794_243392615_243398557_RF	ORF596	151	9
346	ORF596_1_243386248_243390518_243516824_243527512_RF	ORF596	151	9

347	ORF603_18_44885635_44895879_44997556_45002564_FR	ORF603	156	11
348	ORF603_18_44885635_44895879_45014599_45017752_FR	ORF603	156	11
349	ORF605_1_66506442_66514114_66751280_66753550_RF	ORF605	163	8
350	ORF605_1_66578981_66592963_66761002_66762820_RF	ORF605	163	7
351	ORF611_20_1857555_1861228_1955166_1964657_FR	ORF611	59	7
352	ORF611_20_1891489_1897350_1924633_1930962_RR	SIRPA	56	4
353	ORF613_1_160707882_160714935_160743813_160744937_RF	ORF613	27	1
354	ORF618_6_3272293_3273348_3492046_3503752_FF	ORF618	158	8
355	ORF624_2_27626184_27635183_27719544_27726504_RF	ORF624	24	2
356	ORF626_5_150149497_150151091_150181302_150194775_FR	ORF626	34	5
357	ORF626_5_150162904_150166548_150181302_150194775_FR	ORF626	34	5
358	ORF626_5_150162904_150166548_150194890_150198993_FR	ORF626	34	0
359	ORF626_5_150181302_150194775_150230115_150237336_RF	ORF626	34	5
360	ORF626_5_150181302_150194775_150237336_150238718_RF	ORF626	34	5
361	ORF630_17_35287155_35289074_35307929_35312497_FF	ORF630	18	3
362	ORF631_15_67098632_67101498_67199584_67204251_RR	SMAD3	34	2
363	ORF642_16_29613904_29616227_29630194_29632081_RF	SPN	56	4
364	ORF642_16_29613904_29616227_29686079_29687229_RF	SPN	56	4

Table 13.g1

	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr	t
313	0.053424912	0.606428812	17.39	0.356643448	0.356643448	3.960789133
314	0.053424912	0.606428812	17.39	0.285214138	0.285214138	4.609256093
315	0.978491243	0.99999793	4.67	-0.14040288	-0.14040288	-5.186348648
316	2.30E-06	0.000217011	16.04	0.283822723	0.283822723	11.36017484
317	2.30E-06	0.000217011	16.04	0.28622671	0.28622671	10.23998629
318	2.30E-06	0.000217011	16.04	0.312760316	0.312760316	7.112432884
319	0.433763829	1	7.07	0.377286081	0.377286081	4.904828931
320	0.433763829	1	7.07	0.319635014	0.319635014	4.836776666
321	0.18964104	0.954389149	11.43	-0.146341453	-0.146341453	-5.009008006
322	0.18964104	0.954389149	11.43	-0.155897691	-0.155897691	-6.419907226
323	0.587989675	1	6.45	0.162077594	0.162077594	6.758085183
324	0.967461559	0.99999793	3.12	-0.432758998	-0.432758998	-5.571884831
325	0.459116235	1	6.84	0.446838664	0.446838664	12.24134889
326	0.403635377	1	7.58	0.423159851	0.423159851	10.02547665
327	0.06020741	0.646636236	14.71	0.297744446	0.297744446	8.756884365
328	0.337741302	1	11.11	0.196386472	0.196386472	6.01640946
329	0.337741302	1	11.11	0.168913942	0.168913942	6.493464138
330	0.415513464	1	8.11	0.309983092	0.309983092	11.42911374
331	0.415513464	1	8.11	0.355272886	0.355272886	9.89272102
332	0.12838934	0.904598768	10.45	0.289530526	0.289530526	10.39257872
333	0.94351322	0.99999793	3.57	-0.335793252	-0.335793252	-14.59846809
334	0.06020741	0.646636236	14.71	0.301770409	0.301770409	9.8018573
335	0.380387396	1	7.19	0.306584347	0.306584347	2.955558359
336	0.01000538	0.181608098	20	0.319528065	0.319528065	12.82607629
337	0.01000538	0.181608098	20	0.294074256	0.294074256	15.40919841
338	0.000101223	0.003977202	32	0.342315512	0.342315512	4.823515277
339	0.000101223	0.003977202	32	0.381150282	0.381150282	7.660425289
340	0.000101223	0.003977202	32	0.471818762	0.471818762	6.947243306
341	0.432643309	1	6.82	0.334089996	0.334089996	5.008617015
342	0.432643309	1	6.82	0.378448027	0.378448027	6.858042974
343	0.995427013	1	2.54	0.309719719	0.309719719	3.570772465
344	0.019351438	0.304140094	23.53	0.310572354	0.310572354	7.361954056
345	0.617155598	1	5.96	0.388082401	0.388082401	11.1208405
346	0.617155598	1	5.96	0.295082217	0.295082217	6.643633956

347	0.395653632	1	7.05	0.2983925	0.2983925	6.884745917
348	0.395653632	1	7.05	0.286095812	0.286095812	5.99074538
349	0.854051613	1	4.91	0.249385621	0.249385621	2.70486202
350	0.894561341	1	4.29	0.302395192	0.302395192	6.269378105
351	0.076789008	0.731434696	11.86	0.347062258	0.347062258	6.676297968
352	0.659150649	0.99999793	7.14	-0.183746617	-0.183746617	-7.539838325
353	0.858892218	1	3.7	-0.306060504	-0.306060504	-4.552793946
354	0.785606032	1	5.06	0.307291844	0.307291844	7.043291289
355	0.479347944	1	8.33	0.148041193	0.148041193	4.147781826
356	0.085664563	0.667617217	14.71	-0.191241299	-0.191241299	-9.324329472
357	0.085664563	0.667617217	14.71	-0.213609391	-0.213609391	-10.1665293
358	1	1	0	-0.157170259	-0.157170259	-6.502829914
359	0.085664563	0.667617217	14.71	-0.193972875	-0.193972875	-11.86119945
360	0.085664563	0.667617217	14.71	-0.152338864	-0.152338864	-9.193910673
361	0.100654026	0.825363011	16.67	0.309628617	0.309628617	5.989078991
362	0.764125503	0.99999793	5.88	-0.180175335	-0.180175335	-8.471609217
363	0.659150649	0.99999793	7.14	-0.175972335	-0.175972335	-7.054965999
364	0.659150649	0.99999793	7.14	-0.16436617	-0.16436617	-7.773176867

Table 13.g2

	P.Value	adj.P.Val	B	FC	FC_1	LS
313	0.002558481	0.011825242	-1.934224365	1.280443369	1.280443369	1
314	0.000906562	0.005597155	-0.862545562	1.218591124	1.218591124	1
315	0.000378279	0.003044422	0.045441754	0.907265761	-1.102212872	-1
316	0.000000392	0.0000522	7.121810671	1.217416415	1.217416415	1
317	0.00000105	0.0000827	6.131358316	1.219446707	1.219446707	1
318	0.0000286	0.000550434	2.734802175	1.24208191	1.24208191	1
319	0.000575972	0.004077688	-0.391728534	1.298896144	1.298896144	1
320	0.000638673	0.004378379	-0.499072732	1.248014775	1.248014775	1
321	0.000492332	0.003660595	-0.228647352	0.903538855	-1.106759266	-1
322	0.0000684	0.000962212	1.827393464	0.8975737	-1.11411464	-1
323	0.0000443	0.000727991	2.278534173	1.118897278	1.118897278	1
324	0.000216637	0.00207522	0.625787741	0.740843647	-1.34981248	-1
325	0.000000191	0.0000378	7.834376391	1.363050169	1.363050169	1
326	0.00000128	0.0000923	5.92980967	1.340861152	1.340861152	1
327	0.00000448	0.000179825	4.650235925	1.229221108	1.229221108	1
328	0.00011691	0.00138082	1.268397808	1.145824803	1.145824803	1
329	0.0000621	0.000902589	1.926850909	1.124211861	1.124211861	1
330	0.00000037	0.000051	7.179564842	1.239693171	1.239693171	1
331	0.00000145	0.0000986	5.803035818	1.279227525	1.279227525	1
332	0.000000912	0.0000775	6.272306869	1.222242477	1.222242477	1
333	0.0000000344	0.0000161	9.499491123	0.792348352	-1.262071156	-1
334	0.00000158	0.000104705	5.715349753	1.232656145	1.232656145	1
335	0.0140425	0.041914834	-3.663900054	1.236776102	1.236776102	1
336	0.000000122	0.0000302	8.278231076	1.247922262	1.247922262	1
337	0.0000000202	0.0000131	10.00304815	1.226097966	1.226097966	1
338	0.000651715	0.004434959	-0.520065389	1.267789753	1.267789753	1
339	0.0000149	0.000370113	3.408694648	1.302379848	1.302379848	1
340	0.000035	0.000623193	2.524156698	1.386856735	1.386856735	1
341	0.000492621	0.003661363	-0.229256562	1.260582024	1.260582024	1
342	0.0000391	0.000668286	2.408921964	1.299942695	1.299942695	1
343	0.004898278	0.019080854	-2.599525191	1.239466878	1.239466878	1
344	0.0000212	0.000459585	3.046319093	1.240199621	1.240199621	1
345	0.00000048	0.0000579	6.918534793	1.308652814	1.308652814	1
346	0.0000512	0.000797045	2.127594248	1.226954898	1.226954898	1

347	0.0000378	0.000653933	2.443528915	1.229773394	1.229773394	1
348	0.000121059	0.001415354	1.232066621	1.21933607	1.21933607	1
349	0.021686156	0.057998117	-4.095656378	1.188700793	1.188700793	1
350	0.0000833	0.001098005	1.621523674	1.233190082	1.233190082	1
351	0.0000491	0.000776177	2.170852318	1.271967896	1.271967896	1
352	0.0000172	0.000403646	3.263611548	0.880413629	-1.135829759	-1
353	0.000990011	0.005969135	-0.953815343	0.808847426	-1.236327109	-1
354	0.0000311	0.000577254	2.64706744	1.237382765	1.237382765	1
355	0.001886069	0.00947947	-1.620209255	1.108063986	1.108063986	1
356	0.00000251	0.000133818	5.24188899	0.875851812	-1.141745655	-1
357	0.00000112	0.0000854	6.062792551	0.862377002	-1.159585655	-1
358	0.0000614	0.000895467	1.939461051	0.89678232	-1.115097808	-1
359	0.000000259	0.0000428	7.533668036	0.874195057	-1.143909466	-1
360	0.00000286	0.000142904	5.10877376	0.89979056	-1.111369739	-1
361	0.000121333	0.001416487	1.229704368	1.239388612	1.239388612	1
362	0.00000605	0.000215806	4.34015114	0.882595726	-1.133021576	-1
363	0.0000306	0.000572312	2.661925201	0.885170738	-1.129725551	-1
364	0.0000131	0.000338569	3.542755797	0.892320463	-1.120673616	-1

Table 13.g3

		Probe sequence
	Loop detected	**60 mer**
313	PD-L1 Non-responder	CTCATTTTTCCAAAAACGTGAAGAAATCTCGAAGTAAAATTTATTTCAAAGCTATTCTGG
314	PD-L1 Non-responder	TTTAAATTATATTTTTTACTTGCTAAGATCGAGTGACTTTTCTAAATTTTTTGACCCATA
315	PD-L1 responder	TGTTTTTTATTGTTTGATGTCCAATGTATCGAGTCACATGATCAAGCGCTCATTTCTGTT
316	PD-L1 Non-responder	AGAGGCTGAGGTGAAAAGATTGTTTGAGTCGACAACCCAATTTTGTTATTTGAGTTTCTT
317	PD-L1 Non-responder	AGAGGCTGAGGTGAAAAGATTGTTTGAGTCGATAAACAAATTATACAACAAAAGTCTAAG
318	PD-L1 Non-responder	TTTAGTCAAATAATTACAAAGTATAAAATCGAAAGAATTATACTGTATTAATTAATTATC
319	PD-L1 Non-responder	AAAAAGGAAAAATAAAGTATATTTAACATCGAAAAAGAACCACATGGTTAAAAAGAAACT
320	PD-L1 Non-responder	TTTTTTCAATCTTTCTATATCTTTGTCTTCGAGTTCATAAAACTCAGTGATTAACCTGTT
321	PD-L1 responder	GCACTACCCCGGCCTGCCGGAGCCCCAGTCGATGATGGCTTCCTCCCCCAGAGCACCAGC
322	PD-L1 responder	GCACTACCCCGGCCTGCCGGAGCCCCAGTCGAGTTGGTTTCTGGGTCCGCACCCCCTCCC
323	PD-L1 Non-responder	CAGATGGGTGGATCACAAGATCAGGAGTTCGAACAAGTCAGGATGTAATGATAATGAAAA
324	PD-L1 responder	GGATGTATATATATATACTATTTTTATATCGAGCGCTTAATTAGTGCATGTTACCTATGG
325	PD-L1 Non-responder	AGCAGCAGCTAGAAATAATCTTTTCCCTTCGACCATTCTATTTTGAAGGCAAAAGCGACT
326	PD-L1 Non-responder	ATTATGAATACTGTATGTATTATAATTCTCGATCATATTTTCTTTTGCATAGGATTTTTA
327	PD-L1 Non-responder	TTTTTAAAAATCTCAAATGAAAAAGTCTTCGAAAAAAAATTTCTGGTTGGTGGGATAATG
328	PD-L1 Non-responder	GTCAGAGACTCAGCAACGCAAGGTTCTCTCGATGGATGATGTCTGGGATAATGACTGAGG
329	PD-L1 Non-responder	CGCCAAGGACAGAGGTCAGTGCAACGAGTCGATGGATGATGTCTGGGATAATGACTGAGG
330	PD-L1 Non-responder	AAGGTGGGTGGATCATGATGTCAAAAGATCGAAATGTTTGAGAATATTTTTAAGGCTCAG

331	PD-L1 Non-responder	TGAAGAAAATTCTTACTTGGATAAATTATCGAATTTAGAAGAATTAGTGGTATTTTGAAA
332	PD-L1 Non-responder	TAAAATAGAACATTATTTTGAAATTACTTCGAAGAACATTTTTATAGCTGTATTAGCATA
333	PD-L1 responder	GTTCAGCAGCTGCTGAAACTCGGAGTTGTCGACACCCCTCTCTCCCCTCCCTGTTTTTCC
334	PD-L1 Non-responder	TAAATTCTAATTAAATAAAGAAAATACCTCGACTAAATAAAATTAAAAAAAAAATCTTTG
335	PD-L1 Non-responder	AATCCAAGAACAGCTAATTCTTAAGACCTCGAGCAGACTTGGTATATAAGTTGCTTATGG
336	PD-L1 Non-responder	AAGGCAGGCAGATCAGGAGCTCAAGAGATCGAACGCTAAGTGTAGTTTAACACCTACTAG
337	PD-L1 Non-responder	AAGGCAGGCAGATCAGGAGCTCAAGAGATCGAAAGAAAAAAAAAAAAGCATAAAAATCCA
338	PD-L1 Non-responder	AAACTTGGTATGTGTCTAATAAACAGCTTCGAGTGCTGGTTTGGGTCGGAGTGCTGGTTC
339	PD-L1 Non-responder	TGATCACTCCAAACACCCAAAGGTGACTTCGAGTGCTGGTTTGGGTCGGAGTGCTGGTTC
340	PD-L1 Non-responder	AATATAAATTCAATTCATTAAAAAATAATCGAGTGCTGGTTTGGGTCGGAGTGCTGGTTC
341	PD-L1 Non-responder	TGGGTGTGGAAGGCTGGATAATGTCTCCTCGATTTTGCCATTATACTCTCTGTTTACATT
342	PD-L1 Non-responder	TGGGTGTGGAAGGCTGGATAATGTCTCCTCGATCAACCTACATTGGTTTGGTCTGGAAAG
343	PD-L1 Non-responder	GAATATGTGGGAGTGGGTATAAGAAAGATCGAGGTCACATGAAAACCCTCTGTTTAATCT
344	PD-L1 Non-responder	TATCTTAAGTAAATTTATGATAATGTTCTCGAGGACTCAGTACTAGTAGTCTGAGGTCTA
345	PD-L1 Non-responder	TCTTATTAATCTAAAATTTTATATAAAATCGATTCCTTGGAGAAAAGGAAATTGTCAGAA
346	PD-L1 Non-responder	TGTTTTATAATCATTATAATTTTTTCTTTCGAAGCAGGTTTTGAACCCCAGTAAGTTGCC
347	PD-L1 Non-responder	TTTTTGCATTATGAGCTATTTATTAACATCGAGGTTTTTAGACTAATGATTTGATCTCCA
348	PD-L1 Non-responder	TTTTTGCATTATGAGCTATTTATTAACATCGAGGGAACTCAATGTCTGATTCTTGACAGG
349	PD-L1 Non-responder	TGCTCTTTACAAACTATGTAAATGTTGCTCGAAGAGGCTGATTTGAGTAATAATAAACTC
350	PD-L1 Non-responder	TATAGTTAGCAATAATTTATTATATATTTCGAGAGAATTAGGGGGTATATCTACAAGTCA
351	PD-L1 Non-responder	TAAAGTACTGTGTCCCACATATAAGTACTCGAGAAAAGATGCAATAGTGTTGTATTCAGG
352	PD-L1 responder	GCGCCCTATTTCCACCTTGTGCCTTCTGTCGAGACATCTAAGAAGGTCCAGCCAGATGTT
353	PD-L1 responder	CACTCCTAAAGATGAACAAAGAGAGCAGTCGAATAACTATGCAGTAAGCAGTTACTATGT
354	PD-L1 Non-responder	CAGGAAGTAGCCTTTCTGGTTGTGCAGCTCGACAACTTATTTTTTAAAATCATCAAAGAA
355	PD-L1 Non-responder	TTCTGGGCAGACAAAACAATAAGTCTTCTCGATGGCACTTAAAAAAAAAGTTGTCCAAAT
356	PD-L1 responder	GCAGGTTAAAGTTTTCCATTAGTGGTCATCGATCACCCAGGCTAGAATGCAGTGGTGTAA
357	PD-L1 responder	GCAAGCGATTCCCACTCGCAGCGCGGCCTCGATCACCCAGGCTAGAATGCAGTGGTGTAA
358	PD-L1 responder	GCAAGCGATTCCCACTCGCAGCGCGGCCTCGAGCGTACACCAATGGAGGAGGTATGGGCC
359	PD-L1 responder	ATATCTAAACTGGTACTGCTGAGTTCCCTCGATCACCCAGGCTAGAATGCAGTGGTGTAA
360	PD-L1 responder	CCCCTCCCTACCTTTGGTGTCTTCATCCTCGATCACCCAGGCTAGAATGCAGTGGTGTAA
361	PD-L1 Non-responder	ATTGTTTAAGCCAGCCAGCCTATGGTATTCGACGCAAGGAAACTACTAAAGCAATCCAGA
362	PD-L1 responder	GTGGCAGGAGAAAAACGCGGCCCCACCCTCGAAAATACTAGAATTATGCCGCACAGTCAG
363	PD-L1 responder	AGGCGACACTCTTGTCCCCGCCATCTTTTCGAAGGCCCCCGTCCTCCTGCGCCATGGAGA
364	PD-L1 responder	CATCATCACAGTCTACGGCTGTTTCCTCTCGAAGGCCCCCGTCCTCCTGCGCCATGGAGA

Table 13.g4

	Probe Location					4 kb Sequence Location		
	Chr	**Start1**	**End1**	**Start2**	**End2**	**Chr**	**Start1**	**End1**
313	7	77589308	77589337	77658596	77658625	7	77589308	77593307
314	7	77632585	77632614	77651775	77651804	7	77628615	77632614
315	1	198595742	198595771	198775797	198775826	1	198591772	198595771
316	1	198666127	198666156	198697386	198697415	1	198662157	198666156
317	1	198666127	198666156	198749227	198749256	1	198662157	198666156
318	1	198735456	198735485	198786812	198786841	1	198735456	198739455
319	11	82936602	82936631	83048972	83049001	11	82936602	82940601
320	11	82948459	82948488	82974616	82974645	11	82944489	82948488
321	11	64269782	64269811	64288581	64288610	11	64265812	64269811
322	11	64269782	64269811	64296895	64296924	11	64265812	64269811
323	1	174835362	174835391	175017892	175017921	1	174835362	174839361
324	7	6325447	6325476	6392091	6392120	7	6325447	6329446
325	20	20425025	20425054	20459825	20459854	20	20425025	20429024
326	13	97443725	97443754	97487579	97487608	13	97439755	97443754
327	2	33398962	33398991	33442363	33442392	2	33394992	33398991
328	14	75478321	75478350	75491596	75491625	14	75474351	75478350
329	14	75491596	75491625	75577787	75577816	14	75491596	75495595
330	21	14176916	14176945	14268983	14269012	21	14176916	14180915
331	21	14210379	14210408	14236469	14236498	21	14210379	14214378
332	21	34505982	34506011	34574861	34574890	21	34502012	34506011
333	11	65634932	65634961	65654597	65654626	11	65634932	65638931
334	12	18261052	18261081	18364485	18364514	12	18257082	18261081
335	3	16456133	16456162	16499665	16499694	3	16452163	16456162
336	19	48916684	48916713	48935281	48935310	19	48912714	48916713
337	19	48916684	48916713	48971543	48971572	19	48912714	48916713
338	6	3030208	3030237	3146778	3146807	6	3026238	3030237
339	6	3051362	3051391	3146778	3146807	6	3047392	3051391
340	6	3114019	3114048	3146778	3146807	6	3114019	3118018
341	6	166614982	166615011	166826698	166826727	6	166614982	166618981
342	6	166614982	166615011	166877620	166877649	6	166614982	166618981
343	21	35517801	35517830	35775665	35775694	21	35513831	35517830
344	20	50753473	50753502	50888426	50888455	20	50749503	50753502
345	1	243286011	243286040	243398528	243398557	1	243286011	243290010
346	1	243386248	243386277	243527483	243527512	1	243386248	243390247
347	18	44895850	44895879	44997556	44997585	18	44891880	44895879
348	18	44895850	44895879	45014599	45014628	18	44891880	44895879
349	1	66506442	66506471	66753521	66753550	1	66506442	66510441
350	1	66578981	66579010	66762791	66762820	1	66578981	66582980
351	20	1861199	1861228	1955166	1955195	20	1857229	1861228
352	20	1891489	1891518	1924633	1924662	20	1891489	1895488
353	1	160707882	160707911	160744908	160744937	1	160707882	160711881
354	6	3273319	3273348	3503723	3503752	6	3269349	3273348
355	2	27626184	27626213	27726475	27726504	2	27626184	27630183
356	5	150151062	150151091	150181302	150181331	5	150147092	150151091
357	5	150166519	150166548	150181302	150181331	5	150162549	150166548
358	5	150166519	150166548	150194890	150194919	5	150162549	150166548
359	5	150181302	150181331	150237307	150237336	5	150181302	150185301
360	5	150181302	150181331	150238689	150238718	5	150181302	150185301
361	17	35289045	35289074	35312468	35312497	17	35285075	35289074
362	15	67098632	67098661	67199584	67199613	15	67098632	67102631
363	16	29613904	29613933	29632052	29632081	16	29613904	29617903
364	16	29613904	29613933	29687200	29687229	16	29613904	29617903

Table 13.g5

	4 kb Sequence Location		Inner_primers		
	Start2	End2	PCR-Primer1_ID	PCR_Primer1	PCR-Primer2_ID
313	77654626	77658625	OBD117.1.1757	AAGGAAAACAATCTAAAATGTAA	OBD117.1.1759
314	77647805	77651804	OBD117.1.1721	CCTCCCCTACCTGAAAGAACTCC	OBD117.1.1723
315	198771827	198775826	OBD117.1.189	CTTCCCTGTTCTGAGGTCTGGATTAT	OBD117.1.191
316	198697386	198701385	OBD117.1.1237	GGAGAATCACTTGAGCCTAAGAGTTC	OBD117.1.1239
317	198745257	198749256	OBD117.1.1801	GAAGAGATAACTAATGAGAGGTA	OBD117.1.1803
318	198782842	198786841	OBD117.1.1173	GCCAGTCAGTCAATCATTTAGTCAGC	OBD117.1.1175
319	83048972	83052971	OBD117.1.1541	ACTCAAGCAAGCCTCCTGCCTCG	OBD117.1.1543
320	82974616	82978615	OBD117.1.1737	ACCACCACTGACTCTTTACTCTT	OBD117.1.1739
321	64288581	64292580	OBD117.1.341	AGTTTCCCTCGTAAGACAGCGGC	OBD117.1.343
322	64292925	64296924	OBD117.1.245	TGTCGCTGGATGTCAGGCAGAGC	OBD117.1.247
323	175013922	175017921	OBD117.1.689	TTGGGATGCGGCTGGACACAGTG	OBD117.1.691
324	6392091	6396090	OBD117.1.729	GTTCCAGGTGGCCTGTTGT	OBD117.1.731
325	20455855	20459854	OBD117.1.1761	GAAGAGATAACTAATGAGAGGTA	OBD117.1.1763
326	97483609	97487608	OBD117.1.1869	AGCCACTGCCCCTGGTCCTAAAT	OBD117.1.1871
327	33442363	33446362	OBD117.1.1837	GTTGTATTATTATGTTGTTTTGT	OBD117.1.1839
328	75491596	75495595	OBD117.1.617	AAGAAGAGGAGGCAGCAGCCCCT	OBD117.1.619
329	75573817	75577816	OBD117.1.685	CCTTGGTCTACAGTGGCACCTCA	OBD117.1.687
330	14265013	14269012	OBD117.1.1357	CTGTAATCCCAGCACTTTGGTAGGC	OBD117.1.1359
331	14236469	14240468	OBD117.1.1577	GAGAATAAATAGAAATACTCAAGAGA	OBD117.1.1579
332	34574861	34578860	OBD117.1.1709	CCACCTCCCAGGACAAGCAAAGG	OBD117.1.1711
333	65650627	65654626	OBD117.1.017	GCTTTTGGAGGGCTTCAATCCCC	OBD117.1.019
334	18360515	18364514	OBD117.1.1185	GTCTCAGAGTCTCCACACATTGTTCA	OBD117.1.1187
335	16495695	16499694	OBD117.1.1613	CAGCAAATGAAAATCAAGTTCTCTGC	OBD117.1.1615
336	48931311	48935310	OBD117.1.1653	GTAGTCCCAGCACTTTCGGAGGC	OBD117.1.1655
337	48967573	48971572	OBD117.1.1681	GTAGTCCCAGCACTTTCGGAGGC	OBD117.1.1683
338	3146778	3150777	OBD117.1.1813	TTTTGTTGTAGTCACGGTTAGTA	OBD117.1.1815
339	3146778	3150777	OBD117.1.1765	GGCACTGTCACTCCCCAAGAGGA	OBD117.1.1767
340	3146778	3150777	OBD117.1.1825	TTTTGTTGTAGTCACGGTTAGTA	OBD117.1.1827
341	166826698	166830697	OBD117.1.1153	CAGGTGCTCAGGTGTAGACCCCT	OBD117.1.1155
342	166877620	166881619	OBD117.1.1585	GTGTAGACCCCTGGTGTTCTTGG	OBD117.1.1587
343	35771695	35775694	OBD117.1.1349	AAAGTGCTGGGATTACAGGTGTGAG	OBD117.1.1351
344	50888426	50892425	OBD117.1.1609	ACTAAATGTCAAGCCTAACTGTGAAT	OBD117.1.1611
345	243394558	243398557	OBD117.1.1109	GAAGATGTTGATTTACTCCTGTGCTG	OBD117.1.1111
346	243523513	243527512	OBD117.1.1789	ATCTTTTCTAAGTTGTGCTTTAT	OBD117.1.1791
347	44997556	45001555	OBD117.1.1197	TATCTTTTCTTCCCACTGGACAGGTG	OBD117.1.1199
348	45014599	45018598	OBD117.1.1705	GGGAAGGTGGCAATGGTGTTAGGATG	OBD117.1.1707
349	66749551	66753550	OBD117.1.601	GTTCTGGGAAGTCCATTGCTACTACC	OBD117.1.603
350	66758821	66762820	OBD117.1.889	ATGGGGTGAAAAGAAGTTGG	OBD117.1.891
351	1955166	1959165	OBD117.1.1441	CAGCCAAGTCCTGTTCTCACGGG	OBD117.1.1443
352	1924633	1928632	OBD117.1.161	AGAGGGCACAATCTGTCAGCAAATCC	OBD117.1.163
353	160740938	160744937	OBD117.1.557	TTCCTGGCACTATTTGGACTTGACAC	OBD117.1.559
354	3499753	3503752	OBD117.1.1181	TTCTCAGGCAGGTTCTGGTCCCT	OBD117.1.1183
355	27722505	27726504	OBD117.1.589	CACTCATTCCTGTGAACACTGGAGCA	OBD117.1.591
356	150181302	150185301	OBD117.1.961	AACTGAGCACGTTAAGGGGC	OBD117.1.963
357	150181302	150185301	OBD117.1.449	TCTGCGTTGCCCCTCACCTCAAG	OBD117.1.451
358	150194890	150198889	OBD117.1.445	TTGAAGTCTGCGTTGCCCCTCAC	OBD117.1.447
359	150233337	150237336	OBD117.1.1033	ATGTGGTGCGTCAAAACTGC	OBD117.1.1035
360	150234719	150238718	OBD117.1.969	CCAGAAGTCTAAGGGGTCCC	OBD117.1.971
361	35308498	35312497	OBD117.1.1497	GACTTCTTGCCTCCCTAACTGTGAGA	OBD117.1.1499
362	67199584	67203583	OBD117.1.061	ACCAAAGCAAGCCTCCCCAAGTG	OBD117.1.063
363	29628082	29632081	OBD117.1.945	TGGAGCTCTCCTCGTTGTTT	OBD117.1.947
364	29683230	29687229	OBD117.1.985	ATGCTGTTGCAGGACTGTGC	OBD117.1.987

Table 13.g6

	Inner_primers	
	PCR_Primer2	GLMNET
313	TGTAAGTTTGATTTGTATGCCAT	0
314	CCACCAGAAGAGGGCAGCAAAGC	0
315	TTGGCAGGAACTGGTGCTGGAATAGG	-0.020382337
316	GTATTCTAAGGAGCATAGTGCCCCTC	0
317	CATTTACTTGTTATCTATCGTAT	0
318	GTAGGAACTCACTGACAATGAAGACA	0
319	GAGCCACCACACCCAGCATCTTT	0
320	TATCTTATTGTAGAGGCAGTCTG	0
321	CTGCCCATTGAGGATGTGGCTGG	0.007677493
322	TCTGCTGTAAGGGACTGCCTCCT	0.017957539
323	GCCACAGCGTCTCTCTCCGAATA	0
324	AGCTGGTAACGCTCAAAACAC	-0.01057369
325	CATTTACTTGTTATCTATCGTAT	0
326	AGTTGGCTTGTTTCACTAAAATA	0
327	GTAGAAAATCAAAATCACCATTA	0
328	AATCGCAACCACTTCCTCTGCCC	0
329	ATCGCAACCACTTCCTCTGCCCC	-0.005472121
330	ATAGAACATTACACCTGAGAACTGC	0
331	ATAGTCTTCTCACTCTGGATGTTTCA	0
332	TCTTGATTCCCATCTGCCCGTGC	0
333	GAAGGGCTCCAGGCTAAGTGGGA	0.005732814
334	CTTCCCTTGCTTGGTCTAACCTGTAA	0
335	TGTTTCACCAAGCCCTGCCAAAGC	0
336	CTTGGTCTGGGACTGGCTGTCTA	0
337	GCGGGAAAGTCCATAGTTGGGAG	0
338	GAACCAGCACTCCAACCCGAACC	0
339	GAACCAGCACTCCAACCCGAACC	0
340	GAACCAGCACTCCAACCCGAACC	0
341	CCACCTCCCTACCCTTACTAACC	0
342	CCCCTGCTTCAAGTTGTCCCAGC	0
343	GCTAAACCAAATACTAAATACTGCCA	0
344	CCAATGCCTACTCCTTTGTAACATCC	0
345	TAGATAACAAAGAGAAGGCTGGG	0
346	ACTGATTTTCTAAGTTGTCTTTT	0
347	TACAATGGTATGGCTTAGAAGATGCC	0
348	ATGCCATACGGTCCTTGTTTCTTGAC	0
349	GCCAGCCAAGTGGTAGAATAGGAGTT	-0.010880594
350	ATGTAGCTTCGGGAAACAGC	-0.013055638
351	GCAGGGCAAGGTCAGAAAGAGAC	0
352	ACCCACCACTGCTTTTCACCACTAAG	-0.014311214
353	GGGAAGGAGCCACATCTATCTATTGC	0
354	TTGGGAAGGTGGAGGAGGAGGGA	0
355	GCTAAGCCCCTACAAGTTTGAGAAGG	-0.005626404
356	AAGAGTCATGTAGGGCCAGG	-0.013176922
357	GCTGAGGCGGGAAAACAGGAGAA	-0.000113816
358	AGACACCCTCCGACAGGACCTCA	-0.026223064
359	ACTTTATGGGAGGCTGAGGG	0
360	AAGAGTCATGTAGGGCCAGG	0
361	TGCTTATCTCTTCCTTCATTTTCTGG	0
362	CTCTTCACTCTCTGCTGCCCCTGT	0
363	GACGAAGCCTCTTTGGTTTC	-0.016440702
364	CTCCCAGGCTTGACGAGAGG	0

Table 13.g7

	Probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig
365	ORF642_16_29613904_29616227_29699675_29702049_RF	ORF642	17	4
366	ORF642_16_29686079_29687229_29699675_29702049_FF	ORF642	17	4
367	ORF657_2_191108390_191117485_191168431_191171042_FF	ORF657	51	3
368	ORF657_2_191108390_191117485_191182179_191184623_FR	ORF657	51	3
369	ORF657_2_191108390_191117485_191184623_191189153_FF	ORF657	51	3
370	ORF667_20_47635013_47638590_47797013_47801718_FF	ORF667	30	3
371	ORF670_9_90816328_90822228_90852643_90856872_FR	ORF670	44	3
372	ORF671_1_114103465_114105233_114168595_114177937_FR	ORF671	92	9
373	ORF684_8_132829420_132832263_132988146_132998009_RR	ORF684	192	18
374	ORF685_2_70401554_70403744_70565683_70581054_FR	ORF685	79	5
375	ORF690_9_72618535_72623611_72793872_72807440_RR	ORF690	122	6
376	ORF695_6_137822043_137829972_137904022_137905775_FR	ORF695	28	1
377	ORF696_5_119229308_119233411_119299768_119309624_RF	ORF696	24	21
378	ORF696_5_119283840_119286417_119299768_119309624_RF	ORF696	24	21
379	ORF696_5_119299768_119309624_119358022_119362710_FF	ORF696	24	21
380	ORF697_8_22979979_22981340_23078156_23085865_FF	ORF697	13	2
381	ORF697_8_23078156_23085865_23111436_23115456_FF	ORF697	13	2
382	ORF698_18_62280369_62283590_62356961_62362521_RR	ORF698	32	4
383	ORF698_18_62280369_62283590_62420808_62426226_RR	ORF698	32	4
384	ORF698_18_62296384_62304812_62385139_62386748_FF	ORF698	32	2
385	ORF698_18_62296384_62304812_62391728_62393598_FF	ORF698	32	2
386	ORF698_18_62330039_62332469_62356961_62362521_FR	TNFRSF11A	58	4
387	ORF698_18_62356961_62362521_62391728_62393598_RF	ORF698	32	2
388	ORF699_8_118882360_118886789_118946661_118952757_RR	ORF699	33	3
389	ORF699_8_118901885_118906751_118946661_118952757_RR	ORF699	33	2
390	ORF70_22_17690372_17692909_17820737_17823770_FR	ORF70	28	1
391	ORF700_22_41905695_41906846_41942147_41943520_RF	ORF700	17	1
392	ORF700_22_41905695_41906846_41946565_41950791_FR	ORF700	17	2
393	ORF703_1_6450603_6452273_6494588_6498048_RF	TNFRSF25	68	16
394	ORF703_1_6461604_6466207_6481328_6484248_FF	TNFRSF25	68	16
395	ORF703_1_6461604_6466207_6494588_6498048_FF	TNFRSF25	68	16
396	ORF703_1_6461604_6466207_6494588_6498048_FR	TNFRSF25	68	16
397	ORF703_1_6461604_6466207_6514024_6515315_FR	TNFRSF25	68	16
398	ORF705_9_114855753_114859111_114882931_114894596_FF	ORF705	33	0
399	ORF705_9_114855753_114859111_114882931_114894596_RF	ORF705	33	4
400	ORF705_9_114855753_114859111_114920994_114929419_FR	ORF705	33	0
401	ORF705_9_114882931_114894596_114957908_114962933_FR	TNFSF8	50	4
402	ORF706_5_150983477_150991968_151047772_151050718_RF	ORF706	52	6
403	ORF708_1_3611941_3615812_3638742_3642185_FR	TP73	32	4
404	ORF71_11_102291091_102294492_102307526_102311117_RR	ORF71	13	2
405	ORF71_11_102291091_102294492_102337635_102346660_RR	ORF71	13	2
406	ORF712_9_120888366_120893320_120913546_120919710_FR	TRAF1	42	6
407	ORF712_9_120888366_120893320_120913546_120919710_RR	TRAF1	42	6
408	ORF712_9_120888366_120893320_120919710_120922922_FR	TRAF1	42	6
409	ORF712_9_120913546_120919710_120936524_120940468_RF	TRAF1	42	6
410	ORF718_19_6698236_6701303_6781841_6783687_FR	ORF718	13	1
411	ORF722_9_110209817_110214913_110296637_110303915_FF	ORF722	14	2
412	ORF730_3_23901404_23907629_23923438_23926768_FF	ORF730	18	3
413	ORF741_11_75790711_75798287_75817276_75823568_FR	ORF741	159	6
414	ORF76_2_241559192_241566423_241577996_241581000_RR	BOK	44	10
415	ORF762_8_104964347_104973135_105209447_105218050_FR	ORF762	184	14
416	ORF83_6_31852623_31856339_31978950_31986111_RR	ORF83	29	7

Table 13.h1

	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr	t
365	0.027232137	0.337893495	23.53	-0.202471668	-0.202471668	-6.315923973
366	0.027232137	0.337893495	23.53	-0.154927207	-0.154927207	-5.674884507
367	0.63170859	1	5.88	0.519129457	0.519129457	2.977884092
368	0.63170859	1	5.88	0.617640584	0.617640584	2.79135711
369	0.63170859	1	5.88	0.284908892	0.284908892	6.270152298
370	0.292900518	1	10	0.290479186	0.290479186	8.351795594
371	0.530531532	1	6.82	0.307304294	0.307304294	7.829405666
372	0.125670239	0.904598768	9.78	0.329823616	0.329823616	3.977368273
373	0.060363548	0.646636236	9.38	0.300112568	0.300112568	4.039709924
374	0.561965233	1	6.33	0.293122718	0.293122718	7.224786679
375	0.788253399	1	4.92	0.290541179	0.290541179	5.494475001
376	0.868767357	1	3.57	-0.152941022	-0.152941022	-6.293551206
377	2.83E-22	2.66E-19	87.5	0.229344865	0.229344865	11.43247953
378	2.83E-22	2.66E-19	87.5	0.24275565	0.24275565	12.45525285
379	2.83E-22	2.66E-19	87.5	0.177823165	0.177823165	10.17772231
380	0.229466748	1	15.38	-0.179387458	-0.179387458	-9.712191434
381	0.229466748	1	15.38	-0.218037237	-0.218037237	-12.57980453
382	0.182398388	0.960903242	12.5	-0.243101878	-0.243101878	-4.208949606
383	0.182398388	0.960903242	12.5	-0.232725718	-0.232725718	-4.760235812
384	0.607730303	1	6.25	-0.157966119	-0.157966119	-7.417609124
385	0.607730303	1	6.25	0.712949305	0.712949305	4.461764999
386	0.686266831	0.99999793	6.9	-0.351747423	-0.351747423	-2.587519517
387	0.607730303	1	6.25	0.307835206	0.307835206	8.640900231
388	0.345775878	1	9.09	-0.235758677	-0.235758677	-10.84175415
389	0.681942534	1	6.06	-0.194826505	-0.194826505	-6.703691813
390	0.838642022	1	3.57	0.330305388	0.330305388	6.588172922
391	0.66956866	1	5.88	-0.184624561	-0.184624561	-5.89087632
392	0.335769804	1	11.76	-0.161300759	-0.161300759	-7.221684584
393	6.44E-05	0.004967399	23.53	-0.316909254	-0.316909254	-18.81843594
394	6.44E-05	0.004967399	23.53	-0.391557328	-0.391557328	-9.736436082
395	6.44E-05	0.004967399	23.53	-0.347052896	-0.347052896	-12.44559121
396	6.44E-05	0.004967399	23.53	-0.316023276	-0.316023276	-9.967999414
397	6.44E-05	0.004967399	23.53	-0.324809038	-0.324809038	-10.99489816
398	1	1	0	-0.193263231	-0.193263231	-5.150192691
399	0.196893931	0.98238612	12.12	-0.152757686	-0.152757686	-4.644039162
400	1	1	0	-0.211999593	-0.211999593	-11.86064828
401	0.568728839	0.99999793	8	-0.415876997	-0.415876997	-6.927544857
402	0.107675958	0.853264106	11.54	0.293172978	0.293172978	9.456672576
403	0.246707931	0.99999793	12.5	-0.248090073	-0.248090073	-8.279478026
404	0.211981801	1	15.38	0.163726198	0.163726198	4.523059159
405	0.195961879	1	15.38	0.201110561	0.201110561	6.744214044
406	0.112492545	0.789152247	14.29	-0.196616458	-0.196616458	-6.590704313
407	0.112492545	0.789152247	14.29	-0.148665785	-0.148665785	-4.410767412
408	0.112492545	0.789152247	14.29	-0.199273043	-0.199273043	-6.213719238
409	0.112492545	0.789152247	14.29	-0.255423865	-0.255423865	-10.52329131
410	0.571197975	1	7.69	-0.191042683	-0.191042683	-10.87727058
411	0.219619008	1	14.29	0.597573234	0.597573234	13.70784629
412	0.100654026	0.825363011	16.67	0.290493679	0.290493679	4.193084229
413	0.940134463	1	3.77	0.282876057	0.282876057	12.42727971
414	0.001969408	0.075986326	22.73	-0.367707426	-0.367707426	-11.11416276
415	0.272101156	1	7.61	0.365971074	0.365971074	10.70453823
416	0.001789508	0.045608266	24.14	0.361761092	0.361761092	4.073141197

Table 13.h2

	P.Value	adj.P.Val	B	FC	FC_1	LS
365	0.0000783	0.001057554	1.685518605	0.869060387	-1.150668026	-1
366	0.000187328	0.001890561	0.777210943	0.898177691	-1.11336544	-1
367	0.0135104	0.040653116	-3.625275836	1.43309024	1.43309024	1
368	0.018664657	0.051850278	-3.94720067	1.534363795	1.534363795	1
369	0.0000832	0.001097922	1.622590571	1.218333322	1.218333322	1
370	0.00000689	0.000230944	4.20728549	1.223046441	1.223046441	1
371	0.0000123	0.000322648	3.609042444	1.237393443	1.237393443	1
372	0.002489795	0.011583149	-1.906237636	1.256859701	1.256859701	1
373	0.002248311	0.010748006	-1.801247822	1.231240479	1.231240479	1
374	0.0000249	0.000505697	2.876053795	1.225289553	1.225289553	1
375	0.000241882	0.002233638	0.510978947	1.223098996	1.223098996	1
376	0.0000807	0.001076073	1.654796525	0.89941508	-1.111833704	-1
377	0.000000369	0.000051	7.182375543	1.17230248	1.17230248	1
378	0.000000162	0.0000357	7.999309139	1.183250597	1.183250597	1
379	0.00000111	0.0000849	6.073270515	1.131175803	1.131175803	1
380	0.00000172	0.000108368	5.628079247	0.883077855	-1.132402986	-1
381	0.000000147	0.0000335	8.09397041	0.859734296	-1.163150063	-1
382	0.0017087	0.008848343	-1.518311904	0.844926717	-1.183534596	-1
383	0.000717954	0.004728245	-0.62056802	0.851025509	-1.175052908	-1
384	0.0000198	0.000441092	3.114727283	0.896287748	-1.11571312	-1
385	0.001142097	0.006622538	-1.101830789	1.639151616	1.639151616	1
386	0.026579755	0.067536623	-4.295830899	0.783634368	-1.276105338	-1
387	0.00000506	0.000193388	4.525216296	1.237848888	1.237848888	1
388	0.000000611	0.0000645	6.675922138	0.849238289	-1.177525805	-1
389	0.0000475	0.000761747	2.207019697	0.873677956	-1.144586507	-1
390	0.000055	0.000832022	2.053813675	1.257279485	1.257279485	1
391	0.000138772	0.001546149	1.089794369	0.879878021	-1.136521172	-1
392	0.000025	0.000506888	2.872175551	0.894218465	-1.118294958	-1
393	0.00000000279	0.00000683	11.81480874	0.802787883	-1.245659061	-1
394	0.00000168	0.000107198	5.651749271	0.762306283	-1.311808681	-1
395	0.000000163	0.0000357	7.991924175	0.786188466	-1.271959642	-1
396	0.00000135	0.0000949	5.875116011	0.803281037	-1.24489432	-1
397	0.000000535	0.0000603	6.809806578	0.79840406	-1.252498641	-1
398	0.000399013	0.003153947	-0.010076757	0.874625168	-1.143346929	-1
399	0.000858885	0.005371224	-0.806528239	0.899529384	-1.111692423	-1
400	0.000000259	0.0000428	7.533224813	0.863339802	-1.158292479	-1
401	0.0000359	0.000632929	2.498799383	0.749563705	-1.33410942	-1
402	0.00000221	0.000123757	5.375272803	1.225332239	1.225332239	1
403	0.00000745	0.000241272	4.126320504	0.842010382	-1.187633812	-1
404	0.001037188	0.006177722	-1.00204781	1.120176602	1.120176602	1
405	0.0000451	0.000738802	2.260334671	1.149582943	1.149582943	1
406	0.0000548	0.000830816	2.057190334	0.872594655	-1.146007478	-1
407	0.001237916	0.007019121	-1.185214291	0.902084331	-1.108543809	-1
408	0.0000897	0.001156677	1.544601478	0.870989334	-1.148119685	-1
409	0.000000811	0.0000728	6.391477553	0.837740969	-1.193686398	-1
410	0.000000593	0.0000638	6.707137194	0.875972399	-1.141588481	-1
411	0.0000000638	0.0000214	8.907819219	1.513169114	1.513169114	1
412	0.001752953	0.009007702	-1.544700881	1.223058727	1.223058727	1
413	0.000000165	0.0000357	7.977910939	1.216617834	1.216617834	1
414	0.000000483	0.0000579	6.912800589	0.775013085	-1.290300795	-1
415	0.00000069	0.0000687	6.554375143	1.288748791	1.288748791	1
416	0.002129042	0.010339113	-1.745111267	1.284993527	1.284993527	1

Table 13.h3

		Probe sequence
	Loop detected	**60 mer**
365	PD-L1 responder	CCACTGCACTCCACCCCGGGGAACAAGATCGAAGGCCCCCGTCCTCCTGCGCCATGGAGA
366	PD-L1 responder	CATCATCACAGTCTACGGCTGTTTCCTCTCGATCTTGTTCCCCGGGGTGGAGTGCAGTGG
367	PD-L1 Non-responder	CATTAGACTCTATCTTTATTACTGTAAGTCGAATATAACTCCTTGATTTAGTAAAACCAT
368	PD-L1 Non-responder	CATTAGACTCTATCTTTATTACTGTAAGTCGAGTGATATAACTGCATAGTCTCCTACTGA
369	PD-L1 Non-responder	CATTAGACTCTATCTTTATTACTGTAAGTCGAAGGTGGTAATTGTAGTCTCGGGTGCAAT
370	PD-L1 Non-responder	AGAAGGGGATTTTACATTTTATTTCTTTTCGATGTAAGTATTTGTTAAATAAAAATATAG
371	PD-L1 Non-responder	TTTTACTGTTTTTGTAAGAGATATGTTTTCGATTAATGTTAAAAATAAAAGGTAGTATTT
372	PD-L1 Non-responder	AGATAATGACTTCTGGGAGAGAGAAGAGTCGAACTGATACATAGAAACAATCACATTCAG
373	PD-L1 Non-responder	GTACTTTACAATGATTACTTTATTTAATTCGAAAGTCCATCTGCACAGTGGAACTGTTCC
374	PD-L1 Non-responder	GCAGCCATAATCCTCCTAGGGACACAACTCGAAATACTCCTTTCCTTTCAGATGCTCATT
375	PD-L1 Non-responder	TTTATTTATATTTACCTTTATTTCTATCTCGATCAAGTAGCAGCTCTGTAACTCCCTGGA
376	PD-L1 responder	GAGGTTACTGTTTTCCTAACCATTGTATTCGATATTTTCACCATGTAGCCCAGGCTGGTC
377	PD-L1 Non-responder	AGAGCAGGGTGGGTAGTTCTGCACGTGATCGATTTTGTGGTCAGATTGCTTAAAAGGTAA
378	PD-L1 Non-responder	AGAGCAGGGTGGGTAGTTCTGCACGTGATCGAGACAAATAAGGACTTGGGTTAAAAAAAC
379	PD-L1 Non-responder	AGAGCAGGGTGGGTAGTTCTGCACGTGATCGAATGATCTTCCTGATTTTCCCAAGTAGCT
380	PD-L1 responder	ATCATTTTTAAACCTAGGCTGAATTTTATCGAATTCCGGGCCCTCTCTGTCTCTAAGGAA
381	PD-L1 responder	TTCCTTAGAGACAGAGAGGGCCCGGAATTCGATCTTCCTTACCACCCACCCCCTCCCACT
382	PD-L1 responder	GCTTGTCAACTAACGCTTCACTCATGCCTCGATTTTGAGGGCTTCTCACAACTCTAGATT
383	PD-L1 responder	GCTTGTCAACTAACGCTTCACTCATGCCTCGAAGTTCTGTCTGCTCTATCTCACGCACTC
384	PD-L1 responder	GTTGGTGAAAAAGAAAGAAGAAATGGACTCGACCGCTACCACCCCAGCATTTCCAGCAGG
385	PD-L1 Non-responder	GTTGGTGAAAAAGAAAGAAGAAATGGACTCGACTGGAGTTTTATATTTTCAAGAGTACCT
386	PD-L1 responder	GAGAATCAATTCCATTTTTAAAGCTTAGTCGATTTTGAGGGCTTCTCACAACTCTAGATT
387	PD-L1 Non-responder	AGGTACTCTTGAAAATATAAAACTCCAGTCGATTTTGAGGGCTTCTCACAACTCTAGATT
388	PD-L1 responder	ATAAAGCAACTTGTTTTTCCTTGTATTGTCGATATCAGAATTGTGCTCTGGGGGCGGCTT
389	PD-L1 responder	TATCAAGAAATTACAAACCGGTTCCTAATCGATATCAGAATTGTGCTCTGGGGGCGGCTT
390	PD-L1 Non-responder	TTCAACATGTATTCAGTACAAAAAATTATCGATATTATTGCTTTAATTTAAACAAATTTA
391	PD-L1 responder	GAGCTGCCTCGCTCGGATACTAAGTCCTTCGATTTCTCTCTCTCCCCCTCAGCATCTTCC
392	PD-L1 responder	GTGGGCACTAGGAATGAGGTCCCCTGCCTCGACCCACTCCCGGGGGGATCGGGACACCGC
393	PD-L1 responder	GGGCACCGCCGCCCTGACTTCCAACACATCGAAGAATGGGTGGGGCCTTGCACCTCATAC
394	PD-L1 responder	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGAGGCTTTCAAGGGATCCAGGGTGGGGTGC
395	PD-L1 responder	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGATGTGTTGGAAGTCAGGGCGGCGGTGCCC
396	PD-L1 responder	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGACAATGTTATTCTTTGTTTCTCTTACCAA
397	PD-L1 responder	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGAGAAGCATAAAGCAGGGACAGGTATGGAG
398	PD-L1 responder	TTCACTGTTGCCTTTTGTTGTCATTATATCGAAGAAATGCTTAAGTATGTCTAAGTTTCA
399	PD-L1 responder	TGAAACTTAGACATACTTAAGCATTTCTTCGATTTGTCTGTCTGCCAAGACCATTTCTGA
400	PD-L1 responder	TTCACTGTTGCCTTTTGTTGTCATTATATCGAGTAATACTGACACTCCTGGCCCACAGAA
401	PD-L1 responder	TGAAACTTAGACATACTTAAGCATTTCTTCGAAAGCTAATGAGGTATGAGGGGAGAATAC
402	PD-L1 Non-responder	AGTGGCCCAATCTCGGCTCACCACAGCCTCGATATTATACAGTCTTAGAACAGAAAGAAA
403	PD-L1 responder	GCTTCTCCCCTCTTTATCCCACCTGGCCTCGACTCACCCTGCAGACAAGCTTTCGGGTAT

404	PD-L1 Non-responder	GCCAGCTTCCAGAGAGTGGGAACATGTGTCGAGAGTCAATTCACAGCAAACAGTGAGAAG
405	Non-Responder	GCCAGCTTCCAGAGAGTGGGAACATGTGTCGAAGGTGTGCATATATGTTGAATGACATTT
406	PD-L1 responder	ATAAAATGGGGAGGCCTTCCAGAAGCTCTCGACCTCCAGGTCCCCCGCCACTTCCACGGC
407	PD-L1 responder	AGTGCTGGGTTCCACACCTCTCAGCTCTTCGACCTCCAGGTCCCCCGCCACTTCCACGGC
408	PD-L1 responder	ATAAAATGGGGAGGCCTTCCAGAAGCTCTCGACCGCCACCTCCTCCAGGAAGCCCTGCCT
409	PD-L1 responder	TATGAGTAATAATTACAATTTCCCCCTTTCGACCTCCAGGTCCCCCGCCACTTCCACGGC
410	PD-L1 responder	TAAAAAACACACCTCTGGGTGGAGATTTTCGAGTGATCCACCCGTCTTGGCCTCCCAAAG
411	PD-L1 Non-responder	TTTGTAAGATAAAAGATTTAAATGGATATCGATACCAATGTATAAGAGCTCTGAGAAGTT
412	PD-L1 Non-responder	GGTAAAACTGCCGGTACCTTAGTGCAAATCGACCAAAACCTTTTTTCTTAGAAAAGGTGT
413	PD-L1 Non-responder	GAGAATGAAGTGTACAAGCAGGTGATCTTCGAGAGTGTGTGGGATTAGGAAAGAGAAAGC
414	PD-L1 responder	GTTTGCTCCGGGGCCGCCGGGCCCGCCCTCGATTTTAACACCACCATGGTTTGAATGAAT
415	PD-L1 Non-responder	TATATTTAAAAATACATACTGGTATACATCGAATATGCCAATTAGATCAAGTTGGTTAAT
416	PD-L1 Non-responder	GTCCTCACTAGATTAGCTAGATACAGTGTCGACTTGGATGCCCATGGAATTATCTTCACT

Table 13.h4

	Probe Location					**4 kb Sequence Location**		
	Chr	**Start1**	**End1**	**Start2**	**End2**	**Chr**	**Start1**	**End1**
365	16	29613904	29613933	29702020	29702049	16	29613904	29617903
366	16	29687200	29687229	29702020	29702049	16	29683230	29687229
367	2	191117456	191117485	191171013	191171042	2	191113486	191117485
368	2	191117456	191117485	191182179	191182208	2	191113486	191117485
369	2	191117456	191117485	191189124	191189153	2	191113486	191117485
370	20	47638561	47638590	47801689	47801718	20	47634591	47638590
371	9	90822199	90822228	90852643	90852672	9	90818229	90822228
372	1	114105204	114105233	114168595	114168624	1	114101234	114105233
373	8	132829420	132829449	132988146	132988175	8	132829420	132833419
374	2	70403715	70403744	70565683	70565712	2	70399745	70403744
375	9	72618535	72618564	72793872	72793901	9	72618535	72622534
376	6	137829943	137829972	137904022	137904051	6	137825973	137829972
377	5	119229308	119229337	119309595	119309624	5	119229308	119233307
378	5	119283840	119283869	119309595	119309624	5	119283840	119287839
379	5	119309595	119309624	119362681	119362710	5	119305625	119309624
380	8	22981311	22981340	23085836	23085865	8	22977341	22981340
381	8	23085836	23085865	23115427	23115456	8	23081866	23085865
382	18	62280369	62280398	62356961	62356990	18	62280369	62284368
383	18	62280369	62280398	62420808	62420837	18	62280369	62284368
384	18	62304783	62304812	62386719	62386748	18	62300813	62304812
385	18	62304783	62304812	62393569	62393598	18	62300813	62304812
386	18	62332440	62332469	62356961	62356990	18	62328470	62332469
387	18	62356961	62356990	62393569	62393598	18	62356961	62360960
388	8	118882360	118882389	118946661	118946690	8	118882360	118886359
389	8	118901885	118901914	118946661	118946690	8	118901885	118905884
390	22	17692880	17692909	17820737	17820766	22	17688910	17692909
391	22	41905695	41905724	41943491	41943520	22	41905695	41909694
392	22	41906817	41906846	41946565	41946594	22	41902847	41906846
393	1	6450603	6450632	6498019	6498048	1	6450603	6454602
394	1	6466178	6466207	6484219	6484248	1	6462208	6466207
395	1	6466178	6466207	6498019	6498048	1	6462208	6466207
396	1	6466178	6466207	6494588	6494617	1	6462208	6466207

397	1	6466178	6466207	6514024	6514053	1	6462208	6466207
398	9	114859082	114859111	114894567	114894596	9	114855112	114859111
399	9	114855753	114855782	114894567	114894596	9	114855753	114859752
400	9	114859082	114859111	114920994	114921023	9	114855112	114859111
401	9	114894567	114894596	114957908	114957937	9	114890597	114894596
402	5	150983477	150983506	151050689	151050718	5	150983477	150987476
403	1	3615783	3615812	3638742	3638771	1	3611813	3615812
404	11	102291091	102291120	102307526	102307555	11	102291091	102295090
405	11	102291091	102291120	102337635	102337664	11	102291091	102295090
406	9	120893291	120893320	120913546	120913575	9	120889321	120893320
407	9	120888366	120888395	120913546	120913575	9	120888366	120892365
408	9	120893291	120893320	120919710	120919739	9	120889321	120893320
409	9	120913546	120913575	120940439	120940468	9	120913546	120917545
410	19	6701274	6701303	6781841	6781870	19	6697304	6701303
411	9	110214884	110214913	110303886	110303915	9	110210914	110214913
412	3	23907600	23907629	23926739	23926768	3	23903630	23907629
413	11	75798258	75798287	75817276	75817305	11	75794288	75798287
414	2	241559192	241559221	241577996	241578025	2	241559192	241563191
415	8	104973106	104973135	105209447	105209476	8	104969136	104973135
416	6	31852623	31852652	31978950	31978979	6	31852623	31856622

Table 13.h5

	4 kb Sequence Location		**Inner_primers**		
	Start2	**End2**	**PCR-Primer1_ID**	**PCR_Primer1**	**PCR-Primer2_ID**
365	29698050	29702049	OBD117.1.989	TGAGGCCGTGAAAGGTAAAAGC	OBD117.1.991
366	29698050	29702049	OBD117.1.1037	TCCTCATCCCCAATCTCCCC	OBD117.1.1039
367	191167043	191171042	OBD117.1.1093	CATCCTCGGGCATTTCTTCTTGTCCT	OBD117.1.1095
368	191182179	191186178	OBD117.1.1481	CATCCTCGGGCATTTCTTCTTGTCCT	OBD117.1.1483
369	191185154	191189153	OBD117.1.1725	CATCCTCGGGCATTTCTTCTTGTCC	OBD117.1.1727
370	47797719	47801718	OBD117.1.1701	CAGCCTGGGTGACAGAGTGAGAC	OBD117.1.1703
371	90852643	90856642	OBD117.1.1449	CCCCTGAGAAGCGATGGGCTACT	OBD117.1.1451
372	114168595	114172594	OBD117.1.1485	GACCAGCAGGAGGCTACAGTTGTTGA	OBD117.1.1487
373	132988146	132992145	OBD117.1.1189	GCAGTCTTTGGGCAGCACTACGC	OBD117.1.1191
374	70565683	70569682	OBD117.1.1389	CCCTGCTTGTCCACTGTCTGAAAACA	OBD117.1.1391
375	72793872	72797871	OBD117.1.1797	GAAATCTTGGTCCCTAATGGCAT	OBD117.1.1799
376	137904022	137908021	OBD117.1.549	CTGAAACACTCACCAGCCAATGACAA	OBD117.1.551
377	119305625	119309624	OBD117.1.1029	GAAGATGGCTCTCAAGACTATAATG	OBD117.1.1031
378	119305625	119309624	OBD117.1.681	GGCTCGCTCCAGCACATTCTCCA	OBD117.1.683
379	119358711	119362710	OBD117.1.677	GGCTCGCTCCAGCACATTCTCCA	OBD117.1.679
380	23081866	23085865	OBD117.1.461	GCACACCTGCCAGAACTCATTCAAGA	OBD117.1.463
381	23111457	23115456	OBD117.1.541	GTTTGCCTGACACAGTTCCCTGC	OBD117.1.543
382	62356961	62360960	OBD117.1.457	ATCACTGGACAAGGTAACAAGGGC	OBD117.1.459
383	62420808	62424807	OBD117.1.981	GAGCAACCCGCTTGTCAAC	OBD117.1.983
384	62382749	62386748	OBD117.1.505	TGTGTTTATTCCCTACAGAGCAGGTT	OBD117.1.507
385	62389599	62393598	OBD117.1.1625	TGTGTTTATTCCCTACAGAGCAGGTT	OBD117.1.1627
386	62356961	62360960	OBD117.1.053	AATCCTACTGGCACCACTGTGTTGGC	OBD117.1.055
387	62389599	62393598	OBD117.1.1745	CCCGAACCAGCCTTCCCAAGAGC	OBD117.1.1747
388	118946661	118950660	OBD117.1.465	CCACAACCCACACCTGCCACTGT	OBD117.1.467
389	118946661	118950660	OBD117.1.533	GCCTAACTGATGTGGCTGTCTTTGTG	OBD117.1.535
390	17820737	17824736	OBD117.1.1773	TGTGTCATCAGGATTCTTTTCTG	OBD117.1.1775
391	41939521	41943520	OBD117.1.525	ATCCTGTGTCTCCCTCCCCTTCA	OBD117.1.527
392	41946565	41950564	OBD117.1.993	CAGAGGGTTGCCTATGGTGG	OBD117.1.995
393	6494049	6498048	OBD117.1.381	AATAACCTGTGCCCAGACCGAGC	OBD117.1.383
394	6480249	6484248	OBD117.1.193	AGCCTCCTGCGTCTCAACTCACC	OBD117.1.195

395	6494049	6498048	OBD117.1.181	AGCCTCCTGCGTCTCAACTCACC	OBD117.1.183
396	6494588	6498587	OBD117.1.137	AGCCTCCTGCGTCTCAACTCACC	OBD117.1.139
397	6514024	6518023	OBD117.1.745	CTAGCCTCCTGCGTCTCAAC	OBD117.1.747
398	114890597	114894596	OBD117.1.545	GTTGCTCAGGCTGCCCTCTTGCT	OBD117.1.547
399	114890597	114894596	OBD117.1.1049	TCAGGGTAGTGCAGTGTAGTGT	OBD117.1.1051
400	114920994	114924993	OBD117.1.517	TGTTGCTCAGGCTGCCCTCTTGCTAT	OBD117.1.519
401	114957908	114961907	OBD117.1.273	GCACCAGGTCAAGTAGCCTCAGG	OBD117.1.275
402	151046719	151050718	OBD117.1.1385	GTCTCGTTCTGTCACCCAGGCTG	OBD117.1.1387
403	3638742	3642741	OBD117.1.349	CCAAATGTAGATGCCCGCACCCG	OBD117.1.351
404	102307526	102311525	OBD117.1.697	TGCCTTGAACAGATTGCCAGCCTCCT	OBD117.1.699
405	102337635	102341634	OBD117.1.597	TGCCTTGAACAGATTGCCAGCCTCCT	OBD117.1.599
406	120913546	120917545	OBD117.1.021	GACGCTCTCCCTTTGCTCAAGCC	OBD117.1.023
407	120913546	120917545	OBD117.1.301	CCCAGTTGTCCAGGTTGCTGCCT	OBD117.1.303
408	120919710	120923709	OBD117.1.013	GACGCTCTCCCTTTGCTCAAGCC	OBD117.1.015
409	120936469	120940468	OBD117.1.169	GCTGTGTATCTCAGGGCACTCAG	OBD117.1.171
410	6781841	6785840	OBD117.1.949	GGCCCTGAAGGGGACTTATC	OBD117.1.951
411	110299916	110303915	OBD117.1.933	CTGATTGCTCAACCCAAAGC	OBD117.1.935
412	23922769	23926768	OBD117.1.1873	TCATACTACTACCAAAGCCATTT	OBD117.1.1875
413	75817276	75821275	OBD117.1.1233	GACCTGGTTCCCATCTACTCCTTTGG	OBD117.1.1235
414	241577996	241581995	OBD117.1.841	AGCGCCACCTTCTTTCAGAG	OBD117.1.843
415	105209447	105213446	OBD117.1.1649	AGGCATTACTGAAGTTGCTGGTATTC	OBD117.1.1651
416	31978950	31982949	OBD117.1.1013	CCAGAGCGGGATGTCACTAC	OBD117.1.1015

Table 13.h6

	Inner_primers	
	PCR_Primer2	GLMNET
365	GCTCCCAGGCTTGACGAGA	0
366	CTGGGGCACTCAATCTAGAGGT	0
367	CCGTGACTCATCAGAGGAAAACTACG	0
368	GGAAAGAGTAGGAACCTGAAACCTGC	0
369	CCTCTTCCTGGCTCACAGACAGC	0
370	CTCACGCTCTGGTCCTTGTCACT	0
371	GGGCAGGGACTAAGGTCTGACTT	0
372	CTCCCATCTTGAGGCTGTAAACAAAC	0
373	CACACTCCTCCTCCAAGTCACAG	0
374	CCACACAGTTTCCACCTTACCACCAT	0
375	GTAGTGGCAGAGGAACTTTCAGT	0
376	AACAGGCAGGGTGAACTCTTCCAGAC	0.009721306
377	CCAAGCTGGCTAATATGTGTG	0
378	GGGCTAACCAGAGGCAAAAGGCA	0.007305849
379	GGTTGAAGGAGGTGGGTCAGTTG	0.001120789
380	GGCTTAGTGGTTTTGGAGTCCTGGTA	-0.017294821
381	ATGAGCCCTGAGTGTGCTGGTGC	0.000113082
382	ATCATAATCAGGCAACTGGCTGGTGC	0.000110518
383	TGTAGCCAGCCATCCAAAGACA	0
384	TGAGCACTGGTTCCCCGCAAATACTG	0.027764821
385	AACCTTACCCGAACCAGCCTTCCCAA	0
386	GAAGAGCCCAGTTGACATCTAATAAC	0.008919637
387	GTTGACATCTAATAACTCACATT	0
388	GCCAAGAGAGAAGAGTGTGAAGCC	-0.009297019
389	AAGCCAAGAGAGAAGAGTGTGAAGCC	0
390	AGGTCCACATACCACACACCATA	0
391	AGGCTCTTCCCCACCACTCTCAG	-0.016217397
392	GTAGTAGAGAGTGCGGTGCC	0
393	GGGAAAATCGGTGTGGCTGGCTC	0.000134142
394	ATACGGACTGAGCCCTATGACGC	0

395	AATAACCTGTGCCCAGACCGAGC	-0.007419688
396	AGAACAGAGGCAAGGGCAGTCCA	-0.005042919
397	CCTCCATACCTGTCCCTGCT	0.020530456
398	GTCAAGTAGCCTCAGGGTAGTGC	0.013121857
399	TGCCATGTAACCTTGTGTTCAGA	0
400	CCTGTTTGAGATGCTCTGCTTTTGAC	0.012738078
401	AGCCCTCGCTAAAGCCAAATGGG	0.010145959
402	GGCAGTGGTTTGTCCTGTGACCT	0
403	GGATAACCGTCTGGTCCTTGTGC	-0.021145842
404	CCTGGCTTGCTTTTGAATCCTGACTT	0.006301587
405	AAGGTATGGAAAGAGTCTGGGAGTGA	0.01482896
406	TGGAGCAGAACCTGTCAGACCTG	-0.016381908
407	TGGAGCAGAACCTGTCAGACCTG	0.024168377
408	GGAGTCCACCAAGTGCTATGGGA	-0.003508085
409	CCTGGAGCAGAACCTGTCAGACC	-0.01000752
410	TCAGGGATCCAATAGGTTAAGTAAT	-0.018046798
411	GCTGCGAAAATGTTGAGGCT	0.008860872
412	GAAGAATGAACTGCTACAACACC	0
413	GAACTGTTATCAGAGAATAGGCTCCA	0
414	GGGCATTATGTGAGGGTCTC	0.000117272
415	AAGAGCAATAAGGATGTCAAAGTTTT	0
416	CCTGTCTCCCCCAACCTGTG	0

Table 13.h7

	Probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig
417	ORF83_6_31878016_31881028_31925606_31928820_RF	ORF83	29	7
418	ORF83_6_31899557_31901172_31978950_31986111_FR	ORF83	29	7
419	ORF83_6_31918302_31923229_31940368_31942384_FR	ORF83	29	7
420	ORF83_6_31918302_31923229_31942384_31947035_FF	ORF83	29	7
421	ORF83_6_31925606_31928820_31942384_31947035_FF	ORF83	29	7
422	ORF83_6_31925606_31928820_31978950_31986111_FR	ORF83	29	7
423	ORF86_1_56841210_56844685_56902220_56908104_RF	ORF86	113	2
424	ORF99_3_105671315_105675681_105723411_105731672_FR	ORF99	169	24
425	ORF99_3_105671315_105675681_105803937_105818229_RF	ORF99	169	24
426	ORF99_3_105671315_105675681_105828793_105836033_FR	ORF99	169	24
427	ORF99_3_105723411_105731672_105748068_105752264_RF	ORF99	169	24
428	ORF99_3_105723411_105731672_105795346_105800869_RR	ORF99	169	24
429	ORF99_3_105723411_105731672_105803937_105818229_RF	ORF99	169	24
430	ORF99_3_105748068_105752264_105803937_105818229_FF	ORF99	169	24
431	ORF99_3_105803937_105818229_105883590_105884656_RF	CBLB	182	2
432	ORF99_3_105887817_105896306_105908853_105916728_RF	ORF99	169	24
433	PIK3R1_5_68187850_68194388_68215410_68221074_FR	PIK3R1	148	12
434	PIK3R1_5_68195469_68198352_68215410_68221074_RR	PIK3R1	148	12
435	PIK3R1_5_68215410_68221074_68272048_68277769_RF	PIK3R1	148	12
436	PRR5_22_44662780_44666500_44696835_44701888_FF	PRR5	64	4
437	PTPRC_1_198646662_198649713_198659753_198666156_RF	PTPRC	32	11
438	PTPRC_1_198659753_198666156_198768850_198775826_FF	PTPRC	32	11
439	RPTOR_17_80636056_80643737_80661868_80664436_FR	RPTOR	86	6
440	RPTOR_17_80636056_80643737_80661868_80664436_RR	RPTOR	86	6
441	RPTOR_17_80636056_80643737_80793263_80796075_FF	RPTOR	86	6
442	SHH_7_155794440_155798922_155840981_155842935_RF	SHH	36	6
443	SHH_7_155807951_155810124_155829183_155832221_FR	SHH	36	6
444	SPN_16_29613904_29616227_29630194_29632081_RF	SPN	56	4
445	SPN_16_29613904_29616227_29686079_29687229_RF	SPN	56	4

446	STAT5B_17_40403935_40406459_40464294_40468456_FR	STAT5B	20	12
447	SYK_9_90816328_90822228_90852643_90856872_FR	SYK	6	2
448	SYK_9_90816328_90822228_90872966_90875740_FR	SYK	6	2
449	TNFRSF11A_18_62317997_62323752_62391728_62393598_RF	TNFRSF11A	7	1
450	TNFRSF13C_22_41905695_41906846_41946565_41950791_FR	TNFRSF13C	4	1
451	TNFRSF1A_12_6358656_6362143_6379726_6384063_FF	TNFRSF1A	46	2
452	TNFRSF25_1_6450603_6452273_6494588_6498048_RF	TNFRSF25	68	16
453	TNFRSF25_1_6461604_6466207_6481328_6484248_FF	TNFRSF25	68	16
454	TNFRSF25_1_6461604_6466207_6494588_6498048_FF	TNFRSF25	68	16
455	TNFRSF25_1_6461604_6466207_6514024_6515315_FR	TNFRSF25	68	16
456	TNFRSF25_1_6494588_6498048_6514024_6515315_FR	TNFRSF25	68	16
457	TNFSF8_9_114957908_114962933_114975258_114977746_RF	TNFSF8	3	1
458	TRAF1_9_120888366_120893320_120913546_120919710_FR	TRAF1	42	6
459	TRAF1_9_120913546_120919710_120936524_120940468_RF	TRAF1	42	6
460	TRAF2_9_136904007_136906211_136939587_136941363_RF	TRAF2	46	2

Table 13.i1

	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr	t
417	0.001789508	0.045608266	24.14	0.168923652	0.168923652	4.273129747
418	0.002398244	0.056538599	24.14	0.144207368	0.144207368	6.014120556
419	0.002398244	0.056538599	24.14	0.199604737	0.199604737	8.688296791
420	0.002398244	0.056538599	24.14	0.1824608	0.1824608	7.192394868
421	0.002398244	0.056538599	24.14	0.172829165	0.172829165	5.388588036
422	0.002398244	0.056538599	24.14	0.173973685	0.173973685	6.172747925
423	0.994563707	1	1.77	0.295771685	0.295771685	3.019840274
424	0.000164355	0.005961019	14.2	0.340118684	0.340118684	13.02892826
425	0.000164355	0.005961019	14.2	0.313675221	0.313675221	5.453800736
426	0.000164355	0.005961019	14.2	0.308984949	0.308984949	13.67253532
427	0.000164355	0.005961019	14.2	0.370970871	0.370970871	8.877555847
428	0.000164355	0.005961019	14.2	0.293427802	0.293427802	8.432951342
429	0.000164355	0.005961019	14.2	0.30374268	0.30374268	7.655073619
430	0.000164355	0.005961019	14.2	0.355774756	0.355774756	5.513101893
431	0.999995464	0.99999793	1.1	-0.197007746	-0.197007746	-4.723247929
432	0.000164355	0.005961019	14.2	0.30240493	0.30240493	7.643472828
433	0.513477047	0.99999793	8.11	-0.331665721	-0.331665721	-11.91788456
434	0.513477047	0.99999793	8.11	-0.356573442	-0.356573442	-14.85687535
435	0.513477047	0.99999793	8.11	-0.31812964	-0.31812964	-14.30149147
436	0.7582782	0.99999793	6.25	-0.385982839	-0.385982839	-17.18527923
437	2.29E-06	0.000217011	34.38	0.321601025	0.321601025	10.73971674
438	2.29E-06	0.000217011	34.38	0.284709632	0.284709632	9.679151953
439	0.687444338	0.99999793	6.98	-0.140265969	-0.140265969	-6.28050969
440	0.687444338	0.99999793	6.98	-0.187583846	-0.187583846	-5.431560127
441	0.687444338	0.99999793	6.98	-0.139084539	-0.139084539	-6.11708923
442	0.062022042	0.70039526	16.67	-0.174771304	-0.174771304	-4.501723442
443	0.062022042	0.70039526	16.67	-0.140520637	-0.140520637	-6.954162178
444	0.659150649	0.99999793	7.14	-0.169924144	-0.169924144	-7.327193408
445	0.659150649	0.99999793	7.14	-0.153139995	-0.153139995	-6.667140097
446	0.001866853	0.066190912	60	0.870424687	0.870424687	6.817040924
447	0.050279839	0.592673603	33.33	0.289411908	0.289411908	8.185158835
448	0.050279839	0.592673603	33.33	0.421540272	0.421540272	12.7959067
449	0.366131493	1	14.29	0.295150757	0.295150757	5.356815514
450	0.251755367	1	25	-0.152450898	-0.152450898	-7.330250938
451	0.889742685	0.99999793	4.35	-0.200276865	-0.200276865	-7.487088438
452	6.44E-05	0.004967399	23.53	-0.330748028	-0.330748028	-18.17630665
453	6.44E-05	0.004967399	23.53	-0.375198131	-0.375198131	-11.77686613

454	6.44E-05	0.004967399	23.53	-0.342250575	-0.342250575	-12.06306132
455	6.44E-05	0.004967399	23.53	-0.358891419	-0.358891419	-10.66682351
456	6.44E-05	0.004967399	23.53	-0.282267049	-0.282267049	-15.53979703
457	0.177479538	1	33.33	0.138918287	0.138918287	7.319723967
458	0.112492545	0.789152247	14.29	-0.165440732	-0.165440732	-5.606610708
459	0.112492545	0.789152247	14.29	-0.22976066	-0.22976066	-9.762488772
460	0.889742685	0.99999793	4.35	-0.18670662	-0.18670662	-5.163579985

Table 13.i2

	P.Value	adj.P.Val	B	FC	FC_1	LS
417	0.001541322	0.008215323	-1.41185712	1.124219428	1.124219428	1
418	0.000117273	0.001382765	1.265161339	1.10512332	1.10512332	1
419	0.00000481	0.000187071	4.576477583	1.148383683	1.148383683	1
420	0.0000259	0.000518564	2.835496877	1.134817891	1.134817891	1
421	0.000281632	0.002477042	0.352536792	1.127266921	1.127266921	1
422	0.0000947	0.001202019	1.487699995	1.128161559	1.128161559	1
423	0.01256505	0.038542086	-3.55264462	1.227541403	1.227541403	1
424	0.000000105	0.0000268	8.427168566	1.265860726	1.265860726	1
425	0.000256392	0.002326445	0.450307706	1.242869843	1.242869843	1
426	0.0000000654	0.0000214	8.883474649	1.238835774	1.238835774	1
427	0.00000395	0.00016934	4.778806192	1.293222821	1.293222821	1
428	0.00000631	0.000221388	4.297454598	1.225548689	1.225548689	1
429	0.000015	0.000371302	3.4022934	1.234342429	1.234342429	1
430	0.000235533	0.00219625	0.538683933	1.279672607	1.279672607	1
431	0.000759949	0.004919307	-0.679565911	0.872358022	-1.14631834	-1
432	0.0000152	0.000374316	3.388405516	1.233198406	1.233198406	1
433	0.000000248	0.0000426	7.579137577	0.794618496	-1.258465547	-1
434	0.000000029	0.0000153	9.663464141	0.78101738	-1.280381239	-1
435	0.0000000421	0.0000172	9.306864203	0.802109086	-1.246713219	-1
436	0.00000000688	0.0000106	11.00320387	0.765257487	-1.30674971	-1
437	0.000000669	0.0000679	6.585681171	1.249716647	1.249716647	1
438	0.00000178	0.000110226	5.595735187	1.218165062	1.218165062	1
439	0.0000821	0.001088928	1.636855792	0.907351864	-1.102108277	-1
440	0.000264717	0.002374878	0.417032009	0.878075047	-1.138854821	-1
441	0.00010205	0.001261051	1.410021654	0.908095203	-1.101206125	-1
442	0.001072501	0.006331857	-1.036726499	0.885907942	-1.128785456	-1
443	0.0000347	0.000620295	2.533051066	0.907191711	-1.102302841	-1
444	0.0000221	0.000471182	3.003395936	0.888889417	-1.124999331	-1
445	0.0000497	0.000781417	2.158738806	0.899291043	-1.111987056	-1
446	0.000217825	NA	1.17150928	1.82820099	1.82820099	1
447	0.00000826	0.000257888	4.019841765	1.222141989	1.222141989	1
448	0.000000125	0.0000307	8.255863058	1.339356736	1.339356736	1
449	0.000294879	0.00256113	0.304679742	1.22701319	1.22701319	1
450	0.000022	0.000469868	3.00717754	0.899720688	-1.111456047	-1
451	0.0000183	0.000418541	3.199585235	0.870383513	-1.148918821	-1
452	0.00000000394	0.00000864	11.50694716	0.79512411	-1.257665297	-1
453	0.000000277	0.0000445	7.465604014	0.770999521	-1.297017667	-1
454	0.00000022	0.0000394	7.6945755	0.788809824	-1.26773269	-1
455	0.000000713	0.0000695	6.520700487	0.779763527	-1.282440079	-1
456	0.0000000186	0.0000129	10.08124721	0.822297844	-1.216104368	-1
457	0.0000223	0.000473074	2.994152645	1.101079232	1.101079232	1
458	0.000206242	0.002008025	0.677010146	0.891656084	-1.121508638	-1
459	0.00000164	0.000106067	5.677124024	0.852776354	-1.172640394	-1
460	0.000391198	0.003113294	0.010501538	0.87860912	-1.138162554	-1

Table 13.i3

		Probe sequence
	Loop detected	**60 mer**
417	Non-Responder	TCCTATCCCGTGGGTGGCAATGTGAGCTTCGAGAAGGTCCCTCATAGGGGTTCCTTCCCC
418	PD-L1 Non-responder	AGCAGGCGGCCAAGATGACCTTGTGGCCTCGACTTGGATGCCCATGGAATTATCTTCACT
419	PD-L1 Non-responder	CACAGGTCAGGTCATGGTCCTTCCACATTCGATTCCCTCTGGGGAATGTCCCTGGTGGTT
420	PD-L1 Non-responder	CACAGGTCAGGTCATGGTCCTTCCACATTCGAAGTCGTGTGGTCTTGGACAGTGGATTGC
421	PD-L1 Non-responder	TCCTATCCCGTGGGTGGCAATGTGAGCTTCGAAGTCGTGTGGTCTTGGACAGTGGATTGC
422	PD-L1 Non-responder	TCCTATCCCGTGGGTGGCAATGTGAGCTTCGACTTGGATGCCCATGGAATTATCTTCACT
423	PD-L1 Non-responder	AGGTCATTAAAGTATAATCCTGTTGTTATCGAGAGATCAAGACCATCCTGGCCAACATGG
424	PD-L1 Non-responder	AGCAGGGGGATCACATAAGGCCAGGAGTTCGAATAAGAAATACTTCTAAACCAAAGGATA
425	PD-L1 Non-responder	ATGTATTTATAGGTCTAATCATGTAAAATCGATATCTCTGAAAGTACCGTCAATTCTTCT
426	PD-L1 Non-responder	AGCAGGGGGATCACATAAGGCCAGGAGTTCGATTTTAACAAGAAACTGTAGGTCTAAGGA
427	PD-L1 Non-responder	TTATTACTTTATTCTGACTGAATATCATTCGAATAAGAAATACTTCTAAACCAAAGGATA
428	PD-L1 Non-responder	TATCCTTTGGTTTAGAAGTATTTCTTATTCGAAAGAAACCAAAAACACAAGTATACATCA
429	PD-L1 Non-responder	ATGTATTTATAGGTCTAATCATGTAAAATCGAATAAGAAATACTTCTAAACCAAAGGATA
430	PD-L1 Non-responder	TTATTACTTTATTCTGACTGAATATCATTCGATTTTACATGATTAGACCTATAAATACAT
431	PD-L1 responder	CCTAATATTTCATTATGATAAGAAAGATTCGAGAGTAAGTTTCTTCTGTTCACTCAGGAG
432	PD-L1 Non-responder	TTATTTATATCTTCTCTAATTTATTTTATCGATGAACGTTTACCCAATTATTTCTAAACA
433	PD-L1 responder	CTGAGTCTTCATTACCAAAAAAAAAAGTTCGACCTCCCCGAACCCCTCCGCCTCTGCGCT
434	PD-L1 responder	AAATCATAATTGTGCAGATGATTTGCCTTCGACCTCCCCGAACCCCTCCGCCTCTGCGCT
435	PD-L1 responder	GCAGTCAATCACCGAGTTATATGAGGTCTCGACCTCCCCGAACCCCTCCGCCTCTGCGCT
436	PD-L1 responder	CCAAACTGGCAATCAACCCAGATAGTCTTCGACCCCGGCCCCGGAGGTCTCCCTCCACAG
437	PD-L1 Non-responder	AGAGGCTGAGGTGAAAAGATTGTTTGAGTCGATTATTTCTTATCTAGCCAATAGAAACTT
438	PD-L1 Non-responder	AGAGGCTGAGGTGAAAAGATTGTTTGAGTCGAGTCACATGATCAAGCGCTCATTTCTGTT
439	PD-L1 responder	CTTTTCCATTGCTTCCTCAGATCCTCTGTCGAGATTCACTGCGCTGCACACCAGGGCCTC
440	PD-L1 responder	AGCTGGAGTCTTGATTAACACAAAAATCTCGAGATTCACTGCGCTGCACACCAGGGCCTC
441	PD-L1 responder	CTTTTCCATTGCTTCCTCAGATCCTCTGTCGAGAGCACGGCCTCTCTGGCGCCTTGCCAT
442	PD-L1 responder	ACATGAGATGTCCTTCAAGTGAAACTGTTCGACCATGCCCGGGCAGGTGGCTGAGACCTC
443	PD-L1 responder	CGCGCACTGAAACCCTAGCCGCGGGGGATCGAAATCATATCACCAGTCATTCCACTCCTG
444	PD-L1 responder	AGGCGACACTCTTGTCCCCGCCATCTTTTCGAAGGCCCCCGTCCTCCTGCGCCATGGAGA
445	PD-L1 responder	CATCATCACAGTCTACGGCTGTTTCCTCTCGAAGGCCCCCGTCCTCCTGCGCCATGGAGA
446	PD-L1 Non-responder	TTCCATAGATTACTTTTCAAATCATCCTTCGAAGCTGGCGGCTGAGGGCCCGGCGCCAAG
447	PD-L1 Non-responder	TTTTACTGTTTTTGTAAGAGATATGTTTTCGATTAATGTTAAAAATAAAAGGTAGTATTT
448	PD-L1 Non-responder	TTTTACTGTTTTTGTAAGAGATATGTTTTCGACATCATTTTTACAAATAAGACCAGATGT
449	PD-L1 Non-responder	AGGTACTCTTGAAAATATAAAACTCCAGTCGACATTATACAAAGAATTCCCACAAATCCA
450	PD-L1 responder	GTGGGCACTAGGAATGAGGTCCCCTGCCTCGACCCACTCCCGGGGGGATCGGGACACCGC
451	PD-L1 responder	TCCAGGGATGGCAGAGTCTCTGGCAGCCTCGATGCGGGGCGGGAGGGGCGGCCGGGAAAG
452	PD-L1 responder	GGGCACCGCCGCCCTGACTTCCAACACATCGAAGAATGGGTGGGGCCTTGCACCTCATAC
453	PD-L1 responder	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGAGGCTTTCAAGGGATCCAGGGTGGGGTGC
454	PD-L1 responder	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGATGTGTTGGAAGTCAGGGCGGCGGTGCCC
455	PD-L1 responder	CCGCGCCCGCAGGGCCCGCCCCGCGCCGTCGAGAAGCATAAAGCAGGGACAGGTATGGAG
456	PD-L1 responder	GGGCACCGCCGCCCTGACTTCCAACACATCGAGAAGCATAAAGCAGGGACAGGTATGGAG
457	Non-Responder	AGTAGTGCAATCATAGCTCACTGAAACCTCGAAAGCTAATGAGGTATGAGGGGAGAATAC
458	PD-L1 responder	ATAAAATGGGGAGGCCTTCCAGAAGCTCTCGACCTCCAGGTCCCCCGCCACTTCCACGGC
459	PD-L1 responder	TATGAGTAATAATTACAATTTCCCCCTTTCGACCTCCAGGTCCCCCGCCACTTCCACGGC
460	PD-L1 responder	CCGCCTCACCTCCCGCATGGTCTTGAGGTCGAGCATGCAGCGCATCTGAGCAGTGAGGCT

Table 13.i4

	Probe Location					4 kb Sequence Location		
	Chr	**Start1**	**End1**	**Start2**	**End2**	**Chr**	**Start1**	**End1**
417	6	31878016	31878045	31928791	31928820	6	31878016	31882015

418	6	31901143	31901172	31978950	31978979	6	31897173	31901172
419	6	31923200	31923229	31940368	31940397	6	31919230	31923229
420	6	31923200	31923229	31947006	31947035	6	31919230	31923229
421	6	31928791	31928820	31947006	31947035	6	31924821	31928820
422	6	31928791	31928820	31978950	31978979	6	31924821	31928820
423	1	56841210	56841239	56908075	56908104	1	56841210	56845209
424	3	105675652	105675681	105723411	105723440	3	105671682	105675681
425	3	105671315	105671344	105818200	105818229	3	105671315	105675314
426	3	105675652	105675681	105828793	105828822	3	105671682	105675681
427	3	105723411	105723440	105752235	105752264	3	105723411	105727410
428	3	105723411	105723440	105795346	105795375	3	105723411	105727410
429	3	105723411	105723440	105818200	105818229	3	105723411	105727410
430	3	105752235	105752264	105818200	105818229	3	105748265	105752264
431	3	105803937	105803966	105884627	105884656	3	105803937	105807936
432	3	105887817	105887846	105916699	105916728	3	105887817	105891816
433	5	68194359	68194388	68215410	68215439	5	68190389	68194388
434	5	68195469	68195498	68215410	68215439	5	68195469	68199468
435	5	68215410	68215439	68277740	68277769	5	68215410	68219409
436	22	44666471	44666500	44701859	44701888	22	44662501	44666500
437	1	198646662	198646691	198666127	198666156	1	198646662	198650661
438	1	198666127	198666156	198775797	198775826	1	198662157	198666156
439	17	80643708	80643737	80661868	80661897	17	80639738	80643737
440	17	80636056	80636085	80661868	80661897	17	80636056	80640055
441	17	80643708	80643737	80796046	80796075	17	80639738	80643737
442	7	155794440	155794469	155842906	155842935	7	155794440	155798439
443	7	155810095	155810124	155829183	155829212	7	155806125	155810124
444	16	29613904	29613933	29632052	29632081	16	29613904	29617903
445	16	29613904	29613933	29687200	29687229	16	29613904	29617903
446	17	40406430	40406459	40464294	40464323	17	40402460	40406459
447	9	90822199	90822228	90852643	90852672	9	90818229	90822228
448	9	90822199	90822228	90872966	90872995	9	90818229	90822228
449	18	62317997	62318026	62393569	62393598	18	62317997	62321996
450	22	41906817	41906846	41946565	41946594	22	41902847	41906846
451	12	6362114	6362143	6384034	6384063	12	6358144	6362143
452	1	6450603	6450632	6498019	6498048	1	6450603	6454602
453	1	6466178	6466207	6484219	6484248	1	6462208	6466207
454	1	6466178	6466207	6498019	6498048	1	6462208	6466207
455	1	6466178	6466207	6514024	6514053	1	6462208	6466207
456	1	6498019	6498048	6514024	6514053	1	6494049	6498048
457	9	114957908	114957937	114977717	114977746	9	114957908	114961907
458	9	120893291	120893320	120913546	120913575	9	120889321	120893320
459	9	120913546	120913575	120940439	120940468	9	120913546	120917545
460	9	136904007	136904036	136941334	136941363	9	136904007	136908006

Table 13.i5

	4 kb Sequence Location		Inner_primers		
	Start2	**End2**	**PCR-Primer1_ID**	**PCR_Primer1**	**PCR-Primer2_ID**
417	31924821	31928820	OBD117.1.877	CCCAGGTGTTATCCATCCAG	OBD117.1.879
418	31978950	31982949	OBD117.1.637	AGCAGGAACTGGTCCCGCAGGAA	OBD117.1.639
419	31940368	31944367	OBD117.1.657	AGCCAAGGTCGCCCTCATCTGGT	OBD117.1.659
420	31943036	31947035	OBD117.1.565	AGCCAAGGTCGCCCTCATCTGGT	OBD117.1.567
421	31943036	31947035	OBD117.1.629	TGTCCAGCCCCTGTCTCCTTTGA	OBD117.1.631
422	31978950	31982949	OBD117.1.633	GTCCAGCCCCTGTCTCCTTTGAG	OBD117.1.635
423	56904105	56908104	OBD117.1.1685	CTTGGCACAGAACAGGAGCACCA	OBD117.1.1687

424	105723411	105727410	OBD117.1.1297	GCAAAACAATACTCAAATGCTCAT	OBD117.1.1299
425	105814230	105818229	OBD117.1.1537	ATGATGATGAAACTTGCTTCCTGGA	OBD117.1.1539
426	105828793	105832792	OBD117.1.1353	GCAAAACAATACTCAAATGCTCAT	OBD117.1.1355
427	105748265	105752264	OBD117.1.1477	TTCTGCCACAACCCTGATGTTTTCTG	OBD117.1.1479
428	105795346	105799345	OBD117.1.1689	TAATGGTTGAAATGTGAGTCTGAAT	OBD117.1.1691
429	105814230	105818229	OBD117.1.1601	ATGAAAACTTATCCCAAAGAAACTTC	OBD117.1.1603
430	105814230	105818229	OBD117.1.1125	TTTCTGCCACAACCCTGATGTTTTCT	OBD117.1.1127
431	105880657	105884656	OBD117.1.205	CACCTATTGCCTGGAGCATAAAGGGA	OBD117.1.207
432	105912729	105916728	OBD117.1.1369	ATCACTTTGGGTAGTATGACCTTTT	OBD117.1.1371
433	68215410	68219409	OBD117.1.853	CACCATTGTATGGGGAATGAC	OBD117.1.855
434	68215410	68219409	OBD117.1.849	AAGCCAAACTTGCTAGCATCC	OBD117.1.851
435	68273770	68277769	OBD117.1.857	GAACGTCGGCCTACCTAGTG	OBD117.1.859
436	44697889	44701888	OBD117.1.249	TTACACTCCTGGGCACTCTTCCC	OBD117.1.251
437	198662157	198666156	OBD117.1.1437	GGAGAATCACTTGAGCCTAAGAGTTC	OBD117.1.1439
438	198771827	198775826	OBD117.1.1245	CCAGCAAAGGGCAGGTCATCATC	OBD117.1.1247
439	80661868	80665867	OBD117.1.097	ATAAGGAGAAACTGTGGAAGAGAGGC	OBD117.1.099
440	80661868	80665867	OBD117.1.865	CATGAGGTACACGGCATCAC	OBD117.1.867
441	80792076	80796075	OBD117.1.093	ATAAGGAGAAACTGTGGAAGAGAGGC	OBD117.1.095
442	155838936	155842935	OBD117.1.873	ACTTCATGGAAGGGTGGTCA	OBD117.1.875
443	155829183	155833182	OBD117.1.1073	GCGCTGCTGTTAGCTCCTG	OBD117.1.1075
444	29628082	29632081	OBD117.1.1001	CCTCATCCGTCCGCACATCT	OBD117.1.1003
445	29683230	29687229	OBD117.1.1009	ATGCTGTTGCAGGACTGTGC	OBD117.1.1011
446	40464294	40468293	OBD117.009	TCTACAGCCCAAGATCCTGCTTT	OBD117.011
447	90852643	90856642	OBD117.1.1213	CCCCTGAGAAGCGATGGGCTACT	OBD117.1.1215
448	90872966	90876965	OBD117.1.1273	CCCCTGAGAAGCGATGGGCTACT	OBD117.1.1275
449	62389599	62393598	OBD117.1.1793	CCCGAACCAGCCTTCCCAAGAGC	OBD117.1.1795
450	41946565	41950564	OBD117.1.997	CAGAGGGTTGCCTATGGTGG	OBD117.1.999
451	6380064	6384063	OBD117.1.1005	AGGAGACCTGGTTGAAGCGG	OBD117.1.1007
452	6494049	6498048	OBD117.1.421	AATAACCTGTGCCCAGACCGAGC	OBD117.1.423
453	6480249	6484248	OBD117.1.241	AGCCTCCTGCGTCTCAACTCACC	OBD117.1.243
454	6494049	6498048	OBD117.1.029	AGCCTCCTGCGTCTCAACTCACC	OBD117.1.031
455	6514024	6518023	OBD117.1.845	CTAGCCTCCTGCGTCTCAAC	OBD117.1.847
456	6514024	6518023	OBD117.1.861	GCTCTTGCTGCATGTCCTCT	OBD117.1.863
457	114973747	114977746	OBD117.1.917	TTGCTTGTGAGTTTGATGCAG	OBD117.1.919
458	120913546	120917545	OBD117.1.361	GACGCTCTCCCTTTGCTCAAGCC	OBD117.1.363
459	120936469	120940468	OBD117.1.333	GCTGTGTATCTCAGGGCACTCAG	OBD117.1.335
460	136937364	136941363	OBD117.1.869	TGAAGAAGCACTCGTCGTTG	OBD117.1.871

Table 13.i6

	Inner_primers	
	PCR_Primer2	GLMNET
417	GTTCCTGTGAAGGGTGAAGC	0.015890823
418	CTCTGGTCCTGTAGTCCTCAGTG	0.000171766
419	CTCCCTGTCTGAGCATCTCTCTC	-0.007266336
420	AGGAGGGATACACCTAAGGCAGC	0.013024
421	GGAGGGATACACCTAAGGCAGCC	-0.000108617
422	CTCTGGTCCTGTAGTCCTCAGTG	0
423	TCCTGCCTCAGCCTCCCAAGTAG	0
424	TAATGGTTGAAATGTGAGTCTGAAT	0
425	GGTGCTATGTTTGATTTAGGAGGTAT	0
426	TCCTTTGACCTTTCTGGACTCAG	0
427	GTGGAGAATGTAGTATTATGAAGGTT	0
428	AGTTTTGACAGAAAGTAGAGGTTCCT	0
429	GTGGAGAATGTAGTATTATGAAGGTT	0
430	ATGAAAACTTATCCCAAAGAAACTTC	0

431	GCCTAAGAGAAAAGCACACAGACTCC	0.00674446
432	GGACAGGAATCCATAGGGAAGAAGT	0
433	GAGTGCTCTGGCTCTACACG	0.0001037
434	TGCTCTGGCTCTACACGTC	0.000117852
435	AGTGCTCTGGCTCTACACGTC	0.000136129
436	AGCAAATCCTCCAGGCAGCCAGG	-0.013597927
437	GATGATTTGACACTTTCCCCACACAC	0
438	GCAGGAACTGGTGCTGGAATAGGC	0
439	GCAGGAGGATACAACTGTCAAAACTC	0.004679577
440	GCATCTAAAAATCGCCTGGA	-0.006781145
441	CTGTAGTTCTGTAAGCGTCTCCCACG	-0.013087312
442	ATCCCATCCAAGGCATCATA	-0.010277817
443	CCATTGTGCACATACACTGC	0
444	CTCCCAGGCTTGACGAGAGG	-0.000111539
445	CTCCCAGGCTTGACGAGAGG	0.021717076
446	CCCCGAGGGTTGAGAAGCAT	0.000094
447	GGGCAGGGACTAAGGTCTGACTT	0
448	CCGCCACTCAGCCATTGTTTCCA	0
449	GGGTTCTTGTCCTCCTTATGGAT	0
450	GTAGTAGAGAGTGCGGTGCC	0
451	ATCGGGCTTCCGAAGAAGGG	0.000108061
452	GGGAAAATCGGTGTGGCTGGCTC	-0.009810191
453	ATACGGACTGAGCCCTATGACGC	-0.020246781
454	AATAACCTGTGCCCAGACCGAGC	0.016525715
455	GCTGAGACTGTAGACGTGAACC	0.005356938
456	AGACGTGAACCTCCATACCTG	0.000119941
457	AAGCCAAATGGGCCTAGCCA	0.012278549
458	TGGAGCAGAACCTGTCAGACCTG	0.011703991
459	CCTGGAGCAGAACCTGTCAGACC	-0.01117453
460	AGCGGCACACCTCTACTCTC	-0.018227673

Table 13.i7

Gene	Marker	GLMNET
AKT1	OBD117.1.833.835	0.000126471
BAD	OBD117.1.265.267	0
BAX	OBD117.1.781.783	-0.0000963
BBC3	OBD117.1.405.407	-0.012797314
BID	OBD117.1.277.279	-0.001049357
BOK	OBD117.1.737.739	0.000120571
C8A	OBD117.1.817.819	-0.003603391
C8A	OBD117.1.1573.1575	0
C8B	OBD117.1.321.323	-0.002344366
CASP6	OBD117.1.821.823	-0.015124118
CASP9	OBD117.1.121.123	0.003583466
CBLB	OBD117.1.1453.1455	0
CD14	OBD117.1.797.799	0.000119448
CD2	OBD117.1.009.011	0.007257883
CD4	OBD117.1.769.771	-0.007336559
CD6	OBD117.1.345.347	0.013413486
CD6	OBD117.1.373.375	-0.020821569
CD6	OBD117.1.337.339	0.017522073
CD6	OBD117.1.329.331	0.000137163
CD6	OBD117.1.085.087	-0.009581325
CD6	OBD117.1.293.295	-0.003930475
CD82	OBD117.1.393.395	-0.013038403

CD82	OBD117.1.741.743	-0.009743329
CD82	OBD117.1.025.027	-0.015977346
CFP	OBD117.1.941.943	0
CRADD	OBD117.1.109.111	-0.00783453
EGF	OBD117.1.117.119	0.01716512
ELK1	OBD117.1.429.431	0
FAS	OBD117.1.133.135	-0.016360123
FAS	OBD117.1.409.411	-0.006985618
FCGR2B	OBD117.1.713.715	-0.00011137
HLA-DQA1	OBD117.1.385.387	0.001576194
ICOSLG	OBD117.1.353.355	-0.010502797
IGF1R	OBD117.1.777.779	-0.008978891
IGF2	OBD117.1.801.803	0.00011913
IKBKB	OBD117.1.825.827	0.000123838
IKBKB	OBD117.1.201.203	-0.003994085
IKBKB	OBD117.1.417.419	-0.023515041
IKBKB	OBD117.1.753.755	0.01434467
IKBKB	OBD117.1.077.079	-0.001425541
IKBKB	OBD117.1.261.263	0.01710902
IL17D	OBD117.1.645.647	-0.0134076
IL17RA	OBD117.1.537.539	0
IRF1	OBD117.1.805.807	0.006327654
IRF1	OBD117.1.785.787	0.000121603
IRF1	OBD117.1.837.839	0.000116599
IRF2	OBD117.1.1077.1079	0

Table 14.a

Gene	Marker	GLMNET
IRF3	OBD117.1.197.199	0.018616515
ITGAM	OBD117.1.789.791	-0.01814247
ITGAM	OBD117.1.309.311	-0.010425
ITGAM	OBD117.1.937.939	0
ITGAX	OBD117.1.369.371	0.00590703
ITK	OBD117.1.269.271	0.013514368
ITK	OBD117.1.397.399	-0.009002897
ITK	OBD117.1.773.775	0.000108207
ITK	OBD117.1.001.003	-0.006474726
ITK	OBD117.1.041.043	-0.021298663
LYN	OBD117.1.809.811	-0.024082323
MAPKAP1	OBD117.1.257.529	0.017680421
MTOR	OBD117.1.793.795	0.01727269
MYC	OBD117.1.377.379	-0.006220015
MYC	OBD117.1.045.047	-0.010058174
NCK2	OBD117.1.813.815	0.000127348
NFKBIE	OBD117.1.049.051	-0.009744914
NFKBIE	OBD117.1.1069.1071	0
ORF102	OBD117.1.893.895	0.008460581
CCL18	OBD117.1.389.391	-0.011403512
ORF107	OBD117.1.1045.1047	0
CCR6	OBD117.1.185.187	0.005137905
ORF110	OBD117.1.953.955	-0.007948899
CD180	OBD117.1.313.315	0.000116162
CD19	OBD117.1.125.127	-0.011725271
ORF116	OBD117.1.1293.1295	0
ORF117	OBD117.1.433.435	0
ORF118	OBD117.1.1221.1223	0

ORF120	OBD117.1.577.579	0.001022887
ORF120	OBD117.1.625.627	-0.005572532
ORF128	OBD117.1.913.915	0.000119295
CD6	OBD117.1.089.091	0
CD6	OBD117.1.237.139	0.00011596
CD6	OBD117.1.153.155	-0.014829951
ORF136	OBD117.1.1865.1867	0
ORF136	OBD117.1.1501.1503	0
CD86	OBD117.1.253.255	-0.001718735
ORF139	OBD117.1.1305.1307	0
ORF140	OBD117.1.1193.1195	0
ORF140	OBD117.1.1117.1119	0
ORF140	OBD117.1.1517.1519	0
ORF140	OBD117.1.1533.1535	0
ORF140	OBD117.1.1393.1395	0
ORF142	OBD117.1.957 .959	0.009388509
ORF142	OBD117.1.501.503	0
ORF142	OBD117.1.473.475	0
ORF145	OBD117.1.1597.1599	0
ORF146	OBD117.1.1641.1643	0
ORF147	OBD117.1.1633.1635	0
ORF149	OBD117.1.481.483	0
ORF149	OBD117.1.453.455	0
ORF149	OBD117.1.493.495	0
ORF149	OBD117.1.509.511	0
ORF149	OBD117.1.529.531	0

Table 14.b

Gene	Marker	GLMNET
ORF149	OBD117.1.973.975	0
ORF149	OBD117.1.441.443	-0.017184561
ORF149	OBD117.1.469.471	0.001327318
ORF149	OBD117.1.437.439	0
ORF149	OBD117.1.513.515	0
ORF149	OBD117.1.489.491	0
ORF157	OBD117.1.1521.1523	0
ORF159	OBD117.1.1549.1551	0
ORF159	OBD117.1.1169.1171	0
ORF159	OBD117.1.1253.1255	0
ORF159	OBD117.1.1329.1331	0
ORF16	OBD117.1.1309.1311	0
ORF160	OBD117.1.1025.1027	0
ORF160	OBD117.1.609.611	0.011827837
ORF160	OBD117.1.701.703	0.00010841
CRADD	OBD117.1.213.215	0.012057101
CSF2	OBD117.1.225.227	0.002120736
ORF171	OBD117.1.1209.1211	0
ORF171	OBD117.1.1121.1221	0
ORF175	OBD117.1.605.607	-0.005375017
ORF179	OBD117.1.1673.1675	0
ORF185	OBD117.1.909.911	0.019526388
ORF188	OBD117.1.1241.1243	0
ORF189	OBD117.1.1409.1411	0
ORF190	OBD117.1.1805.807	0
ORF190	OBD117.1.1781.1783	0
ORF190	OBD117.1.1769.1771	0

ORF193	OBD117.1.1413.1415	0
ORF195	OBD117.1.1817.1819	0
ORF195	OBD117.1.1097.1099	0
ORF197	OBD117.1.661.663	0.027392782
ORF197	OBD117.1.613.615	0.0000923
ORF20	OBD117.1.1593.1595	0
ORF20	OBD117.1.1265.1267	0
ORF202	OBD117.1.497.499	0
ORF205	OBD117.1.1373.1375	0
ORF206	OBD117.1.1561.1563	0
EGF	OBD117.1.149.151	-0.013629912
ORF211	OBD117.1.1425.1427	0
ORF211	OBD117.1.1433.1435	0
ORF212	OBD117.1.521.523	0
ORF213	OBD117.1.1669.1671	0
ORF214	OBD117.1.1145.1147	0
ORF214	OBD117.1.1105.1107	0
ENDOU	OBD117.1.325.327	0
ORF224	OBD117.1.1261.1263	0
F3	OBD117.1.113.115	0.006221331
ORF229	OBD117.1.1553.1555	0
ORF229	OBD117.1.1365.1367	0
ORF229	OBD117.1.1629.1631	0
ORF233	OBD117.1.1321.1323	0
ORF240	OBD117.1.1557.1559	0
FAS	OBD117.1.305.307	0.011677917
ORF243	OBD117.1.649.651	-0.003930014

Table 14.c

Gene	Marker	GLMNET
ORF243	OBD117.1.717.719	-0.023642297
ORF243	OBD117.1.901.903	0.007197773
ORF243	OBD117.1.905.907	-0.014372166
ORF243	OBD117.1.573.575	-0.000142339
ORF243	OBD117.1.897.899	0.009781389
ORF249	OBD117.1.1317.1319	0
ORF249	OBD117.1.1529.1531	0
ORF25	OBD117.1.1445.1447	0
ORF25	OBD117.1.1165.1167	0
ORF252	OBD117.1.1201.1203	0
ORF257	OBD117.1.1401.1403	0
GAB2	OBD117.1.141.143	-0.007419107
ORF263	OBD117.1.1325.1327	0
ORF264	OBD117.1.1333.1335	0
ORF264	OBD117.1.1833.1835	0
ORF264	OBD117.1.1785.1787	0
ORF264	OBD117.1.1377.1379	0
ORF264	OBD117.1.1741.1743	0
ORF264	OBD117.1.1141.1143	0
ORF264	OBD117.1.1841.1843	0
ORF264	OBD117.1.1845.1847	0
ORF272	OBD117.1.1225.1227	0
ORF276	OBD117.1.1061.1063	0
ORF285	OBD117.1.923.925	0.000121346
ORF290	OBD117.1.1777.1779	0
ORF290	OBD117.1.1101.1103	0

HLA-DQA1	OBD117.1.401.403	0.009992562
HLA-DQA1	OBD117.1.721.723	0.00011425
HLA-DQA1	OBD117.1.413.415	0.002234049
HLA-DQA1	OBD117.1.425.427	0.0000993
ORF30	OBD117.1.1749.1751	0
IGF1R	OBD117.1.209.211	0.012827643
IGF1R	OBD117.1.317.319	-0.010330599
IGF1R	OBD117.1.101.103	0.0000979
IKBKB	OBD117.1.757.759	0.00012094
IKBKB	OBD117.1.281.283	-0.00399849
IKBKB	OBD117.1.037.039	0.002891486
IKBKB	OBD117.1.073.075	0.017565968
ORF313	OBD117.1.693.695	-0.022219432
ORF313	OBD117.1.929.931	-0.015662127
ORF313	OBD117.1.665.667	0.000119444
ORF313	OBD117.1.581.583	-0.027382095
ORF316	OBD117.1.1041.1043	0
ORF316	OBD117.1.485.487	0
IL25	OBD117.1.289.291	0.007589853
ORF319	OBD117.1.1017.1019	0
ORF325	OBD117.1.881.883	0.000113252
ORF325	OBD117.1.1129.1131	0
ORF325	OBD117.1.653.655	0.003005705
IRF1	OBD117.1.765.767	-0.010031296
IRF3	OBD117.1.285.287	-0.025409945
ITGAX	OBD117.1.177.179	0.006986068
ITGAX	OBD117.1.173.175	0.004807037
ITK	OBD117.1.165.167	-0.004038003

Table 14.d

Gene	Marker	GLMNET
ORF344	OBD117.1.585.587	0.000108113
ORF344	OBD117.1.593.595	-0.012488304
ORF346	OBD117.1.1717.1719	0
ORF346	OBD117.1.1617.1919	0
ORF348	OBD117.1.1289.1291	0
ORF348	OBD117.1.1605.1607	0
ORF362	OBD117.1.1513.1515	0
ORF362	OBD117.1.1469.1471	0
ORF368	OBD117.1.1337.1339	0
ORF369	OBD117.1.925.927	0.015771071
ORF375	OBD117.1.1397.1399	0
ORF38	OBD117.1.1113.1115	0
ARHGEF7	OBD117.1.157.159	-0.008898153
ORF38	OBD117.1.1457.1459	0
ARHGEF7	OBD117.1.725.727	0.00011344
ORF380	OBD117.1.1849.1851	0
ORF380	OBD117.1.1829.1831	0
ORF382	OBD117.1.1421.1423	0
ORF385	OBD117.1.977.979	0
ORF385	OBD117.1.965.967	-0.006509693
ORF39	OBD117.1.1821.1823	0
ORF39	OBD117.1.1857.1859	0
ORF390	OBD117.1.1301.1303	0
ORF393	OBD117.1.1229.1231	0
ORF396	OBD117.1.477.479	0.011140328

ORF396	OBD117.1.553.555	0
ORF400	OBD117.1.1177.1179	0
MAPK10	OBD117.1.221.223	-0.009554407
MAPKAP1	OBD117.1.033.035	-0.010767501
ORF404	OBD117.1.1133.1135	0
ORF404	OBD117.1.1285.1287	0
ORF408	OBD117.1.1693.1695	0
ORF41	OBD117.1.1581.1583	0
ORF41	OBD117.1.1637.1639	0
ORF415	OBD117.1.1713.1715	0
ORF415	OBD117.1.1205.1207	0
ORF420	OBD117.1.1729.1731	0
ORF430	OBD117.1.1429.1431	0
ORF430	OBD117.1.1089.1091	0
ORF430	OBD117.1.1589.1591	0
ORF430	OBD117.1.1493.1495	0
ORF430	OBD117.1.1661.1663	0
ORF430	OBD117.1.1081.1083	0
ORF430	OBD117.1.1085.1087	0
ORF430	OBD117.1.1509.1511	0
ORF430	OBD117.1.1489.1491	0
ORF433	OBD117.1.1053.1055	0
ORF439	OBD117.1.1697.1699	0
ORF440	OBD117.1.1149.1151	0
ORF440	OBD117.1.1505.1507	0
PIK3R1	OBD117.1.829.831	0.000114527
ORF442	OBD117.1.1417.1419	0
ORF442	OBD117.1.1677.1679	0
ORF447	OBD117.1.1021.1023	0

Table 14.e

Gene	Marker	GLMNET
ORF447	OBD117.1.885.887	0.019910002
NCK2	OBD117.1.749.751	0.011140328
PVRL1	OBD117.1.057.059	0.002451894
ORF457	OBD117.1.1161.1163	0
ORF457	OBD117.1.1281.1283	0
ORF457	OBD117.1.1665.1667	0
ORF458	OBD117.1.1657.1659	0
ORF458	OBD117.1.1809.1811	0
ORF460	OBD117.1.1341.1343	0
ORF462	OBD117.1.1269.1271	0
NFKBIE	OBD117.1.065.067	0.006729048
NFKBIE	OBD117.1.1065.1067	0
ORF465	OBD117.1.1249.1251	0
ORF472	OBD117.1.641.643	0.000955334
PAG1	OBD117.1.081.083	0.0196745
PAG1	OBD117.1.145.147	0.012784814
PAG1	OBD117.1.129.131	0.000107394
PAG1	OBD117.1.105.107	0.011672595
PAG1	OBD117.1.217.219	0.006914365
ORF48	OBD117.1.709.711	0.000126022
ORF48	OBD117.1.705.707	-0.002734128
PAK1	OBD117.1.297.299	-0.020410863
ORF481	OBD117.1.1545.1547	0
ORF482	OBD117.1.669.671	0.022244309

ORF489	OBD117.1.1645.1647	0
ORF494	OBD117.1.1277.1279	0
ORF500	OBD117.1.1361.1363	0
PIK3R1	OBD117.1.069.071	-0.007209703
PIK3R1	OBD117.1.735.737	0.000117929
ORF505	OBD117.1.569.571	0.000114434
ORF510	OBD117.1.1461.1463	0
ORF510	OBD117.1.1525.1527	0
ORF510	OBD117.1.1381.1383	0
ORF510	OBD117.1.1137.1139	0
ORF514	OBD117.1.561.563	0.010030034
ORF518	OBD117.1.1853.1855	0
ORF52	OBD117.1.1313.1315	0
ORF520	OBD117.1.1473.1475	0
ORF520	OBD117.1.1157.1159	0
ORF527	OBD117.1.1345.1347	0
PRKCQ	OBD117.1.365.367	0.007672168
PRR5	OBD117.1.005.007	0.016924425
ORF532	OBD117.1.1565.1567	0
ORF532	OBD117.1.1217.1219	0
ORF534	OBD117.1.673.675	0.006586768
PTK2	OBD117.1.229.231	-0.017032217
PTK2	OBD117.1.233.235	0.000119638
PTK2	OBD117.1.357.359	-0.01499141
PTPN11	OBD117.1.761.763	0.00011938
ORF541	OBD117.1.1757.1759	0
ORF541	OBD117.1.1721.1723	0
PTPRC	OBD117.1.189.191	-0.020382337
ORF544	OBD117.1.1237.1239	0
ORF544	OBD117.1.1801.1803	0

Table 14.f

Gene	Marker	GLMNET
ORF544	OBD117.1.1173.1175	0
ORF547	OBD117.1.1541.1543	0
ORF547	OBD117.1.1737.1739	0
BAD	OBD117.1.341.343	0.007677493
BAD	OBD117.1.245.247	0.017957539
ORF552	OBD117.1.689.691	0
RAC1	OBD117.1.729.731	-0.01057369
ORF554	OBD117.1.1761.1763	0
ORF556	OBD117.1.1869.1871	0
ORF558	OBD117.1.1837.1839	0
ORF56	OBD117.1.617.619	0
ORF56	OBD117.1.685.687	-0.005472121
ORF560	OBD117.1.1357.1359	0
ORF560	OBD117.1.1577.1579	0
ORF564	OBD117.1.1709.1711	0
RELA	OBD117.1.017.019	0.005732814
ORF568	OBD117.1.1185.1187	0
ORF569	OBD117.1.1613.1615	0
ORF57	OBD117.1.1653.1655	0
ORF57	OBD117.1.1681.1683	0
ORF576	OBD117.1.1813.1815	0
ORF576	OBD117.1.1765.1767	0
ORF576	OBD117.1.1825.1827	0
ORF586	OBD117.1.1153.1155	0

ORF586	OBD117.1.1585.1587	0
ORF589	OBD117.1.1349.1351	0
ORF59	OBD117.1.1609.1611	0
ORF596	OBD117.1.1109.1111	0
ORF596	OBD117.1.1789.1791	0
ORF603	OBD117.1.1197.1199	0
ORF603	OBD117.1.1705.1707	0
ORF605	OBD117.1.601.603	-0.010880594
ORF605	OBD117.1.889.891	-0.013055638
ORF611	OBD117.1.1441.1443	0
SIRPA	OBD117.1.161.163	-0.014311214
ORF613	OBD117.1.557.559	0
ORF618	OBD117.1.1181.1183	0
ORF624	OBD117.1.589.591	-0.005626404
ORF626	OBD117.1.961.963	-0.013176922
ORF626	OBD117.1.449.451	-0.000113816
ORF626	OBD117.1.445.447	-0.026223064
ORF626	OBD117.1.1033.1035	0
ORF626	OBD117.1.969.971	0
ORF630	OBD117.1.1497.1499	0
SMAD3	OBD117.1.061.063	0
SPN	OBD117.1.945.947	-0.016440702
SPN	OBD117.1.985.987	0
ORF642	OBD117.1.989.991	0
ORF642	OBD117.1.1037.1039	0
ORF657	OBD117.1.1093.1095	0
ORF657	OBD117.1.1481.1483	0
ORF657	OBD117.1.1725.1727	0
ORF667	OBD117.1.1701.1703	0
ORF670	OBD117.1.1449.1451	0

Table 14.g

Gene	Marker	GLMNET
ORF671	OBD117.1.1485.1487	0
ORF684	OBD117.1.1189.1191	0
ORF685	OBD117.1.1389.1391	0
ORF690	OBD117.1.1797.1799	0
ORF695	OBD117.1.549.551	0.009721306
ORF696	OBD117.1.1029.1031	0
ORF696	OBD117.1.681.683	0.007305849
ORF696	OBD117.1.677.679	0.001120789
ORF697	OBD117.1.461.463	-0.017294821
ORF697	OBD117.1.541.543	0.000113082
ORF698	OBD117.1.457.459	0.000110518
ORF698	OBD117.1.981.983	0
ORF698	OBD117.1.505.507	0.027764821
ORF698	OBD117.1.1625.1627	0
TNFRSF11A	OBD117.1.053.055	0.008919637
ORF698	OBD117.1.1745.1747	0
ORF699	OBD117.1.465.467	-0.009297019
ORF699	OBD117.1.533.535	0
ORF70	OBD117.1.1773.1775	0
ORF700	OBD117.1.525.527	-0.016217397
ORF700	OBD117.1.993.995	0
TNFRSF25	OBD117.1.381.383	0.000134142
TNFRSF25	OBD117.1.193.195	0
TNFRSF25	OBD117.1.181.183	-0.007419688

TNFRSF25	OBD117.1.137.139	-0.005042919
TNFRSF25	OBD117.1.745.747	0.020530456
ORF705	OBD117.1.545.547	0.013121857
ORF705	OBD117.1.1049.1051	0
ORF705	OBD117.1.517.519	0.012738078
TNFSF8	OBD117.1.273.275	0.010145959
ORF706	OBD117.1.1385.1387	0
TP73	OBD117.1.349.351	-0.021145842
ORF71	OBD117.1.697.699	0.006301587
ORF71	OBD117.1.597.599	0.01482896
TRAF1	OBD117.1.021.023	-0.016381908
TRAF1	OBD117.1.301.303	0.024168377
TRAF1	OBD117.1.013.015	-0.003508085
TRAF1	OBD117.1.169.171	-0.01000752
ORF718	OBD117.1.949.951	-0.018046798
ORF722	OBD117.1.933.935	0.008860872
ORF730	OBD117.1.1873.1875	0
ORF741	OBD117.1.1233.1235	0
BOK	OBD117.1.841.843	0.000117272
ORF762	OBD117.1.1649.1651	0
ORF83	OBD117.1.1013.1015	0
ORF83	OBD117.1.877.879	0.015890823
ORF83	OBD117.1.637.639	0.000171766
ORF83	OBD117.1.657.659	-0.007266336
ORF83	OBD117.1.565.567	0.013024
ORF83	OBD117.1.629.631	-0.000108617
ORF83	OBD117.1.633.635	0
ORF86	OBD117.1.1685.1687	0
ORF99	OBD117.1.1297.1299	0
ORF99	OBD117.1.1537.1539	0

Table 14.h

Gene	Marker	GLMNET
ORF99	OBD117.1.1353.1355	0
ORF99	OBD117.1.1477.1479	0
ORF99	OBD117.1.1689.1691	0
ORF99	OBD117.1.1601.1603	0
ORF99	OBD117.1.1125.1127	0
CBLB	OBD117.1.205.207	0.00674446
ORF99	OBD117.1.1369.1371	0
PIK3R1	OBD117.1.853.855	0.0001037
PIK3R1	OBD117.1.849.851	0.000117852
PIK3R1	OBD117.1.857.859	0.000136129
PRR5	OBD117.1.249.251	-0.013597927
PTPRC	OBD117.1.1437.1439	0
PTPRC	OBD117.1.1245.1247	0
RPTOR	OBD117.1.097.099	0.004679577
RPTOR	OBD117.1.865.867	-0.006781145
RPTOR	OBD117.1.093.095	-0.013087312
SHH	OBD117.1.873.875	-0.010277817
SHH	OBD117.1.1073.1075	0
SPN	OBD117.1.1001.1003	-0.000111539
SPN	OBD117.1.1009.1011	0.021717076
STAT5B	OBD117.009.011	0.000094
SYK	OBD117.1.1213.1215	0
SYK	OBD117.1.1273.1275	0
TNFRSF11A	OBD117.1.1793.1795	0

TNFRSF13C	OBD117.1.997.999	0
TNFRSF1A	OBD117.1.1005.1007	0.000108061
TNFRSF25	OBD117.1.421.423	-0.009810191
TNFRSF25	OBD117.1.241.243	-0.020246781
TNFRSF25	OBD117.1.029.031	0.016525715
TNFRSF25	OBD117.1.845.847	0.005356938
TNFRSF25	OBD117.1.861.863	0.000119941
TNFSF8	OBD117.1.917.919	0.012278549
TRAF1	OBD117.1.361.363	0.011703991
TRAF1	OBD117.1.333.335	-0.01117453
TRAF2	OBD117.1.869.871	-0.018227673

Table 14.i

CD2	CD2 Molecule	Protein coding gene, associated with penis squamous cell carcinoma and immune defect due to absence of thymus, related to Akt signaling and hematopoietic stem cell differentiation pathways and lineage-specific markers
CFP	Complement Factor Properdin	Protein coding gene, associated with properdin deficiency, X-linked and properdin deficiency, related to Immune response Lectin induced complement pathway and O-linked glycosylation
ELK1	ELK1 ETS Transcription Factor	Protein coding gene, associated with Hypervitaminosis A, related to p38 MAPK signaling pathway (WikiPathways) and focal ddhesion.
FCGR2B	Fc Fragment Of IgG Receptor IIb	Protein coding gene, associated with systemic lupus erythematosus and malaria, related to Immune response Fc epsilon RI pathway and Fc-gammaR pathway
IL17D	Interleukin 17D	Protein coding gene, associated with psoriasis, related pathways are IL-17 family signaling pathways and C-type lectin receptor signaling pathway
IL17RA	Interleukin 17 Receptor A	Protein coding gene, associated with immunodeficiency 51 and chronic mucocutaneous candidiasis, related to Akt and ERK signaling
TNFRSF13C	TNF Receptor Superfamily Member 13C	Protein coding gene, associated with immunodeficiency, common variable, 4 and common variable immunodeficiency, related to Akt signaling and NF-kappa B signaling pathway

Table 15

	Probe	GeneLocus	Probe_Count_Total	Probe_Count_Sig
1	IL17RA_22_17555467_17556730_17583829_17589696_RF	IL17RA	23	14
2	TP53_17_7568905_7571771_7590321_7591415_FF	TP53	8	5
3	IL4_5_131966700_131972322_132015552_132017427_FF	IL4	17	10
4	EFNB1_X_68004262_68015195_68068238_68069630_RR	EFNB1	24	12
5	IFNA2_9_21392770_21395335_21414238_21418494_FF	IFNA2	30	8
6	BBC3_19_47759469_47760963_47778641_47780208_FR	BBC3	12	7
7	KLRK1_12_10544349_10549161_10570098_10578163_RF	KLRK1	30	11
8	IFNA1_9_21392770_21395335_21437777_21443318_RR	IFNA1	8	3
9	PIK3CA_3_178832360_178841413_178871576_178873671_FF	PIK3CA	25	13
10	BIRC2_11_102178257_102181848_102266251_102268479_FF	BIRC2	13	4
11	PDCD1_2_242777613_242779346_242826000_242827096_FF	PDCD1	12	6
12	XIAP_X_123017153_123019333_123035293_123038006_FR	XIAP	13	3
13	AKT1_14_105266348_105267359_105305709_105309658_RF	AKT1	18	11
14	ARHGEF7_13_111822569_111834523_111970320_111973116_FF	ARHGEF7	175	56
15	ARHGEF7_13_111908346_111914493_111970320_111973116_FF	ARHGEF7	175	56
16	BCL2_18_60884271_60893545_60998913_61003098_FR	BCL2	193	30
17	C8B_1_57385955_57389539_57428402_57432779_FR	C8B	121	33
18	CBLB_3_105390159_105394525_105442255_105450516_FR	CBLB	168	42
19	CBLB_3_105390159_105394525_105547637_105554877_FR	CBLB	168	42
20	CCL16_17_34304462_34314203_34339929_34346837_RR	CCL16	32	9
21	CCL7_17_32553749_32557219_32574048_32580497_FR	CCL7	17	3
22	CD3E_11_118135384_118142619_118163915_118173402_RR	CD3E	13	2
23	CD3E_11_118144515_118145854_118163915_118173402_FR	CD3E	13	2
24	CD4_12_6876592_6883165_6912128_6913978_FR	CD4	14	7
25	CD40_20_44718691_44720694_44762355_44767158_RF	CD40	24	12
26	CD6_11_60689541_60692498_60785339_60793057_RF	CD6	62	33
27	CD6_11_60699859_60701154_60744556_60751199_FR	CD6	62	33
28	CDKN2A_9_21978375_21981767_22029988_22034038_FF	CDKN2A	14	10
29	FAS_10_90717744_90724423_90745185_90750176_FF	FAS	59	25
30	FCGR2B_1_161519223_161525894_161627152_161631654_RR	FCGR2B	72	28
31	FCGR2B_1_161562782_161569954_161627152_161631654_FR	FCGR2B	72	28
32	IKBKB_8_42099384_42103137_42121759_42128721_RF	IKBKB	24	12
33	IKBKB_8_42121759_42128721_42148497_42149642_FF	IKBKB	24	12
34	IKBKB_8_42121759_42128721_42159959_42162198_FF	IKBKB	24	12
35	IKBKB_8_42121759_42128721_42159959_42162198_FR	IKBKB	24	12
36	MAPK1_22_22117703_22122470_22210841_22217782_RR	MAPK1	48	10
37	MAPKAP1_9_128280753_128289273_128393518_128397379_RF	MAPKAP1	100	22
38	MTOR_1_11245934_11254334_11280008_11283155_FF	MTOR	149	42
39	NCK2_2_106375590_106379449_106403393_106408079_RR	NCK2	164	36
40	NCK2_2_106403393_106408079_106439151_106441507_FR	NCK2	164	36
41	PAK1_11_77141424_77148888_77185846_77188900_FR	PAK1	155	38
42	PTK2_8_141745642_141749152_141773261_141781505_FF	PTK2	152	48
43	PTPRA_20_2797355_2801691_3004582_3011246_RF	PTPRA	137	57
44	PTPRA_20_2853761_2858838_2966772_2970097_RF	PTPRA	137	57
45	PTPRA_20_2853761_2858838_3004582_3011246_RF	PTPRA	137	57
46	PTPRA_20_2943750_2948659_2966772_2970097_RF	PTPRA	137	57
47	PVR_19_45099561_45103576_45113698_45116399_FF	PVR	25	13
48	PVR_19_45099561_45103576_45167560_45168855_FR	PVR	25	13
49	PVRL1_11_119551289_119555164_119570787_119575859_FF	PVRL1	95	44
50	PVRL1_11_119581897_119584757_119599998_119609544_FR	PVRL1	95	44
51	PVRL1_11_119599998_119609544_119620830_119624585_RF	PVRL1	95	44
52	SHH_7_155593268_155595881_155627543_155630456_RR	SHH	25	12
53	SIRPA_20_1830612_1833775_1864775_1869190_RR	SIRPA	56	12
54	SIRPA_20_1830612_1833775_1905279_1911608_RF	SIRPA	56	12

55	SRC_20_35981178_35984981_36049517_36053821_RF	SRC	25	0
56	SYK_9_93529835_93536915_93555880_93559839_RR	SYK	141	48
57	TNFRSF11B_8_119933591_119936942_119958900_119964996_FR	TNFRSF11B	24	12
58	TNFRSF11B_8_119958900_119964996_119985773_119986987_RR	TNFRSF11B	24	12
59	TNFRSF25_1_6521664_6526267_6541388_6544308_RF	TNFRSF25	23	16
60	TP63_3_189395557_189406042_189416264_189422493_FR	TP63	131	44
61	TRBV12-3_HG7_PATCH_142268038_142272453_142299803_142302443_FF	TRBV12-3	21	7
62	TYROBP_19_36380190_36382489_36405491_36408643_FR	TYROBP	8	3
63	YES1_18_703962_705806_820113_825053_RF	YES1	12	2

Table 16.a

	HyperG_Stats	FDR_HyperG	Percent_Sig	logFC	AveExpr	t
1	0.000115042	0.007430257	60.87	-0.013772346	-0.013772346	-0.240285183
2	0.019609346	0.224493201	62.5	0.147930594	0.147930594	1.54773245
3	0.001648192	0.054719962	58.82	-0.09302015	-0.09302015	-0.9155182
4	0.003650795	0.086576007	50	0.22695709	0.22695709	3.4316055
5	0.581066149	1	26.67	-0.42260763	-0.42260763	-7.3816234
6	0.021403774	0.222064153	58.33	0.52026112	0.52026112	8.1265262
7	0.158099772	0.672937493	36.67	-0.45326382	-0.45326382	-5.2822758
8	0.369467375	1	37.5	-0.39902611	-0.39902611	-6.1923548
9	0.006619293	0.146507027	52	-0.44521152	-0.44521152	-7.5310764
10	0.479547592	1	30.77	-0.46394556	-0.46394556	-7.8281466
11	0.07482778	0.443952662	50	-0.33213477	-0.33213477	-5.1973943
12	0.722168484	1	23.08	-0.63653446	-0.63653446	-4.1311757
13	0.002366254	0.071417842	61.11	0.471980659	0.471980659	7.433543962
14	0.075877919	0.443952662	32	0.102617139	0.102617139	1.288701188
15	0.075877919	0.443952662	32	0.050243809	0.050243809	0.810857617
16	0.99994673	1	15.54	0.030761848	0.030761848	0.459625443
17	0.49856502	1	27.27	0.087796109	0.087796109	0.831720025
18	0.739516406	1	25	-0.01141347	-0.01141347	-0.203551326
19	0.739516406	1	25	-0.017865418	-0.017865418	-0.321765089
20	0.505143193	1	28.12	0.084236571	0.084236571	1.302140629
21	0.875581427	1	17.65	-0.045569025	-0.045569025	-0.753475926
22	0.901807168	1	15.38	0.081062908	0.081062908	0.685184811
23	0.901807168	1	15.38	0.060479289	0.060479289	0.503342984
24	0.055268149	0.407756121	50	-0.01956492	-0.01956492	-0.202506703
25	0.01320722	0.182699883	50	0.453964947	0.453964947	4.645992114
26	9.60E-06	0.001593482	53.23	0.465039657	0.465039657	7.987834809
27	9.60E-06	0.001593482	53.23	0.449010255	0.449010255	7.086525198
28	0.000646498	0.035772897	71.43	0.463949032	0.463949032	6.463178912
29	0.007195307	0.149302618	42.37	0.498577819	0.498577819	7.028755206
30	0.017535464	0.207920508	38.89	-0.030766524	-0.030766524	-0.553783792
31	0.017535464	0.207920508	38.89	0.115781119	0.115781119	1.99167408
32	0.01320722	0.182699883	50	0.416374779	0.416374779	4.865919407
33	0.01320722	0.182699883	50	0.418275622	0.418275622	4.359821333
34	0.01320722	0.182699883	50	0.381661827	0.381661827	4.157210523
35	0.01320722	0.182699883	50	0.377780658	0.377780658	5.221207867
36	0.869089583	1	20.83	0.05911233	0.05911233	0.930447108
37	0.891633842	1	22	0.126849618	0.126849618	1.741819751
38	0.391767947	1	28.19	-0.118120085	-0.118120085	-1.681387975
39	0.939603617	1	21.95	-0.03216772	-0.03216772	-0.494246209
40	0.939603617	1	21.95	-0.137021654	-0.137021654	-1.988270617
41	0.776895392	1	24.52	0.032810973	0.032810973	0.504074254
42	0.113105973	0.536445473	31.58	0.12642549	0.12642549	1.328126332

43	0.000126919	0.00842741	41.61	0.59038148	0.59038148	4.747669645
44	0.000126919	0.00842741	41.61	0.662663936	0.662663936	7.095181111
45	0.000126919	0.00842741	41.61	0.62773389	0.62773389	7.960830244
46	0.000126919	0.00842741	41.61	-0.034569831	-0.034569831	-0.540303228
47	0.006619293	0.146507027	52	0.510054367	0.510054367	7.019512745
48	0.006619293	0.146507027	52	0.46085773	0.46085773	5.690775832
49	3.65E-05	0.003027108	46.32	0.079697088	0.079697088	1.242102392
50	3.65E-05	0.003027108	46.32	0.568094527	0.568094527	6.294476998
51	3.65E-05	0.003027108	46.32	0.62095435	0.62095435	6.968998342
52	0.019288384	0.22081874	48	-0.109701651	-0.109701651	-1.612003006
53	0.860606844	1	21.43	0.128697259	0.128697259	2.281706671
54	0.860606844	1	21.43	0.028610792	0.028610792	0.429215356
55	1	1	0	0.091685254	0.091685254	1.589549618
56	0.036032885	0.332806348	34.04	0.022347263	0.022347263	0.277666921
57	0.01320722	0.182699883	50	0.525181749	0.525181749	4.601541756
58	0.01320722	0.182699883	50	0.527381914	0.527381914	9.698751213
59	2.37E-05	0.002619074	69.57	0.108337346	0.108337346	1.637060864
60	0.053257016	0.407756121	33.59	0.027917618	0.027917618	0.428723434
61	0.326841379	1	33.33	0.313249511	0.313249511	3.70351688
62	0.369467375	1	37.5	0.079273829	0.079273829	0.887069778
63	0.874170448	1	16.67	-0.02812739	-0.02812739	-0.494526106

Table 16.b

	P.Value	adj.P.Val	B	FC	FC_1	LS	Loop Detected
1	0.816795568	0.8914063	-6.653954243	0.990499158	-1.009591973	0	Non-Responder
2	0.164353966	0.314486691	-5.52937568	1.107979043	1.107979043	1	Responder
3	0.389499204	0.558346665	-6.2420323	0.937558	-1.066601	0	Non-Responder
4	0.010464785	0.05875152	-2.8122673	1.1703638	1.170364	1	Responder
5	0.000130857	0.00978135	1.6800907	0.7460749	-1.340348	-1	Non-Responder
6	0.0000699	0.009591857	2.2958233	1.4342148	1.434215	1	Responder
7	0.001040222	0.017977033	-0.4221012	0.7303886	-1.369134	-1	Non-Responder
8	0.000397981	0.012391118	0.562249	0.75837	-1.318617	-1	Non-Responder
9	0.000114934	0.00978135	1.8084821	0.7344766	-1.361514	-1	Non-Responder
10	0.0000893	0.00978135	2.0563379	0.7250008	-1.379309	-1	Non-Responder
11	0.001143977	0.018798179	-0.5201626	0.7943602	-1.258875	-1	Non-Responder
12	0.004120455	0.035897704	-1.8475599	0.6432563	-1.55459	-1	Non-Responder
13	0.00012506	0.00978135	1.724980841	1.387012375	1.387012375	1	Responder
14	0.237291965	0.4030718	-5.849682939	1.073719491	1.073719491	0	Responder
15	0.443374677	0.604581249	-6.333671754	1.035439894	1.035439894	0	Responder
16	0.65931764	0.779777623	-6.569484186	1.021551437	1.021551437	0	Non-Responder
17	0.432235131	0.596473312	-6.31612829	1.06274547	1.06274547	0	Non-Responder
18	0.84432778	0.909374308	-6.663031225	0.992119997	-1.007942591	0	Non-Responder

19	0.756754959	0.850026261	-6.628568047	0.987692994	-1.012460356	0	Non-Responder
20	0.232903788	0.397959585	-5.833902583	1.060126607	1.060126607	0	Non-Responder
21	0.475034273	0.631532497	-6.379996896	0.968907587	-1.032090174	0	Non-Responder
22	0.514636091	0.666439232	-6.431327032	1.057797087	1.057797087	0	Non-Responder
23	0.629727466	0.757957974	-6.546630196	1.042812144	1.042812144	0	Non-Responder
24	0.84511434	0.910037934	-6.663267658	0.986530172	-1.013653742	0	Non-Responder
25	0.002174068	0.025916536	-1.184382177	1.369799698	1.369799698	1	Responder
26	0.0000783	0.009721979	2.18565792	1.380355296	1.380355296	1	Responder
27	0.000170122	0.009942962	1.419020174	1.365103422	1.365103422	1	Responder
28	0.000304847	0.011606249	0.83266885	1.379312192	1.379312192	1	Responder
29	0.000179269	0.009942962	1.366705698	1.412820144	1.412820144	1	Responder
30	0.596468127	0.731758241	-6.517870372	0.978900056	-1.021554748	0	Non-Responder
31	0.08546631	0.204154819	-4.920965082	1.08356156	1.08356156	0	Non-Responder
32	0.001674193	0.022692964	-0.913760678	1.334569815	1.334569815	1	Responder
33	0.003086815	0.030845315	-1.547910416	1.336329355	1.336329355	1	Responder
34	0.003985576	0.035412035	-1.81303301	1.302841722	1.302841722	1	Responder
35	0.001113756	0.018506461	-0.492540142	1.2993415	1.2993415	1	Responder
36	0.382223612	0.551023134	-6.228239304	1.041824544	1.041824544	0	Non-Responder
37	0.123810276	0.260011317	-5.270706943	1.091906723	1.091906723	0	Non-Responder
38	0.135302587	0.276375393	-5.352673235	0.92138749	-1.085319706	0	Non-Responder
39	0.635827663	0.762978908	-6.551545554	0.977949776	-1.0225474	0	Non-Responder
40	0.085901221	0.204801549	-4.925826912	0.909394602	-1.099632654	0	Non-Responder
41	0.62923841	0.757540065	-6.546231435	1.023003423	1.023003423	0	Non-Responder
42	0.224617635	0.388210511	-5.803108233	1.091585768	1.091585768	0	Non-Responder
43	0.001925031	0.024132924	-1.0583223	1.50564482	1.50564482	1	Responder
44	0.000168797	0.009942962	1.426824141	1.583002941	1.583002941	1	Responder
45	0.00008	0.00978135	2.163976731	1.545136068	1.545136068	1	Responder
46	0.605261259	0.738428481	-6.525804538	0.976322828	-1.024251376	0	Non-Responder
47	0.000180782	0.009942962	1.358298716	1.424103861	1.424103861	1	Responder
48	0.000667147	0.015161131	0.034631546	1.376359866	1.376359866	1	Responder
49	0.253060559	0.421018665	-5.903603004	1.056796129	1.056796129	0	Non-Responder
50	0.000359565	0.012119064	0.665377174	1.482564146	1.482564146	1	Responder
51	0.000189314	0.010133451	1.312167529	1.537892169	1.537892169	1	Responder
52	0.149729695	0.295448526	-5.445243195	0.9267797	-1.079005075	0	Non-Responder
53	0.055409796	0.154727941	-4.499882988	1.09330601	1.09330601	0	Non-Responder
54	0.680295532	0.796125405	-6.58422725	1.02002944	1.02002944	0	Non-Responder

55	0.154696532	0.302455365	-5.474819603	1.06561423	1.06561423	0	Non-Responder
56	0.789058348	0.871284215	-6.643201491	1.015610533	1.015610533	0	Non-Responder
57	0.00229391	0.026232608	-1.24000317	1.439114867	1.439114867	1	Responder
58	0.0000215	0.008847609	3.417854093	1.441311246	1.441311246	1	Responder
59	0.144361583	0.288372184	-5.412012178	1.077985182	1.077985182	0	Non-Responder
60	0.680637436	0.796222402	-6.58445788	1.019539463	1.019539463	0	Non-Responder
61	0.007222384	0.047648108	-2.429187546	1.242503151	1.242503151	1	Responder
62	0.403646431	0.571190716	-6.267826761	1.056486132	1.056486132	0	Non-Responder
63	0.635639513	0.762924558	-6.551395561	0.980692405	-1.019687717	0	Non-Responder

Table 16.c

	Probe sequence	**Probe Location**	
	60 mer	**Chr**	**Start1**
1	GCGCCGCGGTACCCGCTCATGGACAGGTTCGAACTCCTGAGCTCAGGCACCTTGGCCTCC	22	17555467
2	CAGCAAAGTTTTATTGTAAAATAAGAGATCGAGCTCTTACTTGCTACCCAGCACTGATAT	17	7571740
3	AGTGATAGAAGAGGGACAAGGTGGCAGTTCGATATTAGATAACATCCACTCTGGGCTACA	5	131972291
4	CTCTGCCCATTCCATGTCCACGGCCCCCTCGACTTGAATGGGCTTGGCTGGGCTGGGACA	X	68004262
5	AAGGATATCTAGGGCATAAAAATAAAAATCGATCTCCTGATCTCATGATCCACCTGCCTC	9	21395304
6	GAATCCTTTCGGGGGAGGCGGGAGGCTGTCGAGAGCTCTGTGCTCCACGCCGAGGATGCA	19	47760932
7	CGTGACTGTATATCATGTCCTTTGTTAATCGATTGAATAGAGATTGTCTCTTAAATACAG	12	10544349
8	TATAGTGGGCACACACTTTTACACAATATCGAAGAAAAAAGTCTTGACAATATTTAGGTG	9	21392770
9	ACCAAAATAGCAAGTAGATAATCACACTTCGAATTTTTTTCACCACAGCACACAGCCTC	3	178841382
10	CACCTCACAAAATATGATATCTAAAGTGTCGATATTACTCAGATTTGGGGAAATGACATT	11	102181817
11	GCCCTGTGTCTCATGAAAGCCGTTCACTTCGAACTCCTAAGTTCAAGCAATCCTCCTGCC	2	242779315
12	ACTTTATGACTTGAATGATGTGGTAATGTCGAAGGTTAAAGAAGAAGTTTCAAACTGAGT	X	123019302
13	TAGGCCTGGGGGCCGAAAGGAAGAAGCTTCGACATCCTGCTTGAATGTTTGGAAGAGGGT	14	105266348
14	CGCAGCAGTCTCGTTGATCTTCACGGTGTCGACTCACCTGCGCCTCACATCCCAGGCGGG	13	111834492
15	GTAAATGAATTTGAAATATTACAAAAGATCGACTCACCTGCGCCTCACATCCCAGGCGGG	13	111914462
16	CCATGGGTGGTTTTGGAAAAGGCAACATTCGAAAACAATACATAAGTGTCTATAGGCCAA	18	60893514
17	TCACCTTAGTGAAGGGAAGTCCATCAAATCGATTTTGCTCCCCCCACCTTACCCCCAGAG	1	57389508
18	AGCAGGGGGATCACATAAGGCCAGGAGTTCGATTTTAACAAGAAACTGTAGGTCTAAGGA	3	105394494
19	AGCAGGGGGATCACATAAGGCCAGGAGTTCGAATAAGAAATACTTCTAAACCAAAGGATA	3	105394494
20	ACAATGATCAAAATAAAGGAGAAGTATTTCGAGCTTCCCCACCTTGTATGTCTCTTTTCT	17	34304462
21	AGGAGGGTAGATCACCTGAAGTCAGGATTCGAAGGCTTCATTTCTCTGTCTATAAAACAA	17	32557188

22	GAATTCCGACTCCCGTTTTGAAATTGTATCGACCGCGTCACTCTACTCCAGCCTGGGCGA	11	118135384
23	TTCTCAGCATCTCTCCTGAAAGAAAAAGTCGACCGCGTCACTCTACTCCAGCCTGGGCGA	11	118145823
24	CCGCCTCCGTCTGCGCCTGGGCCAGGCCTCGACTTCGTGATCAGCCCGGCTTGGCCTCCC	12	6883134
25	TTATTGTGAAATAAATCCATACAGATGATCGATCTCCTTGGCAATGAGGGCCCGGGAAGT	20	44718691
26	CAATATGACGGTGACATTAATGATAGCTTCGAGGCCAAGGTGCGAGGGCTGGAACGCCAG	11	60689541
27	GTGTGGGCCCCCCTGCTACCGCTGCGTATCGAACTTTACAGAGGGATCTAGAATGAGTGA	11	60701123
28	AAGCTGCCCCGGATAAAAATTCTGATAATCGAAGTTACACCTTTGATTTTTTAAAAAGCA	9	21981736
29	GGGCAGAGAGATTTTTTGTATCTACTTCTCGAGAGCCGGCCTCCTGCCCTTTCTAAAGGC	10	90724392
30	CAGAATCACTCTGTGGAACCAAAGAGCTTCGACCCTTCTGCTTTCTCTCCAGGGGATGGC	1	161519223
31	AAAAAACAATTATGTAATTGAAAACCCATCGACCCTTCTGCTTTCTCTCCAGGGGATGGC	1	161569923
32	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAACTAATATTAGAGGAGAGAGGTCAGTTA	8	42099384
33	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAAGTGCTGTTGAGTTCCCCCATCTCTCAT	8	42128690
34	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGACAGTCCCAAGAGGTCAGAACTGGCTTCC	8	42128690
35	CCACCCCCGCCCCGGGGGAGTCGCCCGGTCGAAGGCTGGACTTAAAAGAGCAGATGCAAG	8	42128690
36	AAAAAAAGATTTAAAGTGGCAGCTTCACTCGACACAAGGGTTTGTAACAAAAAACAAAAA	22	22117703
37	CACTAATCTTTACTCTTTTTCCACTTATTCGAGACCAGTGAAACCTCGTCGCTACAAAAA	9	128280753
38	AGGCCATATGGTGAATCAGGAAAGAAGTTCGAAGTGTCTTAATTTCCTATAAACTAGTTA	1	11254303
39	AAGGCCCAAGAACCAGGAATCTAGGTATTCGAAGCAGGGGACCTGCGAAACTTCAGCTGG	2	106375590
40	TTTAAACTTCTCTAGAGCAAAGAGCATTTCGACCTTCTTTTCCTTAGATAGAAACTGAAT	2	106408048
41	AGACTTTATTAGATAGGTATAAATGTTTTCGACCCAAAGCTTTCTTTCTCCTGAGCTCAG	11	77148857
42	TCCATACGTCACTAGCTGAGGTAAAACGTCGATCCAGCTTTTTGACTCTAAAATGAGCTT	8	141749121
43	ACAATATTAAGTTCCCAGAGAAAAAAATTCGAACTGGCGGCAACCGCTGCAGCGCCTGCT	20	2797355
44	ACTCCATCTCAAAAAAACAAGAGCTTCCTCGAGTTGCAGGCCGCCCTGGTGGCTAGACAT	20	2853761
45	ACAATATTAAGTTCCCAGAGAAAAAAATTCGAGTTGCAGGCCGCCCTGGTGGCTAGACAT	20	2853761
46	ACTCCATCTCAAAAAAACAAGAGCTTCCTCGAGGTGGAATAAAGGTTGAGAACAGCTATA	20	2943750
47	GTCCCTGAAAATGTTTGTAAATGTGGGGTCGAGGGGTAGATATGAGCATCCCCATTTTCT	19	45103545
48	GTCCCTGAAAATGTTTGTAAATGTGGGGTCGACCTGCTGGGCTCGGGCTATCCTTCCATC	19	45103545
49	GGGCTCCGCCATAAGGGCCTCTGTGAAATCGAGCCCTGCCTGGCCAGCACACACTGCATC	11	119555133

50	GAGGCTTCTGAGTTGCTCTGAGGGTACATCGATGCGCGCCCGCCGGGGCCCGGTCGGAGC	11	119584726
51	TGATCATGGGACCCTGAAATGTCAGCGCTCGATGCGCGCCCGCCGGGGCCCGGTCGGAGC	11	119599998
52	TTGACAGTTCAGTCTGATTTCAAGTCAGTCGACTGGAATCTGCATTCGCTTCGCAGGAGC	7	155593268
53	ACCCCCTCCCAGCCTCCTGGTCAGGAGTTCGACCAGGCTGCAGCGAATCACCTCAGCTCC	20	1830612
54	AATGAGTTTCTGGAAGAATAGGACATTGTCGAACTCCTGACCAGGAGGCTGGGAGGGGGT	20	1830612
55	CTCCACCTGGCTAACTTCTATGCATCCTTCGAGCCGTAGCTATCTTCCTGCCTGACCGGG	20	35981178
56	TTTGCTAAATTACCCAAAATTTTGCTTTTCGATAAATTGAACTTCATCAAAATTAAAAAC	9	93529835
57	TAAGCTTTCCATCAAGCTACGAAGCTGCTCGATATCAGAATTGTGCTCTGGGGGCGGCTT	8	119936911
58	AAGCCGCCCCCAGAGCACAATTCTGATATCGAAGTACACAAGTCAAAAAGACAAAAGAAT	8	119958900
59	GCACCCCACCCTGGATCCCTTGAAAGCCTCGATCTCTGCCTCGCGCAGCCCCAGCGTGCG	1	6521664
60	GTCTTCCTCCATTTTAGAAATGAATAACTCGAAGGGGGAATAGAGAATGTAATGATACCT	3	189406011
61	TTTCCACTTTTCATACTTAGACTCACAATCGATCCTCGGGCATCCCTGAATCATCTATCG	7	142272422
62	ATACTGAGGTTTAAAAAGTTCTTTTTTTTCGATCTCGGCTCATTGCAGCCTCCCCGTCCC	19	36382458
63	CACATACAAGCTTTCTGTTCGTTTATTTTCGACATAGGACGTGCCTGCTCCCCCTTCACC	18	703962

Table 16.d

	Probe Location			4 kb Sequence Location				
	End1	Start2	End2	Chr	Start1	End1	Start2	End2
1	17555498	17589665	17589696	22	17555467	17559468	17585695	17589696
2	7571771	7591384	7591415	17	7567770	7571771	7587414	7591415
3	131972322	132017396	132017427	5	131968321	131972322	132013426	132017427
4	68004293	68068238	68068269	X	68004262	68008263	68068238	68072239
5	21395335	21418463	21418494	9	21391334	21395335	21414493	21418494
6	47760963	47778641	47778672	19	47756962	47760963	47778641	47782642
7	10544380	10578132	10578163	12	10544349	10548350	10574162	10578163
8	21392801	21437777	21437808	9	21392770	21396771	21437777	21441778
9	178841413	178873640	178873671	3	178837412	178841413	178869670	178873671
10	102181848	102268448	102268479	11	102177847	102181848	102264478	102268479
11	242779346	242827065	242827096	2	242775345	242779346	242823095	242827096
12	123019333	123035293	123035324	X	123015332	123019333	123035293	123039294
13	105266379	105309627	105309658	14	105266348	105270349	105305657	105309658
14	111834523	111973085	111973116	13	111830522	111834523	111969115	111973116
15	111914493	111973085	111973116	13	111910492	111914493	111969115	111973116
16	60893545	60998913	60998944	18	60889544	60893545	60998913	61002914
17	57389539	57428402	57428433	1	57385538	57389539	57428402	57432403
18	105394525	105547637	105547668	3	105390524	105394525	105547637	105551638
19	105394525	105442255	105442286	3	105390524	105394525	105442255	105446256
20	34304493	34339929	34339960	17	34304462	34308463	34339929	34343930
21	32557219	32574048	32574079	17	32553218	32557219	32574048	32578049
22	118135415	118163915	118163946	11	118135384	118139385	118163915	118167916
23	118145854	118163915	118163946	11	118141853	118145854	118163915	118167916

24	6883165	6912128	6912159	12	6879164	6883165	6912128	6916129
25	44718722	44767127	44767158	20	44718691	44722692	44763157	44767158
26	60689572	60793026	60793057	11	60689541	60693542	60789056	60793057
27	60701154	60744556	60744587	11	60697153	60701154	60744556	60748557
28	21981767	22034007	22034038	9	21977766	21981767	22030037	22034038
29	90724423	90750145	90750176	10	90720422	90724423	90746175	90750176
30	161519254	161627152	161627183	1	161519223	161523224	161627152	161631153
31	161569954	161627152	161627183	1	161565953	161569954	161627152	161631153
32	42099415	42128690	42128721	8	42099384	42103385	42124720	42128721
33	42128721	42149611	42149642	8	42124720	42128721	42145641	42149642
34	42128721	42162167	42162198	8	42124720	42128721	42158197	42162198
35	42128721	42159959	42159990	8	42124720	42128721	42159959	42163960
36	22117734	22210841	22210872	22	22117703	22121704	22210841	22214842
37	128280784	128397348	128397379	9	128280753	128284754	128393378	128397379
38	11254334	11283124	11283155	1	11250333	11254334	11279154	11283155
39	106375621	106403393	106403424	2	106375590	106379591	106403393	106407394
40	106408079	106439151	106439182	2	106404078	106408079	106439151	106443152
41	77148888	77185846	77185877	11	77144887	77148888	77185846	77189847
42	141749152	141781474	141781505	8	141745151	141749152	141777504	141781505
43	2797386	3011215	3011246	20	2797355	2801356	3007245	3011246
44	2853792	2970066	2970097	20	2853761	2857762	2966096	2970097
45	2853792	3011215	3011246	20	2853761	2857762	3007245	3011246
46	2943781	2970066	2970097	20	2943750	2947751	2966096	2970097
47	45103576	45116368	45116399	19	45099575	45103576	45112398	45116399
48	45103576	45167560	45167591	19	45099575	45103576	45167560	45171561
49	119555164	119575828	119575859	11	119551163	119555164	119571858	119575859
50	119584757	119599998	119600029	11	119580756	119584757	119599998	119603999
51	119600029	119624554	119624585	11	119599998	119603999	119620584	119624585
52	155593299	155627543	155627574	7	155593268	155597269	155627543	155631544
53	1830643	1864775	1864806	20	1830612	1834613	1864775	1868776
54	1830643	1911577	1911608	20	1830612	1834613	1907607	1911608
55	35981209	36053790	36053821	20	35981178	35985179	36049820	36053821
56	93529866	93555880	93555911	9	93529835	93533836	93555880	93559881
57	119936942	119958900	119958931	8	119932941	119936942	119958900	119962901
58	119958931	119985773	119985804	8	119958900	119962901	119985773	119989774
59	6521695	6544277	6544308	1	6521664	6525665	6540307	6544308
60	189406042	189416264	189416295	3	189402041	189406042	189416264	189420265
61	142272453	142302412	142302443	7	142268452	142272453	142298442	142302443
62	36382489	36405491	36405522	19	36378488	36382489	36405491	36409492
63	703993	825022	825053	18	703962	707963	821052	825053

Table 16.e

		Inner_primers
	Probe	**PCR-Primer1_ID**
1	IL17RA_22_17555467_17556730_17583829_17589696_RF	OBD115-385
2	TP53_17_7568905_7571771_7590321_7591415_FF	OBD115-397
3	IL4_5_131966700_131972322_132015552_132017427_FF	OBD115-425
4	EFNB1_X_68004262_68015195_68068238_68069630_RR	OBD115-477
5	IFNA2_9_21392770_21395335_21414238_21418494_FF	OBD117-109
6	BBC3_19_47759469_47760963_47778641_47780208_FR	OBD117-085
7	KLRK1_12_10544349_10549161_10570098_10578163_RF	OBD117-053
8	IFNA1_9_21392770_21395335_21437777_21443318_RR	OBD117-033
9	PIK3CA_3_178832360_178841413_178871576_178873671_FF	OBD117-117
10	BIRC2_11_102178257_102181848_102266251_102268479_FF	OBD117-101
11	PDCD1_2_242777613_242779346_242826000_242827096_FF	OBD117-057
12	XIAP_X_123017153_123019333_123035293_123038006_FR	OBD117-073

13	AKT1_14_105266348_105267359_105305709_105309658_RF	n/a
14	ARHGEF7_13_111822569_111834523_111970320_111973116_FF	n/a
15	ARHGEF7_13_111908346_111914493_111970320_111973116_FF	n/a
16	BCL2_18_60884271_60893545_60998913_61003098_FR	OBD115-429
17	C8B_1_57385955_57389539_57428402_57432779_FR	n/a
18	CBLB_3_105390159_105394525_105547637_105554877_FR	n/a
19	CBLB_3_105390159_105394525_105442255_105450516_FR	n/a
20	CCL16_17_34304462_34314203_34339929_34346837_RR	n/a
21	CCL7_17_32553749_32557219_32574048_32580497_FR	n/a
22	CD3E_11_118135384_118142619_118163915_118173402_RR	n/a
23	CD3E_11_118144515_118145854_118163915_118173402_FR	n/a
24	CD4_12_6876592_6883165_6912128_6913978_FR	n/a
25	CD40_20_44718691_44720694_44762355_44767158_RF	n/a
26	CD6_11_60689541_60692498_60785339_60793057_RF	OBD115-281
27	CD6_11_60699859_60701154_60744556_60751199_FR	n/a
28	CDKN2A_9_21978375_21981767_22029988_22034038_FF	OBD115-277
29	FAS_10_90717744_90724423_90745185_90750176_FF	OBD115-293
30	FCGR2B_1_161519223_161525894_161627152_161631654_RR	n/a
31	FCGR2B_1_161562782_161569954_161627152_161631654_FR	n/a
32	IKBKB_8_42099384_42103137_42121759_42128721_RF	n/a
33	IKBKB_8_42121759_42128721_42148497_42149642_FF	n/a
34	IKBKB_8_42121759_42128721_42159959_42162198_FF	n/a
35	IKBKB_8_42121759_42128721_42159959_42162198_FR	n/a
36	MAPK1_22_22117703_22122470_22210841_22217782_RR	n/a
37	MAPKAP1_9_128280753_128289273_128393518_128397379_RF	n/a
38	MTOR_1_11245934_11254334_11280008_11283155_FF	n/a
39	NCK2_2_106375590_106379449_106403393_106408079_RR	n/a
40	NCK2_2_106403393_106408079_106439151_106441507_FR	n/a
41	PAK1_11_77141424_77148888_77185846_77188900_FR	n/a
42	PTK2_8_141745642_141749152_141773261_141781505_FF	n/a
43	PTPRA_20_2797355_2801691_3004582_3011246_RF	n/a
44	PTPRA_20_2853761_2858838_2966772_2970097_RF	OBD115-165
45	PTPRA_20_2853761_2858838_3004582_3011246_RF	n/a
46	PTPRA_20_2943750_2948659_2966772_2970097_RF	n/a
47	PVR_19_45099561_45103576_45113698_45116399_FF	n/a
48	PVR_19_45099561_45103576_45167560_45168855_FR	n/a
49	PVRL1_11_119551289_119555164_119570787_119575859_FF	n/a
50	PVRL1_11_119581897_119584757_119599998_119609544_FR	n/a
51	PVRL1_11_119599998_119609544_119620830_119624585_RF	n/a
52	SHH_7_155593268_155595881_155627543_155630456_RR	n/a
53	SIRPA_20_1830612_1833775_1864775_1869190_RR	n/a
54	SIRPA_20_1830612_1833775_1905279_1911608_RF	n/a
55	SRC_20_35981178_35984981_36049517_36053821_RF	n/a
56	SYK_9_93529835_93536915_93555880_93559839_RR	n/a
57	TNFRSF11B_8_119933591_119936942_119958900_119964996_FR	n/a
58	TNFRSF11B_8_119958900_119964996_119985773_119986987_RR	n/a
59	TNFRSF25_1_6521664_6526267_6541388_6544308_RF	n/a
60	TP63_3_189395557_189406042_189416264_189422493_FR	n/a
61	TRBV12-3_HG7_PATCH_142268038_142272453_142299803_142302443_FF	n/a
62	TYROBP_19_36380190_36382489_36405491_36408643_FR	n/a
63	YES1_18_703962_705806_820113_825053_RF	n/a

Table 17.a

	Inner_primers		
	PCR_Primer1	**PCR-Primer2_ID**	**PCR_Primer2**
1	CTAAGATCATCGTCCTGTGC	OBD115-387	AGTCAGCAATCTGTGAACC
2	CAGTCTCCAGCCTTTGTTC	OBD115-399	CTCCTTCACAACCCTTATCAC
3	AACCAACATAAGAAGCTGAC	OBD115-427	AGGGTGGTTATGGAGTGAG
4	TGCCACGAGAATCAAATCC	OBD115-479	AGATGTTGACTCTCCAGATTG
5	TGTCACATTTGTGCCTTACTCAGC	OBD117-111	AAGCAAGATACACCTTACCCAGTA
6	GGAAGCCTCGCCAGTGAGTT	OBD117-087	CCGGACCAATCCAGAGACGG
7	TATTCCACTGGCAGCAAGGT	OBD117-055	ACTCTCCCTGGTGCTTAGCTTT
8	GGGGCTCCACTAGGGTGACT	OBD117-035	TGTGACACGCTGACTCCCTT
9	CAGATAAATGACAAACTGGGAAACA	OBD117-119	AGACATTTTGGCAAAGATTGTTAGG
10	CAATGACAGGACTCAACCCAGG	OBD117-103	TTCAGCATGGAGTAAGAGGAGGG
11	ACAGGAAAAGGAAGCTCACAGGT	OBD117-059	TAGGAGGCAGAGGCAGGAGG
12	TCTGCCTGCTTAAATATTACTTTCC	OBD117-075	TTTGGAGGGAGGATGGTCAA
13	n/a	n/a	n/a
14	n/a	n/a	n/a
15	n/a	n/a	n/a
16	GCCAAACTCCTGTCTGAAG	OBD115-431	AATAGTCTTGTACCGTTGGATG
17	n/a	n/a	n/a
18	n/a	n/a	n/a
19	n/a	n/a	n/a
20	n/a	n/a	n/a
21	n/a	n/a	n/a
22	n/a	n/a	n/a
23	n/a	n/a	n/a
24	n/a	n/a	n/a
25	n/a	n/a	n/a
26	CGGATGCTCTAGAAAGGTTG	OBD115-283	GCTCTTTGGTATGACACTGG
27	n/a	n/a	n/a
28	GAGTTCTAGAATAGGATGTTGGG	OBD115-279	GCTTTGTTGGCACTGAATG
29	TTCTTGGTAGAGAGGGAAGG	OBD115-295	GGACAGCCCAGTCAAATG
30	n/a	n/a	n/a
31	n/a	n/a	n/a
32	n/a	n/a	n/a
33	n/a	n/a	n/a
34	n/a	n/a	n/a
35	n/a	n/a	n/a
36	n/a	n/a	n/a
37	n/a	n/a	n/a
38	n/a	n/a	n/a
39	n/a	n/a	n/a
40	n/a	n/a	n/a
41	n/a	n/a	n/a
42	n/a	n/a	n/a
43	n/a	n/a	n/a
44	TGGCTGACTTGGTGAAAC	OBD115-103	CATGACTTGGGCCTTCTTC
45	n/a	n/a	n/a
46	n/a	n/a	n/a
47	n/a	n/a	n/a
48	n/a	n/a	n/a
49	n/a	n/a	n/a
50	n/a	n/a	n/a
51	n/a	n/a	n/a
52	n/a	n/a	n/a
53	n/a	n/a	n/a
54	n/a	n/a	n/a

55	n/a	n/a	n/a
56	n/a	n/a	n/a
57	n/a	n/a	n/a
58	n/a	n/a	n/a
59	n/a	n/a	n/a
60	n/a	n/a	n/a
61	n/a	n/a	n/a
62	n/a	n/a	n/a
63	n/a	n/a	n/a

Table 17.b

Gene	Marker	GLMNET
IL17RA	OBD115-385.387	-0.099598169
TP53	OBD115-397.399	-0.089892616
IL4	OBD115-425.427	-0.095230215
EFNB1	OBD115-477.479	0.091808032
IFNA2	OBD117-109.111	-0.130270706
BBC3	OBD117-085.087	-0.076629581
KLRK1	OBD117-053.055	-0.088944337
IFNA1	OBD117-033.035	0.111911072
PIK3CA	OBD117-117.119	-0.039841311
BIRC2	OBD117-101.103	-0.116970742
PDCD1	OBD117-057.059	0.13271562
XIAP	OBD117-073.075	0.036539075
BCL2	OBD115-429.431	0
CD6	OBD115-281.283	0.031298493
CDKN2A	OBD115-277.279	0
FAS	OBD115-293.295	0.035034651
PTPRA	OBD115-165.103	-0.042684846

Table 18

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 how immunoresponsive individuals are; 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 an immunoresponsive 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 an immunoresponsive subgroup; and

- wherein the chromosome interaction either:

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

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

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

or

a) is present in any one of the regions or genes listed in Table 13; and/or

b) corresponds to any one of the chromosome interactions represented by any probe shown in Table 13, and/or

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

or

(α) is present in any one of the regions or genes listed in Table 16; and/or

(β) corresponds to any one of the chromosome interactions represented by any probe shown in Table 16, and/or

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

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

(i) comprising all of the chromosome interactions represented by the probes in Table 1; and/or

(ii) comprising at least 10, 50, 100, 150, 200 or 300 of the chromosome interactions represented by the probes in Table 1; and/or

(iii) which together are present in at least 10, 50, 100, 150 or 200 of the regions or genes listed in Table 1; 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 by the probes in Table 1.

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

(i) comprising all of the chromosome interactions represented by the probes in Table 13; and/or

(ii) comprising at least 10, 50, 100, 150, 200 or 300 of the chromosome interactions represented by the probes in Table 13; and/or

(iii) which together are present in at least 10, 50, 100, 150 or 200 of the regions or genes listed in Table 13; 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 by the probes in Table 13.

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

(i) comprising all of the chromosome interactions represented by the probes in Table 16; and/or

(ii) comprising at least 10, 20, 30 or 40 of the chromosome interactions represented by the probes in Table 16; and/or

(iii) which together are present in at least 10, 20, 30 or 40 of the regions or genes listed in Table 16; and/or

(iv) wherein at least 10, 20, 30 or 40 chromosome interactions are typed which are present in a 4,000 base region which comprises or which flanks the chromosome interactions represented by the probes in Table 16.

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 1, and/or (ii) by a primer pair which has at least 70% identity to any primer pair in Table 4; or

(a) a probe that has at least 70% identity to any of the specific probe sequences mentioned in Table 13, and/or (b) by a primer pair which has at least 70% identity to any primer pair in Table 13, or

(α) a probe that has at least 70% identity to any of the specific probe sequences mentioned in Table 16, and/or (β) by a primer pair which has at least 70% identity to any primer pair in Table 17, or

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; and/or
- the process is carried out to select an individual for a medical treatment; and/or
- the immunoresponsiveness is responsiveness to immunotherapy or an immunocheckpoint therapy; and/or
- the immunoresponsiveness is responsiveness to cancer immunotherapy, and/or
- the process is carried out to determine immunoresponsiveness at one or more defined time points, wherein optionally at least one of the time points is during the course of therapy.

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 200 different chromosome interactions are typed, preferably in 10 to 200 different regions or genes; and optionally

(a) 50 to 100 different chromosome interactions are typed each of which is in a different gene and/or a different region as defined in Table 1; or

(b) 50 to 100 different chromosome interactions are typed each of which is in a different gene and/or a different region as defined in Table 13; or

(c) 20 to 40 different chromosome interactions are typed each of which is in a different gene and/or a different region as defined in Table 16;

and/or

- which is carried out to select whether or not an individual will receive an immunotherapy, wherein the immunotherapy preferably comprises a small molecule immunotherapy, antibody immunotherapy or cell immunotherapy.

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
(vii) comprises a CTCF binding site.

11. A process according to any one of the preceding claims which is carried out to identify or design a therapeutic agent for immunotherapy;
- wherein preferably 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 level of immunoresponsiveness;
- wherein the chromosomal interaction is represented by any probe in Table 1; and/or
- the chromosomal interaction is present in any region or gene listed in Table 1;
and wherein optionally:

- the chromosomal interaction has been identified by the method of determining which chromosomal interactions are relevant to a chromosome state as defined in claim 1, and/or

- the change in chromosomal interaction is monitored using (i) a probe that has at least 70% identity to any of the probe sequences mentioned in Table 1, and/or (ii) by a primer pair which has at least 70% identity to any primer pair in Table 4.

12. A process according to any one of the preceding claims which is carried out to identify or design a therapeutic agent for immunotherapy;

- wherein preferably 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 level of immunoresponsiveness;
- wherein the chromosomal interaction is represented by any probe in Table 13; and/or
- the chromosomal interaction is present in any region or gene listed in Table 13;

and wherein optionally:

- the chromosomal interaction has been identified by the method of determining which chromosomal interactions are relevant to a chromosome state as defined in claim 1, and/or
- the change in chromosomal interaction is monitored using (i) a probe that has at least 70% identity to any of the probe sequences mentioned in Table 13, and/or (ii) by a primer pair which has at least 70% identity to any primer pair in Table 13.

13. A process according to any one of the preceding claims which is carried out to identify or design a therapeutic agent for immunotherapy;

- wherein preferably 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 level of immunoresponsiveness;
- wherein the chromosomal interaction is represented by any probe in Table 16; and/or
- the chromosomal interaction is present in any region or gene listed in Table 16;

and wherein optionally:

- the chromosomal interaction has been identified by the method of determining which chromosomal interactions are relevant to a chromosome state as defined in claim 1, and/or
- the change in chromosomal interaction is monitored using (i) a probe that has at least 70% identity to any of the probe sequences mentioned in Table 16, and/or (ii) by a primer pair which has at least 70% identity to any primer pair in Table 17.

14. A process according to claim 11, 12 or 13 which comprises selecting a target based on detection of chromosome interactions, and preferably screening for a modulator of the target to identify a therapeutic agent for immunotherapy, wherein said target is optionally a protein.

15. A therapeutic agent for use in a method of immunotherapy in an individual that has been identified as being in need of the therapeutic agent by a process according to any one of claims 1 to 10.

16. A process according to any one of claims 1 to 14 or a therapeutic agent for use according to claim 15, 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.

Figure 1

Patient Annotations For Study

Used For	Sample ID	Response/ Progression	12 weeks sample ID	12 weeks PDL1	Age	Gender	LDH high Y/N	Nr therapies	BRAF Y/N	Chemo	Targeted	immuno IPI=1; others=2
D	1378	R	1432	0.157	62	F	N	6	Y	1	1	2
D	1379	R	1430	5.172	57	F	Y	1		0	0	1
D	1380	R	1434	6.411	73	M	N	3	N	1	0	2
D	1386	P	1438	0.174	70	F	Y	1	N	0	0	1
D	1390	P	1443	12.21	62	M	Y	3	Y	0	1	1
D	1392	R	1439	0.308	62	F	N	2		0	0	2
D	1399	P	1436	0.213	63	F	Y	3	Y	0	1	1
D	1416	R	1459	0.569	49	F	Y	2	Y	0	1	1
V	1370	R	1431	0.324	74	M	N	2	N	1	0	1
V	1372	R	1483	0.607	39	F	Y	2		1		1
V	1393	P	1447	0.222	66	F	Y	3		1	0	1
V	1414	R	1457	0.389	46	M	Y	3	Y	0	1	1
V	1482	P			55	F	Y	2	N	1	0	1
V	1426	P	1469		63	M	Y	1		0	0	1
V	1458	P	1481		52	F	N	4	N	1	0	2
V	1440	P	1508		74	M	N	4	N	1	0	2
		Response was defined based on RECIST 1.1 criteria										

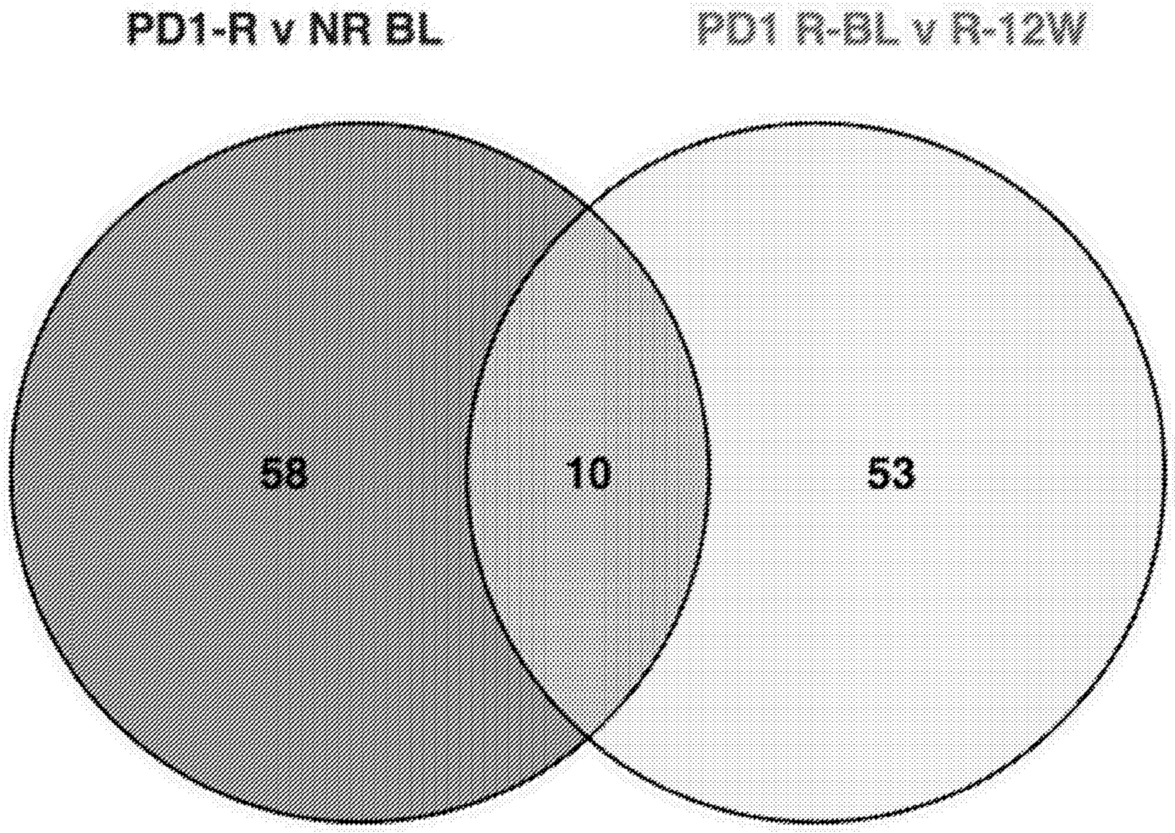
D: indicates the Samples were used in the discovery stage of the study, identifying which EpiSwitch to move to the PCR platform from the array platform

V: indicates samples used to verify the identified EpiSwitch markers on the PCR platform

Figure 2

PCR Probe	**GeneLocus**
69/71	IL15
73/75	STAT5B
85/87	HLA-DQB1
9/11	MYD88
29/31	IL12B
13/15	PVRL1

Figure 3



Analytical Pipeline for anti-PD-1 Array Analysis. 68 EpiSwitch™ Markers identified by statistical processing as strong candidates for predictive biomarkers at baseline for anti-PD-1 therapy. (PD1-R vs NR BL). 63 EpiSwitch™ Markers identified by statistical processing as strong candidates for response biomarkers for anti-PD-1 therapy. (PD1 R-BL v R-12W). 10 Markers are both good candidates for predictive and response markers.

Figure 4

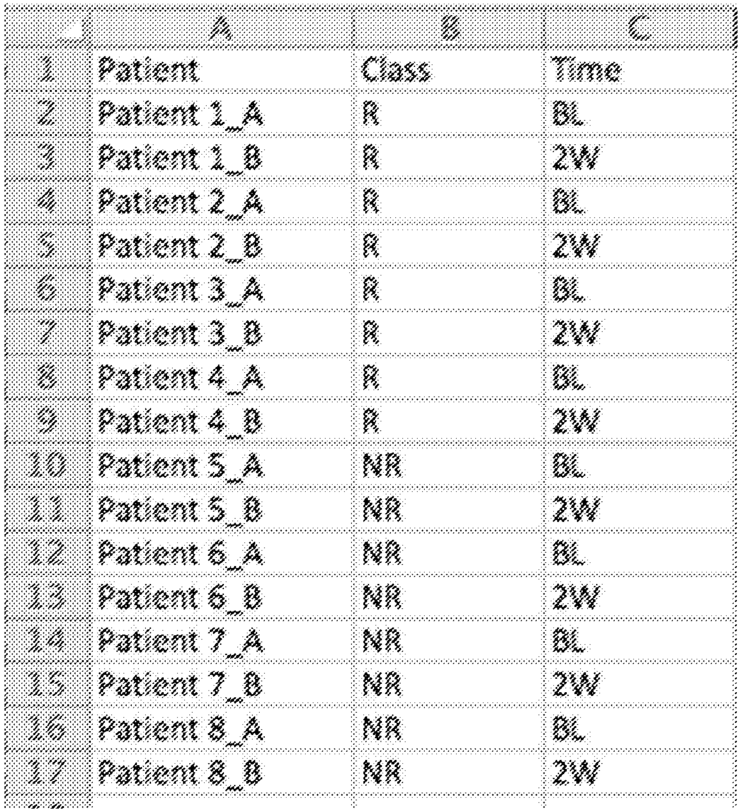
Anti-PD-1 Markers for R-BL v NR-BL:
EpiSwitch™ PCR Data

PCR Probe	GeneLocus	Responder				Non-Responder			
		1370 (BL)	1372 (BL)	1393 (BL)	1414 (BL)	1482 (BL)	1426 (BL)	1458 (BL)	1440 (BL)
69/71	IL15	1	1	1	1	0	0	1	0
73/75	STAT5B	1	1	1	1	0	0	0	1
85/87	HLA-DQB1	1	1	0	1	0	0	0	0
9/11	MYD88	1	1	1	1	1	0	0	0
29/31	IL12B	1	0	0	0	1	1	1	1
13/15	PVRL1	0	0	1	0	1	1	1	1

Array Probe	**Array**
IL15_4_142530356_142539177_142656375_142659066_RF	R
STAT5B_17_40403935_40406459_40464294_40468456_FR	R
HLA-DQB1_6_32607972_32614493_32630138_32632737_RR	R
MYD88_3_38139864_38141788_38192489_38194027_RR	**NR**
IL12B_5_158737480_158738689_158781589_158783887_FF	NR
PVRL1_11_119599998_119609544_119620830_119624585_FR	NR

Patients for aPD-L1 verification of aPD-1 identified markers

Aim: To determine if **30 EpiSwitch™ markers** identified in **Melanoma aPD-1** study **translate to aPD-L1 therapy in NSCLC**



	A	B	C
1	Patient	Class	Time
2	Patient 1_A	R	BL
3	Patient 1_B	R	2W
4	Patient 2_A	R	BL
5	Patient 2_B	R	2W
6	Patient 3_A	R	BL
7	Patient 3_B	R	2W
8	Patient 4_A	R	BL
9	Patient 4_B	R	2W
10	Patient 5_A	NR	BL
11	Patient 5_B	NR	2W
12	Patient 6_A	NR	BL
13	Patient 6_B	NR	2W
14	Patient 7_A	NR	BL
15	Patient 7_B	NR	2W
16	Patient 8_A	NR	BL
17	Patient 8_B	NR	2W

16 **Non-small cell lung carcinoma** (NSCLC) Patients treated with anti PD-L1

2 time points:

Baseline (BL)

2 Weeks (2W)

PBMCs were used in the Study

Figure 5

Complied Statistics for Top discerning EpiSwitch™

Gene	Column	Chi.Square	FT_p_value	sd	LD_p_value	Marker_Class
PDCD1LG2	OBD117_029.OBD117_031_1	4.286	0.079	-0.4	0.0455002	NR
PDCD1	OBD117_057.OBD117_059_1	4.286	0.08	-0.4	0.04550026	NR
ITK	OBD117_089.OBD117_091_0.25	2.637	0.194	-0.3399346	0.11666446	NR
IFNA1	OBD117_033.OBD117_035_0.125	3.281	0.201	-0.4	0.08011831	NR
IRF1	OBD117_045.OBD117_047_0.25	2.143	0.274	-0.4714045	0.15729921	NR
XIAP	OBD117_073.OBD117_075_0.25	2.143	0.278	-0.4714045	0.15729921	NR
IFNA2	OBD117_109.OBD117_111_0.03125	4.286	0.079	0.4	0.04550026	R
STAT5B	OBD117_009.OBD117_011_0.25	3.348	0.115	0.4714045	0.07709987	R
BBC3	OBD117_085.OBD117_087_0.25	3.616	0.122	0.4898979	0.06619258	R
KLRK1	OBD117_053.OBD117_055_0.125	3.233	0.124	0.4988877	0.08235222	R
PIK3CA	OBD117_117.OBD117_119_0.0625	2.637	0.2	0.3399346	0.11666446	R
BIRC2	OBD117_101.OBD117_103_0.25	2.637	0.204	0.3399346	0.11666446	R
CD14	OBD117_105.OBD117_107_0.5	1.759	0.271	0.4422166	0.20004505	R

Figure 6

The table above shows the top **13 out of the 30 aPD-1** markers examined in the **aPD-L1** patients

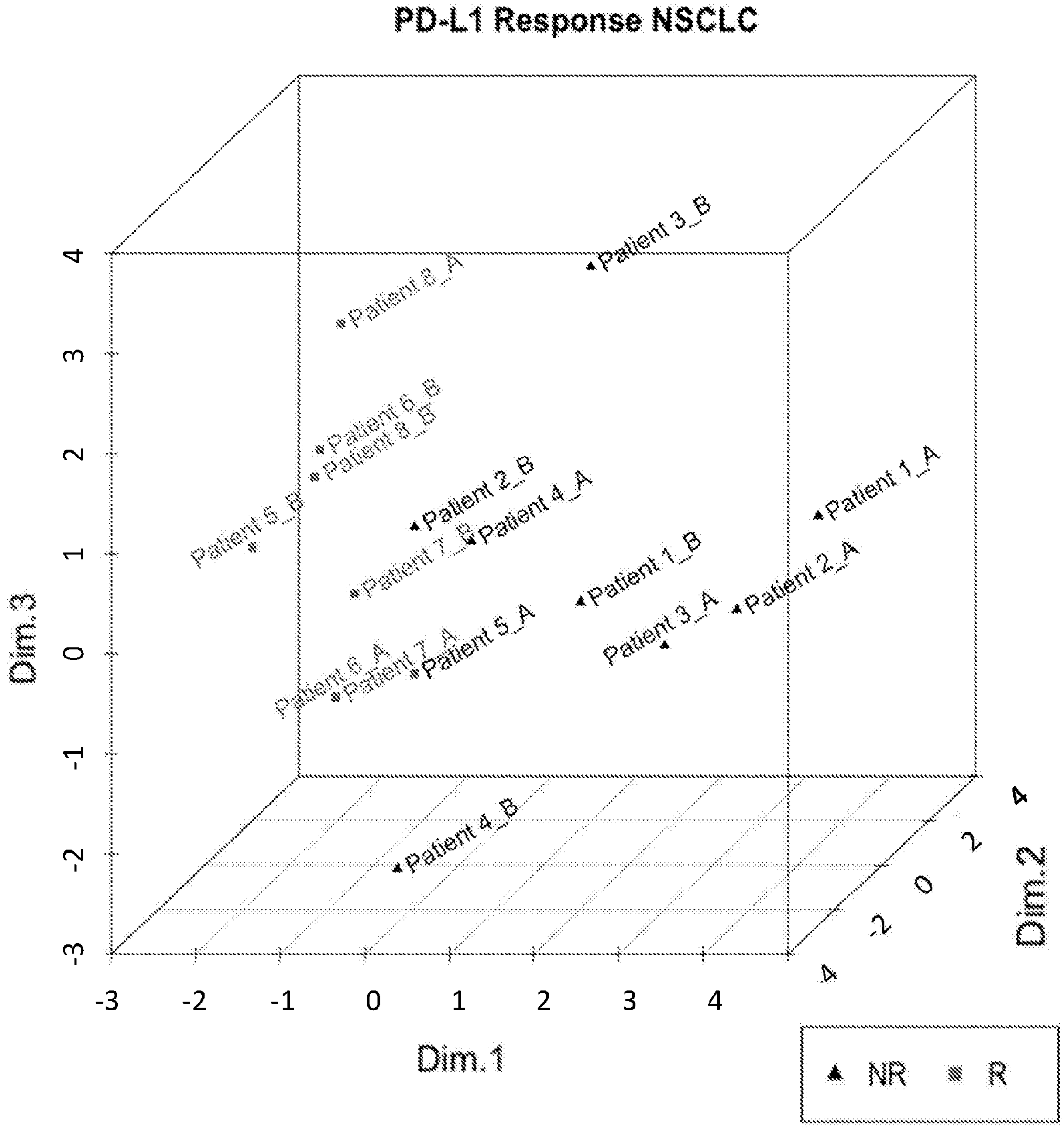
6 NR Markers

7 R Markers

Same **R marker STAT5B** marker was identified in the aPD-L1 patients as in the aPD-1 patients and a **strong NR** marker associated to **PD-L2** was identified

Figure 7A

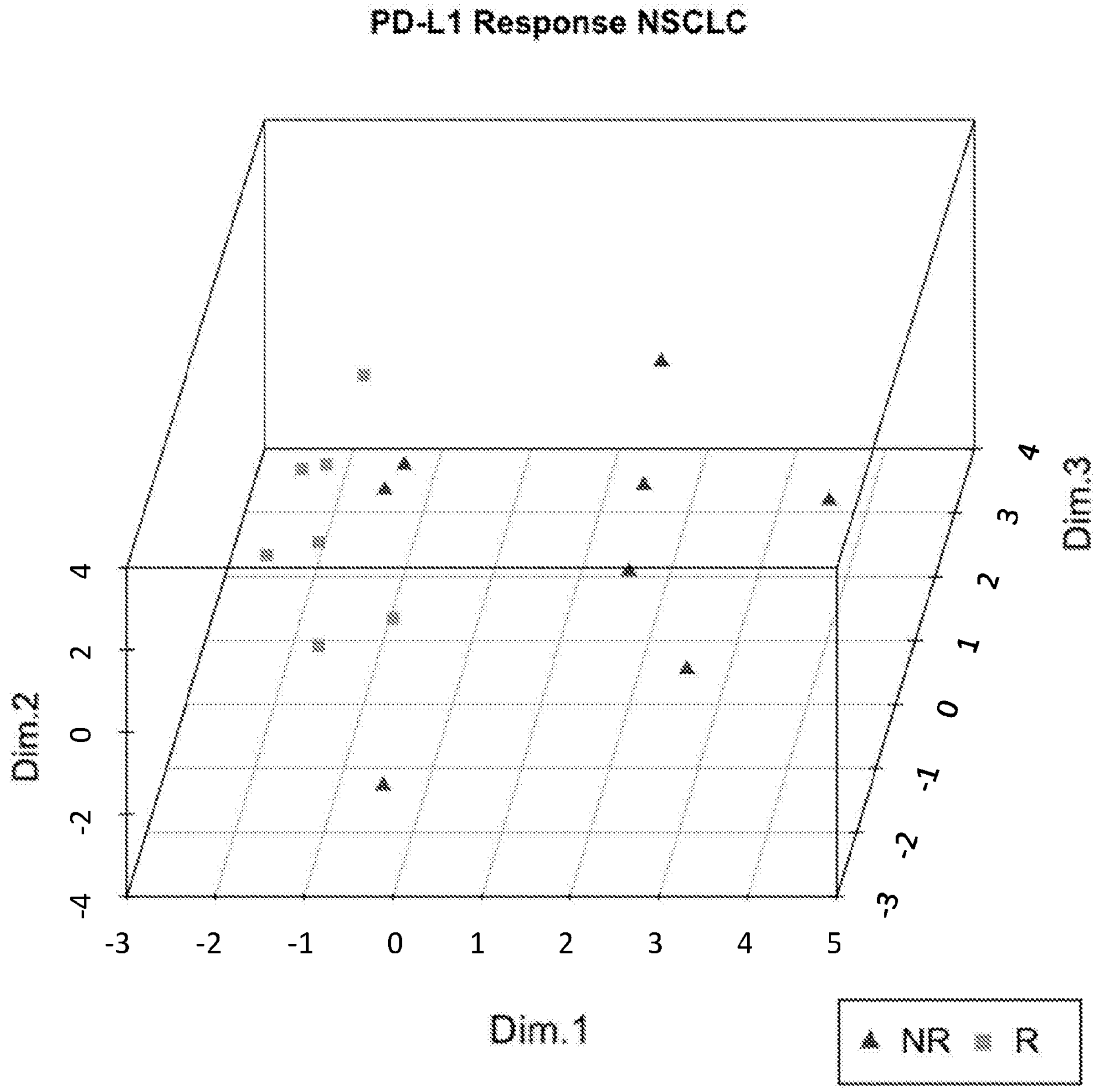
PCA plot of the patients with top 13 EpiSwitch™ markers



These are **3D PCA plots** and show that the spread between the 2 time points (**BL and 2 weeks**) in **Responders and non-Responders** is the similar. This **emphasizes** that the markers are capturing the **difference in response at baseline**

Figure 7B

PCA plot of the patients with top 13 EpiSwitch™ markers



These are **3D PCA plots** and show that the spread between the 2 time points (**BL and 2 weeks**) in **Responders and non-Responders** is the similar. This **emphasizes** that the markers are capturing the **difference in response at baseline**

Figure 8

EpiSwitch™ markers generated from 2 IO studies and used to classify a 3rd IO cohort

Marker	Assoicated_ORF
OBD117_009/OBD117_011	STAT5A-STAT5B
OBD117_045/OBD117_047	IRF1
OBD117_089/OBD117_091	ITK
OBD117_105/OBD117_107	CD14
OBD117_029/OBD117_031	CD274-PDCD1LG2

5 marker model used to classify un-known response NSCLC patients

These were baseline patients for aPD-L1 therapy

Markers were developed from 2 cohorts

8 baseline Melanoma patients (4 R and 4 NR to aPD-1, Pembrolizumab)

24 baseline NSCLC patients (12 R and 12 NR to aPD-L1. This is a different aPD-L1 therapy than the blinded samples**)**

The ORF's associated to the markers are shown in the table above, the last marker forms a loop between PD-L1 (CD274) and PD-L2 (PCD1LG2)

5 EpiSwitch™ Classifier Call for 3rd IO cohort using Random Forest

Marker	Assoicated_ORF
OBD117_009/OBD117_011	STAT5A-STAT5B
OBD117_045/OBD117_047	IRF1
OBD117_089/OBD117_091	ITK
OBD117_105/OBD117_107	CD14
OBD117_029/OBD117_031	CD274-PDCD1LG2

5 marker model used to classify un-known response NSCLC patients

These were baseline patients for aPD-L1 therapy, which is different from the discovery aPD-L1 therapy

inst#,	actual,	predicted,	error,	probabi	lity distribution
1	?	1:R	+	0.621	0.379
2	?	1:R	+	0.699	0.301
3	?	1:R	+	0.621	0.379
4	?	1:R	+	0.621	0.379
5	?	2:NR	+	0.461	0.539
6	?	2:NR	+	0.311	0.689
7	?	1:R	+	0.551	0.449
8	?	1:R	+	0.621	0.379
9	?	2:NR	+	0.461	0.539
10	?	2:NR	+	0.311	0.689
11	?	2:NR	+	0.461	0.539
12	?	2:NR	+	0.311	0.689
13	?	2:NR	+	0.311	0.689
14	?	2:NR	+	0.461	0.539
15	?	2:NR	+	0.461	0.539

Class call for the 15 unknown samples

Random Forest Classifier model was based on the 32 IO samples with known response call

Figure 9

EpiSwitch™ Classifier Call for 3rd IO cohort using Random Forest

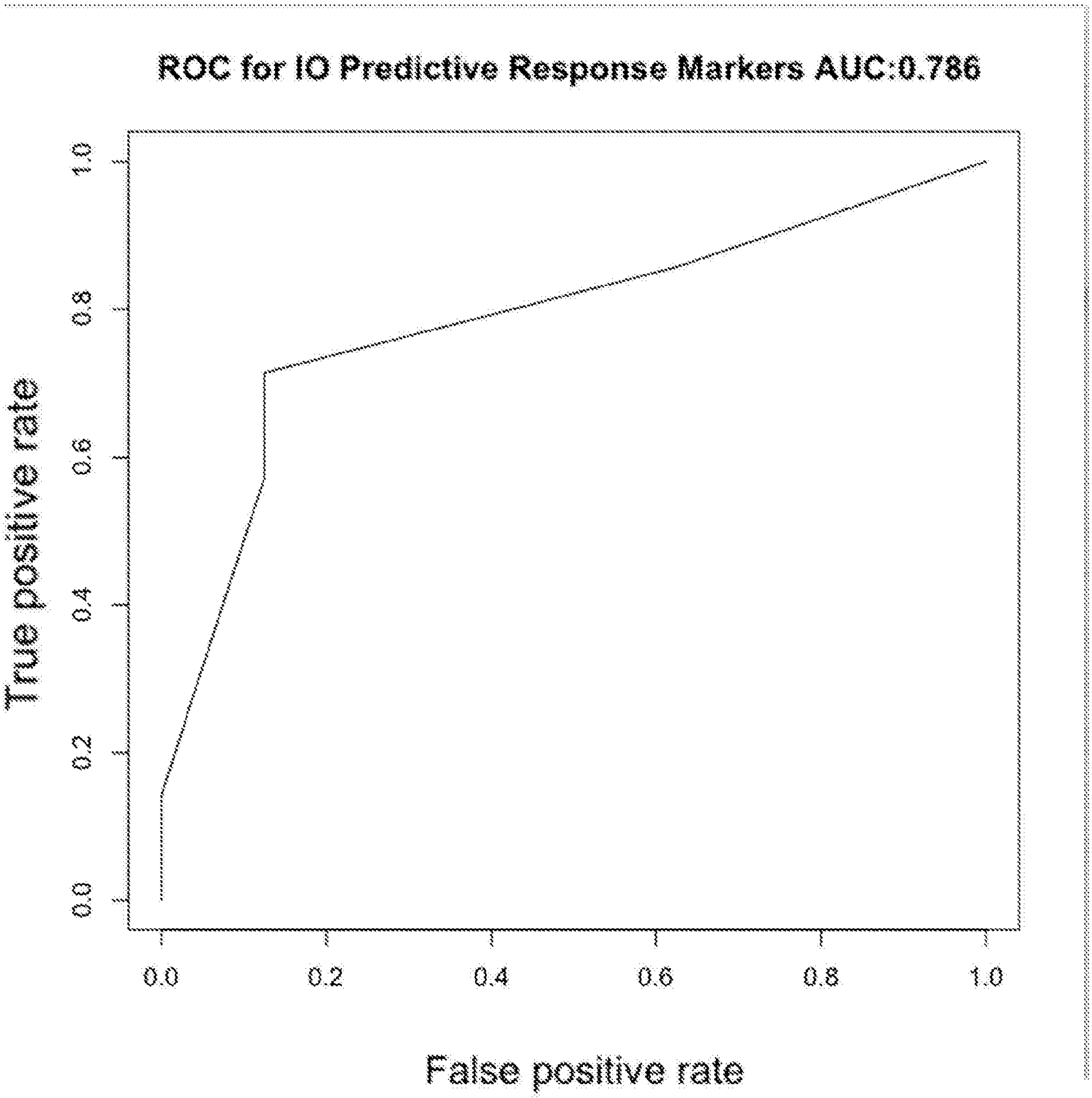
inst#,	actual,	predicted,	error,	probabi	lity distribution	Statistic	Formula	Value	95% CI
1	R	1:R	+	0.621	0.379	Sensitivity	$\frac{a}{a+b}$	71.43%	29.04% to 96.33%
2	R	1:R	+	0.699	0.301				
3	R	1:R	+	0.621	0.379	Specificity	$\frac{d}{c+d}$	87.50 %	47.35% to 99.68%
4	R	1:R	+	0.621	0.379				
5	R	2:NR	+	0.461	0.539	Positive Likelihood Ratio	$\frac{Sensitivity}{1-Specificity}$	5.71	0.86 to 37.91
6	R	2:NR	+	0.311	0.689				
7	R	1:R	+	0.551	0.449	Negative Likehood Ratio	$\frac{1-Sensitivity}{Specificity}$	0.33	0.10 to 1.08
8	NR	1:R	+	0.621	0.379				
9	NR	2:NR	+	0.461	0.539	Disease prevalence	$\frac{a+b}{a+b+c+d}$	46.67% (*)	21.27% to 73.41%
10	NR	2:NR	+	0.311	0.689				
11	NR	2:NR	+	0.461	0.539	Positive Predictive Value	$\frac{a}{a+c}$	83.33% (*)	42.97% to 97.87%
12	NR	2:NR	+	0.311	0.689				
13	NR	2:NR	+	0.311	0.689	Negative Predictive Value	$\frac{d}{b+d}$	77.78 % (*)	51.31% to 92.08%
14	NR	2:NR	+	0.461	0.539				
15	NR	2:NR	+	0.461	0.539				

After un-blinding, the 5 marker model **generated 3 miss calls** which are highlighted.
The test statistics are shown above for the 5 marker model on the 15 blinded samples

Figure 10

Figure 11

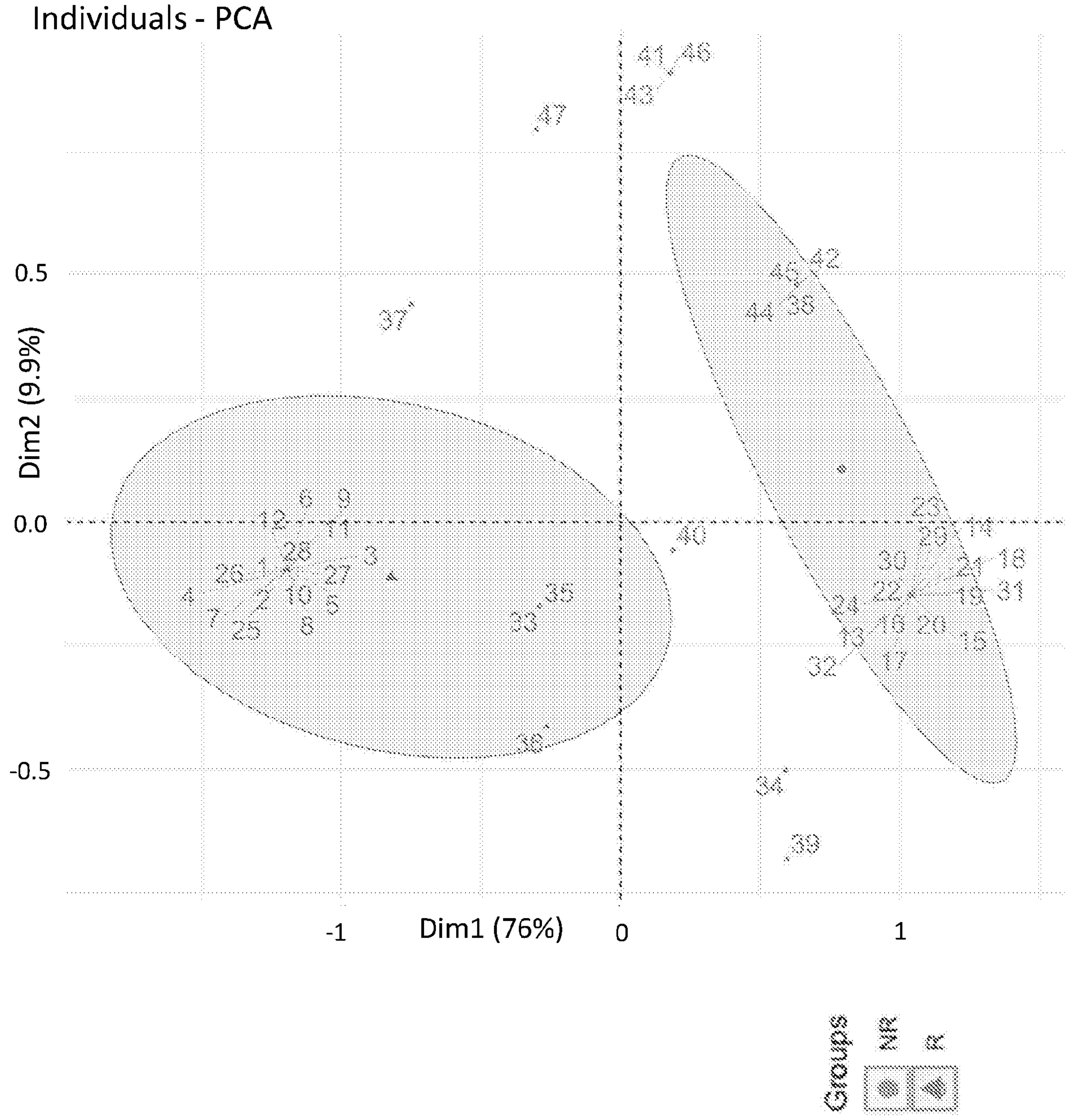
ROC Curve of the 15 baseline aPD-L1 patients



The AUC for the blinded samples was 0.786

Figure 12

PCA of the 47 baseline IO patients using the 5 EpiSwitch™ marker



PCA of the 47 IO baseline Patients, using the EpiSwitch™ binary values 37 (R called NR) and 40 (NR called R are 2 of the miss called samples

Figure 13

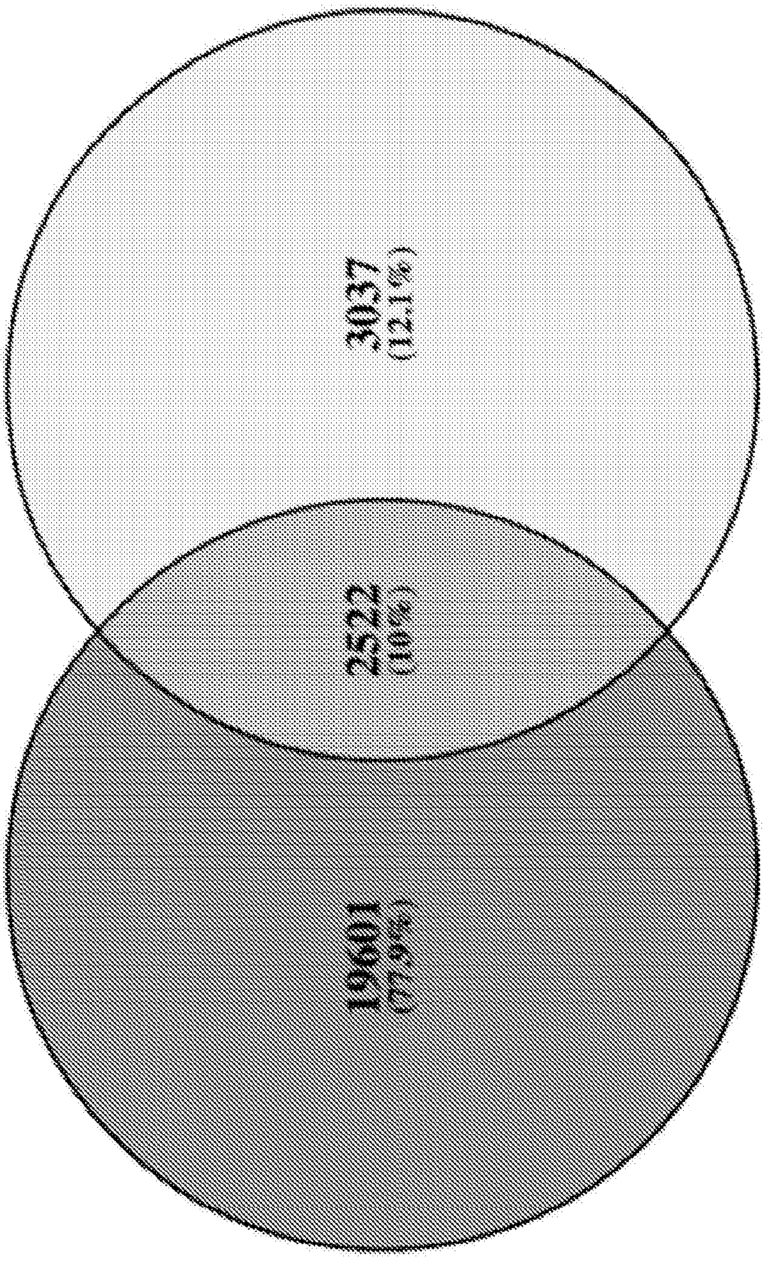
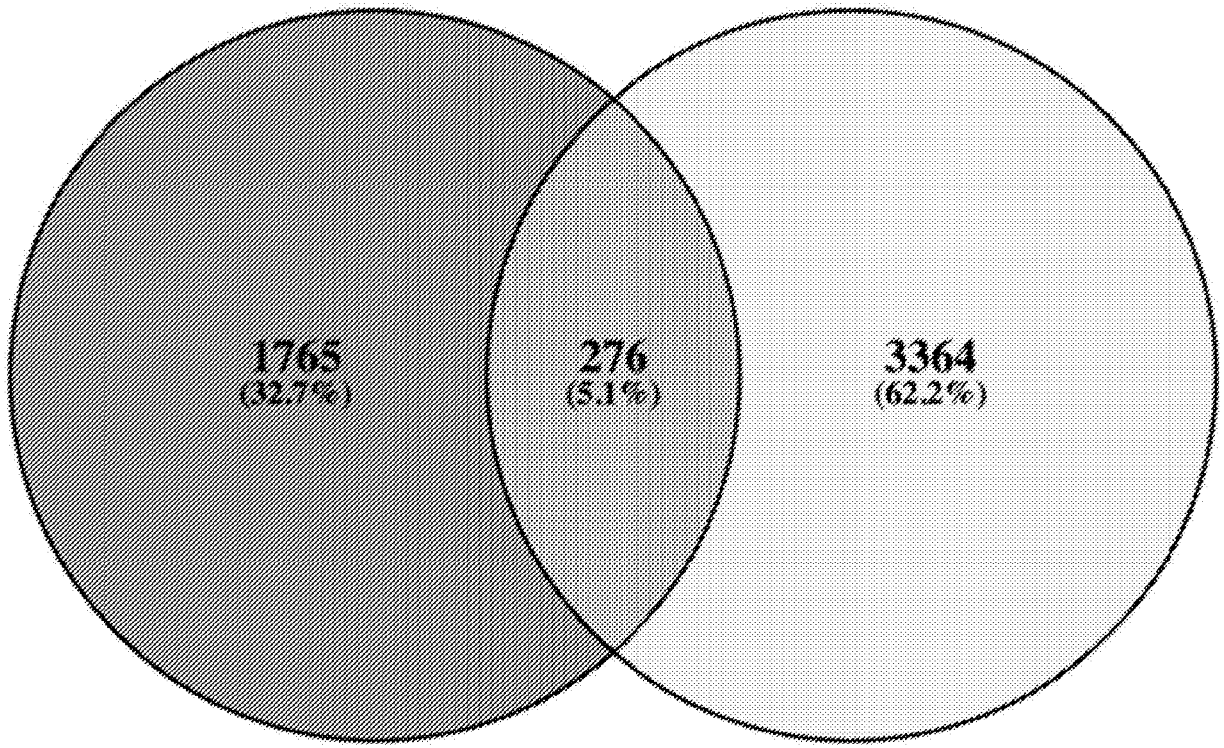
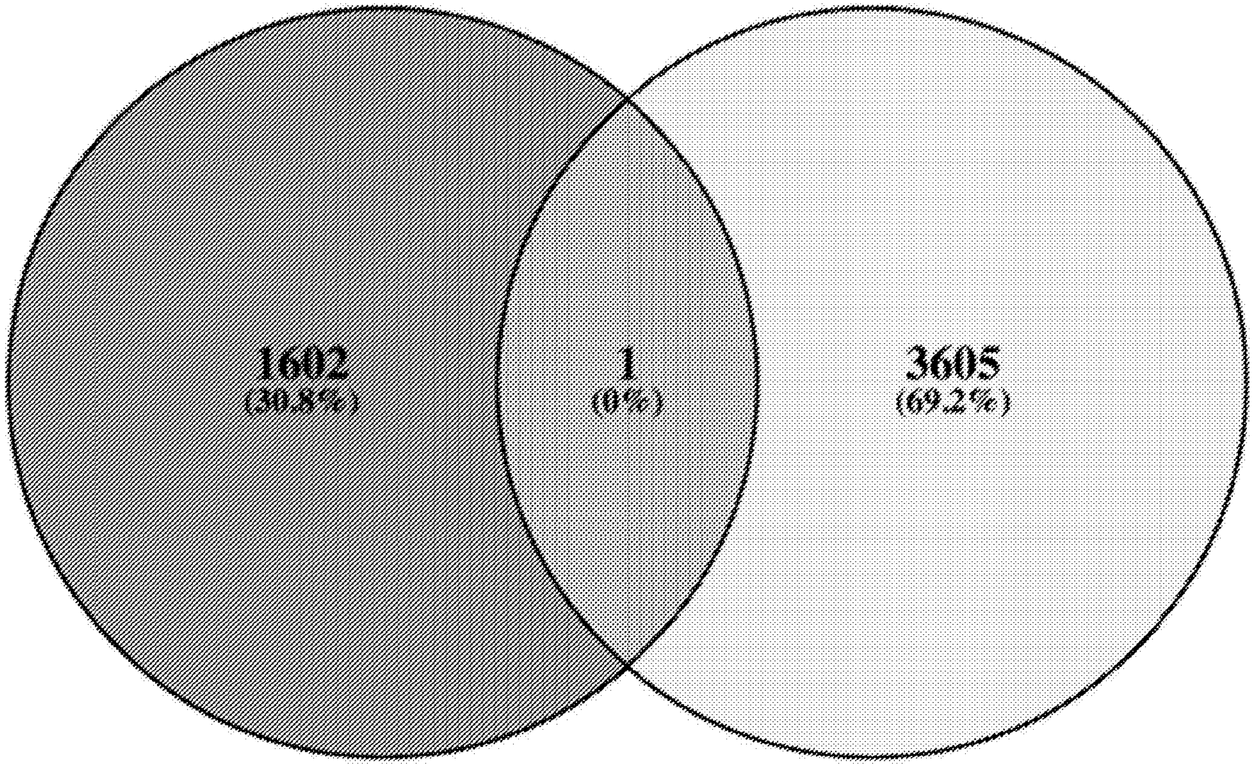


Figure 14



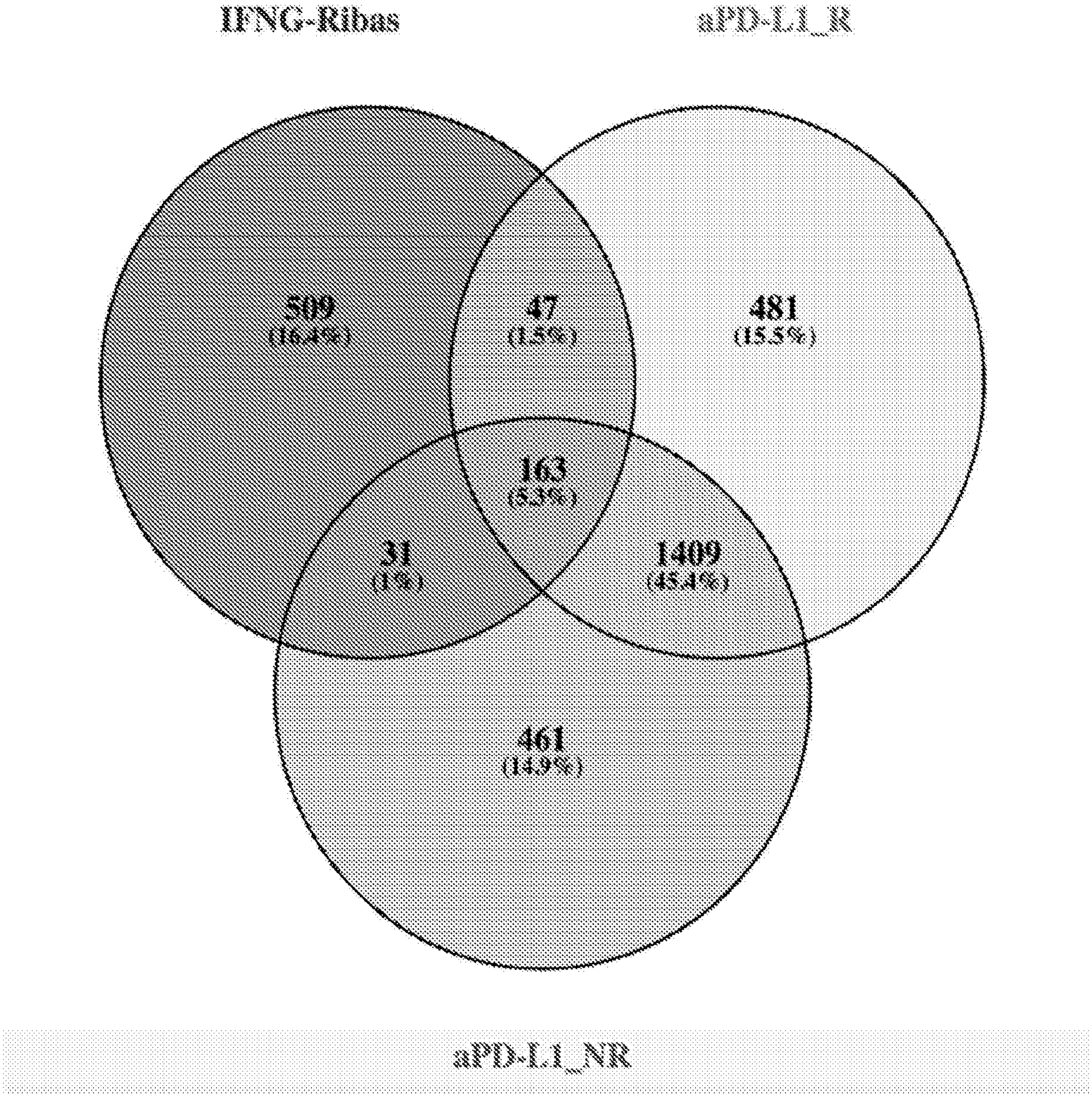
The VENN Diagram shows the overlap between the significant conformations for the Responders at baseline for aPD-1 (melanoma) and aPD-L1 (NSCLC). The 2 responder groups share 276 EpiSwitch CCSs, this equates to 11% of the total number of markers shared on the 2 screening arrays.

Figure 15



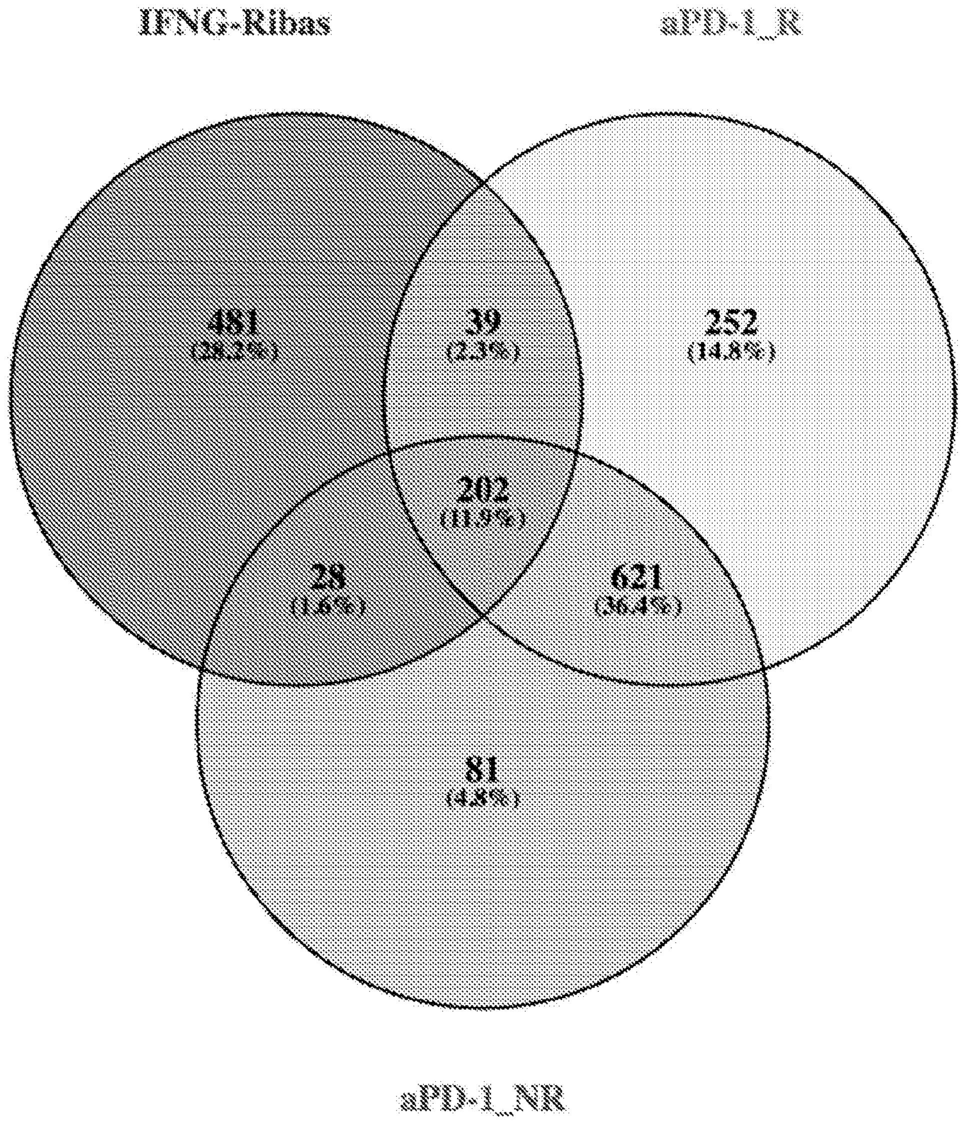
The VENN Diagram shows the overlap between the significant conformations for the Non-Responders at baseline for aPD-1 (melanoma) and aPD-L1 (NSCLC). Only 1 marker is shared between the 2 Non-responder groups.

Figure 16



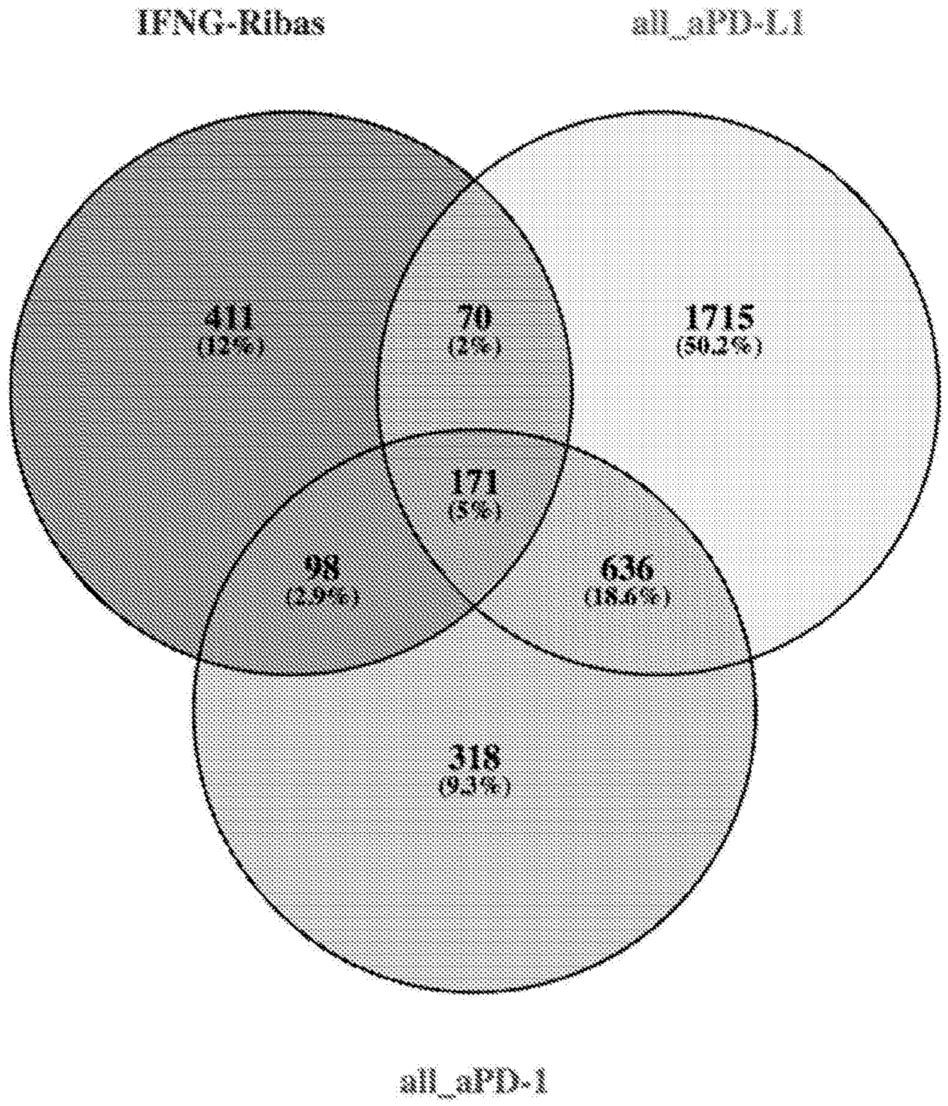
Comparison of ORFs with significant EpiSwitch™ CCSs for R-aPD-L1 and NR-aPD-L1 against the IFNG-Response ORFs. The significant EpiSwitch™ CCSs were compared to Gencode Hg38 annotation using Bedtools window option. All the protein coding regions within 50Kb of significant EpiSwitch™ CCSs were then compared between responders and non-responders for the aPD-L1 study. These 2 list were further compared to a list of IFNG activated ORFs (750), the majority of which are known interferon response genes. The adjacent VENN diagram show the comparison of these 3 lists. 210 IFNG activated ORFs have significant *Responder CCSs* associated to them. 194 IFNG activated ORFs have significant *Non-Responder CCSs* associated to them

Figure 17



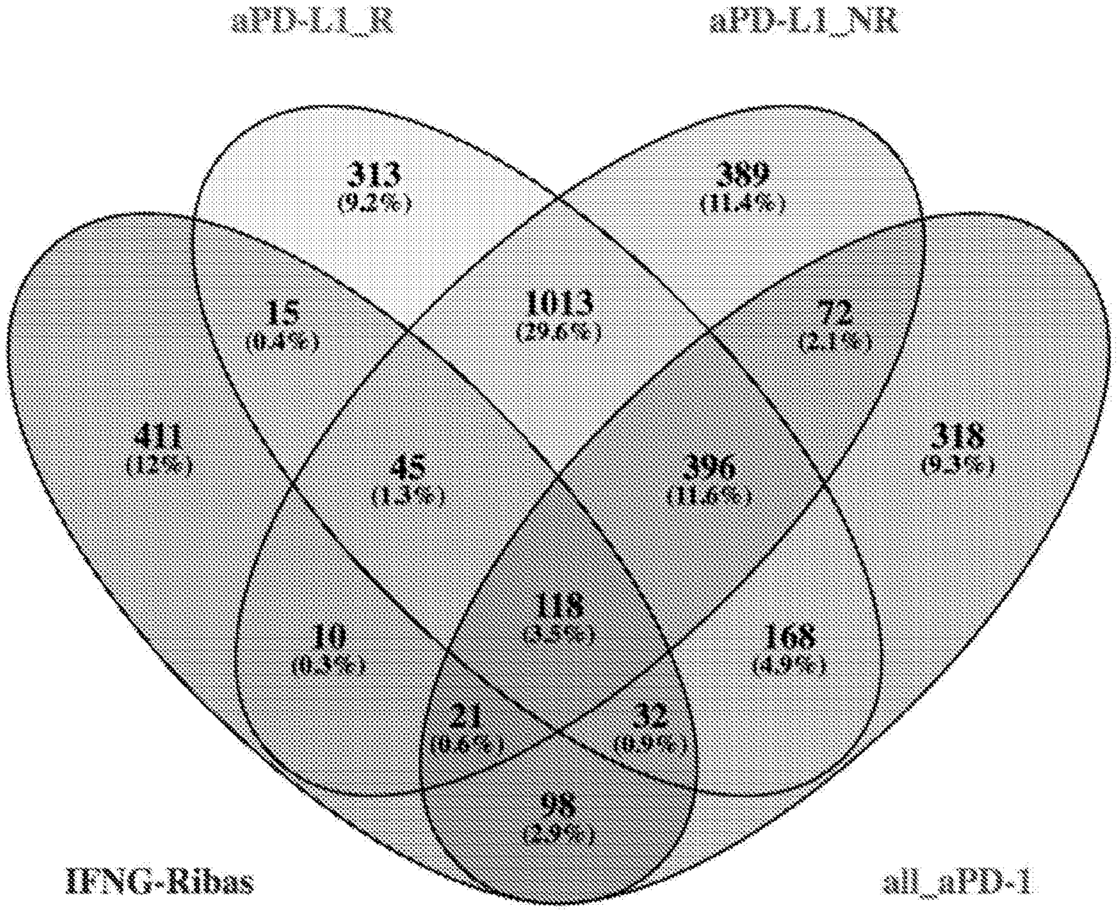
Comparison of ORFs with significant EpiSwitch™ CCSs for R-aPD-1 and NR-aPD-1 against the IFNG-Response ORFs. The same mapping analysis was done using the aPD-1 data. These 2 list were further compared to a list of IFNG activated ORFs (750), the majority of which are known interferon response genes. The adjacent VENN diagram show the comparison of these 3 lists. 241 IFNG activated ORFs have significant Responder CCSs associated to them. 231 IFNG activated ORFs have significant Non-Responder CCSs associated to them.

Figure 18



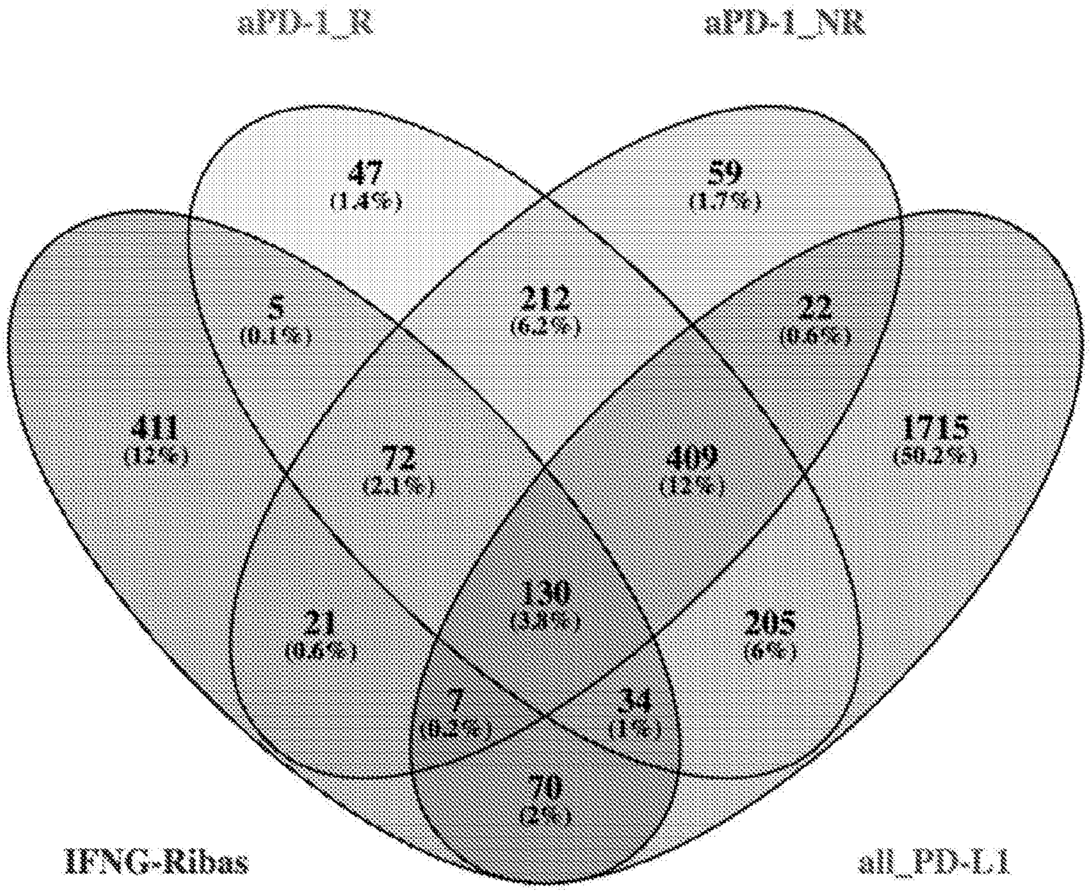
Comparison of ORFs with significant EpiSwitch™ CCSs for all aPD-1 and all aPD-L1 against the IFNG-Response ORFs. The significant CCSs associated ORFs were combined for each study (R and NR as 1 list) and then compared to the IFNG activated ORFs. The adjacent VENN diagram show the comparison of these 3 lists. On the aPD-L1 array there was 260 of the 750 IFNG activated ORFs. On the aPD-1 array there was 274 of the 750 IFNG activated ORFs. 241 of the 260 aPD-L1 IFNG activated ORFs contain significant EpiSwitch™ CCSs. 269 of the 274 aPD-L1 IFNG activated ORFs contain significant EpiSwitch™ CCSs.

Figure 19



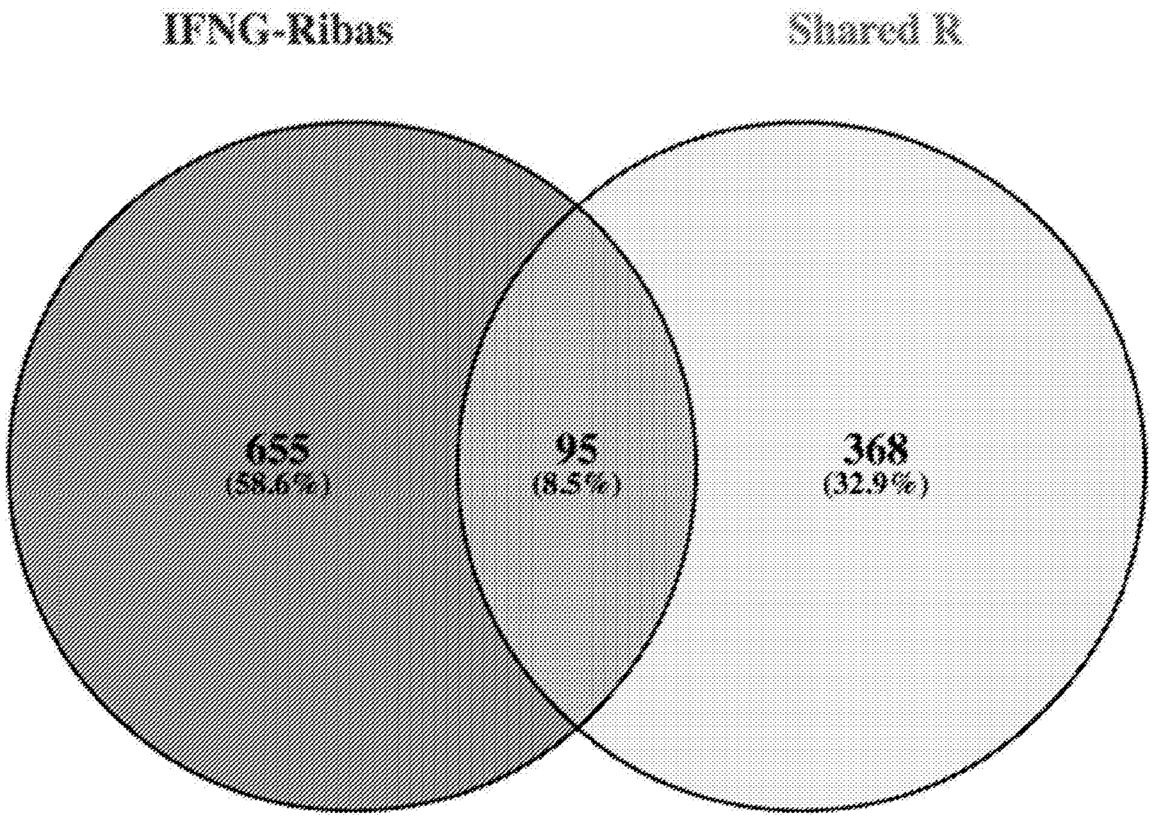
Comparison of ORFs with significant EpiSwitch™ CCSs for aPD-L1 against the aPD-1 and IFNG-Response ORFs. The ORF's containing significant EpiSwitch™ CCSs broken down for the Responders and Non-Responders for aPD-L1 compared to IFNG activated ORFs and the combined significant EpiSwitch™ CCSs ORF's for the aPD-1.

Figure 20



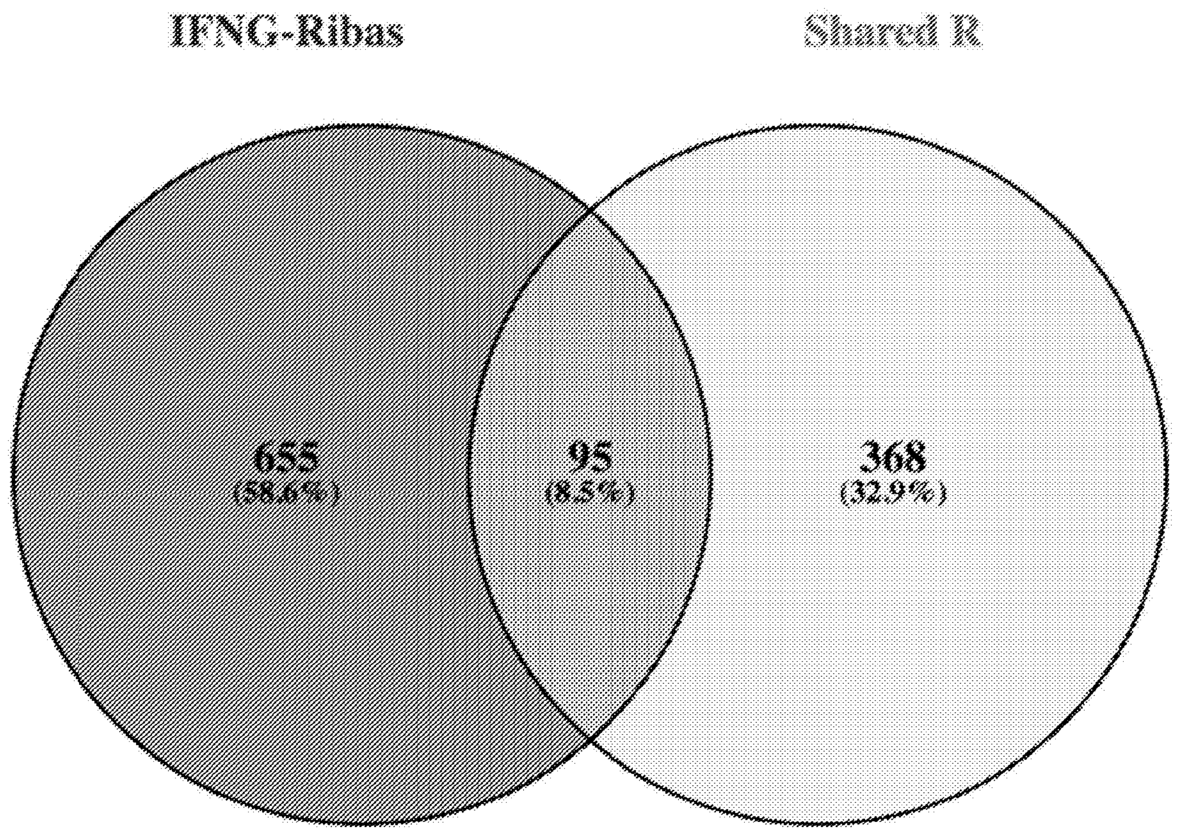
Comparison of ORFs with significant EpiSwitch™ CCSs for aPD-1 against the aPD-L1 and IFNG-Response ORFs. The ORF's containing significant EpiSwitch™ CCSs broken down for the Responders and Non-Responders for aPD-1 compared to IFNG activated ORFs and the combined significant EpiSwitch™ CCSs ORF's for the aPD-L1.

Figure 21



Comparison of ORFs with shared Response EpiSwitch™ CCSs for aPD-L1 and aPD-1 with the IFNG-Response ORFs. The adjacent VENN diagram show the comparison of the ORF's with shared significant Responders EpiSwitch™ CCSs between the aPD-L1 and aPD-1 studies. 95 of the ORFs overlap with the IFNG activated ORFs.

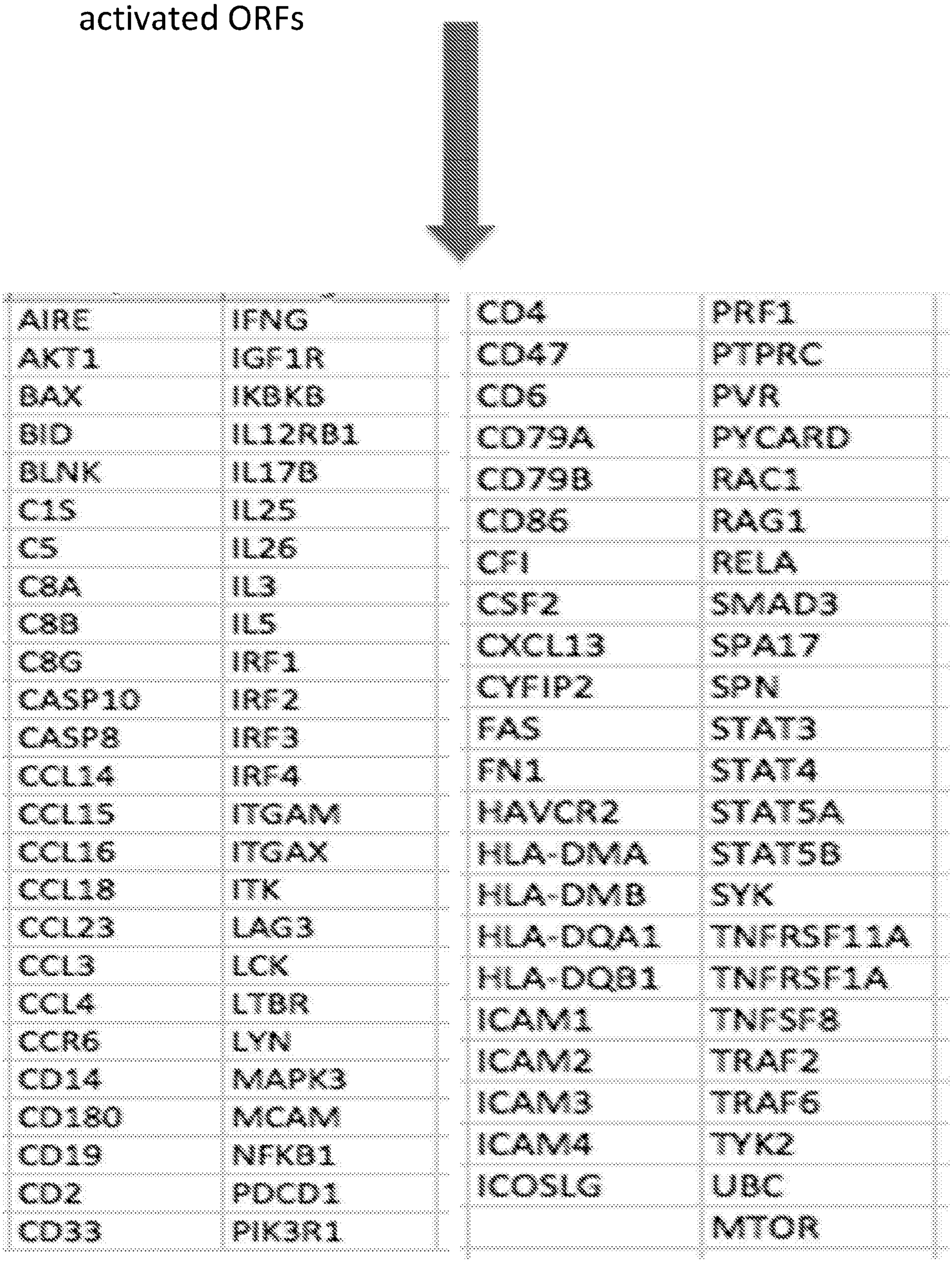
Figure 22A



Comparison of ORFs with shared Response EpiSwitch™ CCSs for aPD-L1 and aPD-1 with the IFNG-Response ORFs.

Figure 22B

The list of the 95 of the ORFs overlap with the IFNG activated ORFs



AIRE	IFNG
AKT1	IGF1R
BAX	IKBKB
BID	IL12RB1
BLNK	IL17B
C1S	IL25
C5	IL26
C8A	IL3
C8B	IL5
C8G	IRF1
CASP10	IRF2
CASP8	IRF3
CCL14	IRF4
CCL15	ITGAM
CCL16	ITGAX
CCL18	ITK
CCL23	LAG3
CCL3	LCK
CCL4	LTBR
CCR6	LYN
CD14	MAPK3
CD180	MCAM
CD19	NFKB1
CD2	PDCD1
CD33	PIK3R1

CD4	PRF1
CD47	PTPRC
CD6	PVR
CD79A	PYCARD
CD79B	RAC1
CD86	RAG1
CFI	RELA
CSF2	SMAD3
CXCL13	SPA17
CYFIP2	SPN
FAS	STAT3
FN1	STAT4
HAVCR2	STAT5A
HLA-DMA	STAT5B
HLA-DMB	SYK
HLA-DQA1	TNFRSF11A
HLA-DQB1	TNFRSF1A
ICAM1	TNFSF8
ICAM2	TRAF2
ICAM3	TRAF6
ICAM4	TYK2
ICOSLG	UBC
	MTOR

Figure 23A

IFNG activated ORFs compared to significant shared Response EpiSwitch™

Gene	Probe_Count_Sig	Probe_Count_Total
IGF1R	16	104
CD6	14	56
CXCL13	14	108
IKBKB	12	46
PIK3R1	12	148
ITK	10	26
PTPRC	10	214
C8B	9	151
C8A	8	166
CCL18	8	42
CYFIP2	8	40
FAS	8	50
ICOSLG	8	40
IRF1	8	42
ITGAM	8	50
ITGAX	8	41
CCL3	7	33
CCL4	7	32
CD14	6	62
CD4	6	42
NFKB1	6	64
SYK	6	78
LAG3	5	29
AKT1	4	60
BLNK	4	66

Figure 23B

C5	4	41
CASP8	4	41
CCR6	4	46
CD180	4	38
CD19	4	56
CD33	4	32
FN1	4	42
HLA-DQA1	4	28
HLA-DQB1	4	22
IL17B	4	44
IL5	4	20
LCK	4	46
MAPK3	4	44
MTOR	4	60
PRF1	4	28
SPN	4	56
TNFRSF11A	4	58
TNFSF8	4	50
TYK2	4	75
AIRE	3	17
ICAM3	3	70
STAT3	3	100
STAT5A	3	99
STAT5B	3	106
BAX	2	52
BID	2	42
C15	2	29
C8G	2	35
CASP10	2	53

Figure 23C

CCL15	2	12
CCL23	2	16
CD2	2	34
CD47	2	46
CD79A	2	44
CD79B	2	20
CD89	2	46
CFI	2	16
CSF2	2	36
HAVCR2	2	10
HLA-DMA	2	16
HLA-DMB	2	26
ICAM1	2	63
IFNG	2	10
IL25	2	74
IL26	2	20
IL3	2	42
IRF2	2	38
IRF3	2	30
IRF4	2	40
LTBR	2	33
LYN	2	48
PDCD1	2	36
PVR	2	65
RAC1	2	64
RAG1	2	51
RELA	2	56
SMAD3	2	34
STAT4	2	58

Figure 23D

TNFRSF1A	2	46
TRAF2	2	46
TRAF6	2	60
UBC	2	64
CCL14	1	9
CCL16	1	9
ICAM2	1	24
ICAM4	1	53
IL12RB1	1	51
MCAM	1	33
PYCARD	1	6
SPA17	1	17

95 of the ORFs overlap with the **IFNG activated ORFs**
The table shows the number of significant EpiSwitch™ in each of the 95 ORFs with the number of total EpiSwitch™ screened at these ORF's on the **aPD-L1 array**
The most enriched ORF for the shared Responder EpiSwitch™ CCSs is **IGF1R** followed by **CD6**

Figure 24

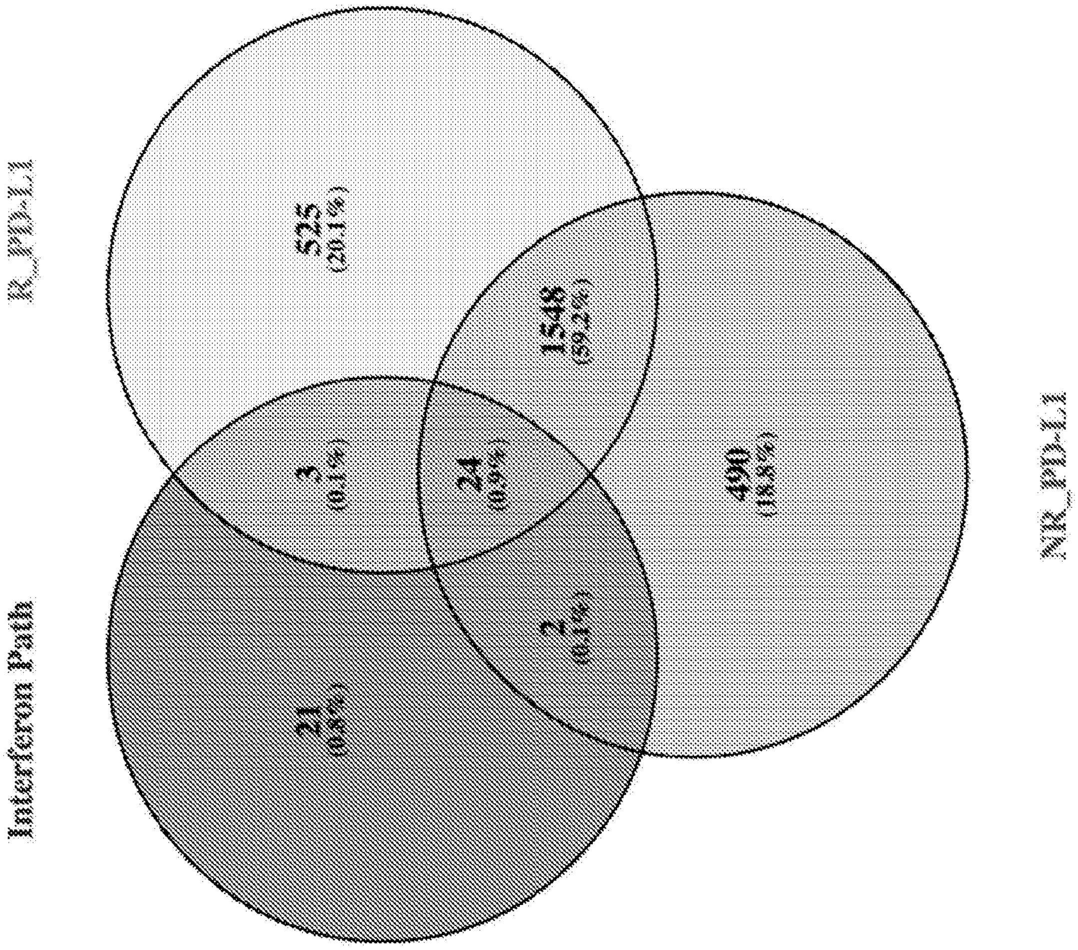
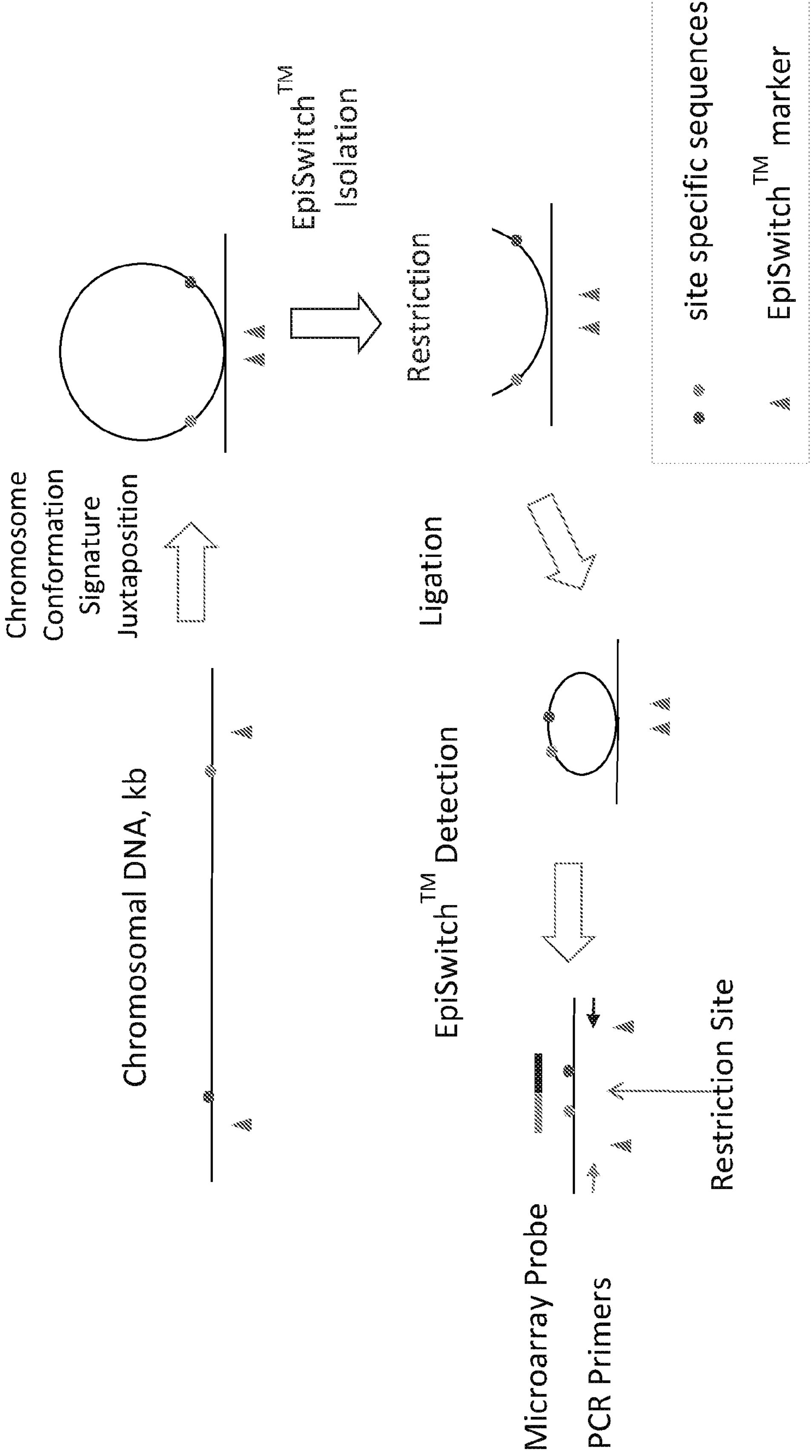

R_PD-L1
NR_PD-L1
Interferon Path
525
(20.1%)
1548
(59.2%)
490
(18.8%)
3
(0.1%)
24
(0.9%)
2
(0.1%)
21
(0.8%)

Figure 25


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