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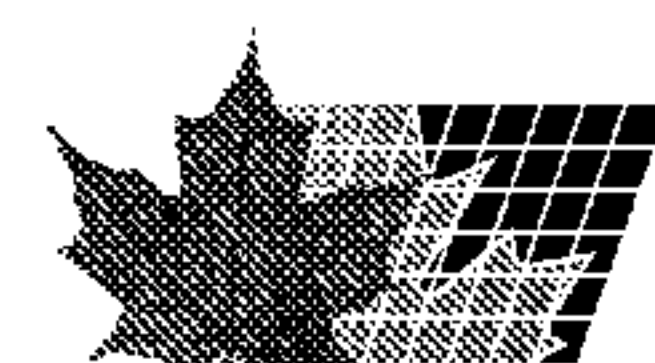
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(57) **Abrégé/Abstract:**

The present invention relates to gene expression profiles, microarrays comprising nucleic acid sequences representing gene expression profiles and new diagnostic kits and methods. The invention further relates to treatment of specific populations of, for example, cancer patients, as characterised by their gene expression profile, suffering from Mage expressing tumours.



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(54) Title: METHOD FOR IDENTIFYING WHETHER A PATIENT WILL BE RESPONDER OR NOT TO IMMUNOTHERAPY

(57) Abstract: The present invention relates to gene expression profiles, microarrays comprising nucleic acid sequences representing gene expression profiles and new diagnostic kits and methods. The invention further relates to treatment of specific populations of, for example, cancer patients, as characterised by their gene expression profile, suffering from Mage expressing tumours.

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Method

Field of the Invention

The present invention relates to gene expression profiles; microarrays comprising nucleic acid sequences for identifying said profiles, for example, by analysing patient derived samples; new
5 diagnostic kits and methods for identification of same. The invention further relates to treatment of specific populations of patients, for example cancer patients, characterised as a responder by their gene expression profile, such as patients suffering from Mage expressing tumours. The invention further includes methods of inducing a responder's profile in a patient initially or originally designated as a non-responder.

10 Background

Melanomas are tumors originating from melanocyte cells in the epidermis. Patients with malignant melanoma in distant metastasis (stage IV according to the American Joint Commission on Cancer (AJCC) classification) have a median survival time of one year, with a long-term survival rate of only 5%. Even the standard chemotherapy for stage IV melanoma has
15 therapeutic response rates of only 8–25%, but with no effect on overall survival. Patients with regional metastases (stage III) have a median survival of two to three years with very low chance of long-term survival, even after an adequate surgical control of the primary and regional metastases (Balch *et al.*, 1992). Most Patients with stage I to III melanoma have their tumour removed surgically, but these patients maintain a substantial risk of relapse. Thus there remains a
20 need to prevent melanoma progression, and to have improved treatment regimes for metastatic melanoma and adjuvant treatments for patients having had a primary tumour removed.

There are two types of lung cancer: non-small cell lung cancer (NSCLC) and small cell lung cancer (SCLC). The names simply describe the type of cell found in the tumours. NSCLC includes squamous-cell carcinoma, adenocarcinoma, and large-cell carcinoma and accounts for
25 around 80% of lung cancers. NSCLC is hard to cure and treatments available tend to have the aim of prolonging life, as far as possible, and relieving symptoms of disease. NSCLC is the most common type of lung cancer and is associated with poor outcomes (Gatzmeier *et al.*, 1994). Of all NSCLC patients, only about 25% have loco-regional disease at the time of diagnosis and are still amenable to surgical excision (stages IB, IIA or IIB according to the AJCC classification).

30 However, more than 50% of these patients will relapse within the two years following the complete surgical resection. There is therefore a need to provide better treatment for these patients.

Traditional chemotherapy is based on administering toxic substances to the patient and relying, in part, on the aggressive uptake of the toxic agent by the tumour/cancer cells. These toxic
35 substances adversely affect the patient's immune system, leaving the individual physically weakened and susceptible to infection.

It is known that not all patients with cancer respond to current cancer treatments. It is thought that only 30% or less of persons suffering from a cancer will respond to any given treatment. The

cancers that do not respond to treatment are described as resistant. In many instances there have not been reliable methods for establishing if the patients will respond to treatment. However, administering treatment to patients who are both responders and non-responders because they cannot be differentiated is an inefficient use of resources and, even worse, can be damaging to the patient because, as discussed already, many cancer treatments have significant side effects, such as severe immunosuppression, emesis and/or alopecia. It is thought that in a number of cases patients receive treatment, when it is not necessary or when it will not be effective.

Cells including cancer/tumour cells express many hundreds even thousands of genes.

A large amount of work has been done in recent times to assist in the diagnosis and prognosis of cancer patients, for example to identify those patients who do not require further treatment because they have no risk of metastasis, recurrence or progression of the disease.

WO 2006/124836 identifies certain gene expression signatures over several oncogenic pathways, thereby defining the prognosis of the patient and sensitivity to therapeutic agents that target these pathways. The specific oncogenes are; Myc, Ras, E2, S3, Src and beta-catenin.

US 2006/0265138 discloses a method of generating a genetic profile, generally for identifying the primary tumour so that appropriate treatment can be given.

US 2006/0240441 and US 2006/0252057 describe methods of diagnosing lung cancer based on the differential expression of certain genes.

US 2006/0234259 relates to the identification and use of certain gene expression profiles of relevance to prostate cancer.

WO 2006/103442 describes gene expression profiles expressed in a subset of estrogen receptor (ER) positive tumours, which act, as a predictive signature for response to certain hormone therapies such as tamoxifen and also certain chemotherapies.

WO 2006/093507 describes a gene profile useful for characterising a patient with colorectal cancer as having a good prognosis or a bad prognosis, wherein patients with a good prognosis are suitable for chemotherapy.

WO 2006/092610 describes a method for monitoring melanoma progression based on differential expression of certain genes and novel markers for the disease, in particular TSBY1, CYBA and MT2A.

WO 2005/049829 describes an isolated set of marker genes that may be employed to predict the sensitivity of certain cancers to a chemotherapeutic agent, which is an erbB receptor kinase inhibitor, such as gefitinib.

Generally, these cases relate to markers for one or more cancers based on biological markers for the identification and/or progression of the cancer. In some instances these pathways are modulated by so-called oncogenes. Diagnosis employing the above techniques allows those patients who are likely to relapse and/or suffer metastasis to be identified and targeted for further therapy. In other instances a specific marker relevant to resistance to a specific treatment is identified.

A new generation of cancer treatments based on antigens, peptides, DNA and the like is currently under investigation by a number of groups. The strategy behind many of these therapies, often referred to as cancer immunotherapy, is to stimulate the patient's immune system into fighting the cancer. These therapies are likely to be advantageous because the side effects, of taking such treatments, are expected to be minimal in comparison to the side effects currently encountered by patients undergoing cancer treatment. An antigen used in a cancer immunotherapy may be referred to as an ASCI, that is antigen-specific cancer immunotherapeutic.

In the early 1980s, Van Pel and Boon published the discovery of cytolytic T cells directed against an antigen presented on tumour cells. This led to the characterization of the first tumour-specific, shared antigen: Melanoma AGE-1 (MAGE-1, subsequently renamed MAGE-A1). It was followed by the identification of a large number of genes sharing the same expression pattern: they are expressed in a wide range of tumour types such as, melanoma, lung, bladder, breast, head and neck cancers. They are not expressed in normal cells, except testis. However, this expression in the testis does not normally lead to antigen expression, as these germ line cells do not express MHC class I molecules. From their peculiar expression profile, the name of Cancer Testis (CT) genes was proposed for these genes.

MAGE antigens are antigens encoded by the family of Melanoma-associated antigen genes (MAGE). MAGE genes are predominately expressed on melanoma cells (including malignant melanoma) and some other cancers including NSCLC (non small cell lung cancer), head and neck squamous cell carcinoma, bladder transitional cell carcinoma and oesophagus carcinoma, but are not detectable on normal tissues except in the testis and the placenta (Gaugler *et al* Human gene MAGE-3 codes for an antigen recognized on a melanoma by autologous cytolytic T lymphocytes *J Exp Med.* 1994 Mar 1;179(3):921-930); Weynants *et al* Expression of mage genes by non-small-cell lung carcinomas *Int. J Cancer.* 1994 Mar 15;56(6):826-829, Patard *et al* Int J. Cancer 64: 60, 1995). MAGE-A3 is expressed in 69% of melanomas (Gaugler, 1994), and can also be detected in 44% of NSCLC (Yoshimatsu 1988), 48% of head and neck squamous cell carcinoma, 34% of bladder transitional cell carcinoma, 57% of oesophageal carcinoma, 32% of colon cancers and 24% of breast cancers (Van Pel, *et al* Genes coding for tumor antigens recognized by cytolytic T lymphocytes *Immunological Reviews* 145, 229-250, 1995, 1995.); Inoue 1995; Fujie 1997; Nishimura 1997). Cancers expressing MAGE proteins are known as Mage associated tumours.

Summary

In one aspect the invention provides a method for detection of a gene signature, indicative of a responder or non-responder to immunotherapy, such as cancer immunotherapy, in a biological sample. Thus the invention provides a method of screening patients to establish if they are suitable for treatment, for example with a cancer immunotherapy.

In one aspect the invention provides a diagnostic kit comprising one or more nucleotide probes capable of hybridising to the mRNA or cDNA of one or more immune activation genes relevant

to the profile.

In one aspect the invention provides one or more probes for identifying said one or more immune activation genes relevant to the profile.

5 In one aspect the invention provides a microarray of said probes suitable for the detection of said gene(s)/profile.

In another aspect the invention provides use of a microarray, including known microarrays, for the identification of said immune gene(s)/profile.

In one aspect the invention provides use of PCR (or other known techniques) for identification of differential expression (such as upregulation) of one or more of said genes.

10 In one aspect the invention provides a method of treating a patient with an appropriate immunotherapy after screening to identify the patient as a responder to said treatment.

In another aspect the invention provides a method of increasing the efficacy of an immunotherapy in a patient population comprising the step of first screening the population for the differential expression of one or more immune genes/said profile, and a second step of
15 characterising the patient as a responder or non-responder.

In a further aspect the invention provides a method of generating a list of differentially expressed immune genes (ie a profile of immune genes) indicative of a responder or non-responder to immunotherapy.

Brief Description of the Figures, Sequences & Tables

20 **Figure 1** is a diagrammatic representation of hierarchical clustering using Spotfire analysis linking the clinical outcome of 31 patients found to be responders (defined herein to include responder, mixed responder and stable disease) or non-responders, to Mage immunotherapy in the MAGE008 clinical trial, with the gene profile identified by microarray analysis and employing the 148 top probe sets.

25 **Figure 2** is a diagrammatic representation of the same analysis as Figure 1, wherein the hierarchical clustering was performed using the BaldiBH analysis using 100 probes sets.

Figure 3 is a diagrammatic representation of the same analysis as Figure 1, wherein the hierarchical clustering was performed using Arrayminer Classmaker gene list.

30 **Figure 4** is a Venn diagram representing the comparison of gene lists used in Figure 1, Figure 2 and Figure 3.

Figure 5 is a visual representation of the expression profile of various genes (36 probe sets) for 30 different patients (patients are along the X-axis and the various probe sets extend along the Y-axis).

35 **Figure 5a** is a visual representation of the expression of 2 genes for 30 different patients (patients along the X-axis).

Figure 6 shows the Principal Component Analysis using PRF1, GZMB, GNLY, CD8A, PRKCQ, FOXP3, IFNG, CCL5, GPR171 and TRBV19 genes.

Figure 7 is a visual representation of the expression profile of various genes (41 probe sets) for

33 different patients (patient identification numbers are along the X-axis) from the MAGE008 clinical trial using the adjuvant AS15.

Figure 8 is a diagrammatic representation of hierarchical clustering for patients in the AS15 arm of the MAGE008 clinical trial.

- 5 **Figure 9** is a visual representation of the expression profile of various genes (41 probe sets) for 33 different patients (patient identification numbers are along the X-axis) from the MAGE008 clinical trial using the adjuvant AS02b.

Figure 10 is a diagrammatic representation of hierarchical clustering for patients in the AS02b arm of the MAGE008 clinical trial.

- 10 In the heat maps herein upregulated genes are represented in red which in greyscale tends to be presented by darker shades. Lighter shades in greyscale tend to present green on the heat map (genes which are not upregulated).

Seq ID No 1	Chromosome 6 open reading frame 190
Seq ID No 2	Hematopoietic cell-specific Lyn substrate 1
Seq ID No 3	Interleukin 2 receptor, gamma (severe combined immunodeficiency)
Seq ID No 4	CD52 antigen (CAMPATH-1 antigen) /// CD52 antigen (CAMPATH-1 antigen)
Seq ID No 5	CD2 antigen (p50), sheep red blood cell receptor /// CD2 antigen (p50), sheep red blood cell receptor
Seq ID No 6	Ubiquitin D
Seq ID No 7	Signal transducer and activator of transcription 4
Seq ID No 8	Granzyme K (granzyme 3; tryptase II) /// granzyme K (granzyme 3; tryptase II)
Seq ID No 9	CD3G antigen, gamma polypeptide (TiT3 complex)
Seq ID No10	G protein-coupled receptor 171
Seq ID No 11	Protein kinase C, beta 1
Seq ID No 12	Major histocompatibility complex, class II, DR alpha /// major histocompatibility complex, class II, DR alpha
Seq ID No 13	Major histocompatibility complex, class II, DQ beta 1 /// Major histocompatibility complex, class II, DQ beta 1
Seq ID No 14	Alcohol dehydrogenase IB (class I), beta polypeptide
Seq ID No 15	T cell receptor alpha constant /// T cell receptor alpha constant
Seq ID No 16	CD69 antigen (p60, early T-cell activation antigen)
Seq ID No 17	Protein kinase C, theta
Seq ID No 18	T cell receptor beta variable 19 /// T cell receptor beta constant 1
Seq ID No 19	T cell receptor alpha locus /// T cell receptor delta variable 2 /// T cell receptor alpha variable 20 /// T cell receptor alpha joining 17 /// T cell receptor alpha constant

Seq ID No 20	T cell receptor gamma constant 2
Seq ID No 21	T cell receptor beta variable 21-1 /// T cell receptor beta variable 19 /// T cell receptor beta variable 5-4 /// T cell receptor beta variable 3-1 /// T cell receptor beta constant 1
Seq ID No 22	T cell receptor alpha locus
Seq ID No 23	T cell receptor beta variable 19 /// T cell receptor beta variable 19 /// T cell receptor beta constant 1 /// T cell receptor beta constant 1
Seq ID No 24	CD3D antigen, delta polypeptide (TiT3 complex)
Seq ID No 25	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// similar to T-cell receptor gamma chain C region PT-gamma-1/2 /// similar to T-cell receptor gamma chain V region PT-gamma-1/2 precursor /// TCR gamma alternate reading frame protein
Seq ID No 26	Pyrin and HIN domain family, member 1
Seq ID No 27	T cell receptor associated transmembrane adaptor 1
Seq ID No 28	SLAM family member 7
Seq ID No 29	Chromosome 4 open reading frame 7
Seq ID No 30	Major histocompatibility complex, class II, DQ alpha 1
Seq ID No 31	Transcribed locus
Seq ID No 32	Amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen)
Seq ID No 33	Dendritic cell-associated lectin-1

Each sequences above is given in Table 1A below.

Seq ID No 34	Nucleotide sequence encoding fusion protein of Lipoprotein D fragment, Mage3 fragment, and histidine tail
Seq ID No 35	Amino acid sequence of the fusion protein of Lipoprotein D fragment, Mage3 fragment and histidine tails

Seq ID No.s 36 to 43 (found in the description) are peptide sequences relevant to MAGE A3.

Seq ID No.s 44 to 48 are examples of oligonucleotide sequences containing a CpG motif.

Seq ID No.s 49 to 84 (listed in Table 1B) are probes sets suitable for hybridising to the genes listed in Table 1.

Seq ID No.s 85 to 97 (listed in Table 3A) are sequences for the genes listed in Table 3.

Tables 1 to 4, 11 and 12 provide lists of genes that are differentially regulated according to the present invention.

Table 1A provides the nucleotide sequence listing for each of the genes listed in Table 1.

Table 1B provides the probe set identifier number (a unique reference number for the probe) of probes (and sequence thereof) wherein each probe is suitable for identifying particular genes listed in Table 1.

Table 3A links the genes (and sequences thereof) of Table 3 and probes suitable for identifying

said genes.

Table 5 provides a list of genes, primers and probes suitable for use in PCR analysis.

Table 6 is a list of gene included in the TaqMan® (Q-PCR) Immune Profiling Array.

Table 7 provides a list of genes according to one aspect of the invention.

5 **Table 7A** provides the geomean ratio between responders and non-responder groups for the genes listed in Table 7.

Table 8 provides a correlation matrix for 30 genes.

Table 9 provides a list of genes according to one aspect of the invention.

Table 9A logistical regression results for certain genes listed in Table 9

10 **Table 10** shows the percentage of correct classification using a logistical regression model for the genes listed in Table 9.

Table 11 provides a list of genes according to one aspect of the invention.

Tables 11A & 11B show the level of gene expression (based on the results of 41 probe sets) for various patients.

15 **Tables 12 and 13** show gene lists that form further aspects of the invention.

Table 14 provides a correlation between the gene expression levels given in Tables 11A & 11B with the clinical outcome for said patients.

Annexes A to C are computer code for assisting with stastical analysis of samples.

20 The MAGE-1 gene belongs to a family of 12 closely related genes, MAGE 1, MAGE 2, MAGE 3, MAGE 4, MAGE 5, MAGE 6, MAGE 7, MAGE 8, MAGE 9, MAGE 10, MAGE 11, MAGE 12, located on chromosome X and sharing with each other 64 to 85% homology in their coding sequence (De Plaen, 1994). These are sometimes known as MAGE A1, MAGE A2, MAGE A3, MAGE A4, MAGE A5, MAGE A6, MAGE A7, MAGE A8, MAGE A9, MAGE A 10, MAGE A11, MAGE A12 (The MAGE A family).

25 Two other groups of proteins are also part of the MAGE family although more distantly related. These are the MAGE B and MAGE C group. The MAGE B family includes MAGE B1 (also known as MAGE Xp1, and DAM 10), MAGE B2 (also known as MAGE Xp2 and DAM 6) MAGE B3 and MAGE B4 – the Mage C family currently includes MAGE C1 and MAGE C2.

30 In general terms, a MAGE A protein can be defined as containing a core sequence signature located towards the C-terminal end of the protein (for example with respect to MAGE A1 a 309 amino acid protein, the core signature corresponds to amino acid 195-279).

It does not simply follow that if the tumour expresses, for example, Mage that the patient will respond to immunotherapy based on a Mage antigen.

35 **Statement of Invention**

Analysis performed on cancers/tumours from patients prior to receiving immunotherapy, such as Mage immunotherapy, identified that certain genes were differentially expressed in patients that responded well to the treatment, in comparison to those patients who did not respond to the

immunotherapy. The present inventors have discovered a gene signature/profile that is predictive of the likely response of the patient to an appropriate immunotherapy. More specifically the present inventors have discovered a gene signature that is predictive of improved survival after treatment with Mage antigen specific immunotherapy.

- 5 Thus the invention provides a gene profile, from a patient derived sample, which is indicative of an increased likelihood that the patient will be a responder (or alternatively a non-responder) to an immunotherapy, for example a cancer immunotherapy, such as Mage immunotherapy, wherein the profile comprises differential expression of at least one immune activation gene. The invention provides a gene profile, from a patient derived sample, which is indicative of an
10 increased likelihood that the patient will be a responder to an immunotherapy, for example a cancer immunotherapy, such as Mage immunotherapy, wherein the profile comprises upregulation of at least one immune activation gene.

The present invention provides a predictive profile in contrast to a diagnostic or prognostic profile.

- 15 Whilst not wishing to be bound by theory it is hypothesised that the gene signature identified is in fact indicative of an immune/inflammatory, such as a T cell infiltration/activation response in the patients who are designated as responders, for example, the signature may represent a T-cell activation marker. The presence of this response is thought to assist the patient's body to fight the disease, such as cancer, after administration of the immunotherapy thereby rendering a patient
20 more responsive to said immunotherapy.

Thus the signature of the present invention does not focus on markers/genes specifically associated with the diagnosis and/or prognosis of the relevant disease, for example cancer such as oncogenes, but rather is predictive of whether the patient will respond to an appropriate immunotherapy, such as cancer immunotherapy.

- 25 The gene profile identified herein for cancer and methods for identifying the same are thought to be indicative of the microenvironment of the tumor. The correct microenvironment of the tumor seems to be key to whether the patient responds to appropriate cancer immunotherapy. Immunotherapy in the context of the invention means therapy based on stimulating an immune response, generally to an antigen, wherein the response results in the treatment, amelioration
30 and/or retardation of the progression of a disease associated therewith. Treatment in this context would not usually include prophylactic treatment.

Cancer immunotherapy in the context of this specification means immunotherapy for the treatment of cancer. In one aspect the immunotherapy is based on a cancer testis antigen, such as Mage (discussed in more detail below).

- 35 This invention may be used for identifying cancer patients that are likely to respond to appropriate immunotherapy, for example patients with melanoma, breast, bladder, lung, NSCLC, head and neck cancer, squamous cell carcinoma, colon carcinoma and oesophageal carcinoma, such as in patients with MAGE-expressing cancers. In an embodiment, the invention may be

used in an adjuvant (post-operative, for example disease-free) setting in such cancers, particularly lung and melanoma. The invention also finds utility in the treatment of cancers in the metastatic setting.

Thus in a first aspect the invention provides a signature indicative of a patient, such as a cancer patient, designated a responder or non-responder to treatment with an appropriate immunotherapy, the signature comprising differential expression of one or more genes selected from immune activation/immune response/inflammatory response genes, for example, the group of genes indicative of T cell infiltration/activation, such as a gene listed (or a gene list comprising or consisting) those listed in Table 1, 2, 3, 4, 7, 9, 11, 12 and/or 13 such as Table 1 or 2.

Differential expression in the context of the present invention means the gene is upregulated or downregulated in comparison to its normal expression. Statistical methods for calculating gene differentiation are discussed below.

Immune activation gene is intended to mean a gene that facilitates, increases or stimulates an appropriate immune response. Immune response gene and immune activation gene are used interchangeably herein.

An important technique for the analysis of the genes expressed by cells, such as cancer/tumour cells, is DNA microarray (also known as gene chip technology), where hundreds or more probe sequences (such as 55, 000 probe sets) are attached to a glass surface. The probe sequences are generally all 25 mers or 60 mers and are sequences from known genes. These probes are generally arranged in a set of 11 individual probes (a probe set) and are fixed in a predefined pattern on the glass surface. Once exposed to an appropriate biological sample these probes hybridise to the relevant RNA or DNA of a particular gene. After washing, the chip is "read" by an appropriate method and a quantity such as colour intensity recorded. The differential expression of a particular gene is proportional to the measure/intensity recorded. This technology is discussed in more detail below.

Once a target gene/profile has been identified there are several analytical methods to measure whether the gene(s) is/are differentially expressed. These analytical techniques include real-time polymerase chain reaction, also called quantitative real time polymerase chain reaction (QRT-PCR or Q-PCR), which is used to simultaneously quantify and amplify a specific part of a given DNA molecule present in the sample.

The procedure follows the general pattern of polymerase chain reaction, but the DNA is quantified after each round of amplification (the "real-time" aspect). Two common methods of quantification are the use of fluorescent dyes that intercalate with double-strand DNA, and modified DNA oligonucleotide probes that fluoresce when hybridized with a complementary DNA.

The basic idea behind real-time polymerase chain reaction is that the more abundant a particular cDNA (and thus mRNA) is in a sample, the earlier it will be detected during repeated cycles of amplification. Various systems exist which allow the amplification of DNA to be followed and

they often involve the use of a fluorescent dye which is incorporated into newly synthesised DNA molecules during real-time amplification. Real-time polymerase chain reaction machines, which control the thermocycling process, can then detect the abundance of fluorescent DNA and thus the amplification progress of a given sample. Typically, amplification of a given cDNA over time follows a curve, with an initial flat-phase, followed by an exponential phase. Finally, as the experiment reagents are used up, DNA synthesis slows and the exponential curve flattens into a plateau.

Alternatively the mRNA or protein product of the target gene(s) may be measured by Northern Blot analysis, Western Blot and/or immunohistochemistry.

In one aspect the analysis to identify the profile/signature is performed on a patient sample wherein a cancer testis antigen is expressed.

If a gene is always upregulated or always down regulated in patients that are deemed to be responders (or alternatively non-responders) then this single gene can be used to establish if the patient is a responder or a non-responder once a threshold is established and provided the separation of the two groups is adequate.

When a single gene is analysed, for example, by Q-PCR then the gene expression can be normalised by reference to a gene that remains constant, for example genes with the symbol H3F3A, GAPDH, TFRC, GUSB or PGK1. The normalisation can be performed by subtracting the value obtained for the constant gene from the value obtained for the gene under consideration.

A threshold may be established by plotting a measure of the expression of the relevant gene for each patient. Generally the responders and the non-responders will be clustered about a different axis/focal point. A threshold can be established in the gap between the clusters by classical statistical methods or simply plotting a "best fit line" to establish the middle ground between the two groups. Values, for example, above the pre-defined threshold can be designated as responders and values, for example below the pre-designated threshold can be designated as non-responders.

In one aspect the invention provides a gene profile for identifying a responder comprising one or more of said genes wherein 50, 60, 70, 75, 80, 85, 90, 95, 99 or 100% of the genes are upregulated.

The genes listed in Table 1, 2, 3, 4, 7, 9, 11, 12 and/or 13 such as Table 1, 2 and/or 3 are generally upregulated in responders.

The robustness of the predictive method of the invention can be further improved for larger sample sizes by employing 2, 3, 4, 5, 6, etc genes from Table 1, 2, 3, 4, 7, 9, 11, 12 and/or 13 such as Table 1 or 2.

Furthermore, once at least two differential expressed genes are included in the signature then statistical clustering methods can be used to differentiate the responders and non-responders. Methods for statistical clustering and software for the same are discussed below.

One parameter used in quantifying the differential expression of genes is the fold change, which

is a metric for comparing a gene's mRNA-expression level between two distinct experimental conditions. Its arithmetic definition differs between investigators. However, the higher the fold change the more likely that the differential expression of the relevant genes will be adequately separated, rendering it easier to decide which category (responder or non-responder) the patient falls into.

The fold change may, for example be at least 10, at least 15, at least 20 or 30.

Another parameter also used to quantify differential expression is the "p" value. It is thought that the lower the p value the more differentially expressed the gene is likely to be, which renders it a good candidate for use in profiles of the invention. P values may for example include 0.1 or less, such as 0.05 or less, in particular 0.01 or less. P values as used herein include corrected "P" values and/or also uncorrected "P" values.

The invention provides a method for the detection of a gene signature in a biological sample, the method comprising the analysis of the expression of at least 5 genes as set forth in Table 1.

Alternatively one or more genes may be selected from Table 1, 2, 3, 4, 7, 9, 11, 12 and/or 13 such as Table 1 or 2.

Thus in one aspect the invention provides a method of identifying whether a cancer patient will be a responder or non-responder to immunotherapy, the method comprising:

1. analysing a sample comprising mRNA or fragments thereof expressed by genes of cancerous cells or DNA or fragments thereof from cancerous cells, for differential expression of one or more genes indicative of T-cell infiltration/activation, for example selected from the group comprising or consisting of genes listed in Table 1, 2, 3, 4, 7, 9, 11, 12 and/or 13 such as Table 1 or 2, and

2. characterising a patient as a responder or a non-responder based on the results of step 1.

Responder in the context of the present invention includes persons where the cancer/tumor(s) is irradiated, reduced or improved (mixed responder or partial responder) or simply stabilised such that the disease is not progressing. In responders where the cancer is stabilised then the period of stabilisation is such that the quality of life and/or patients life expectancy is increased (for example stable disease for more than 6 months) in comparison to a patient that does not receive treatment.

Partial clinical response in respect of cancer is wherein all of the tumors/cancers respond to treatment to some extent, for example where said cancer is reduced by 30, 40, 50, 60% or more. Mixed clinical responder in respect of cancer is defined as wherein some of the tumors/cancers respond to treatment and others remain unchanged or progress.

Standard definitions are available for responders, partial responders and mixed responders to cancer treatment. These standard definitions apply herein unless from the context it is clear that they do not apply.

As used herein, methods to predict a favorable clinical response or to identify subjects more likely to respond to therapy, is not meant to imply a 100% predictive ability, but to indicate that

subjects with certain characteristics are more likely to experience a favorable clinical response to a specified therapy than subjects who lack such characteristics. However, as will be apparent to one skilled in the art, some individuals identified as more likely to experience a favorable clinical response may nonetheless fail to demonstrate measurable clinical response to the treatment.

5 Similarly, some individuals predicted as non-responders may nonetheless exhibit a favorable clinical response to the treatment.

As used herein, a 'favorable response' (or 'favorable clinical response') to, for example, an anticancer treatment refers to a biological or physical response that is recognized by those skilled in the art as indicating a decreased rate of tumor growth, compared to tumor growth that would occur with an alternate treatment or the absence of any treatment. "Favorable clinical response" as used herein is not synonymous with a cure, but includes Partial Response, Mixed Response or Stable Disease. A favorable clinical response to therapy may include a lessening of symptoms experienced by the subject, an increase in the expected or achieved survival time, a decreased rate of tumor growth, cessation of tumor growth (stable disease), regression in the number or mass of metastatic lesions, and/or regression of the overall tumor mass (each as compared to that which would occur in the absence of therapy, or in response to an alternate therapy).

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Patients in need of treatment for, for example, a Mage-expressing tumor, whose tumor cells have a gene signature described herein as a "Responder" signature are more likely to have a favorable clinical response, compared to patients whose tumor cells show a gene signature described herein as a "Non-Responder" signature, when treated with Mage specific immunotherapy.

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Non-responder in the context of this invention includes persons whose symptoms ie cancers/tumors are not improved or stabilised.

Optionally the characterisation of the patient as a responder or non-responder can be performed by reference to a "standard" or a training set. The standard may be the profile of a person/patient who is known to be a responder or non-responder or alternatively may be a numerical value.

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Such pre-determined standards may be provided in any suitable form, such as a printed list or diagram, computer software program, or other media.

Training set in the context of the present specification is intended to refer to a group of samples for which the clinical results can be correlated with the gene profile and can be employed for training an appropriate statistical model/programme to identify responders and/or non-responder for new samples. Tables 11A, 11B and 14 contain the training set information relevant to the 41 probe set model described in Example 4.

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In one aspect a mathematical model/algorithm/statistical method is employed to characterise the patient as responder or non-responder.

In one aspect the invention provides a profile based one or more immune activation genes, such as 5 or more such genes.

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In one aspect the invention provides a profile based on the genes in Table 1, 2, 3, 4, 7, 9, 11, 12 and/or 13 such as Table 1 or 2.

In one aspect the invention provides a profile based on 489 probes (listed in Table 4A) and/or approximately 480 genes as listed in Table 4.

According to one aspect the present invention provides a gene signature indicative of improved survival of patients with Mage expressing cancers following treatment with Mage specific immunotherapy. This gene signature, of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or 31, genes from the genes disclosed in Table 1, is characterised by differential expression compared to the gene signature of MAGE-expressing tumour patients who do not respond to Mage antigen specific cancer immunotherapy. Improved survival is likely to be a corollary of a response to the immunotherapy administered, if the patient is in fact a responder.

TABLES WITH GENE LISTS

In one aspect the invention relates to one or more genes listed in Table 1

Table 1

	Gene Title	Seq Id No
1.1	chromosome 6 open reading frame 190	1
1.2	hematopoietic cell-specific Lyn substrate 1	2
1.3	interleukin 2 receptor, gamma (severe combined immunodeficiency)	3
1.4	CD52 antigen (CAMPATH-1 antigen) /// CD52 antigen (CAMPATH-1 antigen)	4
1.5	CD2 antigen (p50), sheep red blood cell receptor /// CD2 antigen (p50), sheep red blood cell receptor	5
1.6	ubiquitin D	6
1.7	signal transducer and activator of transcription 4	7
1.8	granzyme K (granzyme 3; tryptase II)///granzyme K (granzyme 3; tryptase II)	8
1.9	CD3G antigen, gamma polypeptide (TiT3 complex)	9
1.10	G protein-coupled receptor 171	10
1.11	Protein kinase C, beta 1	11
1.12	major histocompatibility complex, class II, DR alpha /// major histocompatibility complex, class II, DR alpha	12
1.13	Major histocompatibility complex, class II, DQ beta 1 /// Major histocompatibility complex, class II, DQ beta 1	13
1.14	alcohol dehydrogenase IB (class I), beta polypeptide	14
1.15	T cell receptor alpha constant /// T cell receptor alpha constant	15
1.16	CD69 antigen (p60, early T-cell activation antigen)	16
1.17	protein kinase C, theta	17
1.18	T cell receptor beta variable 19 /// T cell receptor beta constant 1	18

1.19	T cell receptor alpha locus /// T cell receptor delta variable 2 /// T cell receptor alpha variable 20 /// T cell receptor alpha joining 17 /// T cell receptor alpha constant	19
1.20	T cell receptor gamma constant 2	20
1.21	T cell receptor beta variable 21-1 /// T cell receptor beta variable 19 /// T cell receptor beta variable 5-4 /// T cell receptor beta variable 3-1 /// T cell receptor beta constant 1	21
1.22	T cell receptor alpha locus	22
1.23	T cell receptor beta variable 19 /// T cell receptor beta variable 19 /// T cell receptor beta constant 1 /// T cell receptor beta constant 1	23
1.24	CD3D antigen, delta polypeptide (TiT3 complex)	24
1.25	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// similar to T-cell receptor gamma chain C region PT-gamma-1/2 /// similar to T-cell receptor gamma chain V region PT-gamma-1/2 precursor /// TCR gamma alternate reading frame protein	25
1.26	pyrin and HIN domain family, member 1	26
1.27	T cell receptor associated transmembrane adaptor 1	27
1.28	SLAM family member 7	28
1.29	chromosome 4 open reading frame 7	29
1.30	Major histocompatibility complex, class II, DQ alpha 1	30
1.31	Transcribed locus	31
1.32	Amphiphysin (Stiff-Man syndrome with breast cancer 128kDa autoantigen)	32
1.33	dendritic cell-associated lectin-1	33

Table 1A at the end of this specification gives the full nucleotide sequence for each of the above genes.

In one aspect the invention provides a profile based on differential expression of 1 or more of 62 genes, identified in the literature, that relate to immune infiltration and activation.

In one aspect the invention provides a profile based on the genes listed in Table 2.

Table 2:

	Gene Symbol	Gene Title	Seq Id No
2.1	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	30
2.2	TRBV3-1	T cell receptor beta variable 3-1	21
2.3	IL2RG	interleukin 2 receptor, gamma (severe combined immunodeficiency)	3
2.4	CD2	CD2 antigen (p50), sheep red blood cell receptor	5

2.5	GPR171	G protein-coupled receptor 171	10
2.6	ADH1B	alcohol dehydrogenase IB (class I), beta polypeptide	14
2.7	CD69	CD69 antigen (p60, early T-cell activation antigen)	16
2.8	TRBV19	T cell receptor beta variable 19	18
2.9	TRAT1	T cell receptor associated transmembrane adaptor 1	27
2.10	C4orf7	chromosome 4 open reading frame 7	29
2.11	PRKCB1	protein kinase C, beta 1	11
2.12	CD3D	CD3D antigen, delta polypeptide (TiT3 complex)	24
2.13	UBD	ubiquitin D	6

In one aspect the invention provides the list of genes in Table 3.

Table 3

	Gene Symbol	Gene Title
3.1	CD52	CD52 molecule /// CD52 molecule
3.2	UBD	gamma-aminobutyric acid (GABA) B receptor, 1 /// ubiquitin D
3.3	STAT4	signal transducer and activator of transcription 4
3.4	GZMK	granzyme K (granzyme 3; tryptase II) /// granzyme K (granzyme 3; tryptase II)
3.5	GPR171	G protein-coupled receptor 171
3.6	PRKCQ	protein kinase C, theta
3.7	TRA@ /// TRDV2 /// TRAV20 /// TRAC	T cell receptor alpha locus /// T cell receptor delta variable 2 /// T cell receptor alpha variable 20 /// T cell receptor alpha constant
3.8	TRGC2 /// TRGV2 /// TRGV9 /// TARP /// LOC642083	T cell receptor gamma constant 2 /// T cell receptor gamma variable 2 /// T cell receptor gamma variable 9 /// TCR gamma alternate reading frame protein /// hypothetical protein LOC642083
3.9	TRBV21-1 /// TRBV19 /// TRBV5-4 /// TRBV3-1 /// TRBC1	T cell receptor beta variable 21-1 /// T cell receptor beta variable 19 /// T cell receptor beta variable 5-4 /// T cell receptor beta variable 3-1 /// T cell receptor beta constant 1 /// similar to T-cell receptor beta chain V region CTL-L17 precursor
3.10	TRBV19 /// TRBC1	T cell receptor beta variable 19 /// T cell receptor beta variable 19 /// T cell receptor beta constant 1 /// T cell receptor beta constant 1
3.11	CD3D	CD3d molecule, delta (CD3-TCR complex)
3.12	TRAT1	T cell receptor associated transmembrane adaptor 1

In one aspect the invention provides a profile based on one or more genes of Table 4

Table 4

	Gene Symbol	Gene Title
4.1	FLJ20647	NA
4.2	NAV1	neuron navigator 1
4.3	GPR171	G protein-coupled receptor 171
4.4	CCL14	chemokine (C-C motif) ligand 14
4.5	C1S	complement component 1, s subcomponent
4.6	CXCL2	chemokine (C-X-C motif) ligand 2
4.7	TRBV3-1	T cell receptor beta variable 3-1
4.8	TRDV2	T cell receptor delta variable 2
4.9	RUFY3	RUN and FYVE domain containing 3
4.10	DOCK8	dedicator of cytokinesis 8
4.11	GCH1	GTP cyclohydrolase 1 (dopa-responsive dystonia)
4.12	CENTD3	centaurin, delta 3
4.13	ACSL5	acyl-CoA synthetase long-chain family member 5
4.14	AMICA1	adhesion molecule, interacts with CXADR antigen 1
4.15	IL2RG	interleukin 2 receptor, gamma (severe combined immunodeficiency)
4.16	TNFAIP3	tumor necrosis factor, alpha-induced protein 3
4.17	PSCDBP	pleckstrin homology, Sec7 and coiled-coil domains, binding protein
4.18	ESR1	estrogen receptor 1
4.19	TRBC1	T cell receptor beta constant 1
4.20	CD52	CD52 antigen (CAMPATH-1 antigen)
4.21	LOC442535	NA
4.22	TRBV19	T cell receptor beta variable 19
4.23	IL7R	interleukin 7 receptor
4.24	TRAC	T cell receptor alpha constant
4.25	NCF2	neutrophil cytosolic factor 2 (65kDa, chronic granulomatous disease, autosomal 2)
4.26	LOC92689	NA
4.27	GZMK	c("granzyme K (granzyme 3", " tryptase II)")
4.28	NA	NA (gene identified by probe 235831_at)
4.29	RAB34	RAB34, member RAS oncogene family
4.30	DPT	dermatopontin
4.31	PVT1	Pvt1 oncogene homolog, MYC activator (mouse)
4.32	TRGC2	T cell receptor gamma constant 2

4.33	GIMAP5	GTPase, IMAP family member 5
4.34	CD52	CD52 antigen (CAMPATH-1 antigen)
4.35	CD3D	CD3d antigen, delta polypeptide (TiT3 complex)
4.36	TMEM132C	transmembrane protein 132C
4.37	NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
4.38	TRA@	T cell receptor alpha locus
4.39	TRAT1	T cell receptor associated transmembrane adaptor 1
4.40	LOC442535 (NA)	NA (duplicate)
4.41	RAB34	RAB34, member RAS oncogene family
4.42	CD69	CD69 antigen (p60, early T-cell activation antigen)
4.43	DOCK8	dedicator of cytokinesis 8
4.44	GIMAP5 (NA)	GTPase, IMAP family member 5 (NA –duplicate)
4.45	IRF8	interferon regulatory factor 8
4.46	KLRB1	killer cell lectin-like receptor subfamily B, member 1
4.47	NA	NA
4.48	ITGA3	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)
4.49	MAP3K8	mitogen-activated protein kinase kinase kinase 8
4.50	C1orf162	chromosome 1 open reading frame 162
4.51	UBD	ubiquitin D
4.52	TRGV9	T cell receptor gamma variable 9
4.53	NAV1 (NA)	neuron navigator 1 (NA- duplicate)
4.54	ARHGAP9	Rho GTPase activating protein 9
4.55	TIFA	NA
4.56	DPT	dermatopontin
4.57	NA	NA (gene identified by probe 1569942_at)
4.58	GIMAP4	GTPase, IMAP family member 4
4.59	HCLS1	hematopoietic cell-specific Lyn substrate 1
4.60	PRKCH	protein kinase C, eta
4.61	STAT4	signal transducer and activator of transcription 4
4.62	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1
4.63	ADRB2	adrenergic, beta-2-, receptor, surface
4.64	NA	NA
4.65	CTSW	cathepsin W (lymphopain)
4.66	MYH11	myosin, heavy polypeptide 11, smooth muscle
4.67	GIMAP6	GTPase, IMAP family member 6
4.68	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1

4.69	CD8A	CD8 antigen, alpha polypeptide (p32)
4.70	TNFAIP3	tumor necrosis factor, alpha-induced protein 3
4.71	CP	ceruloplasmin (ferroxidase)
4.72	SMOC2	SPARC related modular calcium binding 2
4.73	C20orf24	chromosome 20 open reading frame 24
4.74	C16orf54	chromosome 16 open reading frame 54
4.75	CD2	CD2 antigen (p50), sheep red blood cell receptor
4.76	SLIT3	slit homolog 3 (Drosophila)
4.77	BAALC	brain and acute leukemia, cytoplasmic
4.78	TRIB3	tribbles homolog 3 (Drosophila)
4.79	LOC440160	NA
4.80	C6orf190	chromosome 6 open reading frame 190
4.81	TAGAP	T-cell activation GTPase activating protein
4.82	FAM92A1	family with sequence similarity 92, member A1
4.83	PSTPIP2	proline-serine-threonine phosphatase interacting protein 2
4.84	PTPRC	protein tyrosine phosphatase, receptor type, C
4.85	HLA-DRA	major histocompatibility complex, class II, DR alpha
4.86	EFCAB2	EF-hand calcium binding domain 2
4.87	TNFAIP8	tumor necrosis factor, alpha-induced protein 8
4.88	SLIC1	NA
4.89	CD1C	CD1c antigen
4.90	TRAF3IP3	TRAF3 interacting protein 3
4.91	HLA-DQA1 (NA)	MHC, class II, DQ α -1 (NA-duplicate)
4.92	NAV1 (NA)	neuron navigator 1 (NA- duplicate)
4.93	HLA-DQB1 (NA)	MHC, class II, DQ beta 1 (NA- duplicate)
4.94	PTPRC (NA)	protein tyrosine phosphatase, receptor type, C (NA- duplicate)
4.95	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides
4.96	PLEK	pleckstrin
4.97	TRA@ (NA)	T cell receptor alpha locus (NA- duplicate)
4.98	TMEM44	transmembrane protein 44
4.99	TRA@	T cell receptor alpha locus
4.100	EBI2	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)
4.101	SAMSN1	SAM domain, SH3 domain and nuclear localisation signals, 1
4.102	KIAA1794	KIAA1794
4.103	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)
4.104	CDC42SE2	CDC42 small effector 2

4.105	GFRA1	GDNF family receptor alpha 1
4.106	ITK	IL2-inducible T-cell kinase
4.107	HLA-DRA	major histocompatibility complex, class II, DR alpha
4.108	GIMAP7	GTPase, IMAP family member 7
4.109	FLJ20273	NA
4.110	PTPN6	protein tyrosine phosphatase, non-receptor type 6
4.111	PTGER3	prostaglandin E receptor 3 (subtype EP3)
4.112	RAI2	retinoic acid induced 2
4.113	LGALS2	lectin, galactoside-binding, soluble, 2 (galectin 2)
4.114	HMOX1	heme oxygenase (decycling) 1
4.115	NA	NA (gene identified by probe 227995_at)
4.116	ZNFN1A1	zinc finger protein, subfamily 1A, 1 (Ikaros)
4.117	CSF2RB	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)
4.118	PCSK5	proprotein convertase subtilisin/kexin type 5
4.119	CCDC69	coiled-coil domain containing 69
4.120	CDC42SE2	CDC42 small effector 2
4.121	GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)
4.122	C3	complement component 3
4.123	TNFAIP8 (NA)	tumor necrosis factor, alpha-induced protein 8 (NA- duplicate)
4.124	C15orf48	chromosome 15 open reading frame 48
4.125	RARRES3	retinoic acid receptor responder (tazarotene induced) 3
4.126	LOC283537	NA
4.127	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
4.128	NAV1 (NA)	neuron navigator 1 (NA- duplicate)
4.129	NA	NA (gene identified by probe set 231882_at)
4.130	SOD2	superoxide dismutase 2, mitochondrial
4.131	CTSS	cathepsin S
4.132	CTBP2	C-terminal binding protein 2
4.133	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)
4.134	CCL22	chemokine (C-C motif) ligand 22
4.135	ACSL5	acyl-CoA synthetase long-chain family member 5
4.136	DOC1	NA
4.137	SLC31A2	solute carrier family 31 (copper transporters), member 2
4.138	POPDC3	popeye domain containing 3
4.139	DOC1 (NA)	NA (duplicate)

4.140	SQRDL	sulfide quinone reductase-like (yeast)
4.141	RASGEF1B	RasGEF domain family, member 1B
4.142	FGL2	fibrinogen-like 2
4.143	C10orf128	chromosome 10 open reading frame 128
4.144	IL10RA	interleukin 10 receptor, alpha
4.145	EGFL6	EGF-like-domain, multiple 6
4.146	IL18	interleukin 18 (interferon-gamma-inducing factor)
4.147	ARHGAP30	Rho GTPase activating protein 30
4.148	PALMD	palmdelphin
4.149	RASSF5	Ras association (RalGDS/AF-6) domain family 5
4.150	GATA3	GATA binding protein 3
4.151	DKFZP564O0823	NA
4.152	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)
4.153	TXNIP	thioredoxin interacting protein
4.154	DTX4	deltex 4 homolog (Drosophila)
4.155	DARC	Duffy blood group, chemokine receptor
4.156	RNASE6	ribonuclease, RNase A family, k6
4.157	CD86	CD86 antigen (CD28 antigen ligand 2, B7-2 antigen)
4.158	ZFP36	zinc finger protein 36, C3H type, homolog (mouse)
4.159	BASP1	brain abundant, membrane attached signal protein 1
4.160	CKAP1	cytoskeleton associated protein 1
4.161	HCP5	HLA complex P5
4.162	GRB14	growth factor receptor-bound protein 14
4.163	GJA7	gap junction protein, alpha 7, 45kDa (connexin 45)
4.164	FLJ14054	NA
4.165	VNN1	vanin 1
4.166	ADCY7	adenylate cyclase 7
4.167	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A
4.168	CPA3	carboxypeptidase A3 (mast cell)
4.169	PIM1	pim-1 oncogene
4.170	CCL19	chemokine (C-C motif) ligand 19
4.171	SYK	spleen tyrosine kinase
4.172	NAV1 (NA)	neuron navigator 1 (NA- duplicate)
4.173	SIT1	signaling threshold regulating transmembrane adaptor 1
4.174	NA	NA (gene identified by probe set 228812_at)
4.175	NAP1L2	nucleosome assembly protein 1-like 2
4.176	CCL13	chemokine (C-C motif) ligand 13
4.177	SLA	Src-like-adaptor

4.178	NOD3	NA
4.179	PRKCH	protein kinase C, eta
4.180	TRD@	T cell receptor delta locus
4.181	BAALC	brain and acute leukemia, cytoplasmic
4.182	RP1-93H18.5	NA
4.183	FLJ20701	NA
4.184	SH3TC2	SH3 domain and tetratricopeptide repeats 2
4.185	CCR2	chemokine (C-C motif) receptor 2
4.186	CCL5	chemokine (C-C motif) ligand 5
4.187	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1
4.188	MS4A6A (NA)	membrane spanning 4-domains, subfamilyA, member6A (NA-duplicate)
4.189	PECAM1	platelet/endothelial cell adhesion molecule (CD31 antigen)
4.190	AMIGO2	adhesion molecule with Ig-like domain 2
4.191	CCDC69	coiled-coil domain containing 69
4.192	CLEC7A	C-type lectin domain family 7, member A
4.193	P2RY14	purinergic receptor P2Y, G-protein coupled, 14
4.194	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1
4.195	ADH1B	alcohol dehydrogenase IB (class I), beta polypeptide
4.196	TOP1MT	topoisomerase (DNA) I, mitochondrial
4.197	CD276	CD276 antigen
4.198	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1
4.199	JAM2	junctional adhesion molecule 2
4.200	C1S	complement component 1, s subcomponent
4.201	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A
4.202	TGFBR3	transforming growth factor, beta receptor III (betaglycan, 300kDa)
4.203	ITGAL	c("integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1", " alpha polypeptide"))
4.204	IL1R1	interleukin 1 receptor, type I
4.205	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A
4.206	HLA-DRB1	major histocompatibility complex, class II, DR beta 1
4.207	GIMAP2	GTPase, IMAP family member 2
4.208	ZC3H12D	zinc finger CCCH-type containing 12D
4.209	PCDH9	protocadherin 9
4.210	SLAMF7	SLAM family member 7
4.211	MGC7036	NA
4.212	RGS18	regulator of G-protein signalling 18
4.213	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1

4.214	CD53	CD53 antigen
4.215	MPEG1	NA
4.216	SSBP4	single stranded DNA binding protein 4
4.217	NA	NA (gene identified by probe set 231262_at)
4.218	CDH19	cadherin 19, type 2
4.219	CTBP2	C-terminal binding protein 2
4.220	NAV1 (NA)	neuron navigator 1 (NA- duplicate)
4.221	FAM107B	family with sequence similarity 107, member B
4.222	IGKC	immunoglobulin kappa constant
4.223	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)
4.224	CKAP1	cytoskeleton associated protein 1
4.225	HLA-DRB1	major histocompatibility complex, class II, DR beta 1
4.226	CDH19	cadherin 19, type 2
4.227	MGC16291	NA
4.228	DDEF2	development and differentiation enhancing factor 2
4.229	TNFAIP2	tumor necrosis factor, alpha-induced protein 2
4.230	CXCL14	chemokine (C-X-C motif) ligand 14
4.231	CD209	CD209 antigen
4.232	COL9A3	collagen, type IX, alpha 3
4.233	ANKRD22	ankyrin repeat domain 22
4.234	NCKAP1L	NCK-associated protein 1-like
4.235	CMKOR1	chemokine orphan receptor 1
4.236	HLA-DRB5	major histocompatibility complex, class II, DR beta 5
4.237	LCP1	lymphocyte cytosolic protein 1 (L-plastin)
4.238	ADH1B	alcohol dehydrogenase IB (class I), beta polypeptide
4.239	CXXC5	CXXC finger 5
4.240	GJA7	gap junction protein, alpha 7, 45kDa (connexin 45)
4.241	FGD2	FYVE, RhoGEF and PH domain containing 2
4.242	MAN1A1	mannosidase, alpha, class 1A, member 1
4.243	C6orf115	chromosome 6 open reading frame 115
4.244	RP1-93H18.5 (NA)	NA (duplicate)
4.245	CXCL9	chemokine (C-X-C motif) ligand 9
4.246	FAM107B (NA)	family with sequence similarity 107, member B (NA- duplicate)
4.247	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)
4.248	FYB	FYN binding protein (FYB-120/130)
4.249	VCAM1	vascular cell adhesion molecule 1
4.250	FLI1	Friend leukemia virus integration 1

4.251	CXXC5	CXXC finger 5
4.252	TRAM2	translocation associated membrane protein 2
4.253	IGKC (NA)	immunoglobulin kappa constant (NA- duplicate)
4.254	SHC4	SHC (Src homology 2 domain containing) family, member 4
4.255	SLC9A9	solute carrier family 9 (sodium/hydrogen exchanger), member 9
4.256	PTPRC	protein tyrosine phosphatase, receptor type, C
4.257	PTGER4	prostaglandin E receptor 4 (subtype EP4)
4.258	LILRB1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1
4.259	PRDM1	PR domain containing 1, with ZNF domain
4.260	RP1-93H18.5 (NA)	NA (duplicate)
4.261	ARHGAP15	Rho GTPase activating protein 15
4.262	SLC5A3	solute carrier family 5 (inositol transporters), member 3
4.263	DOCK9	dedicator of cytokinesis 9
4.264	GPSM1	G-protein signalling modulator 1 (AGS3-like, C. elegans)
4.265	CCL5	chemokine (C-C motif) ligand 5
4.266	GLIPR1	GLI pathogenesis-related 1 (glioma)
4.267	APOL3	apolipoprotein L, 3
4.268	HLA-DMB	major histocompatibility complex, class II, DM beta
4.269	SYNPO2	synaptopodin 2
4.270	NA	NA (gene identified by probe set 221651_x_at)
4.271	NA	NA (gene identified by probe set 231929_at)
4.272	RP1-93H18.5	NA
4.273	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
4.274	PRKCQ	protein kinase C, theta
4.275	IL1R2	interleukin 1 receptor, type II
4.276	CARD15	caspase recruitment domain family, member 15
4.277	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta
4.278	HLA-DRB4	major histocompatibility complex, class II, DR beta 4
4.279	SART2	squamous cell carcinoma antigen recognized by T cells 2
4.280	LSP1	lymphocyte-specific protein 1
4.281	AMPD3	adenosine monophosphate deaminase (isoform E)
4.282	SEMA4F	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F
4.283	ISOC1	isochorismatase domain containing 1
4.284	CCL5 (NA)	chemokine (C-C motif) ligand 5 (NA- duplicate)
4.285	HPS3	Hermansky-Pudlak syndrome 3

4.286	HLA-DPA1 (NA)	MHC, class II, DP alpha 1 (NA- duplicate)
4.287	HLA-DQB1 (NA)	MHC, class II, DQ beta 1 (NA- duplicate)
4.288	HOXB7	homeobox B7
4.289	FGL2 (NA)	fibrinogen-like 2 (NA-duplicate)
4.290	ZNFN1A1	zinc finger protein, subfamily 1A, 1 (Ikaros)
4.291	ARHGAP9	Rho GTPase activating protein 9
4.292	GATA2	GATA binding protein 2
4.293	AP2B1	adaptor-related protein complex 2, beta 1 subunit
4.294	CTSC	cathepsin C
4.295	PLK2	polo-like kinase 2 (Drosophila)
4.296	CD4	CD4 antigen (p55)
4.297	GGTA1	glycoprotein, alpha-galactosyltransferase 1
4.298	GADD45B	growth arrest and DNA-damage-inducible, beta
4.299	GADD45B (NA)	growth arrest and DNA-damage-inducible, beta (NA- duplicate)
4.300	FLJ10847	NA
4.301	KIF21B	kinesin family member 21B
4.302	CCND2	cyclin D2
4.303	PRG1	proteoglycan 1, secretory granule
4.304	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1
4.305	HLA-DPA1 (NA)	MHC, class II, DP alpha 1 (NA- duplicate)
4.306	SOD2 (NA)	superoxide dismutase 2, mitochondrial (NA- duplicate)
4.307	CRIP1	cysteine-rich protein 1 (intestinal)
4.308	LOC283070	NA
4.309	SIGLEC1	sialic acid binding Ig-like lectin 1, sialoadhesin
4.310	ZNF11B	zinc finger protein 11B
4.311	CXCR4	chemokine (C-X-C motif) receptor 4
4.312	HLA-DMA	major histocompatibility complex, class II, DM alpha
4.313	MRC1	mannose receptor, C type 1
4.314	CASP1 (NA)	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase) (NA- duplicate)
4.315	LMO2	LIM domain only 2 (rhombotin-like 1)
4.315a	DENN2D	DENN/MADD domain containing 2D
4.316	CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)
4.317	P2RY13	purinergic receptor P2Y, G-protein coupled, 13
4.318	CCL18 (NA)	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated) (NA- duplicate)
4.319	ANGPTL1	angiopoietin-like 1

4.320	NA	NA (gene identified by probe set 230391_at)
4.321	ITGAL (NA)	c("integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1", " alpha polypeptide)") (NA- duplicate)
4.322	C8orf51	chromosome 8 open reading frame 51
4.323	GIMAP8	GTPase, IMAP family member 8
4.324	NA	NA (gene identified by probe set 227780_s_at)
4.325	JAK2	Janus kinase 2 (a protein tyrosine kinase)
4.326	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10
4.327	C1R	complement component 1, r subcomponent
4.328	ACPL2	acid phosphatase-like 2
4.329	TNFRSF19	tumor necrosis factor receptor superfamily, member 19
4.330	PCSK5 (NA)	proprotein convertase subtilisin/kexin type 5 (NA- duplicate)
4.331	LRP12	low density lipoprotein-related protein 12
4.332	NA	NA (gene identified by probe set 1557116_at)
4.333	PECAM1 (NA)	platelet/endothelial cam (CD31 antigen) (NA- duplicate)
4.334	PRKCB1	protein kinase C, beta 1
4.335	IPO11	importin 11
4.336	DLGAP1	discs, large (Drosophila) homolog-associated protein 1
4.337	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta
4.338	MAP3K8	mitogen-activated protein kinase kinase kinase 8
4.339	EVI2B	ecotropic viral integration site 2B
4.340	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa
4.341	CXCL10	chemokine (C-X-C motif) ligand 10
4.342	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1
4.343	MED12L	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)-like
4.344	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
4.345	CTBP2	C-terminal binding protein 2
4.346	IGLJ3	immunoglobulin lambda joining 3
4.347	GBP4	guanylate binding protein 4
4.348	LOC439949	NA
4.349	FBXO16	F-box protein 16
4.350	PRF1	perforin 1 (pore forming protein)
4.351	TRAM2	translocation associated membrane protein 2
4.352	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
4.353	CENTD1	centaurin, delta 1

4.354	CASP1 (NA)	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase) (NA- duplicate)
4.355	FLJ20273	NA
4.356	TFEC	transcription factor EC
4.357	PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B
4.358	CD48	CD48 antigen (B-cell membrane protein)
4.359	HLA-DPB1	major histocompatibility complex, class II, DP beta 1
4.360	SHC4 (NA)	SHC family, member 4 (NA- duplicate)
4.361	GTPBP5	GTP binding protein 5 (putative)
4.362	GBP5	guanylate binding protein 5
4.363	MAP1B	microtubule-associated protein 1B
4.364	EXTL3	exostoses (multiple)-like 3
4.365	CORO1A	coronin, actin binding protein, 1A
4.366	PDGFRL	platelet-derived growth factor receptor-like
4.367	RP9	retinitis pigmentosa 9 (autosomal dominant)
4.368	RHOU	ras homolog gene family, member U
4.369	MTAC2D1	membrane targeting (tandem) C2 domain containing 1
4.370	CCL8	chemokine (C-C motif) ligand 8
4.371	CECR1	cat eye syndrome chromosome region, candidate 1
4.372	IGKC (NA)	immunoglobulin kappa constant (NA- duplicate)
4.373	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1
4.374	ADCY6	adenylate cyclase 6
4.375	CP	ceruloplasmin (ferroxidase)
4.376	EDG1	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
4.377	RGS3	regulator of G-protein signalling 3
4.378	CD28 (NA)	CD28 antigen (Tp44) (NA- duplicate)
4.379	NA	NA (gene identified by probe set 228339_at)
4.380	ABHD5	abhydrolase domain containing 5
4.381	MS4A7	membrane-spanning 4-domains, subfamily A, member 7
4.382	PRKCH	protein kinase C, eta
4.383	GBP1 (NA)	guanylate binding protein 1, i-inducible, 67kDa (NA- duplicate)
4.384	LOC286071	NA
4.385	BLNK	B-cell linker
4.386	NA	NA (gene identified by probe set 242546_at)
4.387	PCDHGC3	protocadherin gamma subfamily C, 3
4.388	CCL13 (NA)	chemokine (C-C motif) ligand 13 (NA- duplicate)
4.389	JAK2 (NA)	Janus kinase 2 (a protein tyrosine kinase) (NA- duplicate)

4.390	CAMSAP1L1	calmodulin regulated spectrin-associated protein 1-like 1
4.391	NPY1R	neuropeptide Y receptor Y1
4.392	CD274	CD274 antigen
4.393	PGM5	phosphoglucomutase 5
4.394	PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)
4.395	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10
4.396	SOD2 (NA)	superoxide dismutase 2, mitochondrial (NA- duplicate)
4.397	BTG2	BTG family, member 2
4.398	LAMP3	lysosomal-associated membrane protein 3
4.399	IGLC1	immunoglobulin lambda constant 1 (Mcg marker)
4.400	SIPA1L1	signal-induced proliferation-associated 1 like 1
4.401	AIF1	allograft inflammatory factor 1
4.402	IGLC2	immunoglobulin lambda constant 2 (Kern-Oz- marker)
4.403	B2M	beta-2-microglobulin
4.404	CLEC7A	C-type lectin domain family 7, member A
4.405	MGC17330	NA
4.406	IGF1R	insulin-like growth factor 1 receptor
4.407	HIVBP1	human immunodeficiency virus type I enhancer binding protein 1
4.408	FKBP14	FK506 binding protein 14, 22 kDa
4.409	LAPTM5	lysosomal associated multispinning membrane protein 5
4.410	ABI3BP	ABI gene family, member 3 (NESH) binding protein
4.411	HLA-E	major histocompatibility complex, class I, E
4.412	ARL4C	ADP-ribosylation factor-like 4C
4.413	ASS	argininosuccinate synthetase
4.414	CASP1 (NA)	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase) (NA- duplicate)
4.415	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
4.416	SYK	spleen tyrosine kinase
4.417	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)
4.418	NA	NA (gene identified by probe set 1557222_at)
4.419	CD3G	CD3g antigen, gamma polypeptide (TiT3 complex)
4.420	IGF1	insulin-like growth factor 1 (somatomedin C)
4.421	NA	NA (gene identified by probe set 228858_at)
4.422	CYB5A	cytochrome b5 type A (microsomal)
4.423	TTC25	tetratricopeptide repeat domain 25
4.424	SLAMF6	SLAM family member 6
4.425	ARHGAP21	Rho GTPase activating protein 21

4.426	FLOT1	flotillin 1
4.427	AIF1 (NA)	allograft inflammatory factor 1 (NA- duplicate)
4.428	IBRDC2	IBR domain containing 2
4.429	KIAA1794	KIAA1794
4.430	OLFML1	olfactomedin-like 1
4.431	GMFG	glia maturation factor, gamma
4.432	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B
4.433	NA	NA (gene identified by probe set 217629_at)
4.434	DEF6	differentially expressed in FDCP 6 homolog (mouse)
4.435	HLA-E (NA)	major histocompatibility complex, class I, E (NA- duplicate)
4.436	MAP4K4	mitogen-activated protein kinase kinase kinase 4
4.437	CMKOR1	chemokine orphan receptor 1
4.438	NA	NA (gene identified by probe set 1563461_at)
4.439	CHKA	choline kinase alpha
4.440	NA	NA (gene identified by probe set 226865_at)
4.441	HS3ST3B1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1
4.442	CXorf9	chromosome X open reading frame 9
4.443	EVI2A	ecotropic viral integration site 2A
4.444	GBP1 (NA)	guanylate binding protein 1, i-inducible, 67kDa (NA- duplicate)
4.445	NFAM1	NFAT activating protein with ITAM motif 1
4.446	NA	NA (gene identified by probe set 242874_at)
4.447	ATP5J	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F6
4.448	NAV1 (NA)	neuron navigator 1 (NA- duplicate)
4.449	IGLC2 (NA)	immunoglobulin λ constant 2 (Kern-Oz- marker) (NA- duplicate)
4.450	CYLD	cylindromatosis (turban tumor syndrome)
4.451	GIMAP6	GTPase, IMAP family member 6
4.452	MFAP4	microfibrillar-associated protein 4
4.453	TUBB2B	tubulin, beta 2B
4.454	NELL2	NEL-like 2 (chicken)
4.455	NA	NA
4.456	IL1RN	interleukin 1 receptor antagonist
4.457	KIAA1211 (NA)	NA (duplicate)
4.458	SYK	spleen tyrosine kinase
4.459	ADAMDEC1	ADAM-like, decysin 1
4.460	AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)
4.461	SAMHD1	SAM domain and HD domain 1
4.462	CXCL14 (NA)	chemokine (C-X-C motif) ligand 14 (NA- duplicate)

4.463	SLC22A3	solute carrier family 22 (extraneuronal monoamine transporter), member 3
4.464	IL1R1 (NA)	interleukin 1 receptor, type I (NA- duplicate)
4.465	IGLV3-25	immunoglobulin lambda variable 3-25
4.466	NA	NA (gene identified by probe set 1556185_a_at)
4.467	RAB11FIP1	RAB11 family interacting protein 1 (class I)
4.468	PER2	period homolog 2 (Drosophila)
4.469	TTL	tubulin tyrosine ligase
4.470	SIAHBP1	NA
4.471	LAPTM5	lysosomal associated multispinning membrane protein 5
4.472	FLJ22536	NA
4.473	RP6-213H19.1	NA
4.474	NA	NA (gene identified by probe set 235804_at)
4.475	NCF4	neutrophil cytosolic factor 4, 40kDa
4.476	EPSTI1	epithelial stromal interaction 1 (breast)
4.477	LOC441212	NA
4.478	ANK3	ankyrin 3, node of Ranvier (ankyrin G)
4.479	PCDH9	protocadherin 9
4.480	C21orf86	chromosome 21 open reading frame 86
4.481	DHRS9	dehydrogenase/reductase (SDR family) member 9
4.482	ARHGAP25	Rho GTPase activating protein 25
4.483	TRAF4	TNF receptor-associated factor 4
4.484	LST1	leukocyte specific transcript 1
4.485	PALMD	palmdelphin
4.486	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
4.487	MSX2	msh homeobox homolog 2 (Drosophila)
4.488	SIRPG	signal-regulatory protein gamma

NA = not applicable

In the tables listed herein the given gene may be listed more than once, for example as a specific gene or as a gene cluster. Table 4 above is generated from the probe sets listed in Table 4A below. There are often multiple probe sets for each gene and thus where more than one probe set has been used to indentify a particular gene then the gene appears more than once in Table 4. An attempt has been made to remove the duplication by scoring through genes that appear more than once in Table 4.

In one aspect the invention provides across the various embodiments herein one or more genes selected from Table 1, 2, 3, 4, 7, 9, 11, 12 and/or 13 including combinations thereof. In a further aspect the invention provides all the genes of Table 1, 2, 3, 4, 7, 9, 11, 12 or 13 or indeed combinations thereof.

In a further aspect the invention provides at least 10% of the genes listed in Table 1, 2, 3, 4, 7, 9, 11, 12 and/or 13, for example at least 40%, 50%, 60% or 70% such as 80%, 90% or 100% thereof.

One or more genes includes 1-5, 6-10, 11-15, 16-20, 21-25, 26-30, 31-35, 36-40, 41-45, 46-50, 51-55, 56-60, 61-65, 66-70, 71-75, 76-80, 81-85, 86-90, 91-95, 96-100, 101-105, 106-110, 111-115, 116-120, 121-125, 126-130, 131-135, 136-140, 141-145, 146-150, 151-155, 156-160, 161-165, 166-170, 171-175, 176-180, 181-185, 186-190, 191-195, 196-200, 201-205, 206-210, 211-215, 216-220, 221-225, 226-230, 231-235, 236-240, 241-245, 246-250, 251-255, 256-260, 261-265, 266-270, 271-275, 276-280, 281-285, 286-290, 291-295, 296-300, 301-305, 306-310, 311-315, 316-320, 321-325, 326-330, 331-335, 336-340, 341-345, 346-350, 351-355, 356-360, 361-365, 366-370, 371-375, 376-380, 381-385, 386-390, 391-395, 396-400, 401-405, 406-410, 411-415, 416-420, 421-425, 426-430, 431-435, 436-440, 441-445, 446-450, 451-455, 456-460, 461-465, 466-470, 471-475, 476-480, as appropriate and combinations thereof.

In one or more aspects the invention provides an embodiment as described in any one of paragraphs 1 to 430 below.

1) Thus the invention may employ one or more genes from Table 4.

2) In another aspect the invention employs one or more genes according to paragraph 1, wherein the gene has the symbol FLJ20647, optionally in combination with one or more genes labeled as 4.2 to 4.488 identified in Table 4.

3) In another aspect the invention employs one or more genes according to paragraph 1 or 2, wherein the gene has the NAV1, optionally in combination with one or more genes labeled as 4.3 to 4.488 identified in Table 4.

4) In another aspect the invention employs one or more genes according to any one one of paragraphs 1-3, wherein the gene has the symbol GPR171, optionally in combination with one or more genes labeled as 4.4 to 4.488 identified in Table 4.

5) In another aspect the invention employs one or more genes according to any one one of paragraphs 1-4, wherein the gene has the symbol CCL14, optionally in combination with one or more genes labeled as 4.5 to 4.488 identified in Table 4.

6) In another aspect the invention employs one or more genes according to any one one of paragraphs 1-5, wherein the gene has the symbol C1S, optionally in combination with one or more genes labeled as 4.6 to 4.488 identified in Table 4.

7) In another aspect the invention employs one or more genes according to any one one of paragraphs 1-6, wherein the gene has the symbol CXCL2, optionally in combination with one or more genes labeled as 4.7 to 4.488 identified in Table 4.

8) In another aspect the invention employs one or more genes according to any one one of paragraphs 1-7, wherein the gene has the symbol TRBV3-1, optionally in combination with one or more genes labeled as 4.8 to 4.488 identified in Table 4.

9) In another aspect the invention employs one or more genes according to any one one of

paragraphs 1-8, wherein the gene has the symbol TRDV2, optionally in combination with one or more genes labeled as 4.9 to 4.488 identified in Table 4.

10) In another aspect the invention employs one or more genes according to any one one of paragraphs 1-9, wherein the gene has the symbol RUFY3, optionally in combination with one or more genes labeled as 4.10 to 4.488 identified in Table 4.

11) In another aspect the invention employs one or more genes according to any one one of paragraphs 1-10, wherein the gene has the symbol DOCK8, optionally in combination with one or more genes labeled as 4.11 to 4.488 identified in Table 4.

12) In another aspect the invention employs one or more genes according to any one one of paragraphs 1-11, wherein the gene has the symbol GCH1, optionally in combination with one or more genes labeled as 4.12 to 4.488 identified in Table 4.

13) In another aspect the invention employs one or more genes according to any one one of paragraphs 1-12, wherein the gene has the symbol CENTD3, optionally in combination with one or more genes labeled as 4.13 to 4.488 identified in Table 4.

14) In another aspect the invention employs one or more genes according to any one of paragraphs 1-13, wherein the gene has the symbol ACSL5, optionally in combination with one or more genes labeled as 4.14 to 4.488 identified in Table 4.

15) In another aspect the invention employs one or more genes according to any one of paragraphs 1-14, wherein the gene has the symbol AMICA1, optionally in combination with one or more genes labeled as 4.15 to 4.488 identified in Table 4.

16) In another aspect the invention employs one or more genes according to any one of paragraphs 1-15, wherein the gene has the symbol IL2RG, optionally in combination with one or more genes labeled as 4.16 to 4.488 identified in Table 4.

17) In another aspect the invention employs one or more genes according to any one of paragraphs 1-16, wherein the gene has the symbol TNFAIP3, optionally in combination with one or more genes labeled as 4.17 to 4.488 identified in Table 4.

18) In another aspect the invention employs one or more genes according to any one of paragraphs 1-17, wherein the gene has the symbol PSCDBP, optionally in combination with one or more genes labeled as 4.18 to 4.488 identified in Table 4.

19) In another aspect the invention employs one or more genes according to any one of paragraphs 1-18, wherein the gene has the symbol ESR1, optionally in combination with one or more genes labeled as 4.19 to 4.488 identified in Table 4.

20) In another aspect the invention employs one or more genes according to any one of paragraphs 1-19, wherein the gene has the symbol TRBC1, optionally in combination with one or more genes labeled as 4.20 to 4.488 identified in Table 4.

21) In another aspect the invention employs one or more genes according to any one of paragraphs 1-20, wherein the gene has the symbol CD52, optionally in combination with one or more genes labeled as 4.21 to 4.488 identified in Table 4.

22) In another aspect the invention employs one or more genes according to any one of paragraphs 1-21, wherein the gene has the symbol LOC442535, optionally in combination with one or more genes labeled as 4.22 to 4.488 identified in Table 4.

23) In another aspect the invention employs one or more genes according to any one of paragraphs 1-22, wherein the gene has the symbol TRBV19, optionally in combination with one or more genes labeled as 4.23 to 4.488 identified in Table 4.

24) In another aspect the invention employs one or more genes according to any one of paragraphs 1-23, wherein the gene has the symbol IL7R, optionally in combination with one or more genes labeled as 4.24 to 4.488 identified in Table 4.

25) In another aspect the invention employs one or more genes according to any one of paragraphs 1-24, wherein the gene has the symbol TRAC, optionally in combination with one or more genes labeled as 4.25 to 4.488 identified in Table 4.

26) In another aspect the invention employs one or more genes according to any one of paragraphs 1-25, wherein the gene has the symbol NCF2, optionally in combination with one or more genes labeled as 4.26 to 4.488 identified in Table 4.

27) In another aspect the invention employs one or more genes according to any one of paragraphs 1-26, wherein the gene has the symbol LOC92689, optionally in combination with one or more genes labeled as 4.27 to 4.488 identified in Table 4.

28) In another aspect the invention employs one or more genes according to any one of paragraphs 1-27, wherein the gene has the symbol GZMK, optionally in combination with one or more genes labeled as 4.28 to 4.488 identified in Table 4.

29) In another aspect the invention employs one or more genes according to any one of paragraphs 1-28, wherein the gene is the one identified by probe set 235831, optionally in combination with one or more genes labeled as 4.29 to 4.488 identified in Table 4.

30) In another aspect the invention employs one or more genes according to any one of paragraphs 1-29, wherein the gene has the symbol RAB34, optionally in combination with one or more genes labeled as 4.30 to 4.488 identified in Table 4.

31) In another aspect the invention employs one or more genes according to any one of paragraphs 1-30, wherein the gene has the symbol DPT, optionally in combination with one or more genes labeled as 4.31 to 4.488 identified in Table 4.

32) In another aspect the invention employs one or more genes according to any one of paragraphs 1-31, wherein the gene has the symbol PVT1, optionally in combination with one or more genes labeled as 4.32 to 4.488 identified in Table 4.

33) In another aspect the invention employs one or more genes according to any one of paragraphs 1-32, wherein the gene has the symbol TRGC2, optionally in combination with one or more genes labeled as 4.33 to 4.488 identified in Table 4.

34) In another aspect the invention employs one or more genes according to any one of paragraphs 1-33, wherein the gene has the symbol GIMAP5, optionally in combination with one

or more genes labeled as 4.34 to 4.488 identified in Table 4.

35) In another aspect the invention employs one or more genes according to any one of paragraphs 1-34, wherein the gene has the symbol CD52, optionally in combination with one or more genes labeled as 4.35 to 4.488 identified in Table 4.

5 36) In another aspect the invention employs one or more genes according to any one of paragraphs 1-35, wherein the gene has the symbol CD3D, optionally in combination with one or more genes labeled as 4.36 to 4.488 identified in Table 4.

37) In another aspect the invention employs one or more genes according to any one of paragraphs 1-36, wherein the gene has the symbol TMEM132C, optionally in combination with
10 one or more genes labeled as 4.37 to 4.488 identified in Table 4.

38) In another aspect the invention employs one or more genes according to any one of paragraphs 1-37, wherein the gene has the symbol NFKBIA, optionally in combination with one or more genes labeled as 4.38 to 4.488 identified in Table 4.

39) In another aspect the invention employs one or more genes according to any one of paragraphs 1-38, wherein the gene has the symbol TRA@, optionally in combination with one or
15 more genes labeled as 4.39 to 4.488 identified in Table 4.

40) In another aspect the invention employs one or more genes according to any one of paragraphs 1-39, wherein the gene has the symbol TRAT1, optionally in combination with one or more genes labeled as 4.41 to 4.488 identified in Table 4.

20 41) In another aspect the invention employs one or more genes according to any one of paragraphs 1-40, wherein the gene has the symbol RAB34, optionally in combination with one or more genes labeled as 4.42 to 4.488 identified in Table 4.

42) In another aspect the invention employs one or more genes according to any one of paragraphs 1-41, wherein the gene has the symbol CD69, optionally in combination with one or
25 more genes labeled as 4.43 to 4.488 identified in Table 4.

43) In another aspect the invention employs one or more genes according to any one of paragraphs 1-42, wherein the gene has the symbol DOCK8 optionally in combination with one or more genes labeled as 4.44 to 4.488 identified in Table 4.

44) In another aspect the invention employs one or more genes according to any one of paragraphs 1-43, wherein the gene has the symbol IRF8 optionally in combination with one or
30 more genes labeled as 4.46 to 4.488 identified in Table 4.

45) In another aspect the invention employs one or more genes according to any one of paragraphs 1-44, wherein the gene has the symbol KLRB1 optionally in combination with one or more genes labeled as 4.47 to 4.488 identified in Table 4.

35 46) In another aspect the invention employs one or more genes according to any one of paragraphs 1-45, wherein the gene is identifiable by probe set number 236280_at, optionally in combination with one or more genes labeled as 4.48 to 4.488 identified in Table 4.

47) In another aspect the invention employs one or more genes according to any one of

paragraphs 1-46, wherein the gene has the symbol ITGA3, optionally in combination with one or more genes labeled as 4.49 to 4.488 identified in Table 4.

48) In another aspect the invention employs one or more genes according to any one of paragraphs 1-47, wherein the gene has the symbol MAP3K8, optionally in combination with one or more genes labeled as 4.50 to 4.488 identified in Table 4.

49) In another aspect the invention employs one or more genes according to any one of paragraphs 1-48, wherein the gene has the symbol Clorf162, optionally in combination with one or more genes labeled as 4.51 to 4.488 identified in Table 4.

50) In another aspect the invention employs one or more genes according to any one of paragraphs 1-49, wherein the gene has the symbol UBD, optionally in combination with one or more genes labeled as 4.52 to 4.488 identified in Table 4.

51) In another aspect the invention employs one or more genes according to any one of paragraphs 1-50, wherein the gene has the symbol TRGV9, optionally in combination with one or more genes labeled as 4.54 to 4.488 identified in Table 4.

52) In another aspect the invention employs one or more genes according to any one of paragraphs 1-51, wherein the gene has the symbol NAV1, optionally in combination with one or more genes labeled as 4.54 to 4.488 identified in Table 4.

53) In another aspect the invention employs one or more genes according to any one of paragraphs 1-51, wherein the gene has the symbol ARHGAP9, optionally in combination with one or more genes labeled as 4.55 to 4.488 identified in Table 4.

54) In another aspect the invention employs one or more genes according to any one of paragraphs 1-53, wherein the gene has the symbol TIFA, optionally in combination with one or more genes labeled as 4.56 to 4.488 identified in Table 4.

55) In another aspect the invention employs one or more genes according to any one of paragraphs 1-54, wherein the gene is identified by probe number 1569942_at, optionally in combination with one or more genes labeled as 4.58 to 4.488 identified in Table 4.

56) In another aspect the invention employs one or more genes according to any one of paragraphs 1-55, wherein the gene has the symbol GIMAP4, optionally in combination with one or more genes labeled as 4.59 to 4.488 identified in Table 4.

57) In another aspect the invention employs one or more genes according to any one of paragraphs 1-56, wherein the gene has the symbol HCLS1, optionally in combination with one or more genes labeled as 4.60 to 4.488 identified in Table 4.

58) In another aspect the invention employs one or more genes according to any one of paragraphs 1-57, wherein the gene has the symbol PRKCH, optionally in combination with one or more genes labeled as 4.61 to 4.488 identified in Table 4.

59) In another aspect the invention employs one or more genes according to any one of paragraphs 1-58, wherein the gene has the symbol STAT4, optionally in combination with one or more genes labeled as 4.62 to 4.488 identified in Table 4.

60) In another aspect the invention employs one or more genes according to any one of paragraphs 1-59, wherein the gene has the symbol HLA-DQA1, optionally in combination with one or more genes labeled as 4.63 to 4.488 identified in Table 4.

61) In another aspect the invention employs one or more genes according to any one of paragraphs 1-60, wherein the gene has the symbol ADRB2, optionally in combination with one or more genes labeled as 4.64 to 4.488 identified in Table 4.

62) In another aspect the invention employs one or more genes according to any one of paragraphs 1-61, wherein the gene is identifiable by probe set number 239237_at, optionally in combination with one or more genes labeled as 4.65 to 4.488 identified in Table 4.

63) In another aspect the invention employs one or more genes according to any one of paragraphs 1-62, wherein the gene has the symbol CTSW, optionally in combination with one or more genes labeled as 4.66 to 4.488 identified in Table 4.

64) In another aspect the invention employs one or more genes according to any one of paragraphs 1-63, wherein the gene has the symbol MYH11, optionally in combination with one or more genes labeled as 4.67 to 4.488 identified in Table 4.

65) In another aspect the invention employs one or more genes according to any one of paragraphs 1-64, wherein the gene has the symbol GIMAP6, optionally in combination with one or more genes labeled as 4.68 to 4.488 identified in Table 4.

66) In another aspect the invention employs one or more genes according to any one of paragraphs 1-65, wherein the gene has the symbol HLA-DQB1,, optionally in combination with one or more genes labeled as 4.69 to 4.488 identified in Table 4.

67) In another aspect the invention employs one or more genes according to any one of paragraphs 1-66, wherein the gene has the symbol CD8A,, optionally in combination with one or more genes labeled as 4.70 to 4.488 identified in Table 4.

68) In another aspect the invention employs one or more genes according to any one of paragraphs 1-67, wherein the gene has the symbol TNFAIP3, optionally in combination with one or more genes labeled as 4.71 to 4.488 identified in Table 4.

69) In another aspect the invention employs one or more genes according to any one of paragraphs 1-68, wherein the gene has the symbol CP, optionally in combination with one or more genes labeled as 4.72 to 4.488 identified in Table 4.

70) In another aspect the invention employs one or more genes according to any one of paragraphs 1-69, wherein the gene has the symbol SMOC2, optionally in combination with one or more genes labeled as 4.73 to 4.488 identified in Table 4.

71) In another aspect the invention employs one or more genes according to any one of paragraphs 1-70, wherein the gene has the symbol C20orf24, optionally in combination with one or more genes labeled as 4.74 to 4.488 identified in Table 4.

72) In another aspect the invention employs one or more genes according to any one of paragraphs 1-71, wherein the gene has the symbol C16orf54, optionally in combination with one

or more genes labeled as 4.75 to 4.488 identified in Table 4.

73) In another aspect the invention employs one or more genes according to any one of paragraphs 1-72, wherein the gene has the symbol CD2, optionally in combination with one or more genes labeled as 4.76 to 4.488 identified in Table 4.

5 74) In another aspect the invention employs one or more genes according to any one of paragraphs 1-73, wherein the gene has the symbol SLIT3, optionally in combination with one or more genes labeled as 4.77 to 4.488 identified in Table 4.

75) In another aspect the invention employs one or more genes according to any one of paragraphs 1-74, wherein the gene has the symbol BAALC, optionally in combination with one
10 or more genes labeled as 4.78 to 4.488 identified in Table 4.

76) In another aspect the invention employs one or more genes according to any one of paragraphs 1-75, wherein the gene has the symbol TRIB3, optionally in combination with one or more genes labeled as 4.79 to 4.488 identified in Table 4.

77) In another aspect the invention employs one or more genes according to any one of
15 paragraphs 1-76, wherein the gene has the symbol LOC440160, optionally in combination with one or more genes labeled as 4.80 to 4.488 identified in Table 4.

78) In another aspect the invention employs one or more genes according to any one of paragraphs 1-77, wherein the gene has the symbol C6orf190, optionally in combination with one or more genes labeled as 4.81 to 4.488 identified in Table 4.

20 79) In another aspect the invention employs one or more genes according to any one of paragraphs 1-78, wherein the gene has the symbol TAGAP, optionally in combination with one or more genes labeled as 4.82 to 4.488 identified in Table 4.

80) In another aspect the invention employs one or more genes according to any one of paragraphs 1-79, wherein the gene has the symbol FAM92A1, optionally in combination with
25 one or more genes labeled as 4.83 to 4.488 identified in Table 4.

81) In another aspect the invention employs one or more genes according to any one of paragraphs 1-80, wherein the gene has the symbol PSTPIP2, optionally in combination with one or more genes labeled as 4.84 to 4.488 identified in Table 4.

82) In another aspect the invention employs one or more genes according to any one of
30 paragraphs 1-81, wherein the gene has the symbol PTPRC, optionally in combination with one or more genes labeled as 4.85 to 4.488 identified in Table 4.

83) In another aspect the invention employs one or more genes according to any one of paragraphs 1-82, wherein the gene has the symbol HLA-DRA, optionally in combination with one or more genes labeled as 4.86 to 4.488 identified in Table 4.

35 84) In another aspect the invention employs one or more genes according to any one of paragraphs 1-83, wherein the gene has the symbol EFCAB2, optionally in combination with one or more genes labeled as 4.87 to 4.488 identified in Table 4.

85) In another aspect the invention employs one or more genes according to any one of

paragraphs 1-84, wherein the gene has the symbol TNFAIP8, optionally in combination with one or more genes labeled as 4.88 to 4.488 identified in Table 4.

86) In another aspect the invention employs one or more genes according to any one of paragraphs 1-85, wherein the gene has the symbol SLIC1, optionally in combination with one or more genes labeled as 4.89 to 4.488 identified in Table 4.

87) In another aspect the invention employs one or more genes according to any one of paragraphs 1-86, wherein the gene has the symbol CD1C, optionally in combination with one or more genes labeled as 4.90 to 4.488 identified in Table 4.

88) In another aspect the invention employs one or more genes according to any one of paragraphs 1-87, wherein the gene has the symbol TRAF3IP3, optionally in combination with one or more genes labeled as 4.91 to 4.488 identified in Table 4.

89) In another aspect the invention employs one or more genes according to any one of paragraphs 1-88, wherein the gene has the symbol IGJ, optionally in combination with one or more genes labeled as 4.96 to 4.488 identified in Table 4.

90) In another aspect the invention employs one or more genes according to any one of paragraphs 1-89, wherein the gene has the symbol PLEK, optionally in combination with one or more genes labeled as 4.98 to 4.488 identified in Table 4.

91) In another aspect the invention employs one or more genes according to any one of paragraphs 1-90, wherein the gene has the symbol TMEM44, optionally in combination with one or more genes labeled as 4.100 to 4.488 identified in Table 4.

92) In another aspect the invention employs one or more genes according to any one of paragraphs 1-91, wherein the gene has the symbol EBI2, optionally in combination with one or more genes labeled as 4.101 to 4.488 identified in Table 4.

93) In another aspect the invention employs one or more genes according to any one of paragraphs 1-92, wherein the gene has the symbol SAMSN1, optionally in combination with one or more genes labeled as 4.102 to 4.488 identified in Table 4.

94) In another aspect the invention employs one or more genes according to any one of paragraphs 1-93, wherein the gene has the symbol KIAA1794, optionally in combination with one or more genes labeled as 4.103 to 4.488 identified in Table 4.

95) In another aspect the invention employs one or more genes according to any one of paragraphs 1-94, wherein the gene has the symbol ALDH2, optionally in combination with one or more genes labeled as 4.104 to 4.488 identified in Table 4.

96) In another aspect the invention employs one or more genes according to any one of paragraphs 1-95, wherein the gene has the symbol CDC42SE2, optionally in combination with one or more genes labeled as 4.105 to 4.488 identified in Table 4.

97) In another aspect the invention employs one or more genes according to any one of paragraphs 1-96, wherein the gene has the symbol GFRA1, optionally in combination with one or more genes labeled as 4.106 to 4.488 identified in Table 4.

98) In another aspect the invention employs one or more genes according to any one of paragraphs 1-97, wherein the gene has the symbol ITK, optionally in combination with one or more genes labeled as 4.107 to 4.488 identified in Table 4.

99) In another aspect the invention employs one or more genes according to any one of paragraphs 1-98, wherein the gene has the symbol GIMAP7, optionally in combination with one or more genes labeled as 4.109 to 4.488 identified in Table 4.

100) In another aspect the invention employs one or more genes according to any one of paragraphs 1-99, wherein the gene has the symbol FLJ20273, optionally in combination with one or more genes labeled as 4.110 to 4.488 identified in Table 4.

101) In another aspect the invention employs one or more genes according to any one of paragraphs 1-100, wherein the gene has the symbol PTPN6, optionally in combination with one or more genes labeled as 4.111 to 4.488 identified in Table 4.

102) In another aspect the invention employs one or more genes according to any one of paragraphs 1-101, wherein the gene has the symbol PTGER3, optionally in combination with one or more genes labeled as 4.112 to 4.488 identified in Table 4.

103) In another aspect the invention employs one or more genes according to any one of paragraphs 1-102, wherein the gene has the symbol RAI2, optionally in combination with one or more genes labeled as 4.113 to 4.488 identified in Table 4.

104) In another aspect the invention employs one or more genes according to any one of paragraphs 1-103, wherein the gene has the symbol LGALS2, optionally in combination with one or more genes labeled as 4.114 to 4.488 identified in Table 4.

105) In another aspect the invention employs one or more genes according to any one of paragraphs 1-104, wherein the gene has the symbol HMOX1, optionally in combination with one or more genes labeled as 4.115 to 4.488 identified in Table 4.

106) In another aspect the invention employs one or more genes according to any one of paragraphs 1-105, wherein the gene is identifiable by probe set number 227995_at, optionally in combination with one or more genes labeled as 4.116 to 4.488 identified in Table 4.

107) In another aspect the invention employs one or more genes according to any one of paragraphs 1-106, wherein the gene has the symbol ZNFN1A1, optionally in combination with one or more genes labeled as 4.117 to 4.488 identified in Table 4.

108) In another aspect the invention employs one or more genes according to any one of paragraphs 1-107, wherein the gene has the symbol CSF2RB, optionally in combination with one or more genes labeled as 4.118 to 4.488 identified in Table 4.

109) In another aspect the invention employs one or more genes according to any one of paragraphs 1-108, wherein the gene has the symbol PCSK5, optionally in combination with one or more genes labeled as 4.119 to 4.488 identified in Table 4.

110) In another aspect the invention employs one or more genes according to any one of paragraphs 1-109, wherein the gene has the symbol CCDC69, optionally in combination with one

or more genes labeled as 4.120 to 4.488 identified in Table 4.

111) In another aspect the invention employs one or more genes according to any one of paragraphs 1-110, wherein the gene has the symbol CDC42SE2, optionally in combination with one or more genes labeled as 4.121 to 4.488 identified in Table 4.

5 112) In another aspect the invention employs one or more genes according to any one of paragraphs 1-111, wherein the gene has the symbol GZMA, optionally in combination with one or more genes labeled as 4.122 to 4.488 identified in Table 4.

113) In another aspect the invention employs one or more genes according to any one of paragraphs 1-112, wherein the gene has the symbol C3, optionally in combination with one or
10 more genes labeled as 4.123 to 4.488 identified in Table 4.

114) In another aspect the invention employs one or more genes according to any one of paragraphs 1-113, wherein the gene has the symbol C15orf48, optionally in combination with one or more genes labeled as 4.125 to 4.488 identified in Table 4.

115) In another aspect the invention employs one or more genes according to any one of
15 paragraphs 1-114, wherein the gene has the symbol RARRES3, optionally in combination with one or more genes labeled as 4.126 to 4.488 identified in Table 4.

116) In another aspect the invention employs one or more genes according to any one of paragraphs 1-115, wherein the gene has the symbol LOC283537, optionally in combination with one or more genes labeled as 4.127 to 4.488 identified in Table 4.

20 117) In another aspect the invention employs one or more genes according to any one of paragraphs 1-116, wherein the gene has the symbol CXCL12, optionally in combination with one or more genes labeled as 4.129 to 4.488 identified in Table 4.

118) In another aspect the invention employs one or more genes according to any one of paragraphs 1-117, wherein the gene is identifiable by probe set number 231882_at, optionally in
25 combination with one or more genes labeled as 4.130 to 4.488 identified in Table 4.

119) In another aspect the invention employs one or more genes according to any one of paragraphs 1-118, wherein the gene has the symbol SOD2, optionally in combination with one or more genes labeled as 4.131 to 4.488 identified in Table 4.

120) In another aspect the invention employs one or more genes according to any one of
30 paragraphs 1-119, wherein the gene has the symbol CTSS, optionally in combination with one or more genes labeled as 4.132 to 4.488 identified in Table 4.

121) In another aspect the invention employs one or more genes according to any one of paragraphs 1-120, wherein the gene has the symbol CTBP2, optionally in combination with one or more genes labeled as 4.133 to 4.488 identified in Table 4.

35 122) In another aspect the invention employs one or more genes according to any one of paragraphs 1-121, wherein the gene has the symbol BCL11B, optionally in combination with one or more genes labeled as 4.134 to 4.488 identified in Table 4.

123) In another aspect the invention employs one or more genes according to any one of

paragraphs 1-122, wherein the gene has the symbol CCL22, optionally in combination with one or more genes labeled as 4.135 to 4.488 identified in Table 4.

124) In another aspect the invention employs one or more genes according to any one of paragraphs 1-123, wherein the gene has the symbol ACSL5, optionally in combination with one or more genes labeled as 4.136 to 4.488 identified in Table 4.

125) In another aspect the invention employs one or more genes according to any one of paragraphs 1-124, wherein the gene has the symbol DOC1, optionally in combination with one or more genes labeled as 4.137 to 4.488 identified in Table 4.

126) In another aspect the invention employs one or more genes according to any one of paragraphs 1-125, wherein the gene has the symbol SLC31A2, optionally in combination with one or more genes labeled as 4.138 to 4.488 identified in Table 4.

127) In another aspect the invention employs one or more genes according to any one of paragraphs 1-126, wherein the gene has the symbol POPDC3, optionally in combination with one or more genes labeled as 4.139 to 4.488 identified in Table 4.

128) In another aspect the invention employs one or more genes according to any one of paragraphs 1-127, wherein the gene has the symbol SQRDL, optionally in combination with one or more genes labeled as 4.141 to 4.488 identified in Table 4.

129) In another aspect the invention employs one or more genes according to any one of paragraphs 1-128, wherein the gene has the symbol RASGEF1B, optionally in combination with one or more genes labeled as 4.142 to 4.488 identified in Table 4.

130) In another aspect the invention employs one or more genes according to any one of paragraphs 1-129, wherein the gene has the symbol FGL2, optionally in combination with one or more genes labeled as 4.143 to 4.488 identified in Table 4.

131) In another aspect the invention employs one or more genes according to any one of paragraphs 1-130, wherein the gene has the symbol C10orf128, optionally in combination with one or more genes labeled as 4.144 to 4.488 identified in Table 4.

132) In another aspect the invention employs one or more genes according to any one of paragraphs 1-131, wherein the gene has the symbol IL10RA, optionally in combination with one or more genes labeled as 4.145 to 4.488 identified in Table 4.

133) In another aspect the invention employs one or more genes according to any one of paragraphs 1-132, wherein the gene has the symbol EGFL6, optionally in combination with one or more genes labeled as 4.146 to 4.488 identified in Table 4.

134) In another aspect the invention employs one or more genes according to any one of paragraphs 1-133, wherein the gene has the symbol IL18, optionally in combination with one or more genes labeled as 4.147 to 4.488 identified in Table 4.

135) In another aspect the invention employs one or more genes according to any one of paragraphs 1-134, wherein the gene has the symbol ARHGAP30, optionally in combination with one or more genes labeled as 4.148 to 4.488 identified in Table 4.

136) In another aspect the invention employs one or more genes according to any one of paragraphs 1-135, wherein the gene has the symbol PALMD, optionally in combination with one or more genes labeled as 4.149 to 4.488 identified in Table 4.

137) In another aspect the invention employs one or more genes according to any one of paragraphs 1-136, wherein the gene has the symbol RASSF5, optionally in combination with one or more genes labeled as 4.150 to 4.488 identified in Table 4.

138) In another aspect the invention employs one or more genes according to any one of paragraphs 1-137, wherein the gene has the symbol GATA3, optionally in combination with one or more genes labeled as 4.151 to 4.488 identified in Table 4.

139) In another aspect the invention employs one or more genes according to any one of paragraphs 1-138, wherein the gene has the symbol DKFZP564O0823, optionally in combination with one or more genes labeled as 4.152 to 4.488 identified in Table 4.

140) In another aspect the invention employs one or more genes according to any one of paragraphs 1-139, wherein the gene has the symbol TXNIP, optionally in combination with one or more genes labeled as 4.154 to 4.488 identified in Table 4.

141) In another aspect the invention employs one or more genes according to any one of paragraphs 1-140, wherein the gene has the symbol DTX4, optionally in combination with one or more genes labeled as 4.155 to 4.488 identified in Table 4.

142) In another aspect the invention employs one or more genes according to any one of paragraphs 1-141, wherein the gene has the symbol DARC, optionally in combination with one or more genes labeled as 4.156 to 4.488 identified in Table 4.

143) In another aspect the invention employs one or more genes according to any one of paragraphs 1-142, wherein the gene has the symbol RNASE6, optionally in combination with one or more genes labeled as 4.157 to 4.488 identified in Table 4.

144) In another aspect the invention employs one or more genes according to any one of paragraphs 1-143, wherein the gene has the symbol CD86, optionally in combination with one or more genes labeled as 4.158 to 4.488 identified in Table 4.

145) In another aspect the invention employs one or more genes according to any one of paragraphs 1-144, wherein the gene has the symbol ZFP36, optionally in combination with one or more genes labeled as 4.159 to 4.488 identified in Table 4.

146) In another aspect the invention employs one or more genes according to any one of paragraphs 1-145, wherein the gene has the symbol BASP1, optionally in combination with one or more genes labeled as 4.160 to 4.488 identified in Table 4.

147) In another aspect the invention employs one or more genes according to any one of paragraphs 1-146, wherein the gene has the symbol CKAP1, optionally in combination with one or more genes labeled as 4.161 to 4.488 identified in Table 4.

148) In another aspect the invention employs one or more genes according to any one of paragraphs 1-147, wherein the gene has the symbol HCP5, optionally in combination with one or

more genes labeled as 4.162 to 4.488 identified in Table 4.

149) In another aspect the invention employs one or more genes according to any one of paragraphs 1-148, wherein the gene has the symbol GRB14, optionally in combination with one or more genes labeled as 4.163 to 4.488 identified in Table 4.

5 150) In another aspect the invention employs one or more genes according to any one of paragraphs 1-149, wherein the gene has the symbol GJA7, optionally in combination with one or more genes labeled as 4.164 to 4.488 identified in Table 4.

151) In another aspect the invention employs one or more genes according to any one of paragraphs 1-150, wherein the gene has the symbol FLJ14054, optionally in combination with
10 one or more genes labeled as 4.165 to 4.488 identified in Table 4.

152) In another aspect the invention employs one or more genes according to any one of paragraphs 1-151, wherein the gene has the symbol VNN1, optionally in combination with one or more genes labeled as 4.166 to 4.488 identified in Table 4.

153) In another aspect the invention employs one or more genes according to any one of paragraphs 1-152, wherein the gene has the symbol ADCY7, optionally in combination with one or more genes labeled as 4.167 to 4.488 identified in Table 4.

154) In another aspect the invention employs one or more genes according to any one of paragraphs 1-153, wherein the gene has the symbol MS4A6A, optionally in combination with one or more genes labeled as 4.168 to 4.488 identified in Table 4.

20 155) In another aspect the invention employs one or more genes according to any one of paragraphs 1-154, wherein the gene has the symbol CPA3, optionally in combination with one or more genes labeled as 4.169 to 4.488 identified in Table 4.

156) In another aspect the invention employs one or more genes according to any one of paragraphs 1-155, wherein the gene has the symbol PIM1, optionally in combination with one or
25 more genes labeled as 4.170 to 4.488 identified in Table 4.

157) In another aspect the invention employs one or more genes according to any one of paragraphs 1-156, wherein the gene has the symbol CCL19, optionally in combination with one or more genes labeled as 4.171 to 4.488 identified in Table 4.

158) In another aspect the invention employs one or more genes according to any one of paragraphs 1-157, wherein the gene has the symbol SYK, optionally in combination with one or
30 more genes labeled as 4.172 to 4.488 identified in Table 4.

159) In another aspect the invention employs one or more genes according to any one of paragraphs 1-158, wherein the gene has the symbol SIT1, optionally in combination with one or more genes labeled as 4.174 to 4.488 identified in Table 4.

35 160) In another aspect the invention employs one or more genes according to any one of paragraphs 1-159, wherein the gene is identifiable by probe set number 228812_at, optionally in combination with one or more genes labeled as 4.175 to 4.488 identified in Table 4.

161) In another aspect the invention employs one or more genes according to any one of

paragraphs 1-160, wherein the gene has the symbol NAP1L2 , optionally in combination with one or more genes labeled as 4.176 to 4.488 identified in Table 4.

162) In another aspect the invention employs one or more genes according to any one of paragraphs 1-161, wherein the gene has the symbol CCL13, optionally in combination with one or more genes labeled as 4.177 to 4.488 identified in Table 4.

163) In another aspect the invention employs one or more genes according to any one of paragraphs 1-162, wherein the gene has the symbol SLA, optionally in combination with one or more genes labeled as 4.178 to 4.488 identified in Table 4.

164) In another aspect the invention employs one or more genes according to any one of paragraphs 1-163, wherein the gene has the symbol NOD3, optionally in combination with one or more genes labeled as 4.179 to 4.488 identified in Table 4.

165) In another aspect the invention employs one or more genes according to any one of paragraphs 1-164, wherein the gene has the symbol PRKCH , optionally in combination with one or more genes labeled as 4.180 to 4.488 identified in Table 4.

166) In another aspect the invention employs one or more genes according to any one of paragraphs 1-165, wherein the gene has the symbol TRD@ , optionally in combination with one or more genes labeled as 4.181 to 4.488 identified in Table 4.

167) In another aspect the invention employs one or more genes according to any one of paragraphs 1-166, wherein the gene has the symbol BAALC, optionally in combination with one or more genes labeled as 4.182 to 4.488 identified in Table 4.

168) In another aspect the invention employs one or more genes according to any one of paragraphs 1-167, wherein the gene has the symbol RP1-93H18.5, optionally in combination with one or more genes labeled as 4.183 to 4.488 identified in Table 4.

169) In another aspect the invention employs one or more genes according to any one of paragraphs 1-168, wherein the gene has the symbol FLJ20701, optionally in combination with one or more genes labeled as 4.184 to 4.488 identified in Table 4.

170) In another aspect the invention employs one or more genes according to any one of paragraphs 1-169, wherein the gene has the symbol SH3TC2, optionally in combination with one or more genes labeled as 4.185 to 4.488 identified in Table 4.

171) In another aspect the invention employs one or more genes according to any one of paragraphs 1-170, wherein the gene has the symbol CCR2, optionally in combination with one or more genes labeled as 4.186 to 4.488 identified in Table 4.

172) In another aspect the invention employs one or more genes according to any one of paragraphs 1-171, wherein the gene has the symbol CCL5, optionally in combination with one or more genes labeled as 4.187 to 4.488 identified in Table 4.

173) In another aspect the invention employs one or more genes according to any one of paragraphs 1-172, wherein the gene has the symbol HLA-DPA1, optionally in combination with one or more genes labeled as 4.189 to 4.488 identified in Table 4.

174) In another aspect the invention employs one or more genes according to any one of paragraphs 1-173, wherein the gene has the symbol PECAM1, optionally in combination with one or more genes labeled as 4.190 to 4.488 identified in Table 4.

175) In another aspect the invention employs one or more genes according to any one of paragraphs 1-174, wherein the gene has the symbol AMIGO2, optionally in combination with one or more genes labeled as 4.192 to 4.488 identified in Table 4.

176) In another aspect the invention employs one or more genes according to any one of paragraphs 1-175, wherein the gene has the symbol CLEC7A, optionally in combination with one or more genes labeled as 4.193 to 4.488 identified in Table 4.

177) In another aspect the invention employs one or more genes according to any one of paragraphs 1-176, wherein the gene has the symbol P2RY14, optionally in combination with one or more genes labeled as 4.194 to 4.488 identified in Table 4.

178) In another aspect the invention employs one or more genes according to any one of paragraphs 1-177, wherein the gene has the symbol PIK3AP1, optionally in combination with one or more genes labeled as 4.195 to 4.488 identified in Table 4.

179) In another aspect the invention employs one or more genes according to any one of paragraphs 1-178, wherein the gene has the symbol ADH1B, optionally in combination with one or more genes labeled as 4.196 to 4.488 identified in Table 4.

180) In another aspect the invention employs one or more genes according to any one of paragraphs 1-179, wherein the gene has the symbol TOP1MT, optionally in combination with one or more genes labeled as 4.197 to 4.488 identified in Table 4.

181) In another aspect the invention employs one or more genes according to any one of paragraphs 1-180, wherein the gene has the symbol CD276, optionally in combination with one or more genes labeled as 4.199 to 4.488 identified in Table 4.

182) In another aspect the invention employs one or more genes according to any one of paragraphs 1-181, wherein the gene has the symbol JAM2, optionally in combination with one or more genes labeled as 4.200 to 4.488 identified in Table 4.

183) In another aspect the invention employs one or more genes according to any one of paragraphs 1-182, wherein the gene has the symbol C1S, optionally in combination with one or more genes labeled as 4.202 to 4.488 identified in Table 4.

184) In another aspect the invention employs one or more genes according to any one of paragraphs 1-183, wherein the gene has the symbol TGFBR3, optionally in combination with one or more genes labeled as 4.203 to 4.488 identified in Table 4.

185) In another aspect the invention employs one or more genes according to any one of paragraphs 1-184, wherein the gene has the symbol ITGAL, optionally in combination with one or more genes labeled as 4.204 to 4.488 identified in Table 4.

186) In another aspect the invention employs one or more genes according to any one of paragraphs 1-185, wherein the gene has the symbol IL1R1, optionally in combination with one or

more genes labeled as 4.206 to 4.488 identified in Table 4.

187) In another aspect the invention employs one or more genes according to any one of paragraphs 1-186, wherein the gene has the symbol HLA-DRB1, optionally in combination with one or more genes labeled as 4.207 to 4.488 identified in Table 4.

5 188) In another aspect the invention employs one or more genes according to any one of paragraphs 1-187, wherein the gene has the symbol GIMAP2, optionally in combination with one or more genes labeled as 4.208 to 4.488 identified in Table 4.

189) In another aspect the invention employs one or more genes according to any one of paragraphs 1-188, wherein the gene has the symbol ZC3H12D, optionally in combination with
10 one or more genes labeled as 4.209 to 4.488 identified in Table 4.

190) In another aspect the invention employs one or more genes according to any one of paragraphs 1-189, wherein the gene has the symbol PCDH9, optionally in combination with one or more genes labeled as 4.210 to 4.488 identified in Table 4.

191) In another aspect the invention employs one or more genes according to any one of
15 paragraphs 1-190, wherein the gene has the symbol SLAMF7, optionally in combination with one or more genes labeled as 4.211 to 4.488 identified in Table 4.

192) In another aspect the invention employs one or more genes according to any one of paragraphs 1-191, wherein the gene has the symbol MGC7036, optionally in combination with one or more genes labeled as 4.212 to 4.488 identified in Table 4.

20 193) In another aspect the invention employs one or more genes according to any one of paragraphs 1-192, wherein the gene has the symbol RGS18, optionally in combination with one or more genes labeled as 4.214 to 4.488 identified in Table 4.

194) In another aspect the invention employs one or more genes according to any one of paragraphs 1-193, wherein the gene has the symbol CD53, optionally in combination with one or
25 more genes labeled as 4.215 to 4.488 identified in Table 4.

195) In another aspect the invention employs one or more genes according to any one of paragraphs 1-194, wherein the gene has the symbol MPEG1, optionally in combination with one or more genes labeled as 4.216 to 4.488 identified in Table 4.

196) In another aspect the invention employs one or more genes according to any one of
30 paragraphs 1-195, wherein the gene has the symbol SSBP4, optionally in combination with one or more genes labeled as 4.217 to 4.488 identified in Table 4.

197) In another aspect the invention employs one or more genes according to any one of paragraphs 1-196, wherein the gene is identifiable by probe set number 231262_at, optionally in combination with one or more genes labeled as 4.218 to 4.488 identified in Table 4.

35 198) In another aspect the invention employs one or more genes according to any one of paragraphs 1-197, wherein the gene has the symbol CDH19, optionally in combination with one or more genes labeled as 4.219 to 4.488 identified in Table 4.

199) In another aspect the invention employs one or more genes according to any one of

paragraphs 1-198, wherein the gene has the symbol CTBP2, optionally in combination with one or more genes labeled as 4.221 to 4.488 identified in Table 4.

200) In another aspect the invention employs one or more genes according to any one of paragraphs 1-199, wherein the gene has the symbol FAM107B, optionally in combination with one or more genes labeled as 4.222 to 4.488 identified in Table 4.

201) In another aspect the invention employs one or more genes according to any one of paragraphs 1-200, wherein the gene has the symbol IGKC, optionally in combination with one or more genes labeled as 4.223 to 4.488 identified in Table 4.

202) In another aspect the invention employs one or more genes according to any one of paragraphs 1-201, wherein the gene has the symbol ITGAM, optionally in combination with one or more genes labeled as 4.224 to 4.488 identified in Table 4.

203) In another aspect the invention employs one or more genes according to any one of paragraphs 1-202, wherein the gene has the symbol CKAP1, optionally in combination with one or more genes labeled as 4.227 to 4.488 identified in Table 4.

204) In another aspect the invention employs one or more genes according to any one of paragraphs 1-203, wherein the gene has the symbol MGC16291, optionally in combination with one or more genes labeled as 4.228 to 4.488 identified in Table 4.

205) In another aspect the invention employs one or more genes according to any one of paragraphs 1-204, wherein the gene has the symbol DDEF2, optionally in combination with one or more genes labeled as 4.229 to 4.488 identified in Table 4.

206) In another aspect the invention employs one or more genes according to any one of paragraphs 1-205, wherein the gene has the symbol TNFAIP2, optionally in combination with one or more genes labeled as 4.230 to 4.488 identified in Table 4.

207) In another aspect the invention employs one or more genes according to any one of paragraphs 1-206, wherein the gene has the symbol CXCL14, optionally in combination with one or more genes labeled as 4.231 to 4.488 identified in Table 4.

208) In another aspect the invention employs one or more genes according to any one of paragraphs 1-207, wherein the gene has the symbol CD209, optionally in combination with one or more genes labeled as 4.232 to 4.488 identified in Table 4.

209) In another aspect the invention employs one or more genes according to any one of paragraphs 1-208, wherein the gene has the symbol COL9A3, optionally in combination with one or more genes labeled as 4.233 to 4.488 identified in Table 4.

210) In another aspect the invention employs one or more genes according to any one of paragraphs 1-209, wherein the gene has the symbol ANKRD22, optionally in combination with one or more genes labeled as 4.234 to 4.488 identified in Table 4.

211) In another aspect the invention employs one or more genes according to any one of paragraphs 1-210, wherein the gene has the symbol NCKAP1L, optionally in combination with one or more genes labeled as 4.235 to 4.488 identified in Table 4.

212) In another aspect the invention employs one or more genes according to any one of paragraphs 1-211, wherein the gene has the symbol CMKOR1, optionally in combination with one or more genes labeled as 4.236 to 4.488 identified in Table 4.

5 213) In another aspect the invention employs one or more genes according to any one of paragraphs 1-212, wherein the gene has the symbol HLA-DRB5, optionally in combination with one or more genes labeled as 4.237 to 4.488 identified in Table 4.

214) In another aspect the invention employs one or more genes according to any one of paragraphs 1-213, wherein the gene has the symbol LCP1, optionally in combination with one or more genes labeled as 4.239 to 4.488 identified in Table 4.

10 215) In another aspect the invention employs one or more genes according to any one of paragraphs 1-214, wherein the gene has the symbol CXXC5, optionally in combination with one or more genes labeled as 4.240 to 4.488 identified in Table 4.

15 216) In another aspect the invention employs one or more genes according to any one of paragraphs 1-215, wherein the gene has the symbol GJA7, optionally in combination with one or more genes labeled as 4.241 to 4.488 identified in Table 4.

217) In another aspect the invention employs one or more genes according to any one of paragraphs 1-216, wherein the gene has the symbol FGD2, optionally in combination with one or more genes labeled as 4.242 to 4.488 identified in Table 4.

20 218) In another aspect the invention employs one or more genes according to any one of paragraphs 1-217, wherein the gene has the symbol MAN1A1, optionally in combination with one or more genes labeled as 4.243 to 4.488 identified in Table 4.

219) In another aspect the invention employs one or more genes according to any one of paragraphs 1-218, wherein the gene has the symbol C6orf115, optionally in combination with one or more genes labeled as 4.245 to 4.488 identified in Table 4.

25 220) In another aspect the invention employs one or more genes according to any one of paragraphs 1-219, wherein the gene has the symbol CXCL9, optionally in combination with one or more genes labeled as 4.247 to 4.488 identified in Table 4.

30 221) In another aspect the invention employs one or more genes according to any one of paragraphs 1-220, wherein the gene has the symbol NPR3, optionally in combination with one or more genes labeled as 4.248 to 4.488 identified in Table 4.

222) In another aspect the invention employs one or more genes according to any one of paragraphs 1-221, wherein the gene has the symbol FYB, optionally in combination with one or more genes labeled as 4.249 to 4.488 identified in Table 4.

35 223) In another aspect the invention employs one or more genes according to any one of paragraphs 1-222, wherein the gene has the symbol VCAM1, optionally in combination with one or more genes labeled as 4.250 to 4.488 identified in Table 4.

224) In another aspect the invention employs one or more genes according to any one of paragraphs 1-223, wherein the gene has the symbol FLI1, optionally in combination with one or

more genes labeled as 4.251 to 4.488 identified in Table 4.

225) In another aspect the invention employs one or more genes according to any one of paragraphs 1-224, wherein the gene has the symbol CXXC5, optionally in combination with one or more genes labeled as 4.252 to 4.488 identified in Table 4.

5 226) In another aspect the invention employs one or more genes according to any one of paragraphs 1-225, wherein the gene has the symbol TRAM2, optionally in combination with one or more genes labeled as 4.254 to 4.488 identified in Table 4.

227) In another aspect the invention employs one or more genes according to any one of paragraphs 1-226, wherein the gene has the symbol SHC4, optionally in combination with one or
10 more genes labeled as 4.255 to 4.488 identified in Table 4.

228) In another aspect the invention employs one or more genes according to any one of paragraphs 1-227, wherein the gene has the symbol SLC9A9, optionally in combination with one or more genes labeled as 4.256 to 4.488 identified in Table 4.

229) In another aspect the invention employs one or more genes according to any one of
15 paragraphs 1-228, wherein the gene has the symbol PTPRC, optionally in combination with one or more genes labeled as 4.257 to 4.488 identified in Table 4.

230) In another aspect the invention employs one or more genes according to any one of paragraphs 1-229, wherein the gene has the symbol PTGER4, optionally in combination with one or more genes labeled as 4.258 to 4.488 identified in Table 4.

20 231) In another aspect the invention employs one or more genes according to any one of paragraphs 1-230, wherein the gene has the symbol LILRB1, optionally in combination with one or more genes labeled as 4.259 to 4.488 identified in Table 4.

232) In another aspect the invention employs one or more genes according to any one of paragraphs 1-231, wherein the gene has the symbol PRDM1, optionally in combination with one
25 or more genes labeled as 4.261 to 4.488 identified in Table 4.

233) In another aspect the invention employs one or more genes according to any one of paragraphs 1-232, wherein the gene has the symbol ARHGAP15, optionally in combination with one or more genes labeled as 4.262 to 4.488 identified in Table 4.

234) In another aspect the invention employs one or more genes according to any one of
30 paragraphs 1-233, wherein the gene has the symbol SLC5A3, optionally in combination with one or more genes labeled as 4.263 to 4.488 identified in Table 4.

235) In another aspect the invention employs one or more genes according to any one of paragraphs 1-234, wherein the gene has the symbol DOCK9, optionally in combination with one or more genes labeled as 4.264 to 4.488 identified in Table 4.

35 236) In another aspect the invention employs one or more genes according to any one of paragraphs 1-235, wherein the gene has the symbol GPSM1, optionally in combination with one or more genes labeled as 4.265 to 4.488 identified in Table 4.

237) In another aspect the invention employs one or more genes according to any one of

paragraphs 1-236, wherein the gene has the symbol CCL5, optionally in combination with one or more genes labeled as 4.266 to 4.488 identified in Table 4.

238) In another aspect the invention employs one or more genes according to any one of paragraphs 1-237, wherein the gene has the symbol GLIPR1, optionally in combination with one or more genes labeled as 4.267 to 4.488 identified in Table 4.

239) In another aspect the invention employs one or more genes according to any one of paragraphs 1-238, wherein the gene has the symbol APOL3, optionally in combination with one or more genes labeled as 4.268 to 4.488 identified in Table 4.

240) In another aspect the invention employs one or more genes according to any one of paragraphs 1-239, wherein the gene has the symbol HLA-DMB, optionally in combination with one or more genes labeled as 4.269 to 4.488 identified in Table 4.

241) In another aspect the invention employs one or more genes according to any one of paragraphs 1-240, wherein the gene has the symbol SYNPO2, optionally in combination with one or more genes labeled as 4.270 to 4.488 identified in Table 4.

242) In another aspect the invention employs one or more genes according to any one of paragraphs 1-241, wherein the gene is identifiable by probe set number 221651_x_at, optionally in combination with one or more genes labeled as 4.271 to 4.488 identified in Table 4.

243) In another aspect the invention employs one or more genes according to any one of paragraphs 1-242, wherein the gene is identifiable by probe set number 231929_at, optionally in combination with one or more genes labeled as 4.273 to 4.488 identified in Table 4.

244) In another aspect the invention employs one or more genes according to any one of paragraphs 1-243, wherein the gene has the symbol CASP1, optionally in combination with one or more genes labeled as 4.274 to 4.488 identified in Table 4.

245) In another aspect the invention employs one or more genes according to any one of paragraphs 1-244, wherein the gene has the symbol PRKCQ, optionally in combination with one or more genes labeled as 4.275 to 4.488 identified in Table 4.

246) In another aspect the invention employs one or more genes according to any one of paragraphs 1-245, wherein the gene has the symbol IL1R2, optionally in combination with one or more genes labeled as 4.276 to 4.488 identified in Table 4.

247) In another aspect the invention employs one or more genes according to any one of paragraphs 1-246, wherein the gene has the symbol CARD15, optionally in combination with one or more genes labeled as 4.277 to 4.488 identified in Table 4.

248) In another aspect the invention employs one or more genes according to any one of paragraphs 1-247, wherein the gene has the symbol ARHGDIB, optionally in combination with one or more genes labeled as 4.278 to 4.488 identified in Table 4.

249) In another aspect the invention employs one or more genes according to any one of paragraphs 1-248, wherein the gene has the symbol HLA-DRB4, optionally in combination with one or more genes labeled as 4.279 to 4.488 identified in Table 4.

250) In another aspect the invention employs one or more genes according to any one of paragraphs 1-249, wherein the gene has the symbol SART2, optionally in combination with one or more genes labeled as 4.280 to 4.488 identified in Table 4.

5 251) In another aspect the invention employs one or more genes according to any one of paragraphs 1-250, wherein the gene has the symbol LSP1, optionally in combination with one or more genes labeled as 4.281 to 4.488 identified in Table 4.

252) In another aspect the invention employs one or more genes according to any one of paragraphs 1-251, wherein the gene has the symbol AMPD3, optionally in combination with one or more genes labeled as 4.282 to 4.488 identified in Table 4.

10 253) In another aspect the invention employs one or more genes according to any one of paragraphs 1-252, wherein the gene has the symbol SEMA4F, optionally in combination with one or more genes labeled as 4.283 to 4.488 identified in Table 4.

15 254) In another aspect the invention employs one or more genes according to any one of paragraphs 1-253, wherein the gene has the symbol ISOC1, optionally in combination with one or more genes labeled as 4.285 to 4.488 identified in Table 4.

255) In another aspect the invention employs one or more genes according to any one of paragraphs 1-254, wherein the gene has the symbol HPS3, optionally in combination with one or more genes labeled as 4.288 to 4.488 identified in Table 4.

20 256) In another aspect the invention employs one or more genes according to any one of paragraphs 1-255, wherein the gene has the symbol HOXB7, optionally in combination with one or more genes labeled as 4.290 to 4.488 identified in Table 4.

257) In another aspect the invention employs one or more genes according to any one of paragraphs 1-256, wherein the gene has the symbol ZNFN1A1, optionally in combination with one or more genes labeled as 4.291 to 4.488 identified in Table 4.

25 258) In another aspect the invention employs one or more genes according to any one of paragraphs 1-257, wherein the gene has the symbol ARHGAP9, optionally in combination with one or more genes labeled as 4.292 to 4.488 identified in Table 4.

30 259) In another aspect the invention employs one or more genes according to any one of paragraphs 1-258, wherein the gene has the symbol GATA2, optionally in combination with one or more genes labeled as 4.293 to 4.488 identified in Table 4.

260) In another aspect the invention employs one or more genes according to any one of paragraphs 1-259, wherein the gene has the symbol AP2B1, optionally in combination with one or more genes labeled as 4.294 to 4.488 identified in Table 4.

35 261) In another aspect the invention employs one or more genes according to any one of paragraphs 1-260, wherein the gene has the symbol CTSC, optionally in combination with one or more genes labeled as 4.295 to 4.488 identified in Table 4.

262) In another aspect the invention employs one or more genes according to any one of paragraphs 1-261, wherein the gene has the symbol PLK2, optionally in combination with one or

more genes labeled as 4.296 to 4.488 identified in Table 4.

263) In another aspect the invention employs one or more genes according to any one of paragraphs 1-262, wherein the gene has the symbol CD4, optionally in combination with one or more genes labeled as 4.297 to 4.488 identified in Table 4.

5 264) In another aspect the invention employs one or more genes according to any one of paragraphs 1-263, wherein the gene has the symbol GGTA1, optionally in combination with one or more genes labeled as 4.298 to 4.488 identified in Table 4.

265) In another aspect the invention employs one or more genes according to any one of paragraphs 1-264, wherein the gene has the symbol GADD45B, optionally in combination with
10 one or more genes labeled as 4.300 to 4.488 identified in Table 4.

266) In another aspect the invention employs one or more genes according to any one of paragraphs 1-265, wherein the gene has the symbol FLJ10847, optionally in combination with one or more genes labeled as 4.301 to 4.488 identified in Table 4.

267) In another aspect the invention employs one or more genes according to any one of
15 paragraphs 1-266, wherein the gene has the symbol KIF21B, optionally in combination with one or more genes labeled as 4.302 to 4.488 identified in Table 4.

268) In another aspect the invention employs one or more genes according to any one of paragraphs 1-267, wherein the gene has the symbol CCND2, optionally in combination with one or more genes labeled as 4.303 to 4.488 identified in Table 4.

20 269) In another aspect the invention employs one or more genes according to any one of paragraphs 1-268, wherein the gene has the symbol PRG1, optionally in combination with one or more genes labeled as 4.304 to 4.488 identified in Table 4.

270) In another aspect the invention employs one or more genes according to any one of paragraphs 1-269, wherein the gene has the symbol SLC40A1, optionally in combination with
25 one or more genes labeled as 4.307 to 4.488 identified in Table 4.

271) In another aspect the invention employs one or more genes according to any one of paragraphs 1-270, wherein the gene has the symbol CRIP1, optionally in combination with one or more genes labeled as 4.308 to 4.488 identified in Table 4.

272) In another aspect the invention employs one or more genes according to any one of
30 paragraphs 1-271, wherein the gene has the symbol LOC283070, optionally in combination with one or more genes labeled as 4.309 to 4.488 identified in Table 4.

273) In another aspect the invention employs one or more genes according to any one of paragraphs 1-272, wherein the gene has the symbol SIGLEC1, optionally in combination with one or more genes labeled as 4.310 to 4.488 identified in Table 4.

35 274) In another aspect the invention employs one or more genes according to any one of paragraphs 1-273, wherein the gene has the symbol ZNF11B, optionally in combination with one or more genes labeled as 4.311 to 4.488 identified in Table 4.

275) In another aspect the invention employs one or more genes according to any one of

paragraphs 1-274, wherein the gene has the symbol CXCR4, optionally in combination with one or more genes labeled as 4.312 to 4.488 identified in Table 4.

276) In another aspect the invention employs one or more genes according to any one of paragraphs 1-275, wherein the gene has the symbol HLA-DMA, optionally in combination with one or more genes labeled as 4.313 to 4.488 identified in Table 4

277) In another aspect the invention employs one or more genes according to any one of paragraphs 1-276, wherein the gene has the symbol MRC1, optionally in combination with one or more genes labeled as 4.315 to 4.488 identified in Table 4.

278) In another aspect the invention employs one or more genes according to any one of paragraphs 1-277, wherein the gene has the symbol LMO2, optionally in combination with one or more genes labeled as 4.315a to 4.488 identified in Table 4.

279) In another aspect the invention employs one or more genes according to any one of paragraphs 1-278, wherein the gene has the symbol DENND2D, optionally in combination with one or more genes labeled as 4.316 to 4.488 identified in Table 4.

280) In another aspect the invention employs one or more genes according to any one of paragraphs 1-279, wherein the gene has the symbol CCL18, optionally in combination with one or more genes labeled as 4.317 to 4.488 identified in Table 4.

281) In another aspect the invention employs one or more genes according to any one of paragraphs 1-280, wherein the gene has the symbol P2RY13, optionally in combination with one or more genes labeled as 4.319 to 4.488 identified in Table 4.

282) In another aspect the invention employs one or more genes according to any one of paragraphs 1-281, wherein the gene has the symbol ANGPTL1, optionally in combination with one or more genes labeled as 4.320 to 4.488 identified in Table 4.

283) In another aspect the invention employs one or more genes according to any one of paragraphs 1-282, wherein the gene is identifiable by probe set number 230391_at, optionally in combination with one or more genes labeled as 4.322 to 4.488 identified in Table 4.

284) In another aspect the invention employs one or more genes according to any one of paragraphs 1-283, wherein the gene has the symbol C8orf51, optionally in combination with one or more genes labeled as 4.323 to 4.488 identified in Table 4.

285) In another aspect the invention employs one or more genes according to any one of paragraphs 1-284, wherein the gene has the symbol GIMAP8, optionally in combination with one or more genes labeled as 4.324 to 4.488 identified in Table 4.

286) In another aspect the invention employs one or more genes according to any one of paragraphs 1-285, wherein the gene is identifiable by probe set number 2277880_s_at, optionally in combination with one or more genes labeled as 4.325 to 4.488 identified in Table 4.

287) In another aspect the invention employs one or more genes according to any one of paragraphs 1-286, wherein the gene has the symbol JAK2, optionally in combination with one or more genes labeled as 4.326 to 4.488 identified in Table 4.

- 288) In another aspect the invention employs one or more genes according to any one of paragraphs 1-287, wherein the gene has the symbol TNFSF10, optionally in combination with one or more genes labeled as 4.327 to 4.488 identified in Table 4.
- 289) In another aspect the invention employs one or more genes according to any one of paragraphs 1-288, wherein the gene has the symbol C1R, optionally in combination with one or more genes labeled as 4.328 to 4.488 identified in Table 4.
- 290) In another aspect the invention employs one or more genes according to any one of paragraphs 1-289, wherein the gene has the symbol ACPL2, optionally in combination with one or more genes labeled as 4.329 to 4.488 identified in Table 4.
- 291) In another aspect the invention employs one or more genes according to any one of paragraphs 1-290, wherein the gene has the symbol TNFRSF19, optionally in combination with one or more genes labeled as 4.331 to 4.488 identified in Table 4.
- 292) In another aspect the invention employs one or more genes according to any one of paragraphs 1-291, wherein the gene has the symbol LRP12, optionally in combination with one or more genes labeled as 4.332 to 4.488 identified in Table 4.
- 293) In another aspect the invention employs one or more genes according to any one of paragraphs 1-292, wherein the gene is identifiable by probe set number 1557116_at, optionally in combination with one or more genes labeled as 4.334 to 4.488 identified in Table 4.
- 294) In another aspect the invention employs one or more genes according to any one of paragraphs 1-293, wherein the gene has the symbol PRKCB1, optionally in combination with one or more genes labeled as 4.335 to 4.488 identified in Table 4.
- 295) In another aspect the invention employs one or more genes according to any one of paragraphs 1-294, wherein the gene has the symbol IPO11, optionally in combination with one or more genes labeled as 4.336 to 4.488 identified in Table 4.
- 296) In another aspect the invention employs one or more genes according to any one of paragraphs 1-295, wherein the gene has the symbol DLGAP1, optionally in combination with one or more genes labeled as 4.337 to 4.488 identified in Table 4.
- 297) In another aspect the invention employs one or more genes according to any one of paragraphs 1-296, wherein the gene has the symbol PRKAR2B, optionally in combination with one or more genes labeled as 4.338 to 4.488 identified in Table 4.
- 298) In another aspect the invention employs one or more genes according to any one of paragraphs 1-297, wherein the gene has the symbol MAP3K8, optionally in combination with one or more genes labeled as 4.339 to 4.488 identified in Table 4.
- 299) In another aspect the invention employs one or more genes according to any one of paragraphs 1-298, wherein the gene has the symbol EVI2B, optionally in combination with one or more genes labeled as 4.340 to 4.488 identified in Table 4.
- 300) In another aspect the invention employs one or more genes according to any one of paragraphs 1-299, wherein the gene has the symbol GBP1, optionally in combination with one or

more genes labeled as 4.341 to 4.488 identified in Table 4.

301) In another aspect the invention employs one or more genes according to any one of paragraphs 1-300, wherein the gene has the symbol CXCL10, optionally in combination with one or more genes labeled as 4.342 to 4.488 identified in Table 4.

5 302) In another aspect the invention employs one or more genes according to any one of paragraphs 1-301, wherein the gene has the symbol CAMK2N1, optionally in combination with one or more genes labeled as 4.343 to 4.488 identified in Table 4

10 303) In another aspect the invention employs one or more genes according to any one of paragraphs 1-302, wherein the gene has the symbol MED12L, optionally in combination with one or more genes labeled as 4.344 to 4.488 identified in Table 4.

304) In another aspect the invention employs one or more genes according to any one of paragraphs 1-303, wherein the gene has the symbol ID2, optionally in combination with one or more genes labeled as 4.345 to 4.488 identified in Table 4.

15 305) In another aspect the invention employs one or more genes according to any one of paragraphs 1-304, wherein the gene has the symbol CTBP2, optionally in combination with one or more genes labeled as 4.346 to 4.488 identified in Table 4.

306) In another aspect the invention employs one or more genes according to any one of paragraphs 1-305, wherein the gene has the symbol IGLJ3, optionally in combination with one or more genes labeled as 4.347 to 4.488 identified in Table 4.

20 307) In another aspect the invention employs one or more genes according to any one of paragraphs 1-306, wherein the gene has the symbol GBP4, optionally in combination with one or more genes labeled as 4.348 to 4.488 identified in Table 4.

25 308) In another aspect the invention employs one or more genes according to any one of paragraphs 1-307, wherein the gene has the symbol LOC439949, optionally in combination with one or more genes labeled as 4.349 to 4.488 identified in Table 4.

309) In another aspect the invention employs one or more genes according to any one of paragraphs 1-308, wherein the gene has the symbol FBXO16, optionally in combination with one or more genes labeled as 4.350 to 4.488 identified in Table 4.

30 310) In another aspect the invention employs one or more genes according to any one of paragraphs 1-309, wherein the gene has the symbol PRF1, optionally in combination with one or more genes labeled as 4.351 to 4.488 identified in Table 4.

311) In another aspect the invention employs one or more genes according to any one of paragraphs 1-310, wherein the gene has the symbol TRAM2, optionally in combination with one or more genes labeled as 4.352 to 4.488 identified in Table 4.

35 312) In another aspect the invention employs one or more genes according to any one of paragraphs 1-311, wherein the gene has the symbol LYN, optionally in combination with one or more genes labeled as 4.353 to 4.488 identified in Table 4.

313) In another aspect the invention employs one or more genes according to any one of

paragraphs 1-312, wherein the gene has the symbol CENTD1, optionally in combination with one or more genes labeled as 4.355 to 4.488 identified in Table 4.

314) In another aspect the invention employs one or more genes according to any one of paragraphs 1-313, wherein the gene has the symbol FLJ20273, optionally in combination with one or more genes labeled as 4.356 to 4.488 identified in Table 4.

315) In another aspect the invention employs one or more genes according to any one of paragraphs 1-314, wherein the gene has the symbol TFEC, optionally in combination with one or more genes labeled as 4.357 to 4.488 identified in Table 4.

316) In another aspect the invention employs one or more genes according to any one of paragraphs 1-315, wherein the gene has the symbol PPP1R16B, optionally in combination with one or more genes labeled as 4.358 to 4.488 identified in Table 4.

317) In another aspect the invention employs one or more genes according to any one of paragraphs 1-316, wherein the gene has the symbol CD48, optionally in combination with one or more genes labeled as 4.359 to 4.488 identified in Table 4.

318) In another aspect the invention employs one or more genes according to any one of paragraphs 1-317, wherein the gene has the symbol HLA-DPB1, optionally in combination with one or more genes labeled as 4.361 to 4.488 identified in Table 4.

319) In another aspect the invention employs one or more genes according to any one of paragraphs 1-318, wherein the gene has the symbol GTPBP5, optionally in combination with one or more genes labeled as 4.362 to 4.488 identified in Table 4.

320) In another aspect the invention employs one or more genes according to any one of paragraphs 1-319, wherein the gene has the symbol GBP5, optionally in combination with one or more genes labeled as 4.363 to 4.488 identified in Table 4.

321) In another aspect the invention employs one or more genes according to any one of paragraphs 1-320, wherein the gene has the symbol MAP1B, optionally in combination with one or more genes labeled as 4.364 to 4.488 identified in Table 4.

322) In another aspect the invention employs one or more genes according to any one of paragraphs 1-321, wherein the gene has the symbol EXTL3, optionally in combination with one or more genes labeled as 4.365 to 4.488 identified in Table 4.

323) In another aspect the invention employs one or more genes according to any one of paragraphs 1-322, wherein the gene has the symbol CORO1A, optionally in combination with one or more genes labeled as 4.366 to 4.488 identified in Table 4.

324) In another aspect the invention employs one or more genes according to any one of paragraphs 1-323, wherein the gene has the symbol PDGFRL, optionally in combination with one or more genes labeled as 4.367 to 4.488 identified in Table 4.

325) In another aspect the invention employs one or more genes according to any one of paragraphs 1-324, wherein the gene has the symbol RP9, optionally in combination with one or more genes labeled as 4.368 to 4.488 identified in Table 4.

326) In another aspect the invention employs one or more genes according to any one of paragraphs 1-325, wherein the gene has the symbol RHOU, optionally in combination with one or more genes labeled as 4.369 to 4.488 identified in Table 4.

327) In another aspect the invention employs one or more genes according to any one of paragraphs 1-326, wherein the gene has the symbol MTAC2D1, optionally in combination with one or more genes labeled as 4.370 to 4.488 identified in Table 4.

328) In another aspect the invention employs one or more genes according to any one of paragraphs 1-327, wherein the gene has the symbol CCL8, optionally in combination with one or more genes labeled as 4.371 to 4.488 identified in Table 4.

329) In another aspect the invention employs one or more genes according to any one of paragraphs 1-328, wherein the gene has the symbol CECR1, optionally in combination with one or more genes labeled as 4.373 to 4.488 identified in Table 4.

330) In another aspect the invention employs one or more genes according to any one of paragraphs 1-329, wherein the gene has the symbol SLC40A1, optionally in combination with one or more genes labeled as 4.374 to 4.488 identified in Table 4.

331) In another aspect the invention employs one or more genes according to any one of paragraphs 1-330, wherein the gene has the symbol ADCY6, optionally in combination with one or more genes labeled as 4.375 to 4.488 identified in Table 4.

332) In another aspect the invention employs one or more genes according to any one of paragraphs 1-331, wherein the gene has the symbol CP, optionally in combination with one or more genes labeled as 4.376 to 4.488 identified in Table 4.

333) In another aspect the invention employs one or more genes according to any one of paragraphs 1-332, wherein the gene has the symbol EDG1, optionally in combination with one or more genes labeled as 4.377 to 4.488 identified in Table 4.

334) In another aspect the invention employs one or more genes according to any one of paragraphs 1-333, wherein the gene has the symbol RGS3, optionally in combination with one or more genes labeled as 4.379 to 4.488 identified in Table 4.

335) In another aspect the invention employs one or more genes according to any one of paragraphs 1-334, wherein the gene is identifiable by probe set number 228339_at, optionally in combination with one or more genes labeled as 4.380 to 4.488 identified in Table 4.

336) In another aspect the invention employs one or more genes according to any one of paragraphs 1-335, wherein the gene has the symbol ABHD5, optionally in combination with one or more genes labeled as 4.381 to 4.488 identified in Table 4.

337) In another aspect the invention employs one or more genes according to any one of paragraphs 1-336, wherein the gene has the symbol MS4A7, optionally in combination with one or more genes labeled as 4.382 to 4.488 identified in Table 4.

338) In another aspect the invention employs one or more genes according to any one of paragraphs 1-337, wherein the gene has the symbol PRKCH, optionally in combination with one

or more genes labeled as 4.384 to 4.488 identified in Table 4.

339) In another aspect the invention employs one or more genes according to any one of paragraphs 1-338, wherein the gene has the symbol LOC286071, optionally in combination with one or more genes labeled as 4.385 to 4.488 identified in Table 4.

5 340) In another aspect the invention employs one or more genes according to any one of paragraphs 1-339, wherein the gene has the symbol BLNK, optionally in combination with one or more genes labeled as 4.386 to 4.488 identified in Table 4.

10 341) In another aspect the invention employs one or more genes according to any one of paragraphs 1-340, wherein the gene is identifiable by the probe set number 242546_at, optionally in combination with one or more genes labeled as 4.387 to 4.488 identified in Table 4.

342) In another aspect the invention employs one or more genes according to any one of paragraphs 1-341, wherein the gene has the symbol PCDHGC3, optionally in combination with one or more genes labeled as 4.390 to 4.488 identified in Table 4.

15 343) In another aspect the invention employs one or more genes according to any one of paragraphs 1-342, wherein the gene has the symbol CAMSAP1L1, optionally in combination with one or more genes labeled as 4.391 to 4.488 identified in Table 4.

344) In another aspect the invention employs one or more genes according to any one of paragraphs 1-343, wherein the gene has the symbol NPY1R, optionally in combination with one or more genes labeled as 4.392 to 4.488 identified in Table 4.

20 345) In another aspect the invention employs one or more genes according to any one of paragraphs 1-344, wherein the gene has the symbol CD274, optionally in combination with one or more genes labeled as 4.393 to 4.488 identified in Table 4.

25 346) In another aspect the invention employs one or more genes according to any one of paragraphs 1-345, wherein the gene has the symbol PGM5, optionally in combination with one or more genes labeled as 4.394 to 4.488 identified in Table 4.

347) In another aspect the invention employs one or more genes according to any one of paragraphs 1-346, wherein the gene has the symbol PLCG2, optionally in combination with one or more genes labeled as 4.395 to 4.488 identified in Table 4.

30 348) In another aspect the invention employs one or more genes according to any one of paragraphs 1-347, wherein the gene has the symbol TNFSF10, optionally in combination with one or more genes labeled as 4.397 to 4.488 identified in Table 4.

349) In another aspect the invention employs one or more genes according to any one of paragraphs 1-348, wherein the gene has the symbol BTG2, optionally in combination with one or more genes labeled as 4.398 to 4.488 identified in Table 4.

35 350) In another aspect the invention employs one or more genes according to any one of paragraphs 1-349, wherein the gene has the symbol LAMP3, optionally in combination with one or more genes labeled as 4.399 to 4.488 identified in Table 4.

351) In another aspect the invention employs one or more genes according to any one of

paragraphs 1-350, wherein the gene has the symbol IGLC1, optionally in combination with one or more genes labeled as 4.400 to 4.488 identified in Table 4.

352) In another aspect the invention employs one or more genes according to any one of paragraphs 1-351, wherein the gene has the symbol SIPA1L1, optionally in combination with one or more genes labeled as 4.401 to 4.488 identified in Table 4.

353) In another aspect the invention employs one or more genes according to any one of paragraphs 1-352 wherein the gene has the symbol AIF1, optionally in combination with one or more genes labeled as 4.402 to 4.488 identified in Table 4.

354) In another aspect the invention employs one or more genes according to any one of paragraphs 1-353, wherein the gene has the symbol IGLC2, optionally in combination with one or more genes labeled as 4.403 to 4.488 identified in Table 4.

355) In another aspect the invention employs one or more genes according to any one of paragraphs 1-354, wherein the gene has the symbol B2M, optionally in combination with one or more genes labeled as 4.404 to 4.488 identified in Table 4.

356) In another aspect the invention employs one or more genes according to any one of paragraphs 1-355, wherein the gene has the symbol CLEC7A, optionally in combination with one or more genes labeled as 4.405 to 4.488 identified in Table 4.

357) In another aspect the invention employs one or more genes according to any one of paragraphs 1-356, wherein the gene has the symbol MGC17330, optionally in combination with one or more genes labeled as 4.406 to 4.488 identified in Table 4.

358) In another aspect the invention employs one or more genes according to any one of paragraphs 1-357, wherein the gene has the symbol IGF1R, optionally in combination with one or more genes labeled as 4.407 to 4.488 identified in Table 4.

359) In another aspect the invention employs one or more genes according to any one of paragraphs 1-358, wherein the gene has the symbol HIVEP1, optionally in combination with one or more genes labeled as 4.408 to 4.488 identified in Table 4.

360) In another aspect the invention employs one or more genes according to any one of paragraphs 1-359, wherein the gene has the symbol FKBP14, optionally in combination with one or more genes labeled as 4.409 to 4.488 identified in Table 4.

361) In another aspect the invention employs one or more genes according to any one of paragraphs 1-360, wherein the gene has the symbol LAPTM5, optionally in combination with one or more genes labeled as 4.410 to 4.488 identified in Table 4.

362) In another aspect the invention employs one or more genes according to any one of paragraphs 1-361, wherein the gene has the symbol AB13BP, optionally in combination with one or more genes labeled as 4.411 to 4.488 identified in Table 4.

363) In another aspect the invention employs one or more genes according to any one of paragraphs 1-362, wherein the gene has the symbol HLA-E, optionally in combination with one or more genes labeled as 4.412 to 4.488 identified in Table 4.

364) In another aspect the invention employs one or more genes according to any one of paragraphs 1-363, wherein the gene has the symbol ARL4C, optionally in combination with one or more genes labeled as 4.413 to 4.488 identified in Table 4.

365) In another aspect the invention employs one or more genes according to any one of paragraphs 1-364, wherein the gene has the symbol ASS, optionally in combination with one or more genes labeled as 4.415 to 4.488 identified in Table 4.

366) In another aspect the invention employs one or more genes according to any one of paragraphs 1-365, wherein the gene has the symbol ITGB3, optionally in combination with one or more genes labeled as 4.417 to 4.488 identified in Table 4.

367) In another aspect the invention employs one or more genes according to any one of paragraphs 1-366, wherein the gene has the symbol SYK, optionally in combination with one or more genes labeled as 4.417 to 4.488 identified in Table 4.

368) In another aspect the invention employs one or more genes according to any one of paragraphs 1-366, wherein the gene has the symbol RAC2, optionally in combination with one or more genes labeled as 4.418 to 4.488 identified in Table 4.

369) In another aspect the invention employs one or more genes according to any one of paragraphs 1-368, wherein the gene is identifiable by probe set number 1557222_at, optionally in combination with one or more genes labeled as 4.419 to 4.488 identified in Table 4.

370) In another aspect the invention employs one or more genes according to any one of paragraphs 1-369, wherein the gene has the symbol CD3G, optionally in combination with one or more genes labeled as 4.420 to 4.488 identified in Table 4.

371) In another aspect the invention employs one or more genes according to any one of paragraphs 1-370, wherein the gene has the symbol IGF1, optionally in combination with one or more genes labeled as 4.421 to 4.488 identified in Table 4.

372) In another aspect the invention employs one or more genes according to any one of paragraphs 1-371, wherein the gene is identifiable by probe set number 228858_at, optionally in combination with one or more genes labeled as 4.422 to 4.488 identified in Table 4.

373) In another aspect the invention employs one or more genes according to any one of paragraphs 1-372, wherein the gene is has the symbol CYB5A, optionally in combination with one or more genes labeled as 4.423 to 4.488 identified in Table 4.

374) In another aspect the invention employs one or more genes according to any one of paragraphs 1-373, wherein the gene is has the symbol TTC25, optionally in combination with one or more genes labeled as 4.424 to 4.488 identified in Table 4.

375) In another aspect the invention employs one or more genes according to any one of paragraphs 1-374, wherein the gene is has the symbol SLAMF6, optionally in combination with one or more genes labeled as 4.425 to 4.488 identified in Table 4.

376) In another aspect the invention employs one or more genes according to any one of paragraphs 1-375, wherein the gene is has the symbol ARHGAP21, optionally in combination

with one or more genes labeled as 4.426 to 4.488 identified in Table 4.

377) In another aspect the invention employs one or more genes according to any one of paragraphs 1-376, wherein the gene is has the symbol FLOT1, optionally in combination with one or more genes labeled as 4.428 to 4.488 identified in Table 4.

5 378) In another aspect the invention employs one or more genes according to any one of paragraphs 1-377, wherein the gene is has the symbol IBRDC2 optionally in combination with one or more genes labeled as 4.429 to 4.488 identified in Table 4.

379) In another aspect the invention employs one or more genes according to any one of paragraphs 1-378, wherein the gene is has the symbol KIAA1794, optionally in combination with
10 one or more genes labeled as 4.430 to 4.488 identified in Table 4.

380) In another aspect the invention employs one or more genes according to any one of paragraphs 1 -379, wherein the gene is has the symbol OLFML1, optionally in combination with one or more genes labeled as 4.431 to 4.488 identified in Table 4.

381) In another aspect the invention employs one or more genes according to any one of paragraphs 1-380, wherein the gene is has the symbol GMFG, optionally in combination with one
15 or more genes labeled as 4.432 to 4.488 identified in Table 4.

382) In another aspect the invention employs one or more genes according to any one of paragraphs 1-381, wherein the gene is has the symbol TNFRSF1B, optionally in combination with one or more genes labeled as 4.433 to 4.488 identified in Table 4.

20 383) In another aspect the invention employs one or more genes according to any one of paragraphs 1-382, wherein the gene is identifiable by probe set number 217629_at, optionally in combination with one or more genes labeled as 4.434 to 4.488 identified in Table 4.

384) In another aspect the invention employs one or more genes according to any one of paragraphs 1-383, wherein the gene is has the symbol DEF6, optionally in combination with one
25 or more genes labeled as 4.436 to 4.488 identified in Table 4.

385) In another aspect the invention employs one or more genes according to any one of paragraphs 1-384, wherein the gene is has the symbol MAP4K4, optionally in combination with one or more genes labeled as 4.437 to 4.488 identified in Table 4.

386) In another aspect the invention employs one or more genes according to any one of paragraphs 1-385, wherein the gene is has the symbol CMKOR1, optionally in combination with
30 one or more genes labeled as 4.438 to 4.488 identified in Table 4.

387) In another aspect the invention employs one or more genes according to any one of paragraphs 1-386, wherein the gene is identifiable by probe set number 1563461_at, optionally in combination with one or more genes labeled as 4.439 to 4.488 identified in Table 4.

35 388) In another aspect the invention employs one or more genes according to any one of paragraphs 1-387, wherein the gene is has the symbol CHKA, optionally in combination with one or more genes labeled as 4.440 to 4.488 identified in Table 4.

389) In another aspect the invention employs one or more genes according to any one of

paragraphs 1-388, wherein the gene is identifiable by probe set number 226865_at, optionally in combination with one or more genes labeled as 4.441 to 4.488 identified in Table 4.

390) In another aspect the invention employs one or more genes according to any one of paragraphs 1-389, wherein the gene has the symbol HS3ST3B1, optionally in combination with one or more genes labeled as 4.442 to 4.488 identified in Table 4.

391) In another aspect the invention employs one or more genes according to any one of paragraphs 1-390, wherein the gene has the symbol CXorf9, optionally in combination with one or more genes labeled as 4.443 to 4.488 identified in Table 4.

392) In another aspect the invention employs one or more genes according to any one of paragraphs 1-391, wherein the gene has the symbol EVI2A, optionally in combination with one or more genes labeled as 4.445 to 4.488 identified in Table 4.

393) In another aspect the invention employs one or more genes according to any one of paragraphs 1-392, wherein the gene has the symbol NFAM1, optionally in combination with one or more genes labeled as 4.446 to 4.488 identified in Table 4.

394) In another aspect the invention employs one or more genes according to any one of paragraphs 1-393, wherein the gene is identifiable by probe set number 242874_at, optionally in combination with one or more genes labeled as 4.447 to 4.488 identified in Table 4.

395) In another aspect the invention employs one or more genes according to any one of paragraphs 1-394, wherein the gene has the symbol ATP5J, optionally in combination with one or more genes labeled as 4.450 to 4.488 identified in Table 4.

396) In another aspect the invention employs one or more genes according to any one of paragraphs 1-395, wherein the gene has the symbol CYLD, optionally in combination with one or more genes labeled as 4.451 to 4.488 identified in Table 4.

397) In another aspect the invention employs one or more genes according to any one of paragraphs 1-396, wherein the gene has the symbol GIMAP6, optionally in combination with one or more genes labeled as 4.452 to 4.488 identified in Table 4.

398) In another aspect the invention employs one or more genes according to any one of paragraphs 1-397, wherein the gene has the symbol MFAP4, optionally in combination with one or more genes labeled as 4.453 to 4.488 identified in Table 4.

399) In another aspect the invention employs one or more genes according to any one of paragraphs 1-398, wherein the gene has the symbol TUBB2B, optionally in combination with one or more genes labeled as 4.454 to 4.488 identified in Table 4.

400) In another aspect the invention employs one or more genes according to any one of paragraphs 1-399, wherein the gene has the symbol NELL2, optionally in combination with one or more genes labeled as 4.455 to 4.488 identified in Table 4.

401) In another aspect the invention employs one or more genes according to any one of paragraphs 1-400, wherein the gene is identifiable by probe set number 236583_at, optionally in combination with one or more genes labeled as 4.456 to 4.488 identified in Table 4.

402) In another aspect the invention employs one or more genes according to any one of paragraphs 1-401, wherein the gene has the symbol IL1RN, optionally in combination with one or more genes labeled as 4.457 to 4.488 identified in Table 4.

403) In another aspect the invention employs one or more genes according to any one of paragraphs 1-402, wherein the gene has the symbol KIAA1211, optionally in combination with one or more genes labeled as 4.459 to 4.488 identified in Table 4.

404) In another aspect the invention employs one or more genes according to any one of paragraphs 1-403, wherein the gene has the symbol ADAMDEC1, optionally in combination with one or more genes labeled as 4.460 to 4.488 identified in Table 4.

405) In another aspect the invention employs one or more genes according to any one of paragraphs 1-404, wherein the gene has the symbol AOC3, optionally in combination with one or more genes labeled as 4.461 to 4.488 identified in Table 4.

406) In another aspect the invention employs one or more genes according to any one of paragraphs 1-405, wherein the gene has the symbol SAMHD1, optionally in combination with one or more genes labeled as 4.463 to 4.488 identified in Table 4.

407) In another aspect the invention employs one or more genes according to any one of paragraphs 1-406, wherein the gene has the symbol SLC22A3, optionally in combination with one or more genes labeled as 4.465 to 4.488 identified in Table 4.

408) In another aspect the invention employs one or more genes according to any one of paragraphs 1-407, wherein the gene has the symbol IGLV3-25, optionally in combination with one or more genes labeled as 4.466 to 4.488 identified in Table 4.

409) In another aspect the invention employs one or more genes according to any one of paragraphs 1-408, wherein the gene is identifiable by probe set number 1556185_a_at, optionally in combination with one or more genes labeled as 4.467 to 4.488 identified in Table 4.

410) In another aspect the invention employs one or more genes according to any one of paragraphs 1-409, wherein the gene has the symbol RAB11FIP1, optionally in combination with one or more genes labeled as 4.468- to 4.488 identified in Table 4.

411) In another aspect the invention employs one or more genes according to any one of paragraphs 1-410, wherein the gene has the symbol PER2, optionally in combination with one or more genes labeled as 4.469 to 4.488 identified in Table 4.

412) In another aspect the invention employs one or more genes according to any one of paragraphs 1-411, wherein the gene has the symbol TTL, optionally in combination with one or more genes labeled as 4.470 to 4.488 identified in Table 4.

413) In another aspect the invention employs one or more genes according to any one of paragraphs 1-412, wherein the gene has the symbol SLAHBP1, optionally in combination with one or more genes labeled as 4.472 to 4.488 identified in Table 4.

414) In another aspect the invention employs one or more genes according to any one of paragraphs 1-413, wherein the gene has the symbol FLJ22536, optionally in combination with

one or more genes labeled as 4.473 to 4.488 identified in Table 4.

415) In another aspect the invention employs one or more genes according to any one of paragraphs 1-414, wherein the gene has the symbol RP6-213H19.1, optionally in combination with one or more genes labeled as 4.474 to 4.488 identified in Table 4.

5 416) In another aspect the invention employs one or more genes according to any one of paragraphs 1-415, wherein the gene is identifiable by probe set number 235804_at, optionally in combination with one or more genes labeled as 4.475 to 4.488 identified in Table 4.

417) In another aspect the invention employs one or more genes according to any one of paragraphs 1-416, wherein the gene has the symbol NCF4, optionally in combination with one or
10 more genes labeled as 4.476 to 4.488 identified in Table 4.

418) In another aspect the invention employs one or more genes according to any one of paragraphs 1-417, wherein the gene has the symbol EPSTI1, optionally in combination with one or more genes labeled as 4.477 to 4.488 identified in Table 4.

419) In another aspect the invention employs one or more genes according to any one of
15 paragraphs 1-418, wherein the gene has the symbol LOC441212, optionally in combination with one or more genes labeled as 4.478 to 4.488 identified in Table 4.

420) In another aspect the invention employs one or more genes according to any one of paragraphs 1-419, wherein the gene has the symbol ANK3, optionally in combination with one or more genes labeled as 4.479 to 4.488 identified in Table 4.

20 421) In another aspect the invention employs one or more genes according to any one of paragraphs 1-420, wherein the gene has the symbol PCDH9, optionally in combination with one or more genes labeled as 4.480 to 4.488 identified in Table 4.

422) In another aspect the invention employs one or more genes according to any one of paragraphs 1-421, wherein the gene has the symbol C21orf86, optionally in combination with one
25 or more genes labeled as 4.481 to 4.488 identified in Table 4.

423) In another aspect the invention employs one or more genes according to any one of paragraphs 1-422, wherein the gene has the symbol DHRS9, optionally in combination with one or more genes labeled as 4.482 to 4.488 identified in Table 4.

424) In another aspect the invention employs one or more genes according to any one of
30 paragraphs 1-423, wherein the gene has the symbol ARHGAP25, optionally in combination with one or more genes labeled as 4.483 to 4.488 identified in Table 4.

425) In another aspect the invention employs one or more genes according to any one of paragraphs 1-424, wherein the gene has the symbol TRAF4, optionally in combination with one or more genes labeled as 4.484 to 4.488 identified in Table 4.

35 426) In another aspect the invention employs one or more genes according to any one of paragraphs 1-425, wherein the gene has the symbol LST1, optionally in combination with one or more genes labeled as 4.485 to 4.488 identified in Table 4.

427) In another aspect the invention employs one or more genes according to any one of

paragraphs 1-426, wherein the gene has the symbol PALMD, optionally in combination with one or more genes labeled as 4.486 to 4.488 identified in Table 4.

428) In another aspect the invention employs one or more genes according to any one of paragraphs 1-427, wherein the gene has the symbol TAP1, optionally in combination with one or more genes labeled as 4.487 to 4.488 identified in Table 4.

429) In another aspect the invention employs one or more genes according to any one of paragraphs 1-428, wherein the gene has the symbol MSX2, optionally in combination with one or more genes labeled as 4.448 identified in Table 4.

430) In another aspect the invention employs one or more genes according to any one of paragraphs 1-429, wherein the gene has the symbol SIRPG.

In one aspect the invention employs a gene listed in Table 7.

Table 7

Gene Symbol

CCL5

FASLG

GNLY

GZMB

PRF1

IFNG

ICOS

TBX21

CD8A

CD3E

CXCL11

CXCL10

CXCR3

CD20

FOXP3

INDO

CD45Ro

CD45R

CD69

TRBV19

TRAT1

TRDV2

STAT4
PRKCQ
GMZK
GPR171
UBD
CD52
CD3D
IL7R
IRF1
TLR7

In one aspect the invention employs one or more genes selected from Table 9.

Table 9

Gene Symbol

PRF1
IRF1
GZMB
GNLY
CD8A
PRKCQ
FOXP3
IFNG
CCL5
GPR171
TRBV19
CD3E
TBX21
FASLG
CXCL10
ICOS
CXCR3
CXCL11

In one aspect the invention employs one or more genes selected from Table 11.

Table 11

Gene Symbol	Gene Title
CCL5	chemokine (C-C motif) ligand 5
UCHL1	Ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
PVT1 /// LOC441378	Pvt1 oncogene homolog, MYC activator (mouse) /// LOC441378
---	CDNA clone IMAGE:4796388
CD52	CD52 antigen (CAMPATH-1 antigen) /// CD52 antigen (CAMPATH-1 antigen)
UBD	ubiquitin D
STAT4	signal transducer and activator of transcription 4
GZMK	granzyme K (granzyme 3; tryptase II) /// granzyme K (granzyme 3; tryptase II)
IL18RAP	interleukin 18 receptor accessory protein
GPR171	G protein-coupled receptor 171
PSCDBP	pleckstrin homology, Sec7 and coiled-coil domains, binding protein /// pleckstrin homology, Sec7 and coiled-coil domains, binding protein
NCF2	neutrophil cytosolic factor 2 (65kDa, chronic granulomatous disease, autosomal 2)
PRKCQ	protein kinase C, theta
LST1	leukocyte specific transcript 1
TRA@ /// TRDV2 /// TRAV20 /// TRAJ17 /// TRAC	T cell receptor alpha locus /// T cell receptor delta variable 2 /// T cell receptor alpha variable 20 /// T cell receptor alpha joining 17 /// T cell receptor alpha constant
TRGC2	T cell receptor gamma constant 2
TRBV21-1 /// TRBV19 /// TRBV5-4 /// TRBV3-1 /// TRBC1	T cell receptor beta variable 21-1 /// T cell receptor beta variable 19 /// T cell receptor beta variable 5-4 /// T cell receptor beta variable 3-1 /// T cell receptor beta constant 1
HLA-DQA1 /// HLA-DQA2	major histocompatibility complex, class II, DQ alpha 1 /// major histocompatibility complex, class II, DQ alpha 2
TRBV19 /// TRBC1	T cell receptor beta variable 19 /// T cell receptor beta variable 19 /// T cell receptor beta constant 1 /// T cell receptor beta constant 1
CD3D	CD3D antigen, delta polypeptide (TiT3 complex)
GADD45B	Growth arrest and DNA-damage-inducible, beta
ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
TRAT1	T cell receptor associated transmembrane adaptor 1
HLA-DMA	major histocompatibility complex, class II, DM alpha
CENTD3	centaurin, delta 3

SAMSN1	SAM domain, SH3 domain and nuclear localisation signals, 1
CLEC4E	C-type lectin domain family 4, member E
TNFRSF19	tumor necrosis factor receptor superfamily, member 19
NAV1	neuron navigator 1
LOXL4	lysyl oxidase-like 4
TNFRSF19	tumor necrosis factor receptor superfamily, member 19
TAGAP	T-cell activation GTPase activating protein
GIMAP2	GTPase, IMAP family member 2
IGF1R	Insulin-like growth factor 1 receptor
C17orf63	Chromosome 17 open reading frame 63
CD52	CD52 antigen (CAMPATH-1 antigen)

In one aspect the invention employs one or more genes selected from Table 12.

Table 12

Gene symbol	Gene title
CCL5	chemokine (C-C motif) ligand 5
TRAT1	T cell receptor associated transmembrane adaptor 1
STAT4	signal transducer and activator of transcription 4
PRKCQ	protein kinase C, theta
GPR171	G protein-coupled receptor 171
UBD	ubiquitin D
CD52	CD52 molecule
CD3D	CD3d molecule, delta (CD3-TCR complex)
PRF1	perforin 1 (pore forming protein)
CD8A	CD8a molecule
CXCL10	chemokine (C-X-C motif) ligand 10
CD69	CD69 molecule
TRBV19	T cell receptor beta variable 19
TRDV2	T cell receptor delta variable 2
IL7R	interleukin 7 receptor
GZMK	granzyme K
	PROTEIN-TYROSINE PHOSPHATASE, RECEPTOR-TYPE, C
CD45R	(PTPRC)

5 In one aspect the invention provides one or more genes selected from Table 13.

Table 13

Gene symbol	Gene title
FASLG	Fas ligand (TNF superfamily, member 6)
GNLY	granulysin
GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)
IFNG	interferon, gamma
ICOS	inducible T-cell co-stimulator
TBX21	T-box 21
CD3E	CD3e molecule, epsilon (CD3-TCR complex)
CXCL11	chemokine (C-X-C motif) ligand 11
CXCR3	chemokine (C-X-C motif) receptor 3
CD20	CD20 molecule
FOXP3	forkhead box P3
INDO	indoleamine-pyrrole 2,3 dioxygenase
IRF1	interferon regulatory factor 1
TLR7	toll-like receptor 7

PCR is a more sensitive technique than microarray and therefore can detect lower levels of differentially expressed genes.

- 5 In particular the following genes are suitable for PCR analysis: IL7R, CD3D, CD3E, CD52, UBD, GPR171, GMZK, PRKCQ, STAT4, TRDV2, TRAT1, TRBV19, CD69, INDO, CD45R, CD45RO, FOXP3, CD20, CCL5, FASLG, GNLY, GZMB, PRF1, IFNG, ICOS, TBX21, CD8A, CD3E, CXCL10, CXCL11, IRF1, TLR7 and CXCR3.

In one aspect the gene(s) employed are selected from the group comprising or consisting of:

- 10 CCL5, TRAT1, STAT4, PRKCQ, GPR171, UBD, CD52, CD3D, PRF1, CD8A, CXCL10, CD69, TRBV19, TRDV2, IL7R, GZMK and CD45R.

In one aspect the gene(s) employed are selected from the comprising or consisting of:

FASLG, GNLY, GZMB, IFNG, ICOS, TBX21, CD3E, CXCL11, CXCR3, CD20, FOXP3, INDO, IRF1 and TLR7.

- 15 The gene(s) FOXP3 and/or PRF1 is/are particularly suitable for PCR analysis according to the invention.

Suitable targets for immunohistochemistry include CD3, CD8, CD86, LAMP, CD20, CD45RO, CXCR3, CXL10/11, CD69, granzyme B, IDO, B cells and gene products from one or more genes from the NK family, HLA family, T cell receptor family and/or activated T cell.

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In a further aspect of the invention there is provided a gene signature indicative of a non-responder, for example wherein one or more of immune genes such as those listed herein are NOT differentially expressed and/or are down regulated and/or are NOT upregulated.

In one aspect the gene is NOT FOXP3.

- 5 According to a further aspect the present invention provides a gene signature indicative of an increased likelihood of a patients responding favourably to appropriate immunotherapy, which in turn is likely to result in an improved survival of patients, for example with Mage expressing cancers following treatment with Mage specific immunotherapy. This gene signature, of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or 31
10 genes from the genes disclosed in Table 1, is characterised by differential expression compared to the gene signature of Mage-expressing tumour patients who do not respond to Mage antigen specific cancer immunotherapy.

In one aspect the invention provides a profile based on differential expression of 1 or more of 62 known genes that relate to immune infiltration and activation.

- 15 The predictive genes correspond mainly to expression of and often upregulation of genes related to immune infiltration and activation. These genes include HLA class II, Interleukin-2 receptor gamma, T cell receptor genes (TRBV19, TRAT1, TRGC2), granzyme, and CD69.

- In one embodiment there is provided a gene signature, present in patients, for example with or who have had MAGE-expressing tumours, who respond to treatment, in which one or more, for
20 example at least 5, suitably 6, 7, 8, 9, 10 of the genes of Table 2 are differentially expressed: As shown in Fig 5a below, characterisation of responders and non-responders may be based on the differential expression on only one or two genes, such as TCR, CD3 and/or IL-7.

- Other genes that are thought to be particularly suitable in methods employing only one or two genes include: IL7R, CD3D, CD3E, CD52, UBD, GPR171, GMZK, PRKCQ, STAT4, TRDV2,
25 TRAT1, TRBV19, CD69, INDO, CD45R, CD45RO, FOXP3, CD20, CCL5, FASLG, GNLY, GZMB, PRF1, IFNG, ICOS, TBX21, CD8A, CD3E, CXCL10, CXCL11, TRF1, TLR7 and CXCR3, which may require the use of appropriately sensitive analytical techniques.

The invention herein extends to use of all permutations of the genes listed herein for identification of said signature/profile.

- 30 The invention also extends to embodiments according to the invention described herein, which comprise, consist essentially of, or consists of the components/elements described.

- The invention extends to the functional equivalents of genes listed herein, for example as characterised by hierarchical classification of genes such as described by Hongwei Wu *et al* 2007(Hierarchical classification of equivalent genes in prokaryotes-*Nucliec Acid Research*
35 *Advance Access*).

Whilst not wishing to be bound by theory, it is thought that is not necessarily the gene *per se* that is characteristic of the signature but rather it is the gene function which is fundamentally important. Thus a functionally equivalent gene to an immune activation gene such as those listed

above, for example in Table 1, 2, 3, 4, 7, 9, 11, 12 or 13 may be employed in the signature, see for example, *Journal of the National Cancer Institute* Vol 98, No. 7 April 5 2006.

The genes were identified by specific probes and thus a skilled person will understand that the description of the genes above is a description based on current understanding of what hybridises to the probe. However, regardless of the nomenclature used for the genes by repeating the hybridisation to the relevant probe under the prescribed conditions the requisite gene can be identified.

The invention extends to use of the profile(s) according to the invention for predicting or identifying a patient as a responder or non-responder to immunotherapy, such as cancer immunotherapy, for example cancer testis immunotherapy.

Thus the invention includes a method of analyzing a patient derived sample, based on differential expression of the profile/gene(s) according to the invention for the purpose of characterising the patient from which the sample was derived as a responder or non-responder to immunotherapy.

In one aspect the invention provides a method of identifying a profile according to the invention comprising the steps:

- a) analyzing a patient derived sample for differential expression of one or more immune response genes, and
 - b) characterising the patient from which the sample was derived as a responder or non-responder to appropriate immunotherapy, based on the results of step (a),
- wherein the characterisation step is optionally performed by reference or comparison to a standard.

Suitable standards are described above.

The present invention therefore, generally relates, in one aspect, to a method for the detection of a gene signature in a biological sample, the method comprising the analysis of the expression of one or more genes of Tables 1, 2, 3, 4, 7, 9, 11, 12 or 13, for example at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or 31 genes (eg for genes set forth in Table 1). In an embodiment, the analysis comprises the expression of at least 5, suitably 6, 7, 8, 9 or 10 genes set forth in Table 2.

In one aspect the invention provides a method for measuring expression levels of polynucleotides from immune activation genes such as one or more genes listed in Tables 1, 2, 3, 4, 7, 9, 11, 12 and/or 13 in a sample for the purpose of identifying if the patient, from whom the sample was derived, is likely to be a responder or non-responder to immunotherapy such a cancer immunotherapy comprising the steps:

- isolating the RNA from the sample,
- optionally amplifying the copies of the cDNA from the sample for said genes, and
- quantifying the levels of cDNA in the sample.

In one embodiment, the diagnostic method comprises determining whether a subject expresses any of the gene products of the genes set forth in Table 1 or any other embodiment of the

invention described herein by, for example, detecting the level of the corresponding mRNA and/or protein level of the gene products of the genes set forth in Table 1 etc. For example, by using techniques such as by Northern blot analysis, reverse transcription-polymerase chain reaction (RT-PCR), in situ hybridization, immunoprecipitation, Western blot hybridization, or immunohistochemistry. According to the method, cells may be obtained from a subject and the levels of the protein, or mRNA, of the analyzed genes, compared to that of a non-responder patient. Patients who differentially express one or more, for example, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or 31 genes selected from Table 1 or another embodiment of the invention are those which can be predicted to benefit from immunotherapy, for example cancer immunotherapy, such as Mage antigen specific cancer immunotherapy. For example, a nucleic acid molecule which hybridizes to a given location on a microarray is said to be differentially expressed if the hybridization signal is, for example, higher than the hybridization signal at the same location on an identical array hybridized with a nucleic acid sample obtained from a subject that does not clinically respond to Mage specific immunotherapy.

The results of 30 patients who have been subjected to gene profiling are shown in figure 5. This pictorially demonstrates that the gene signature of the present invention is aligned with clinical response to MAGE-antigen specific cancer immunotherapy.

Alternatively the cancer patient may be characterised as a responder or non-responder to immunotherapy from a visual inspection of a tissue section derived from the cancer or tumour. A responder is likely to be a patient with an infiltration of immune response cells into the cancer/tumour microenvironment.

The invention also provides a method of generating a new gene profile not specifically recited herein, based on differential expression of one or more immune response/activation genes, for indicating whether a patient is likely to be a responder or non-responder to appropriate immunotherapy, for example cancer immunotherapy such as Mage immunotherapy comprising the steps:

- a) analysing at least two patient derived samples for differential expression of one or more of immune activation genes, where the sample group comprises both responders and non-responders to appropriate immunotherapy, and
- b) correlating same with clinical outcome, after appropriate treatment, of patients from which the samples were derived, and
- c) identifying one or more genes which are differentially expressed in responders and/or non-responders.

After the new profile has been identified the invention also extends to analysis of a previously uncharacterised sample, designating same as responders or non-responders (as appropriate) and if desired administering a therapeutically effective amount of an appropriate immunotherapy, for example cancer immunotherapy such as Mage immunotherapy to one or more patients designated

as responders.

The invention also provides a method of generating a gene profile based on differential expression of one or more gene sequences recited in Table 1, 2, 3, 4, 7, 9, 11, 12 and/or 13 for indicating whether a patient is likely to be a responder or non-responder to immunotherapy

5 comprising the steps:

- a) analyzing at least two patient derived samples for differential expression of
 - (i) one or more gene sequences recited in Table 1, 2, 3, 4, 7, 9, 11, 12 and/or 13 and
 - (ii) optionally one or more gene sequences not recited in Table 1, 2, 3, 4, 7, 9, 11,

10

12 and/or 13, where the sample group comprises both responders and non-responders to appropriate immunotherapy;

- b) correlating differential expression of said one or more gene sequences with clinical outcome, after appropriate treatment, of patients from which the samples were

15

- derived, and
- c) identifying one or more genes which are differentially expressed in responders and non-responders.

After the profile has been identified the invention also extends to analysis of a previously uncharacterised sample, designating same as responders or non-responders (as appropriate) and if

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desired administering a therapeutically effective amount of an appropriate immunotherapy, for example cancer immunotherapy such as Mage immunotherapy to one or more patients designated as responders.

The invention provides a diagnostic kit comprising at least one component for performing an analysis on a patient derived sample to identify a profile according to the invention, the results of

25

which may be used to designate a patient from which the sample was derived as a responder or non-responder to immunotherapy.

The kit may comprise materials/reagents for PCR (such as QPCR), microarray analysis, immunohistochemistry or other analytical technique that may be used for accessing differential expression of one or more genes.

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The invention also provides a diagnostic kit comprising a set of probes capable of hybridising to the mRNA or cDNA of one or more, such as at least 5 genes as set forth in Table 1 or alternatively Tables 2, 3, 4, 7, 9, 11, 12 and/or 13, for example a diagnostic kit comprising a set of probes capable of hybridising to the mRNA or its cDNA of at least 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or 31 genes as set forth in Table 1.

35

In another embodiment this invention relates to diagnostic kits. For example, diagnostic kits containing such microarrays comprising a microarray substrate and probes that are capable of hybridising to mRNA or cDNA expressed from, for example, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or 31 genes from, for example Table 1

or any other embodiment of the invention that are capable of demonstrating the gene signature of the invention.

In one aspect the invention provides microarrays adapted for identification of a signature according to the invention.

- 5 The invention also extends to substrates and probes suitable for hybridising to an mRNA or cDNA moiety expressed from one or more genes employed in the invention, for example from Table 1, 2, 3, 4, 7, 9, 11, 12 or 13.

Commercially available microarrays contain many more probes than are required to characterise the differential expression of the genes under consideration at any one time, to aid the accuracy of
10 the analysis. Thus one or more probe sets may recognise the same gene.

Thus in one embodiment multiple probes or probe sets are used to identify if an immune activation gene is differentially expressed, such as upregulated.

The diagnostic kit may, for example comprise probes, which are arrayed in a microarray.

Specifically, prepared microarrays, for example, containing one or more probe sets described
15 herein can readily be prepared by companies such as Affimetrix, thereby providing a specific test and optionally reagents for identifying the profile, according to the invention.

In an embodiment the microarrays or diagnostic kits will additionally be able to test for the presence or absence of the relevant cancer testis antigen expressing gene such as the Mage gene.

Thus in one aspect the invention provides a probe and/or probe set suitable for said hybridisation,
20 under appropriate conditions. The invention also extends to use of probes, for example as described herein or functional equivalents thereof, for the identification of a gene profile according to the present invention.

The invention herein described extends to use of all permutations of the probes listed herein (or functional analogues thereof) for identification of the said signature.

25 In one aspect the invention provides use of a probe for the identification of differential expression of at least one gene product of an immune activation gene for establishing if a gene profile according to the present invention is present in a patient derived sample.

Table 1B discloses probe sets from which probes of typically 25 mer in length may be designed and which are suitable for identifying the mRNA (or its cDNA) expressed from, for example the
30 genes of Table 1 (or alternatively Table 2, 3, 4, 7, 9, 11, 12 or 13). Such probes and probe sets are an aspect of the invention. Typically each probe set may comprise about or exactly 11 individual sequences of about or exactly 25 nucleotides, which correspond precisely to a run of sequences from the probe set.

Accordingly, in one aspect, this invention relates to oligonucleotide probes and primers capable
35 of recognising the mRNA (or its cDNA) expressed from the genes from Table 1, (or alternatively Table 2, 3, 4, 7, 9, 11, 12 or 13) and diagnostic kits based on these probes and primers. Such kits may include probes or kits for the detection of a Mage gene.

In an aspect the invention provides a profile based on the differential expression of one or more

of the genes of Table 3 identifiable by one or more of following 13 probes:

204661_at, 205890_s_at, 206118_at, 206666_at, 207651_at, 210038_at,
210972_x_at, 211144_x_at, 211796_s_at, 213193_x_at, 213539_at, 217147_s_at,
34210_at.

- 5 Further details of these probes and the target genes of the same are given in Table 3A below.
Hybridisation will generally be preformed under stringent conditions, such as 3X SSC, 0.1%
SDS, at 50 °C.

Once the target gene(s)/profile has/have been identified then it is well within the skilled person's
ability to design alternative probes that hybridise to the same target. Therefore the invention also
10 extends to probes, which under appropriate conditions measure the same differential expression
of the gene(s) of the present invention to provide a signature/profile as described.

The invention also extends to use of the relevant probe in analysis of whether a cancer patient
will be a responder or non-responder to treatment with an appropriate immunotherapy.

- 15 The invention also extends to use (and processes employing same) of known microarrays for
identification of said signature.

A nucleic acid probe may be at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100 or more nucleotides in
length and may comprise the full length gene. Probes for use in the invention are those that are
able to hybridise specifically to the mRNA (or its cDNA) expressed from the genes listed in
Table 1 (or Table 2, 3, 4, 7, 9, 11, 12 or 13) under stringent conditions.

- 20 The present invention further relates to a method of screening the effects of a drug on a tissue or
cell sample comprising the step of analysing the expression profile of, for example 5, 6, 7, 8, 9,
10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 21, 22, 23, 24, 25, 26, 27, 28 , 29, 30 or 31 genes
selected from Table 1 or any other embodiment of the invention described herein before and after
drug treatment. The invention therefore provides a method for screening for a drug, which would
25 alter the gene profile to that of a patient having improved survival following treatment with, for
example, Mage antigen specific cancer immunotherapy (ie. to alter the gene profile to that of a
responder), to enable the patient to benefit from, for example, Mage antigen specific cancer
immunotherapy.

- 30 The present invention further provides a method of patient diagnosis comprising, for example, the
step of analysing the expression profile of, for example, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17,
18, 19, 20 21, 22, 23, 24, 25, 26, 27, 28 , 29, 30 or 31 genes selected from Table 1 or any other
embodiment of the invention described herein and comparing it with a standard to diagnose
whether the patient would benefit from Mage specific immunotherapy.

- 35 The invention includes a method of patient diagnosis comprising the step of analysing the
expression profile of at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 21, 22, 23, 24,
25, 26, 27, 28, 29, 30 or 31 genes selected from Table 1 or other embodiment of the invention
from a tumour tissue sample given by a patient and assessing whether 5 or more of said genes are
expressed.

Thus in clinical applications, tissue samples from a human patient may be screened for the presence and/or absence of the expression of, for example 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or 31 genes selected from Table 1 or any other embodiment of the invention described herein.

5 In the context of the present invention, the sample may be of any biological tissue or fluid derived from a patient potentially in need of treatment. The sample maybe derived from sputum, blood, urine, or from solid tissues such as biopsy from a primary tumour or metastasis, or from sections of previously removed tissues.

Samples could comprise or consist of, for example, needle biopsy cores, surgical resection
10 samples or lymph node tissue. These methods include obtaining a biopsy, which is optionally fractionated by cryostat sectioning to enrich tumour cells to about 80% of the total cell population. In certain embodiments, nucleic acids extracted from these samples may be amplified using techniques well known in the art. The levels of selected markers (eg the gene products of table 1) can be detected and can be compared with statistically valid groups of, for example,

15 Mage positive non responder patients.

For cancer, the biological sample will contain cancer or tumour cells and may, for example, be derived from the cancer or tumour such as a fresh sample (including frozen samples) or a sample that has been preserved in paraffin. Having said this, samples preserved in paraffin can suffer from degradation and the profile observed may be modified. A person working the in field is
20 well able to compensate of these changes observed by recalibrating the parameters of the profile.

Microarrays

A microarray is an array of discrete regions, typically nucleic acids, which are separate from one another and are typically arrayed at a density of between, about 100/cm² to 1000/cm², but can be arrayed at greater densities such as 10000 /cm². The principle of a microarray experiment, is that
25 mRNA from a given cell line or tissue is used to generate a labeled sample typically labeled cDNA, termed the 'target', which is hybridized in parallel to a large number of, nucleic acid sequences, typically DNA sequences, immobilised on a solid surface in an ordered array.

Tens of thousands of transcript species can be detected and quantified simultaneously. Although many different microarray systems have been developed the most commonly used systems today
30 can be divided into two groups, according to the arrayed material: complementary DNA (cDNA) and oligonucleotide microarrays. The arrayed material has generally been termed the probe since it is equivalent to the probe used in a northern blot analysis. Probes for cDNA arrays are usually products of the polymerase chain reaction (PCR) generated from cDNA libraries or clone collections, using either vector-specific or gene-specific primers, and are printed onto glass slides
35 or nylon membranes as spots at defined locations. Spots are typically 10–300 µm in size and are spaced about the same distance apart. Using this technique, arrays consisting of more than 30,000 cDNAs can be fitted onto the surface of a conventional microscope slide. For oligonucleotide arrays, short 20–25mers are synthesized *in situ*, either by photolithography onto silicon wafers

(high-density-oligonucleotide arrays from Affymetrix or by ink-jet technology (developed by Rosetta Inpharmatics, and licensed to Agilent Technologies). Alternatively, presynthesized oligonucleotides can be printed onto glass slides. Methods based on synthetic oligonucleotides offer the advantage that because sequence information alone is sufficient to generate the DNA to be arrayed, no time-consuming handling of cDNA resources is required. Also, probes can be designed to represent the most unique part of a given transcript, making the detection of closely related genes or splice variants possible. Although short oligonucleotides may result in less specific hybridization and reduced sensitivity, the arraying of presynthesized longer oligonucleotides (50–100mers) has recently been developed to counteract these disadvantages.

Thus in performing a microarray to ascertain whether a patient presents with a gene signature of the present invention, the following steps are performed: obtain mRNA from the sample and prepare nucleic acids targets, contact the array under conditions, typically as suggested by the manufactures of the microarray (suitably stringent hybridisation conditions such as 3X SSC, 0.1% SDS, at 50 °C) to bind corresponding probes on the array, wash if necessary to remove unbound nucleic acid targets and analyse the results.

It will be appreciated that the mRNA may be enriched for sequences of interest such as those in Table 1 or 2 (or other embodiment of the invention) by methods known in the art, such as primer specific cDNA synthesis. The population may be further amplified, for example, by using PCR technology. The targets or probes are labeled to permit detection of the hybridisation of the target molecule to the microarray. Suitable labels include isotopic or fluorescent labels which can be incorporated into the probe.

In an alternative embodiment, a patient may be diagnosed to ascertain whether his/her tumor expresses the gene signature of the invention utilising a diagnostic kit based on PCR technology, in particular Quantative PCR (For a review see Ginzinger D Experimental haematology 30 (2002) p 503 – 512 and Giuliette et al Methods, 25 p 386 (2001).

In an alternative aspect the invention provides a method further comprising the steps of analyzing a tumour derived sample to determine which antigen(s) are expressed by the tumour and hence enabling administration of an a therapeutically effective amount of an appropriate antigen specific cancer immunotherapeutic, for example where the tumour is found to be MAGE (such as Mage A3) positive, appropriate treatment may, for example, include administration of Mage A3 antigen specific immunotherapy.

A sample such as tumour tissue of a patient is deemed to present the gene signature of the invention if one or more genes of Table 1, 2, 3, 4, 7, 9, 11, 12 and/or 13 are differentially expressed (such as upregulated), for example, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or 31 genes from for example Table 1 or other embodiment of the invention are expressed and can be detected by microarray analysis or other appropriate analysis for example as described herein. The tumour tissue preferably shows expression of at least 5 genes selected from Table 1, 2, 3, 4, 7, 9, 11, 12 and/or 13, more

preferably 10 genes, particularly 5, 6, 7, 8, 9 or 10 genes from Table 1, 2, 3, 4, 7, 9, 11, 12 or 13.

Immunotherapeutics

In a further aspect the invention provides a method of treating a responder patient with an appropriate immunotherapy, for example cancer immunotherapy such as cancer testis

5 immunotherapy, after identification of the same as a responder thereto.

Thus the invention provides a method of treating a patient comprising the step of administering a therapeutically effective amount of an appropriate immunotherapy (for example cancer immunotherapy, such as Mage cancer immunotherapy), after first characterising the patient as a responder based on differential expression of at least one immune activation gene, for example as

10 shown by appropriate analysis of a sample derived from the patient. In particular wherein the patient is characterised as a responder based on one or more embodiments described herein. In one aspect the immunotherapy comprises an appropriate adjuvant (immunostimulant), see description below.

In yet a further embodiment of the invention there is provided a method of treating a patient

15 suffering from, for example, a Mage expressing tumour, the method comprising determining whether the patient expresses the gene signature of the invention and then administering, for example, a Mage specific immunotherapeutic. In a further embodiment, the patient is treated with, for example, the Mage specific immunotherapy to prevent or ameliorate recurrence of disease, after first receiving treatment such as resection by surgery of any tumour or other

20 chemotherapeutic or radiotherapy treatment.

A further aspect of the invention is a method of treating a patient suffering from a Mage expressing tumour, the method comprising determining whether the patient's tumour expresses at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or 31 genes selected from Table 1 (or other embodiment of the invention) from a tumour tissue

25 sample given by a patient and then administering a Mage specific immunotherapeutic to said patient.

Also provided is a method of treating a patient susceptible to recurrence of Mage expressing tumour having been treated to remove/treat a Mage expressing tumour, the method comprising determining whether the patient's tumour expresses at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15,

30 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or 31 genes selected from Table 1 (or other embodiment of the invention) from a tumour tissue sample given by a patient and then administering a Mage specific immunotherapeutic.

The invention also provides as method of treatment or use employing:

- MAGE specific immunotherapeutic comprising a MAGE antigen or peptide thereof,
- 35 • MAGE antigen comprising a MAGE-A3 protein or peptide,
- MAGE antigen comprising the peptide EVDPIGHLV,

- MAGE antigen or peptide fused or conjugated to a carrier protein, for example in which the carrier protein is selected from protein D, NS1 or CLytA or fragments thereof, and/or
- MAGE specific immunotherapeutic further comprises an adjuvant, for example in which the adjuvant comprises one or more or combinations of: 3D-MPL; aluminium salts; CpG containing oligonucleotides; saponin-containing adjuvants such as QS21 or ISCOMs; oil-in-water emulsions; and liposomes.

The invention also extends to use of an immunotherapy such as a cancer immunotherapy, in particular Mage immunotherapy in the manufacture of a medicament for the treatment of a patient such as a cancer patient designated as a responder, thereto.

It was observed that one patient initially characterised as a non-responder was subsequently characterised as responder after radiation therapy. Interestingly the inventors also believe that it may be possible to induce a responders profile in at least some non-responders, for example by subjecting the patient to radiation therapy, or administering an inflammatory stimulant such as interferon (for example imiquimod such as administered topically) or a TLR 3 (for example as described in WO 2006/054177), 4, 7, 8 or TLR 9 agonist (for example containing a CpG motif, in particular administering a high dose thereof such as 0.1 to 75 mg per Kg administered, for example weekly). See for example Krieg, A. M., Efler, S. M., Wittpoth, M., Al Adhami, M. J. & Davis, H. L. Induction of systemic TH1-like innate immunity in normal volunteers following subcutaneous but not intravenous administration of CPG 7909, a synthetic B-class CpG oligodeoxynucleotide TLR9 agonist. *J. Immunother.* 27, 460–471 (2004).

The high dose of CpG may, for example be inhaled or given subcutaneously.

Whilst not wishing to be bound by theory, it is hypothesised that the radiation therapy stimulated a systemic inflammatory response/immune response, which once triggered rendered the patient (or tumour tissue therein) more responsive to immunotherapy.

Accordingly, the invention further provides a method of inducing a responders profile by stimulating a systemic immune response, for example by administering an immunostimulant.

The invention further provides the use of Mage specific immunotherapy in the manufacture of a medicament for the treatment of patients suffering from Mage expressing tumour or patients who have received treatment (e.g. surgery, chemotherapy or radiotherapy) to remove/treat a Mage expressing tumour, said patient expressing the gene signature of the invention.

The immunotherapy may then be administered once the responders profile has been induced.

In one aspect the invention provides use of Mage specific immunotherapy in the manufacture of a medicament for the treatment of patients suffering from Mage expressing tumour, said patient characterised by their tumour expressing at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or 31 genes selected from Table 1, or alternatively other embodiments of the invention.

The invention also provides use of Mage specific immunotherapy in the manufacture of a

medicament for the treatment of patients susceptible to recurrence from Mage expressing tumour said patient characterised by their tumour expressing at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or 31 genes selected from Table 1 or alternatively other embodiments of the invention.

5 Advantageously, the invention may allow medics to target those populations of patients that will obtain a clinical benefit from receiving an appropriate immunotherapy. It is expected that after screening that at least 60% of patients such as 70, 75, 80, 85% or more of patients deemed/characterised as responders will receive a clinical benefit from the immunotherapy, which is a significant increase over the current levels observed with therapy such as cancer
10 therapy generally.

Advantageously if the cancer immunotherapy is given concomitantly or subsequent to chemotherapy it may assist in raising the patient's immune responses, which may have been depleted by the chemotherapy.

Antigen Specific Cancer Immunotherapeutics (ASCIs) suitable for use in the invention may, for
15 example include those capable of raising a Mage specific immune response. Such immunotherapeutics may be capable of raising an immune response to a Mage gene product, for example a Mage-A antigen such as Mage-A3. The immunotherapeutic will generally contain at least one epitope from a Mage gene product. Such an epitope may be present as a peptide antigen optionally linked covalently to a carrier and optionally in the presence of an adjuvant.
20 Alternatively larger protein fragments may be used. For example, the immunotherapeutic for use in the invention may comprise an antigen that corresponds to or comprises amino acids 195-279 of MAGE-A1. The fragments and peptides for use must however, when suitably presented be capable of raising a Mage specific immune response. Examples of peptides that may be used in the present invention include the MAGE-3.A1 nonapeptide EVDPIGHLY [Seq. ID No 36] (see
25 Marchand *et al.*, International Journal of Cancer 80(2), 219-230), and the following MAGE-A3 peptides:

	FLWGPRALV;	[Seq. ID No 37]
	MEVDPIGHLY;	[Seq. ID No 38]
	VHFLLLKYRA;	[Seq. ID No 39]
30	LVHFLLLKYR;	[Seq. ID No 40]
	LKYRAREPVT;	[Seq. ID No 41]
	ACYEFLWGPRALVETS; and	[Seq. ID No 42]
	TQHFVQENYLEY;	[Seq. ID No 43]

35 Alternative ASCIs include cancer testis antigens such as PRAME, LAGE 1, LAGE 2, and others, for example details of which can be obtained from www.cancerimmunity.org/CTdatabase. The cancer immunotherapy may be based, for example on one or more of the antigens discussed below.

In one embodiment of the present invention, the antigen to be used may consist or comprise a MAGE tumour antigen, for example, MAGE 1, MAGE 2, MAGE 3, MAGE 4, MAGE 5, MAGE 6, MAGE 7, MAGE 8, MAGE 9, MAGE 10, MAGE 11 or MAGE 12. The genes encoding these MAGE antigens are located on chromosome X and share with each other 64 to 85% homology in their coding sequence (De Plaen, 1994). These antigens are sometimes known as MAGE A1, MAGE A2, MAGE A3, MAGE A4, MAGE A5, MAGE A6, MAGE A7, MAGE A8, MAGE A9, MAGE A 10, MAGE A11 and/or MAGE A12 (The MAGE A family). In one embodiment, the antigen is MAGE A3.

In one embodiment, an antigen from one of two further MAGE families may be used: the MAGE B and MAGE C group. The MAGE B family includes MAGE B1 (also known as MAGE Xp1, and DAM 10), MAGE B2 (also known as MAGE Xp2 and DAM 6) MAGE B3 and MAGE B4 – the MAGE C family currently includes MAGE C1 and MAGE C2.

In general terms, a MAGE protein can be defined as containing a core sequence signature located towards the C-terminal end of the protein (for example with respect to MAGE A1 a 309 amino acid protein, the core signature corresponds to amino acid 195-279).

The consensus pattern of the core signature is thus described as follows wherein x represents any amino acid, lower case residues are conserved (conservative variants allowed) and upper case residues are perfectly conserved.

Core sequence signature

LixvL(2x)I(3x)g(2x)apEExiWexl(2x)m(3-4x)Gxe(3-4x)gxp(2x)llt(3x)VqexYLxYxqVPxsxP(2x)ye**FLWG**prA(2x)Et(3x)kv

Conservative substitutions are well known and are generally set up as the default scoring matrices in sequence alignment computer programs. These programs include PAM250 (Dayhoff M.O. *et al.*, (1978), "A model of evolutionary changes in proteins", In "Atlas of Protein sequence and structure" 5(3) M.O. Dayhoff (ed.), 345-352), National Biomedical Research Foundation, Washington, and Blosum 62 (Steven Henikoff and Jorja G. Henikoff (1992), "Amino acid substitution matrices from protein blocks"), Proc. Natl. Acad. Sci. USA 89 (Biochemistry): 10915-10919.

In general terms, substitution within the following groups are conservative substitutions, but substitutions between groups are considered non-conserved. The groups are:

- i) Aspartate/asparagine/glutamate/glutamine
- ii) Serine/threonine
- iii) Lysine/arginine
- iv) Phenylalanine/tyrosine/tryptophane
- v) Leucine/isoleucine/valine/methionine
- vi) Glycine/alanine

In general and in the context of this invention, a MAGE protein will be approximately 50% or more identical, such as 70, 80, 90, 95 or 99% identical, in this core region with amino acids 195

to 279 of MAGE A1.

MAGE protein derivatives are also known in the art, see: WO 99/40188. Such derivatives are suitable for use in therapeutic vaccine formulations (Immunotherapeutic) which are suitable for the treatment of a range of tumour types.

5 Several CTL epitopes have been identified on the MAGE-3 protein. One such epitope, MAGE-3.A1, is a nonapeptide sequence located between amino acids 168 and 176 of the MAGE-3 protein which constitutes an epitope specific for CTLs when presented in association with the MHC class I molecule HLA.A1. Recently two additional CTL epitopes have been identified on the peptide sequence of the MAGE-3 protein by their ability to mount a CTL response in a mixed
10 culture of melanoma cells and autologous lymphocytes. These two epitopes have specific binding motifs for the HLA.A2 (Van der Bruggen, 1994) and HLA.B44 (Herman, 1996) alleles respectively.

In a further embodiment of the invention, the tumour antigen may comprise or consist of one of the following antigens, or an immunogenic portion thereof which is able to direct an immune
15 response to the antigen:

SSX-2; SSX-4; SSX-5; NA17; MELAN-A; Tyrosinase; LAGE-1; NY-ESO-1; PRAME; P790; P510; P835; B305D; B854; CASB618 (as described in WO00/53748); CASB7439 (as described in WO01/62778); C1491; C1584; and C1585.

In one embodiment, the antigen may comprise or consist of P501S (also known as prostein). The
20 P501S antigen may be a recombinant protein that combines most of the P501S protein with a bacterial fusion protein comprising the C terminal part of protein LytA of *Streptococcus pneumoniae* in which the P2 universal T helper peptide of tetanus toxoid has been inserted, ie. a fusion comprising CLytA-P2-CLytA (the "CPC" fusion partner), as described in WO03/104272; In one embodiment, the antigen may comprise or consist of WT-1 expressed by the Wilm's
25 tumor gene, or its N-terminal fragment WT-1F comprising about or approximately amino acids 1-249; the antigen expressed by the Her-2/neu gene, or a fragment thereof. In one embodiment, the Her-2/neu antigen may be one of the following fusion proteins which are described in WO00/44899.

In a further embodiment, the antigen may comprise or consist of "HER-2/neu ECD-ICD fusion protein," also referred to as "ECD-ICD" or "ECD-ICD fusion protein," which refers to a fusion
30 protein (or fragments thereof) comprising the extracellular domain (or fragments thereof) and the intracellular domain (or fragments thereof) of the HER-2/neu protein. In one embodiment, this ECD-ICD fusion protein does not include a substantial portion of the HER-2/neu transmembrane domain, or does not include any of the HER-2/neu transmembrane domain.

35 In a further embodiment, the antigen may comprise or consist of "HER-2/neu ECD-PD fusion protein," also referred to as "ECD-PD" or "ECD-PD fusion protein," or the "HER-2/neu ECD-APD fusion protein," also referred to as "ECD-APD" or "ECD-APD fusion protein," which refers to fusion proteins (or fragments thereof) comprising the extracellular domain (or fragments

thereof) and phosphorylation domain (or fragments thereof, *e.g.*, Δ PD) of the HER-2/neu protein. In one embodiment, the ECD-PD and ECD- Δ PD fusion proteins do not include a substantial portion of the HER-2/neu transmembrane domain, or does not include any of the HER-2/neu transmembrane domain.

- 5 In one embodiment, the antigen may comprise a Mage or other appropriate protein linked to an immunological fusion or expression enhancer partner. Fusion proteins may include a hybrid protein comprising two or more antigens relevant to a given disease or may be a hybrid of an antigen and an expression enhancer partner.

The antigen and partner may be chemically conjugated, or may be expressed as a recombinant fusion protein. In an embodiment in which the antigen and partner are expressed as a recombinant fusion protein, this may allow increased levels to be produced in an expression system compared to non-fused protein. Thus the fusion partner may assist in providing T helper epitopes (immunological fusion partner), preferably T helper epitopes recognised by humans, and/or assist in expressing the protein (expression enhancer) at higher yields than the native recombinant protein. In one embodiment, the fusion partner may be both an immunological fusion partner and expression enhancing partner.

In one embodiment of the invention, the immunological fusion partner that may be used is derived from protein D, a surface protein of the gram-negative bacterium, *Haemophilus influenza* B (WO 91/18926) or a derivative thereof. The protein D derivative may comprise the first 1/3 of the protein, or approximately or about the first 1/3 of the protein, in particular it may comprise the first N-terminal 100-110 amino acids or approximately the first N-terminal 100-110 amino acids.

In one embodiment the fusion protein comprises the first 109 residues (or 108 residues therefrom) or amino acids 20 to 127 of protein D.

- 25 Other fusion partners that may be used include the non-structural protein from *influenzae* virus, NS1 (hemagglutinin). Typically the N terminal 81 amino acids of NS1 may be utilised, although different fragments may be used provided they include T-helper epitopes.

In another embodiment the immunological fusion partner is the protein known as LytA. LytA is derived from *Streptococcus pneumoniae* which synthesise an N-acetyl-L-alanine amidase, amidase LytA, (coded by the LytA gene (Gene, 43 (1986) page 265-272) an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LytA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of E.coli C-LytA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LytA fragment at its amino terminus has been described (Biotechnology: 10, (1992) page 795-798). In one embodiment, the C terminal portion of the molecule may be used. The embodiment may utilise the repeat portion of the LytA molecule found in the C terminal end starting at residue 178. In one embodiment, the LytA portion may incorporate residues 188 - 305.

In one embodiment of the present invention, the Mage protein may comprise a derivatised free thiol. Such antigens have been described in WO 99/40188. In particular carboxyamidated or carboxymethylated derivatives may be used.

In one embodiment of the present invention, the tumour associated antigen comprises a Mage-A3-protein D molecule. The nucleotide and amino acid sequences for this molecule are shown in seq ID No 35. This antigen and those summarised below are described in more detail in WO 99/40188.

In further embodiments of the present invention, the tumour associated antigen may comprise any of the following fusion proteins:

A fusion protein of Lipoprotein D fragment, MAGE1 fragment, and histidine tail; fusion protein of NS1-MAGE3, and Histidine tail; fusion protein of CLYTA-MAGE1-Histidine; fusion protein of CLYTA-MAGE3-Histidine.

A further embodiment of the present invention comprises utilising a nucleic acid immunotherapeutic, which comprises a nucleic acid molecule encoding a Mage specific tumour associated antigens as described herein. Such sequences may be inserted into a suitable expression vector and used for DNA/RNA vaccination. Microbial vectors expressing the nucleic acid may also be used as vectored delivered immunotherapeutics. Such vectors include for example, poxvirus, adenovirus, alphavirus and listeria.

Conventional recombinant techniques for obtaining nucleic acid sequences, and production of expression vectors of are described in Maniatis *et al.*, Molecular Cloning - A Laboratory Manual; Cold Spring Harbor, 1982-1989.

For protein based immunotherapeutics the proteins of the present invention are provided either in a liquid form or in a lyophilised form.

It is generally expected that each human dose will comprise 1 to 1000 µg of protein, and preferably 30 - 300 µg.

The method(s) as described herein may comprise a composition further comprises a vaccine adjuvant, and/or immunostimulatory cytokine or chemokine.

Suitable vaccine adjuvants for use in the present invention are commercially available such as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminium salts such as aluminium hydroxide gel (alum) or aluminium phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatised polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, and chemokines may also be used as adjuvants.

In formulations it may be desirable that the adjuvant composition induces an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN-γ, TNFα, IL-2 and IL-12) tend to favour the induction of cell mediated immune responses to an administered

antigen. According to one embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

5 Accordingly, suitable adjuvants that may be used to elicit a predominantly Th1-type response include, for example a combination of monophosphoryl lipid A, such as 3-de-O-acylated monophosphoryl lipid A (3D-MPL) together with an aluminium salt. 3D-MPL or other toll like receptor 4 (TLR4) ligands such as aminoalkyl glucosaminide phosphates as disclosed in WO 98/50399, WO 01/34617 and WO 03/065806 may also be used alone to generate a predominantly
10 Th1-type response.

Other known adjuvants, which may preferentially induce a TH1 type immune response, include TLR9 agonists such as unmethylated CpG containing oligonucleotides. The oligonucleotides are characterised in that the CpG dinucleotide is unmethylated. Such oligonucleotides are well known and are described in, for example WO 96/02555.

15 Suitable oligonucleotides include:

OLIGO 1: TCC ATG ACG TTC CTG ACG TT (CpG 1826) [Seq ID No 44]

OLIGO 2: TCT CCC AGC GTG CGC CAT (CpG 1758) [Seq ID No 45]

OLIGO 3: ACC GAT GAC GTC GCC GGT GAC GGC ACC ACG [Seq ID No 46]

OLIGO 4 TCG TCG TTT TGT CGT TTT GTC GTT (CpG 2006, CpG 7909) [Seq ID No
20 47]

OLIGO 5 TCC ATG ACG TTC CTG ATG CT (CpG 1668) [Seq ID No 48]

CpG-containing oligonucleotides may also be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a CpG-containing oligonucleotide
25 and a saponin derivative particularly the combination of CpG and QS21 as disclosed in WO 00/09159 and WO 00/62800.

The formulation may additionally comprise an oil in water emulsion and/or tocopherol.

Another suitable adjuvant is a saponin, for example QS21 (Aquila Biopharmaceuticals Inc., Framingham, MA), that may be used alone or in combination with other adjuvants. For example,
30 an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other suitable formulations comprise an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in, for
35 example, an oil-in-water emulsion is described in WO 95/17210.

In another embodiment, the adjuvants may be formulated in a liposomal composition.

The amount of 3D-MPL used is generally small, but depending on the immunotherapeutic formulation may be in the region of 1-1000µg per dose, preferably 1-500µg per dose, and more

preferably between 1 to 100µg per dose.

In an embodiment, the adjuvant system comprises three immunostimulants: a CpG oligonucleotide, 3D-MPL, & QS21 either presented in a liposomal formulation or an oil in water emulsion such as described in WO 95/17210.

- 5 The amount of CpG or immunostimulatory oligonucleotides in the adjuvants or immunotherapeutics of the present invention is generally small, but depending on the immunotherapeutic formulation may be in the region of 1-1000µg per dose, preferably 1-500µg per dose, and more preferably between 1 to 100µg per dose.

- 10 The amount of saponin for use in the adjuvants of the present invention may be in the region of 1-1000µg per dose, preferably 1-500µg per dose, more preferably 1-250µg per dose, and most preferably between 1 to 100µg per dose.

- Generally, it is expected that each human dose will comprise 0.1-1000 µg of antigen, preferably 0.1-500 µg, preferably 0.1-100 µg, most preferably 0.1 to 50 µg. An optimal amount for a particular immunotherapeutic can be ascertained by standard studies involving observation of
15 appropriate immune responses in vaccinated subjects. Following an initial vaccination, subjects may receive one or several booster immunisation adequately spaced.

Other suitable adjuvants include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), Ribi Detox, RC-529 (GSK, Hamilton, MT) and other aminoalkyl glucosaminide 4-phosphates (AGPs).

- 20 Accordingly there is provided an immunogenic composition for use in the method of the present invention comprising an antigen as disclosed herein and an adjuvant, wherein the adjuvant comprises one or more of 3D-MPL, QS21, a CpG oligonucleotide, a polyethylene ether or ester or a combination of two or more of these adjuvants. The antigen within the immunogenic composition may be presented in an oil in water or a water in oil emulsion vehicle or in a
25 liposomal formulation.

In one embodiment, the adjuvant may comprise one or more of 3D-MPL, QS21 and an immunostimulatory CpG oligonucleotide. In an embodiment all three immunostimulants are present. In another embodiment 3D-MPL and QS21 are presented in an oil in water emulsion, and in the absence of a CpG oligonucleotide.

- 30 A composition for use in the method of the present invention may comprise a pharmaceutical composition comprising tumour associated antigen as described herein, or a fusion protein, in a pharmaceutically acceptable excipient.

EXAMPLES

EXAMPLE 1

- 35 MAGE008 Mage melanoma clinical trial:

In this on-going trial, the recMAGE-A3 protein (recombinant mage fusion protein as shown in Seq Id No 35) is combined with two different immunological adjuvants: either AS02B (QS21, MPL) or AS15 (QS21, MPL and CpG7909). The objectives were to discriminate between the

adjuvants in terms of safety profile, clinical response and immunological response.

In this experiment two adjuvant compositions are made up of mixtures of two immunostimulants:

1. QS21 (Purified, naturally occurring saponin molecule from the South-American tree *Quillaja Saponaria* Molina), and
- 5 2. MPL (3 de-O-acetylated monophosphoryl lipid A - detoxified derivative of lipid A, derived from *S. minnesota* LPS).

AS02B is an oil-in-water emulsion of QS21 and MPL.

In animal models these adjuvants have been successfully shown to induce both humoral and TH1 types of cellular-mediated immune responses, including CD4 and CD8 T-cells producing IFN α (Moore *et al.*, 1999; Gérard *et al.*, 2001). Moreover, the injection of recombinant protein formulated in this type of adjuvant leads to the induction of a systemic anti-tumor response: indeed, vaccinated animals were shown to be protected against challenges with murine tumor cells genetically engineered to express the tumor antigen, and regressing tumors were shown to be highly infiltrated by CD8, CD4 and NK cells and by macrophages.

15 The second adjuvant system is AS15: it contains a third immunostimulant, namely CpG7909 (otherwise known as CpG 2006 supra), in addition to MPL and QS21, in a liposome formulation. In animal models (mainly mice), it has been shown that the addition of CpG7909 further improves the induced immune and anti-tumor responses (Krieg and Davis, 2001; Ren *et al.*, 2004). CpG oligodeoxynucleotides (ODNs) directly stimulate dendritic-cell activation through
20 TLR9 triggering. In addition, in mice, the systemic application of CpG7909 greatly increases the infiltration of transferred T-cells into tumors (Meidenbauer *et al.*, 2004).

Study overview

1. Design

The MAGE008 trial is:

- 25 • open
- randomized
- two-arm (AS02B vs. AS15)
- with 68 patients in total.

As described above, the recMAGE-A3 protein is combined with either AS02B or AS15 adjuvant
30 system.

2. Patients population

The recMAGE-A3 protein is administered to patients with progressive metastatic melanoma with regional or distant skin and/or lymph-node lesions (unresectable stage III and stage IV M1a). The expression of the MAGE-A3 gene by the tumor was assessed by quantitative PCR. The selected
35 patients did not receive previous treatment for melanoma (recMAGE-A3 is given as first-line treatment) and had no visceral disease.

3. Schedule of immunization

Method of treatment schedules

Adjuvant setting

The method of treatment schedule for use in disease in an adjuvant (post-operative) setting may comprise administration of an antigen as described herein according to the following schedules:

Administration of antigen at three week intervals for the first 5 to 8 vaccinations, followed at 3 month intervals for the next 8, 9 or more vaccinations.

The antigen may be administered at the exact time frame indicated, or the antigen may be given 1, 2, 3 or 4 days before or after the exact interval, as required or as practical. An example of this schedule is shown in the table below:

Induction: 5 vaccinations at intervals of 3 weeks for example Weeks 0, 3, 6, 9, 12 or Weeks 0, 6, 9, 12

Maintenance: 9 vaccinations at intervals of 3 months

Alternatively, the vaccinations may be given initially at 2 week intervals, for example 6 injections at two week intervals followed by appropriate maintenance therapy.

Active disease

The method of treatment schedule for use in active or unresectable disease, for example in melanoma cancer, comprising: administration of an antigen as described herein at two or three week intervals for the first six months to one year of treatment. A schedule may comprise the following pattern of injections: the antigen may be given at two week intervals for the first 4 to 10 vaccinations, followed by 3 week intervals for the next 4 to 10 vaccinations, then at 6 week intervals for the next 3 to 7 vaccinations. Long term treatment may then continue with vaccinations at 3 month intervals for 3 to 5 vaccinations, followed by 6 month intervals for the next 3 to 5 vaccinations.

The antigen may be administered at the exact time frame indicated, or the antigen may be given 1, 2, 3 or 4 days before or after the exact interval, as required or as practical.

An example of this schedule is shown in the table below:

Cycle 1:	6 vaccinations at intervals of 2 weeks (Weeks 1, 3, 5, 7, 9, 11)
Cycle 2:	6 vaccinations at intervals of 3 weeks (Weeks 15, 18, 21, 24, 27, 30)
Cycle 3:	4 vaccinations at intervals of 6 weeks (Weeks 34, 40, 46, 52)
Long Term Treatment:	4 vaccinations at intervals of 3 months, for example followed by 4 vaccinations at intervals of 6 months

For both of the above treatment regimes additional vaccinations may be given after treatment, as required.

In order to screen potential participants in the above clinical trial we received biopsies of the tumor, prior to any immunization, as frozen tumor samples. From these samples we extracted RNA for the quantitative PCR. The quality of this purified RNA was extremely high and it was suitable for microarray analysis. We therefore analyzed the tumor samples by microarrays. The goal was to identify a set of genes associated with the clinical response so that patients likely to

benefit from this antigen-specific cancer immunotherapeutic are properly identified and selected. Gene profiling has been performed only on biopsies from patients who signed the informed consent for microarray analysis.

Materials and Methods

5 Tumor specimens

30 tumor specimens (pre-vaccination) were used from the Mage008 Mage-3 melanoma clinical trial. These were fresh frozen preserved in the RNA stabilizing solution RNAlater.

RNA purification

10 Tumoral total RNA was purified using the Tripure method - Tripure extraction (Roche Cat. No. 1 667 165). The protocols provided were followed subsequently by the use of an RNeasy Mini kit - clean-up protocol with DNase treatment (Qiagen Cat. No. 74106).

http://www1.qiagen.com/literature/handbooks/PDF/RNAStabilizationAndPurification/FromAnimalAndPlantTissuesBacteriaYeastAndFungi/RNY_Mini/1035969_HB.pdf.

15 www.roche-applied-science.com/PROD_INF/MANUALS/napi_man/pdf/chapter4/page_152-158.pdf

RNA quality control

Quantification of RNA was initially completed using optical density at 260nm and Quant-IT RiboGreen RNA assay kit (Invitrogen - Molecular probes R11490).

<http://probes.invitrogen.com/media/pis/mp11490.pdf>.

20 The Quality of the 28s and 18s ribosomal RNA peaks were assessed by use of the Agilent bioanalyser.

RNA labeling and amplification for microarray analysis

Due to the small biopsy size received during the clinical study an amplification method was used in conjunction with the labeling of the RNA for microarray analysis.

25 The Nugen 3' ovation biotin kit (Labelling of 50 ng of RNA - Ovation biotin system Cat; 2300-12, 2300-60) http://www.nugeninc.com/html/03_products2.html

A starting input of 50ng of total RNA was used.

Microarray chips

30 The Affymetrix HU-U133.Plus 2.0 gene chips were utilized as these were the most up to date chips (based on the human genome project) available from the supplier. These chips cover about 47,000 potential gene transcripts.

Microarray hybridization and scanning

35 The hybridized chips were washed and scanned according to the standard Affymetrix protocols: Affymetrix gene chip expression analysis protocols can be downloaded from http://www.affymetrix.com/support/technical/manual/expression_manual.affx.

The scanner that has to be used with the Affymetrix microarray workstation is http://www.affymetrix.com/products/instruments/specific/scanner_3000.affx

Data normalization

The fluorescent scanned data was then normalized using RMA to allow comparisons between individual chips. The following reference describes this method.

Irizarry RA, Hobbs B, Collin F, Beazer-Barclay YD, Antonellis KJ, Scherf U, Speed TP.

Exploration, normalization, and summaries of high density oligonucleotide array probe level data. *Biostatistics*. 2003 Apr;4(2):249-64.

Data analysis

Three independent methods were used to generate gene lists to distinguish responder from non-responding patients. The methods are 1. Spotfire, 2. Baldi BH and 3. Arrayminer.

The Baldi analysis method is available from the following website.

http://www.igb.uci.edu/~pfbaldi/software_and_servers.htm.

The spotfire software can be purchased from this site <http://www.spotfire.com>. The arrayminer software is available for purchase at

<http://www.optimaldesign.com/ArrayMiner/ArrayMiner.htm>.

All data analysis was performed with the use of the R statistics software (available at www.r-project.org) and various Bioconductor packages for R (available at www.bioconductor.org).

The raw data were pre-processed for background correction, normalisation and probe summarisation by the RMA (Irizarry RA, Hobbs B, Collin F, Beazer-Barclay YD, Antonellis KJ, Scherf U, Speed TP. Exploration, normalization, and summaries of high density oligonucleotide array probe level data. *Biostatistics*. 2003 Apr;4(2):249-64)

The differential gene expression between any two groups was computed by two different statistical methods, the RankProduct (Breitling, R., Armengaud, P., Amtmann, A., and Herzyk, P.(2004) Rank Products: A simple, yet powerful, new method to detect differentially regulated genes in replicated microarray experiments, *FEBS Letter*, 57383-92) and the CyberT (P. Baldi and A.D. Long, "A Bayesian Framework for the Analysis of Microarray Expression Data: Regularized t-Test and Statistical Inferences of Gene Changes", *Bioinformatics*, 17, 6, 509-519, (2001)) methods.

In each of them, a correction for multiple testing was done with the method of Benjamini-Hochberg (Y. Benjamini and Y. Hochberg, Controlling the false discovery rate: a practical and powerful approach to multiple testing, *J. Roy. Stat. Soc. B* 57 (1995)), and the threshold of 5% was chosen for the false discovery rate; thus, the genes had to have a corrected p-value less or equal to 0.05 to be considered as differentially expressed.

Baldi-BH is equivalent to CyberT followed by Benjamini-Hochberg correction.

1. Spotfire analysis

The results of the analysis of patient samples (from the clinical research program named Mage008) are summarized in the figure 1.

As a first step, a supervised comparison was performed in order to find a group of genes able to cluster. Two patients that showed clinical response (patient 67 and 59) fell within the cluster of non-reponders. Two patients who were non-responders (patient 3 and 39) fell within the cluster

designated as responders. The responding patients are also found within cross over cluster (ie the areas of overlap in the figure). However, there are two patients who are non-responders that fall within this area of overlap.

In Figure 1 RESPONDERS were patients 27 and 38 (full/complete clinical responders), patients 2, 10, 20, 26-1, 26-2, 59 & 67 (mixed responders) and patients 19, 23, 65 and 75 (stable disease). NON-RESPONDERS in Figure 1 were patients 3, 5, 8, 9, 13, 14, 15, 16, 28, 30, 36, 37, 39, 52, 55, 56, 60 and 66.

2. Baldi BH analysis

This software is designed for statistical supervised gene classification in microarray experiments.

A list of 100 most significant genes were identified that define the two groups. See figure 2 below. The clustering is a more effective than with spotfire with the majority of the responders found in the responder cluster. However we still see the same patients non responding (patients 3, 39), and the responding patients (67 and 59) that are located within the wrong clusters.

In Figure 2 RESPONDERS were patients 27 and 38 (full/complete clinical responders), patients 2, 10, 20, 26-1, 26-2, 59 & 67 (mixed responders) and patients 19, 23, 65 and 75 (stable disease). NON-RESPONDERS in Figure 2 were patients 3, 5, 8, 9, 13, 14, 15, 16, 28, 30, 36, 37, 39, 52, 55, 56, 60 and 66.

3. Arrayminer analysis

This software is classifies genes by using a "train and test" method. In this method the software first identifies a discriminant set of markers for the training classes, similar to a classical cross-validation study.

Here due to the analysis there is only the responder or non-responder cluster, with no area of overlap. Here again there is mis-classification of samples, in particular patients 59 and 67 who both responded to treatment but in this analysis were in the cluster of non-responders. Patients 3, 14, 39, 52 and 66 were non-responders but were located in the cluster for responders using this analysis.

In Figure 3 RESPONDERS were patients 27 and 38 (full/complete clinical responders), patients 10, 20, 26-1, 26-2, 59 & 67 (mixed responders and patients) 19, 23, 65 and 75 (stable disease). NON-RESPONDERS in Figure 3 were patients 3, 5, 8, 9, 13, 14, 15, 16, 28, 30, 36, 37, 39, 52, 55, 56, 60 and 66.

Combination of the three methods

The three methods were used together to find a common set of gene probes that will define the signature with high significance. A venn diagram was created comparing all of the results. See figure 4. A list of 36 probesets was found that are common with all three programs. (Table 1B).

These 36 probesets were then used for a supervised clustering of the responding and non-reponding patients. The genes which are identified by the 36 probes sets form a specific aspect of the invention.

Fold change definition

In programs such as Arrayminer, Fold change of gene expression can be calculated. This is shown in Table 1B and is the change in average gene expression between two groups, for example responder vs non-responder. The statistical value attached to the fold change is calculated and is the more significant in genes where the level of expression is less variable between patients in each group, and difference between groups is larger.

Gene expression shown on a heat map

Figure 5 is a heat map (a diagrammatic representation of the expression level of various genes for a given patient), on which can be seen individual expression of genes represented in the Y-Axes by a coloured box and the patients in the X-axes. The expression values of each gene in all samples are normalized to a mean of zero and a standard deviation of 1, and these normalized values are coded into a gradient of colors.

Affymetrix arrays have 11 probe pairs available to interrogate each gene. Ideally, the signal intensity from all of these 11 probes should be equal as they all interrogate the same gene. However, there are enormous differences between individual probes in a probe set. The pattern of the probe signals in a probe set is called a "probe response pattern". The Robust Multi-array Average" (RMA) software uses, model-based algorithms to incorporate information from multiple microarrays to calculate the expression of a gene. After proper correction for background, and quantile normalisation of the probe intensities, the probe response pattern is fitted over multiple arrays an additive model in RMA software. These algorithms use the fitted models to detect abnormally behaving probes, which are subsequently excluded for calculating gene expression. Therefore, gene expression from these model-based algorithms can be expected to provide more reproducible results. RMA use a stochastic model to estimate gene expression which is potentially a better way of estimating gene expression. Algorithms are implemented in RMA software.

Figure 4: The predictive 36 probesets correspond mainly to upregulation of genes related to immune infiltration and activation. These genes include HLA class II, Interleukin-2 receptor gamma, T cell receptor genes (TRBV19, TRAT1, TRGC2), granzyme, and CD69.

Increase in treatment efficacy

As described herein, gene profiling has allowed the identification of a subset of patients likely to respond to recMAGE-A3 treatment. This subset corresponds to ~30% of the patient population. Patients having the gene profile show far higher efficacy levels could be obtained. Indeed, with the early identification of patients susceptible for anti-MAGE-A3 immunization, the efficacy of the treatment will probably increase to levels far higher than other current cancer treatments. This may also lead to a better compliance by the patient. For example, in 100 patients with melanoma, 60 will be found to express MAGE-A3. If these patients all receive recMAGE-A3 injections, 10 out of them will respond; leading to a 15% efficacy rate. However, if gene profile is performed on the 60 MAGE-A3-expressing patients, only the 14 out of them who are predicted to be susceptible to this treatment will receive recMAGE-A3 injections. The other 46 patients

will receive another treatment. 10 out of these 14 patients will respond to the treatment, leading to a 71% efficacy rate.

Gene profile in other tumour types

This gene profiling has also been performed in a NSCLC study. However, as this study is blinded, only preliminary data are available. It is thought that the signature observed in melanoma is also present in NSCLC, stages IB and II. Preliminary data suggests approximately 30% of the patients present a gene profile signature characteristic of immune response and immune cell infiltration and that suggests they will respond to ASCI treatment.

Figure 5 shows and expression profile for 30 individual patients for a number of genes.

Fig 5a shows the expression profiles for 31 patients of two genes.

EXAMPLE 2:

Predicting the clinical outcome of patients using machine learning approaches.

Materials & Methods.

15 Tumor specimens, RNA purification, quality control, labeling and amplification for microarray analysis

Tumor specimens (pre-vaccination) were used from a Mage-3 melanoma clinical trial (MAGE008). These were preserved, RNA prepared, labeled and amplified as in Example 1 above. The quality of the RNA samples was checked prior to hybridization to the genechip. Only data from samples that were deemed to adequately hybridize to the genechip were used in this Example (61 samples in total).

Microarray chips, hybridizations and scanning.

As in the material and methods section of the first example above (referred to herein as Example 1), Affymetrix HG-U133.Plus2.0 genechips were employed, and hybridized and scanned as described therein.

Data processing & normalization.

The fluorescent scanned data image was processed and normalized using a R 2.3.1 [1] implementation of GCRMA algorithm [2, 3].

Unspecific filtering of gene expression matrix

30 Prior to calculation of differential expression gene expression matrix was filtered in an unspecific (i.e. independently of experimental groups) manner. 4 processes were used:

1. panp filtering: calls indicating whether a gene is expressed in a given sample (present call, P) or not (absent call, A) were derived for all array measures using the panp method implemented in the panp R package [4]. Only probe sets showing at least one P call throughout experimental samples were kept for subsequent calculations.
2. SD filtering: standard deviation (SD) of each probe sets were calculated throughout samples, were only kept probe sets having SDs above the 75th percentile of all SDs.

3. IQR filtering: interquartile range (IQR) of each probe sets were calculated throughout samples, were only kept probe sets having IQRs above the 7th quantile of all IQRs.
4. SH filtering: SD of each probe sets were calculated throughout samples, the midpoint of the SD shorth (the shortest interval containing all of the data) as calculated using the shorth function of genefilter package [5] under R 2.3.1, were only kept probes sets having SD above the shorth for subsequent calculations.

Calculation of differential expression.

The differential expression between the groups of patients showing a clinical benefit after vaccination or not (subsequently called Responder (R) or Non-Responder (NR) groups) was calculated in R 2.3.1 program according to 2 statistical procedures:

1. Regular t-test, as implemented in the genefilter package, and
2. A modified (regularized, moderated) t-test, to account for poor estimates of gene-specific variance under standard t-test, such as the method of Jain et al [6], implemented the LPE R package [7], or the method of Smyth [8], implemented in the limma R package [9], or the method of Baldi and Long [10], also known as Cyber-T [11].

Correction for multiple testing by controlling the false discovery rate (FDR) at 5% was done under R 2.3.1 with Benjamini-Hochberg method [12] implemented in the multtest package [13].

Gene profile normalizations

To make the probe sets having low and high levels of expression comparable and to put an emphasis on differential profiles rather than absolute profiles, data was further normalized at the probe set level. Two gene-level normalizations schemes were used:

1. IQR normalization, where each probe set measure is subtracted by its median over samples and divided by its IQR.
2. Z-score normalization, where each probe set measure is subtracted by its mean over samples and divided by its SD.

Machine learning algorithms

The 14 machine learning algorithms (or predictive rules) interfaced in MLInterfaces package [14] running under R 2.3.1 program were used to train clinical outcome predictive models and to predict the Mage008 patient clinical outcomes, under the reporter lists calculated by the unspecific filtering, differential expression, gene normalization processes. These algorithms were, knn (k-nearest neighbour, kNN, function of class package), nnet (neural network), gbm (generalized boost regression), lvq1 (learning vector quantization 1), naiveBayes (naïve bayes classifier), svm (support vector machine), lda (linear discriminant algorithm), rpart (recursive partitioning), stat.diag.da (diagonal discriminant analysis), randomforest (random forest), bagging, ipredknn (k-nearest neighbour function form ipred package, equivalent to knn form class package), slda (stabilized linear discriminant analysis), pamr (partition around medoids, also known as nearest shrunken centroid classifier). Default parameters were used for all algorithms except for kNN rule where even values of k ranging from 1 to 7 were tested.

Leave-one-out (LOO) scheme of MLinterfaces coded in the xval function was used for cross-validation when appropriate, without re-calculation of reporter list at each cross-validation loop. The misclassification rate was calculated by averaging the number of wrongly predicted samples to the total number of samples of each patient group or class (either R or NR).

5 Some of the MLinterfaces interfaced predictive rules (nnet, lda, naiveBayes) were used outside of the MLInterfaces package as direct calling to make the related classifiers usable on external data sets independently of the data used to train the models.

The MiPP algorithm [15, 16], implemented in the MiPP R library and ran under R 2.3.1, was employed to reduce the number of probe sets involved in the reporter lists. The best reporters out
10 of the submitted list were selected as optimizing the 10-fold cross-validation of linear discriminant analysis predictions of a training set and further reduced to reporters giving an optimized global misclassification error of linear discriminant analysis predictions of a testing set. Global misclassification error or rate was calculated as the ratio of the total number of misclassified patients to the total of set patients.

15 **Results**

Patient sample stratification for training and testing section definitions.

A 31 sample subpart of the full 61 sample data set was used to train and test the classifying model in a first attempt; the remaining 30 samples were kept for subsequent model evaluations. Several training and testing sections were defined from the 31 sample data set subpart. The
20 training sections were used to calculate the reporter list (i.e. the differentially expressed genes to be used in clinical outcome prediction of patient samples) and to set the machine learning algorithm weights for clinical outcome prediction. The testing sections allowed evaluation of the model performance independently of the patients used to construct the predictive model. Model evaluations were also undertaken on the training sections according to a cross-validation
25 procedure.

Training and testing sections from the 31 sample data set subpart were defined as follows:

1. A first training section containing 5 Responders and 5 Non-Responders, leaving 21 patients for the testing section;
2. A second training section of 10 Responders and 11 Non-Responders, leaving 10 patients for
30 the testing section;
3. A last training section containing all 31 patients (13 Responders and 18 Non-Responders). In this last stratification there is no patient left for a testing section, classifying model would only be evaluated by a cross-validation procedure.

35 **Identification of the differential expression calculation process performing best for classification.**

Gene expression data was pre-processed and normalized according to Material & Methods taking into account the full data set. Differential expressions (DE) between the Responder and Non-Responder groups were calculated for each training / testing section according to various

processes.

The DE calculation framework was constructed as follows:

1. Unspecific filtering of gene expression matrix: panp filtering, or not, followed by either SD, IQR or SH filtering, or none.
- 5 2. Calculation of DE : either t-test or a modified (regularized, moderated) t-test, such as the method of Jain *et al*, implemented the LPE R package, or the method of Smyth, implemented in the limma R package, or the method of Baldi and Long (Cyber-T), followed by multiple testing correction, or not.
3. Gene profile normalizations: Either IQR or Z-score normalizations, or none.
- 10 The processes minimizing the overall misclassification rates in both training and testing sections in at least two out of the three available training / testing stratifications were selected. The misclassification rate was obtained by comparing the predicted clinical outcome given by a kNN predictive rule to the given clinical outcome.

Seven DE processes were found as minimizing the overall misclassification rate according to the kNN rule:

- t-test without correction for multiple testing and irrespective of panp filtering;
- SH filter, t-test without correction for multiple testing and irrespective of panp filtering;
- SD filter, t-test without correction for multiple testing;
- SD filter, t-test without correction for multiple testing, Z-score normalization;
- 20 – IQR filter, t-test without correction for multiple testing, IQR normalization.

The minimized overall misclassification rates for these processes were as follows:

- 0% in the 5 Responders to 5 Non-Responders stratification, as evaluated by leave-one-out cross-validation, all patients were therefore correctly classified.
- 20% in the 21 patients testing section, given by the direct prediction of these patients from the model defined from the 5 Responders to 5 Non-Responders training set. 80% of patients were correctly predicted.
- 25 – 12% for the 13 Responders to 18 Non-Responders segregation, as assessed by cross-validation, being 88% of patient correctly predicted.

The performances for the other training/testing stratification was not found to be informative (i.e. no DE process converging to a minimized misclassification rate), hence not mentioned.

The last process, IQR filter, t-test without correction for multiple testing, IQR normalization, was preferred since the minimized misclassification rates were obtained with a higher value of k (k=5) than other six processes (k=3). It was anticipated that working with higher values of k would facilitate the transposition of the predictive model in further settings, since high k values generate simpler models supposed to be less biased towards a training set.

This process generated a reporter list of 489 Affymetrix probe sets. The reporter list is given in Table 4A, as Affymetrix probe set identifications along with gene names and symbols.

External validation: independent evaluation of the best clinical outcome predicting model.

The best DE calculation and gene expression treatment process (IQR filter, t-test without correction for multiple testing, IQR normalization) was used to build a kNN predictive model (k=5) from 13 Responders/18 Non-responders training section.

The clinical outcome of the independent patients that were previously left away was then directly predicted from this model. Of these 30 independent patients only 15 were informative (i.e. having a characterized clinical outcome). Misclassification rate was calculated on the basis on these 15 informative patients for the model evaluation.

According to this predictive model, misclassification rate was 34%, hence 66% of independent patients had their clinical outcome correctly predicted.

Improvement of clinical outcome predicting model through other classification rules.

On the basis of the best DE (and expression normalization) process as selected with a kNN rule, further classification (predictive) rules were tried to eventually increase the predictive model performance. Beside kNN, 13 other rules were assessed. For each selected DE process that performed for the kNN rule, each further rule was trained on the 13 Responders/18 Non-responders section of the data set, its predictive performance evaluated on the training set by cross-validation and on the independent set of 30 patient samples by direct prediction.

Further classification rules did not improve the misclassification rate, as assessed by cross-validation on the training set, the lowest remaining unchanged at 12% of samples miss-predicted (88% of patient assigned to their correct clinical outcome).

However, for the above mentioned preferred DE process, the neural network rule did improve the misclassification rate on the independent set of 15 informative patients out of the 30 available, by reducing it from 34%, as given by KNN rule, to 30% (i.e. one additional patient correctly predicted), while keeping it the lowest on the cross-validation evaluation of the training set.

Neural network rule then allows the correct prediction of 70% of patient independently of those used to train the model.

Furthermore, in a further evaluation of the predictive modeling performance, when clinical outcomes were available for all 30 external patient samples, i.e. when all the independent patients were informative for misclassification rate calculation, the lowest misclassification error became 26%, which is 74% of patients were correctly classified. This best performance obtained on a wider data set in terms of informative sample number was given by a lda rule. A naiveBayes rule was also able to give a 28% misclassification rate, correctly prediction the clinical outcome of 72% of patients. However, the misclassification rate using kNN and nnet rules became 35% and 41%, respectively. This performance is based on the use of the gene list and probes of Table 4A.

Implementation of the preferred classifiers, predicting the clinical outcome of further patient biopsies.

To make use on further metastatic melanoma samples of the exemplified neural network classifier, yielding 30% of misclassification on the 15 informative sample external set, the following R code can be used in a R session (a stastical programme):

```
library(nnet)
set.seed(1234)
predict(nn, data, type="class")
where
```

- 5 – data is a data frame containing the 489 reporter (Table 4A) expression data of the samples to classify (GCRMA sample normalized and IQR gene normalized). Samples are organized in columns and reporters in rows;

– nn is the R object of class nnet shown in **Appendix A**.

- the lda (linear discriminant analysis) classifier would be reproduced by programming the
10 following R code chunk :

```
library(MASS)
predict(lda, data, type="class")
where
```

- data is as previously;
- 15 – lda is the R object of class lda shown in **Appendix B**.

The naïve Bayes classifier works under the following R coding:

```
library(e1071)
predict(nb, data, type="class")
where
```

- 20 – data is as previously;
- nb is the R object of class naiveBayes shown in **Appendix C**.

Down-sizing the 489 probe set reporter list while maintaining an identical classification performance.

- 25 The MiPP algorithm was used to determine if it was possible to reduce the number of reporters involved in the IQR filter, t-test without correction for multiple testing, IQR normalization, based predictive model while keeping the same misclassification rate. Indeed, working under a shorter reporter list would be more convenient for classifier follow-up purposes for instance such as transposition from a microarray based format to a quantitative RT-PCR format.

- 30 The 489 probe set microarray data was submitted to the MiPP process: 11 classifying probe sets were selected on the 13 R / 18 NR training section as being sufficient to achieve a lowest global misclassification error, and 4 probe sets out of these were further identified as minimal on the 30 informative external sample data set to obtain the lowest global misclassification rate for the independent patients.

- 35 The 4 probe set reporter list was then used in leave-one-out cross-validation predictions of the 13 R / 18 NR stratification of data as training set and direct prediction the 30 informative patient section as external testing set under all 14 predictive rules. LOO performance was increased for most of the rules (being as high as 3% of misclassification rate for lda and naiveBayes among other), while misclassification rate stayed 28% on the external data set under svm and gbm rules.

The following table depicts the identity of the genes involved in the 4 probe set model :

Probe	Gene	Gene
Set ID	Symbol	Name
207651_at	GPR171	G protein-coupled receptor 171
5 205392_s_at	CCL14	chemokine (C-C motif) ligand 14
212233_at	MAP1B	microtubule-associated protein 1B
206204_at	GRB14	growth factor receptor-bound protein 14.

EXAMPLE 3:

10 Predicting the clinical outcome of patients using Quantitative Polymerase Chain Reaction (Q-PCR)

Material & Methods

Tumor specimens and RNA purification.

30 tumor specimens (pre-vaccination) were used from MAGE-A3 melanoma clinical trial (MAGE008). These were preserved and RNA extracted as in Example 1 above.

cDNA synthesis and quantitative PCR amplification

2 µg of total RNA were retro-transcribed into cDNA using M-MLV reverse transcriptase (Invitrogen) and oligo(dT) or random primers.

The different interesting genes were amplified by quantitative PCR using TaqMan chemistry and 7900 sequence detection system (Applied Biosystems).

Genes were amplified using standard 96 well plates or the TaqMan® Immune Profiling Array (TaqMan Low density arrays - TLDA - Applied Biosystems). TLDA are ready to use 384 well plates pre-coated with primers and probes.

The 7900 apparatus is a fully integrated system for real-time detection of PCR including a 96-well or a TLDA thermal cycler, a laser to induce fluorescence, a charge-coupled device detector, a computer and a real-time sequence detection software.

In standard 96 well plates, cDNA corresponding to 50 ng of total RNA was amplified by polymerase-chain-reaction using the TF,TAQMAN,PCR REAGENT CORE KIT (Applied Biosystems). Primers and probes are listed in **Table 5**.

30 For the TaqMan® Immune Profiling Array, cDNA corresponding to only 1 ng of RNA was amplified by polymerase-chain-reaction using the TF,TAQMAN,PCR CORE REAGENT KIT (Applied Biosystems). The genes included in the array are listed in **Table 6**.

Data processing and normalization

35 All PCR data were normalized against H3F3A (standard 96 Well plates) or the geometric mean of GUSB and PGK1 (TLDA) house keeping genes (also referred to as constant genes).

Expression values were afterwards log transformed.

Univariate statistical analysis

Analyses of variance (ANOVA1) were performed using the SAS software to significantly select

the genes able to differentiate responder from non-responder groups. The first group was composed of 14 responder patients, the second one was composed of 15 non-responder patients. Each gene was analyzed independently from the others.

IL7R, CD3D, CD52, UBD, GPR171, GMZK, PRKCQ, STAT4, TRDV2, TRAT1, TRBV19, CD69, INDO1, CD45R, CD45RO, FoxP3, CD20, CCL5, FASLG, GNLY, GZMB, PRF1, IFNG, ICOS, TBX21, CD8A, CD3E, CXCL10, CXCL11, IRF1, TLR7 and CXCR3 genes were selected for their capacity to differentiate both groups. The p-value was <0.0001 for every gene. For every gene, a significant difference was proven between mean (responder/non-responder). The Geomean ratios between both groups were also calculated for all genes (Table 7A) and range from 3.4 to 21.2.

Correlation analysis

A correlation matrix (Table 8) was calculated between 30 genes showing that all these genes are pretty well correlated.

Logistic regression model

An analysis by logistic regression was performed using Proc logistic (SAS Software). Logistic regression analysis is often used to investigate the relationship between binary responses and a set of explanatory variables.

The number of predictors is too large and the use of all possible regression is not feasible. So, stepwise selection was employed. This procedure gives a model with a good value (high) for a specified criterion: Score Chi-square. This is analogous to the use of SSE or R^2 in multiple linear regression.

The model information are:

Data: 29 patients and 111 genes.

Response variable: clinical status

Number of response level: 2 (responder – non responder)

Mode: binary logit

Optimization technique: Fisher's scoring

The model giving the best value of score Chi-square (Chi-square = 16 and pvalue <0.0001) is :

Logit (p) = $7.69 + 5.07 \log(\text{PRF1})$, with p the probability to be responder

Coefficient B0 (7.69) & B1 (5.07) are significant ($p < 0.005$)

Other criterion can be used to test goodness of fit

Likelihood Ratio	:	23.1429 (chi-square) and	<0.001 (p-value)
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Wald	:	6.9250 (chi-square) and	<0.001 (p-value)
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Like in linear regression, a R^2 is computed: 0.55.

From the 111 genes, 18 (with only one predictor) are listed in the Table 9. Higher the $R^2(\%)$ and chi-square score are the better the model/gene.

Using the PRF1 model, it is possible to classify correctly 86.6 % of patients.

Table 10 gives the percentage of correct classification calculated using the logistic regression model for some other genes.

Combining more than 1 gene didn't improve the classification performance.

Genex analysis

- 5 The 30 patients were also classified using the PCA (Principal Component Analysis) and neural network analysis from Genex software with the genes PRF1, GZMB, GNLY, CD8A, PRKCQ, FOXP3, IFNG, CCL5, GPR171 and TRBV19.
- For the neural network analysis, 5 responder patients (Patient ID No.s 27, 53, 65, 119, 127) and 5 non responder patients (Patient ID No.s 8, 60, 66, 81, 160) were used as training set. The
- 10 remaining 20 patients were used as testing set.
- Figure 6 shows the Principal Component Analysis using PRF1, GZMB, GNLY, CD8A, PRKCQ, FOXP3, IFNG, CCL5, GPR171 and TRBV19 genes.
- It can be seen the responders are clustered on the left-hand side of Figure 6 and the non-responders are clustered on the right-hand side of the figure. Patients labeled 85, 3 and 154 are
- 15 miss-classified. Therefore, the percentage of "correct" classification is 85% using the PCA. The neural network approach confirms a correct classification range of 85%.
- Comparison: Microarray to Q-PCR data.
- 17 genes (Table 12) evaluated by the Q-PCR technology were already present in the microarray gene lists. These genes are therefore able to discriminate responder from non responder patients
- 20 whatever the technology used to detect them. These genes form a specific aspect of the invention.

Table 12 Genes present in microarray and Q-PCR list.

Gene symbol	Gene title
CCL5	chemokine (C-C motif) ligand 5
TRAT1	T cell receptor associated transmembrane adaptor 1
STAT4	signal transducer and activator of transcription 4
PRKCQ	protein kinase C, theta
GPR171	G protein-coupled receptor 171
UBD	ubiquitin D
CD52	CD52 molecule
CD3D	CD3d molecule, delta (CD3-TCR complex)
PRF1	perforin 1 (pore forming protein)
CD8A	CD8a molecule
CXCL10	chemokine (C-X-C motif) ligand 10
CD69	CD69 molecule
TRBV19	T cell receptor beta variable 19
TRDV2	T cell receptor delta variable 2
IL7R	interleukin 7 receptor

GZMK	granzyme K
	PROTEIN-TYROSINE PHOSPHATASE, RECEPTOR-TYPE, C
CD45R	(PTPRC)

Fourteen genes (Table 13) were able to discriminate responder from non-responder patients using Q-PCR technology were not present in the microarray gene lists. This may be due to the increased sensitivity of the Q-PCR technology compared to the microarray.

5 **Table 13. Gene used to classify patients using Q-PCR technology, absent in Microarray gene lists.**

Gene symbol	Gene title
FASLG	Fas ligand (TNF superfamily, member 6)
GNLY	granulysin
	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine
GZMB	esterase 1)
IFNG	interferon, gamma
ICOS	inducible T-cell co-stimulator
TBX21	T-box 21
CD3E	CD3e molecule, epsilon (CD3-TCR complex)
CXCL11	chemokine (C-X-C motif) ligand 11
CXCR3	chemokine (C-X-C motif) receptor 3
CD20	CD20 molecule
FOXP3	forkhead box P3
INDO	indoleamine-pyrrole 2,3 dioxygenase
IRF1	interferon regulatory factor 1
TLR7	toll-like receptor 7

Some genes absent in the microarray signature but are known to be expressed by immunological cells and thus are also able to predict the clinical outcome of the patients.

10 The presence of an immune infiltration into the tumoral tissue seems to be the most important biological event to predict the clinical outcome of the patients rather than only a limited list of genes.

For example, PRF1 and CD8A are present in the microarray gene lists and are expressed by CD8 T lymphocytes. CD8 T lymphocytes express also IFNG that is absent in the microarray gene lists. Nevertheless, a good prediction of the clinical response was achieved using this gene by Q-PCR.

15 The number of miss-classified patients using the q-PCR data remains in the same range than clustering and KNN approaches using microarray data. Therefore different technologies and

softwares can be used to classify the patients.

Example 4:

Predicting the clinical outcome of patients using hierarchical clustering approach.

5 Material & Methods

Tumor specimens and RNA purification.

67 tumor specimens (pre-vaccination) were used from MAGE-A3 melanoma clinical trial (MAGE008). These were preserved, RNA prepared, quality controlled, labeled and amplified as in Example 1 above. The quality of the RNA samples was checked prior to hybridization to the
10 genechip.

Microarray chips, hybridizations and scanning

As in the material and methods section of the first example above (referred to herein as Example 1), Affymetrix HG-U133.Plus2.0 genechips were employed, and hybridized and scanned as described in Example 1.

15 Data processing & normalization.

The fluorescent scanned data image was processed and normalized using a R 2.3.1 implementation of GCRMA algorithm as described in Example 2.

Selection of the gene list

41 Probe Sets were selected to discriminate responder from non responder patients using
20 Arrayminer software described in Example 1.

Analysis parameters were:

- Train and test evaluation
- Pre-definition of 2 class
 - a. Responder class : PID2, PID65, PID75, PID20, PID10, PID19, PID23, PID26,
25 PID27, PID38, PID67
 - b. Non Responder class : PID14, PID52, PID66, PID37, PID16, PID13, PID55,
PID56, PID5, PID60, PID8

wherein PID stands for patient identification No (ie the numerical label given to the patient)

- 30 • Maximum number of markers per class: 25
- Number of markers per couple: 1
- Allow multi-class markers : Yes
- Use KNN classification: No – Proprietary voting method was used.

A list of 50 probe sets was obtained. 9 Probe sets were removed due the Absence status in all
35 samples. The intensities of the 41 probe sets for the 22 patients listed above are listed in Tables 11A and 11B.

Prediction of the clinical status

The clinical status of the 67 patients was predicted using the hierarchical clustering approach of

Spotfire software.

Data were normalized regarding the genes using a Z-score calculation available in Spotfire before performing the Hierarchical clustering.

Calculation options of the hierarchical clustering were:

- 5 • Clustering method: complete linkage
- Similarity measure: Euclidean distance
- Ordering function: average value

This clustering was performed for patients included into the AS15 (Figure 7 and 8) or the AS02B (Figure 9 and 10) arms.

10 Using the hierarchical clustering approach, about 58% of patients have the responder signature whatever the adjuvant group.

100% and 87.5% of patients with a clinical benefit are well clustered respectively in AS15 and in AS02b groups.

71% and 52% of patients with a progressive disease are well clustered respectively in AS15 and
15 in AS02b groups.

In the clinical benefit cluster, 28% and 55% of patients have a progressive disease respectively in AS15 and in AS02b groups. The percentage of patients with a responder gene profile according to the invention who achieved a clinical benefit to the MAGE-A3 vaccination when the AS15 adjuvant was used was larger than the percentage who achieved a clinical benefit to the MAGE-
20 A3 vaccination when AS02b adjuvant was employed in the formulation.

Example 5

Inducing a responder's profile.

Initial biopsy (sampled before irradiation) of patient 59 did not have the responder signature
25 while his second biopsy (sampled after irradiation) had the responder signature (data not shown) suggesting that irradiation of lesions may induce the responder signature.

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Table 1A Gene sequences for and Seq ID No.s for the genes of Table 1

Seq ID No.	Gene name	Full gene sequence
1	chromosome 6 open reading frame 190	>gi 58218985 ref NM_001010923.1 Homo sapiens chromosome 6 open reading frame 190 (C6orf190), mRNA ATACTTACAATTACGAGATTATATATTGTCATTAGTCCTTTGGCTGGGTAGGGTGAGAGGCTCTTC CTGGATCCCTTATTTCTACAGGAGAGGAGGAAACACCTGGGATGCTCCAGTGCTCTTACGCAGATAAT GATCATTAACATCAGCCTCTCTGATCAAAAGAGCTACTCCACCCCACTCTGGCTGTAGTGTGACATTCCCTG CCTGCCGTGAGGAAGAAATGGTGAGCAGGGCTGCAATTGCAGACAAGTGTCAACCAGAAAGCCACAAGTTT CTGTGAGCACCAAGTCTACAAACTACCCAAGGCATAGCAATGGCATTATCACTGGAAGAATTCGTCCACT CCCTTGACCTCAGGACCTACCCAGGGTTCTAGAAATCCAGGCAGGCATCTATCTTGAAGGCTCTATTTA TGAAATGTTTGGAAATGAATGCTGTTTTTCAACAGGAGAAAGTGATTAATAATTACTGGTCTCAAAAGTTAAG AAGATCATAGCTGAAATTTGTGAGCAGATTGAAGGTTGTGAGTCTCTACAGCCATTTGAACTGCCCTATGA ATTTCCAGGCTTTTTTAAGATTGTGGCTGATAAAACTCCATACCTTACTATGGAAGAAATCACAAAGGAC CATTCATATTGGACCAAGTAGACTAGGGCATCCTTGCTTCTATCATCAGAAGGATATAAACTAGAGAAC CTCATATAAAGCAGGTGAGCAAAATCATGCTCAACTCAGTTGAAGAGATTGATGGAGAAAATAATGGTGA GCTGTGCAGTAGCAAGGAATCATCAAACTCACTCATTTAAATTTGCCTTTGTCAACAAGAAGGAGAAATTTCTA CGAGTGTGAAGATGAACGTAATTTACACTCTAAAGGAGATTGTTGAATGGAAGATTCTTAAGAACAGAAACA AGAACTGTAAACCTTACAGATTTTTCAAAATAAGTGGGACTCAACGAATCCATTTCCTAAAGACTTTTATG GTACCCCTGATTCTCAAGCCTGTTTATGAAATTCAAGGTGTGATGAAATTTCGAAAAGATATAATCCGCAT CCTCCCCAGTCTAGATGTCGAAGTCAAAGACATCACTGATTCTTACGATGCTAACTGGTTTCTTCAGCTG TTATCAACAGAAAGATCTTTTGAATGACTAGTAAAGAGTTCCCCATAGTGAAGTCAAGTCAAGAGCAC CTGAAGGAAACCACTGCCCCCAAAGCAATTTTACAGCCTGGGAAACCAATTTGTGATCCACAAAAGTACCA GGCATCAAGAATCTTAGCTTCAGAAATTAGAAGCAATTTTCCTAAAGACACTTCTTGATCCCCACTAGC TATAAAGGCAAGTTCAGCGCGGACCGAGGAGTTCCCAACGGCCTATGACCTAGAGATCGCTAAGAGTG AAAAGGAGCCCTCTTCAAGTGGTGCCCAACCAAGCGTTTCAATCCCCCTCATGACAAGCTGTCTATCCGTATC TGTGCGGACCAAGTTTCTGGTGTCATCAGTCAGAGACGACTGAAGTCCCTCTGTGAGGGAATAAAAAAGTG GTGAATGTTCTGGCCTGTGAAAAAATCCTCAAAAAGTCCCTATGAGGCTGCGTCCCTTTGTACATGG AAGGAGGTTTGTAGAGGTGATTCTATGATAAGAAAACAGTACCAGATTCTGAGCTCTGTAACAGTTCCG TTTGGCCCTTCAATGTGAAGGTGTCTGTCAAGGGATCTTTCCATTGAAGAGGACGTGTTGGCTGCCACACCA GGACTGCAGTTGGAGGAGGACATTACAGACTCTTACCTACTCATAGTGAATTTTGCCCAACCCACGGAGT GCTGGGAAATTCCCTGTGGGCCGCTTGAATATGACTGTTTCAAGTTAGTTAGTAATTTCTCTAGGGATGCAGA

		ACCATTTCTAGTCAGGACTCTGGTAGAAGAGATCACTGAAGAGCAATATTACATGATGCGGAGATATGAA AGCTCAGCCTCACATCCCCACCTCGCCCTCCGAAACACCCCTCAGTAGAGGAAACAAAGTTAACCTGC TAACCTTAGCAGAAAGGACGGTAGACCTGCCCAAGTCTCCCAAGCTCATCAGTAGACATAACCAA GAAACTTCACCCAAATCAAGCTGGCTGGATTCAAAAAGTACTGATTGGTAGTCAGAATGATTTGGTGGAT GAAGAGAAAGAAAGGAGCAACCGTGGGGCCACAGCAATAGCAGAAACATTCAAAAATGAAAAACATCAAA AATAACAAGATGTGACAGAAAGCCACTTAGCGAGCAACATAAATGTTGCAGTGAAAAAAGAGCTAGCCT TCTAGCTGAAAAACGAGTATTCGCCAATGGACTCCAGAAAGAACTTGATTCACTGCTGCAAGAAAGAA CAACCTTAAAACCTTTTAAACAGATAAAACTTAACAGAAACCTATGATATAGAAATTCATATAGTCTATCTGT TGTGCTAAATCTGTAGGCATTGTGTGTTCTTTAGGACGTAATTTAATTTAACTTGCACATTTTTTCA GATTCCTTATTTCTACTACCAACAACATAAGTAATTTGGAAATAATTCGTATTTTCAGTTTCTGAGTAAAC CAGTCTGAAATAGGATAAAAGCCACCAATAATTTCTTTTTCAGAAATTTGTTTTGCCATTTTTTAG TGCTATCATCATTCCTAAACAAGACTAACTTAACAGAAAAATAATTATATCTGACTGATTTAAAAATGTTTCA GTTTCTTATCCAAATCCCTTTGGAACATAAGAAAGGAGTTTGATTTTCACATTCACAGTGTATTTACAAAAT ACGCTGTGTCATAAATATGTTTGAAATTCCAAACAGCCAAAGCCATTGAGAGTCAATAGGAGTTTTCATAAC CTTCTCTCTATGACCCAAACAAGCTCATGACTGAAATTTCAACAGATTTCTGAGACGATGCTCTAAT ATTCTATGTGCTATGTACCAGATAAATCTTTTAGATGAATGTTTCTTAGGATTGTAGGAAAAATTATCTAGT TAATCATAAATATTGATGGAAGAAAAAGACAAATAAATTTGTAATAATAAATTTGGCTGACAAAGAAAC CAAAGTGATTTCTTAAATTAGTATAACATCAGAAATGATGCTCTTATAGTTGTACCATCTATAAAAAATTACTTT AAGGCTCTCACATTTTAAATAATTTATCTTATGATTAAGTATACAGGAACAATAATTATTTTTCCTT TAACAAAATGAAGAGACAGGCTATCTGGTTAATGTACATAGGAAATTTAATAGTAATGCTTGAACCTTCAT CCATAGATCATCTCTGTACAAAATTTGTTAGCTAACATCCTATCTCATAATTTATTTATGTTTGTGGA GAAATTTGTTGATTTTGTACCAAAGTGTTTCTGAAGACAAATAAATTTGTGAGTCAACTTTAGAAACAAAAA AATTAGAGTTTTCATGTTTATATCTGATTAAGCTTACTTTACCTTACATTTTCTAAGTAACAAT GAATCCTGATTTCTAGTGTCCTAAAAATTGCTTAGTGATTTGATTTGTTGCTGTTGTCAGATAAGAAACAGAAAC ATGTCCTAAAGTTTATGGGACAGTTTTCCTTTTATTTTATTTTGCCTGTTTGTGAGATAAGAAACAGAAAC TTTTCTAAGACCCACATTTGTTTATTTGAAGGCCACAGCGAATCTTAACCTAACAGCCTTGACAAACTGCA CCATAGGTGTTTTTAGACTCATATAAATTTGTTTATTTTCAAAACAATAGTGAATAAATAATTTTGTGTTT GGAATTTGAGAAACAATAAATTTGTACTTTTAGTAACCTACCATTTCTTTGATTAGAAAAATTAAGAGATGC ATATCTTACTTTGGTTGTAAATTTATCAAGGGCTTTCTAATAGAAATCATATATAACATTTCTAAATATAA GTCCCTTTCACATACTGTGTTTCCAGTTGCTTGATATTGAAAAAGTGAATAAACTTCATGCTCACCTATT GGAGATTGGGAAGGTTGAAAAATAAACTTCCTAATTTTAAAAAAAAA
2	hematopoietic cell-	>gi 37059786 ref NM_005335.3 Homo sapiens hematopoietic cell-specific Lyn substrate 1 (HCLS1), mRNA

	specific Lyn substrate 1	GTGGACGCGAGAGCCGGGCGCTTAGAACAGAGGCTTGACAGGTGGAGATGTGGAAGTCTGTAGTGGC CATGATGTGTCTGTTTCCGTGGAGACCCAGGGTGATGATTTGGGACACAGATCCTGACTTTTGTGAATGACA TCTCTGAATAAGGAGCAACGATGGGAGCCAAAGACCATCGAGGGTCTGGACGCACAGAACACATCAACAT CCACCAGCTGAGGAACAAAGTATCAGAGGAGCATGATGTTCTCAGGAAGAAAGAGATGGAGTCAGGGCCC AAAGCATCCCATGGCTATGGAGGTCGGTTTGGAGTAGAAAGAGACCGAATGGACAAGAGTGCAGTGGGCC ATGAGTATGTTGCCGAGGTGAGAAAGCACTCTTCTCAGACGGATGCTGCCAAAGGCTTTGGGGCAAGTA CGGAGTTGAGAGGGACAGGGCAGACAAAGTCAGCAGTCGGCTTTGATTATAAAGGAGAAAGTGGAGAACAT ACATCTCAGAAAGATTACTCTCGTGGCTTTGGTGGCCGGTACGGGTGGAGAGGATAAATGGGACAAAG CAGCTCTGGGATATGACTACAAGGGAGAGACGGAGAAACACGAGTCCCAGAGAGATTATGCCAAGGCTTT TGGTGGCCAGTATGGAATCCAGAGGACCGAGTGGATAAGAGCGCTGTCCGGCTTCAATGAAATGGAGGCC CCGACCACAGCTTATAAGAAAGACGACGCCCATAGAACCCGCTTCTAGTGTGCCCTGCTGGCTGAAGCGGA AATTGAGTCCATGGCTGAGGAGAAAGAGAAAGCGAGAGGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAG GCAACAGAGCGAAAGGCTGTGACAAAGAGGAGCCCTGAGGCTCCACAGCCAGTGATAGCTATGGAAAGAG CCAGCAGTACCGGCCCACTGCCCAAGAAAATCTCTCAGAGGCTGCGCTCCAGTTGGGACTCCTCCAT CATCAGAGTCTGAGCCTGTGAGAACACAGAGGGAACACCCAGTGCCTTGTGCCCATTAGGCAGACTCT CCGGAGGACAAATGAGGAGCCCCAGCTCTGCCCTTAGGACTCTGGAAGGCTCCAGGTGGAGGAAGAG CCAGTGTACGAAGCAGAGCCTGAGCCTGAGCCCGAGCCTGAGCCCGAGCCTGAGATGACTATGAGGACG TTGAGGAGATGGACAGGCATGAGCAGGAGGATGAACAGAGGGGACTATGAGGAGGTGCTCGAGCCTGA AGATTCTTCTTTTCTGCTCTGGCTGGATCATCAGGCTGCCCGGCTGGGCTGGGCTGGGCTGTG GCTCTGGGGATCTCAGCTGTGGCTCTATATGATTACCAAGGAGAGGGAAGTATGAGCTTTCTTTTGATC CGGACGACGTAATCACTGACATGAGATGGTGGACGAGGCTGGTGGCGGGACGTTGCCATGGCCACTT TGGACTCTTCCCTGCAAAATTATGTCAAGCTTCTGGAGTGACTAGAGCTCACTGTCTACTGCAACTGTGAT TTCCCATGTCCAAAGTGGCTCTGCCCTCCACCCCTCCCTATTCTGTATGCAAAATGCTAAACCAGATGAGT TTCTGGACAGACTTCCCTCTCCTGCTTCATTAAAGGCTTGGGCGAGAGACAGCATGGGGAAGGAGTCCC CTTCCCCAAGAGTCTCTCTATCTGGATGAGCTCATGAACATTTCTCTTGTGTTCTGACTCCTTCCCA ATGAACACCTCTCTGCCACCCCAAGCTCTGCTCTCTCTCTGTGAGCTCTGGGCTTCCAGTTTGTTTA CCCGGGAAGTACGTCTAGATTGTGTGGTTTGGCTCATTTGTGCTATTTGCCCCACTTTCCCTTCCCTGAAGA AATATCTGTGAACCTTCTTTCTGTTCACTCCATAAATTCGAAATAAAGTGAGACTATGTTTCACTGTAA AAAAA >gi 4557881 ref NM_000206.1 Homo sapiens interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG), mRNA GAAGAGCAAGCGCCATGTTGAAGCCATCATACCATTCACATCCCTCTTATTCTGCAGCTGCCCTGCT GGGAGTGGGCTGAACACGACAAATTCTGACGCCCAATGGGAATGAAGACACACAGCTGATTTCTTCCTG ACCACTATGCCCACTGACTCCCTCAGTGTCTTCCACTCTGCCCTCCAGAGGTTTCAGTGTTTTGTGTTCA
3	interleukin 2 receptor, gamma (severe combined immunodeficiency)	

		ATGTCGAGTACATGAATTGCACTTGGAACAGCAGCTCTGAGCCCCAGCCTACCAACCTCACTCTGCATTATTGGTACAAGAACTCGGATAATGATAAAGTCCAGAAGTGCAGCCACTATCTATTCTCTGAAGAAATCACTTCTGGCTGTAGTTGCAAAAAGAGAGATCCACCTCTACCAAAACATTTGTGTTCAAGCTCCAGGACCCACGGAAACCCAGGAGACAGGCCACACAGATGCTAAAACCTGCAGAACTCTGTGATCCCTGGGCTCCAGAGAACCTAACACTTCACAAACTGAGTGAATCCAGCTAGAACTGAACTGGAAACAACAGATTCTTGAAACCACTGTTGGAGCACTTGGTGCAGTACCGGACTGACTGGGACCAAGCTGGACTGAACAATCAGTGGATTATAGACATAAGTTCTCCTTGCCTAGTGTGGATGGGCAGAAACGCTACACGTTTCGTGTTTCGGAGCCGCTTTAACCCACTCTGTGGAAGTGCTCAGCAATTGGAGTGAATGGAGCCACCAATCCACTGGGGAGCAATACTTCAAAAAGAAATCCTTTCTGTTTGCATTGGAAGCCGTGGTTATCTCTGTGGCTCCATGGGATTGATTATCAGCCTTCTCTGTGTGTTTCTGGCTGGAACGGACGATGCCCGAATTCACACCTGAAGAACCTAGAGGATCTTGTTACTGAATACCAACGGGAACTTTTCGGCCTGGAGTGGTGTCTAAGGGACTGGCTGAGAGTCTGCAGCCAGACTACAGTGAACGACTCTGCCCTCGTCAGTGAATTCGCCCAAAAGAGGGGCCCTTGGGGAGGGGCTGGGGCCTCCCCATGCAACCAAGCATAGCCCCCTACTGGGCCCCCCCATGTTACACCTAAAGCCTGAAACCTGAACCCCAATCCTCTGACAGAGAAGAACCCAGGGTCTCTGTAGCCCTAAGTGGTACTAACTTTCCTTCATTCAACCCACCTGCGTCTCATACTACCTCACCCCACTGTGGCTGATTTTGTGCCCCCATGTAAGCACCCCTTCATTTGGCATTTCCCACTTGAGAAATTACCCCTTTTGCCCCGAACATGTTTCTCTCCCTCAGTCTGGCCCTTCCCTTTTCGCAGGATTTCTTCCCTCCCTCCCTCTCTTCCCTCTTCCATCTACCCTCCGATTGTTCTGAAACCGATGAGAAATAAAGTTTCTGTGTGATAATCATC
4	CD52 antigen (CAMPATH-1 antigen) /// CD52 antigen (CAMPATH-1 antigen)	>gi 68342029 ref NM_001803.2 Homo sapiens CD52 molecule (CD52), mRNA CTCCTGGTTCAAAAGCAGCTAAACCAAAAGAGCCTCCAGACAGCCCTGAGATCACTAAAGCTGCTACCAAGACAGCCACGAAGATCCTACCAAAATGAAGCGCTTCCTCTTCTCTCTACTCACCATCAGCCTCCTGGTTATGGTACAGATACAAACTGGACTCTCAGGACAAACGACACCAAGCAGCAGCCCTCAGCATCCAGCAACATAAGCGGAGGCATTTTCTTCTTCGTGGCCAATGCCATAATCCACCTCTTCTGCTTCAGTTGAGGTGACACGTCTCAGCCTTAGCCCTGTGCCCTGAAACAGCTGCCACCATCACTCGCAAGAGAATCCCCCTCCATCTTTGGGAGGGTTGATGCCAGACATCACCAAGTTGTAGAAGTTGACAGGCAGTGCCATGGGGCAACAGCCAAATAGGGGGGTAATGATGTAGGGGCCAAGCAGTGCCAGCTGGGGTCAATAAAGTTACCCCTTGTTACTTGCAAAAAAATAAAAAA
5	CD2 antigen (p50), sheep red blood cell receptor ///	>gi 31542293 ref NM_001767.2 Homo sapiens CD2 molecule (CD2), mRNA ACCAACCCCTAAGATGAGCTTTCATGTAAATTTGTAGCCAGCTTCCTTCTGATTTTCAATGTTCTTCCAAAGTGTCAGTCTCCAAAGAGATTACGAATGCCCTTGGAAACCTGGGGTGCTTGGGTGAGGACATCAACTTGGACATTCCCTAGTTTTCAAATGAGTGATGATATTGACGATATAAATGGGAAAAAACTTCAGACAAGAA

109

7	signal transducer and activator of transcription 4	ATTAAGTGACATGATTTTACTAATGTATTACTGAGACTAGTAAATAAATTTTAAAGCCAA >gi 21618332 ref NM_003151.2 Homo sapiens signal transducer and activator of transcription 4 (STAT4), mRNA AGAGGACGCCCGGTGAAGGGCTCCAGCCCTGGCAGTTTCTGCGTGTAGCATTTCTAGAATAGAGTGGGTGGAACTGACCCAAAGTAAAGTCCAGAGACTCGAACACTGACGACAGGAAAGCCTCAAGTGGAGGAGAATGCAAAATCCCTACTGATGATGGCTCAGCGGCTTCTCCTAGGACTGTGAGGGCGCTTCTGACTTTGGACTTGAGCACTGCCCTGGACCTGTGCTGAGAGAGCGCTAGCATGTCTCAGTGAATCAAGTCCAAAGTTAGAAATCAAGTTTCTGGAGCAGGTGGATCAATTTCTATGATGACAACTTTCCCATGGAAATTCGGCATCTGTTGGCCCCAATGGATTGAAAATCAAGACTGGGAGGCAGCTTCTAACAATGAACCATGGCAACGATTCCTTTCAAAACTTGTAAATACAACTGGATGAACAGTTAGTCTGTGTTTCCAAAGAGAAACCTACTCTTGATACACAAATCTAAAAAGAAATTAGGAAGGTCTTTCAGGGAAAAATTTTCATGGAAATCCAATGCATGTAGCTGTGGTTATTTCAAACTGTTTAAGGGAAGAGAGAGAAATATTTGGCTGCAGCCAAACATGCCCTGTCCAGGGGCTCTTAGAGAAATCCTTACAAAGTTCTTCAGTTTCAGAAAGACAGAGGAATGTGGAGCACAAAGTGGCTGCATTAATAAACAAATTCAGACAAATGGATCAGAGTGACAAAGAAATAGTGCCCATGGTGAATCAGGAAGTTTGTACACTGCAGGAAATGCTTAACAGCCTCGATTTCAAGAGAAAGGAGGCTCTCAGTAAATGACCCAAATCATCCATGAGACAGACCTGTTAATGAACACCATGTCTCATAGAGAGCTGCAAGACTGGAAGCGCGGCAGCAAATCGCCTGCATCGGGGGTCCACTCCACAATGGCTCGACAGCTTCAGAACTGCTTTACACTATTGGCAGAAAGTCTTTCCAACTGAGAAAGGCAATTGGAGAAACTAGAGGAGCAATCTACCAAAATGACATATGAAGTGATCCCATTCCAATGCAAAAGAACTCACATGCTAGAAAGAGTCACTTCTTGATCTACAACTTTTCAGAACTCATTTGTGTTGAGCGACAGCCCATGTATGCCAAACCCACCTCAGAGGCCGTTGGTACTTTAAAAAAGTAAATTCAGTTCACTGTAAACTAATAAAATGCCAGAACTAAACTATCAGGTAAAGGTAAAGCATCAATTGACAAAGAAATGTTTCAACTCTAAGCAACCGAAGATTGTACTTTGTGGAACATAATGTCAAAGCCATGTCTATTGAAGAATCTTCCAAATGGGAGTCTCTCAGTAGAAATTTTCGACATTTGCAACCAAGGAAATGAAGTCCAGTGTGAGGTTAAAGGAAATGAGGGCTGTACACATGGTGAATGAAGAACTTTCATTTCCATAACGTTTGAAACACAGATCTGCCCTCTATGGCCTGACCAATAGATTGGAGACCAGCTCATTTGCCCTGTGGTGATGATTTCCAATGTCAAGTTACCTAATGCTTGGGCATCCATCATTTGGTACAACGTTGTCAACCAACGATTCCAGAACTTGGTTTCTTTAATAATCCTCCACCTGACATTTGAGTCAACTACTGAGGTGATGAGCTGGCAGTTTTCATCGTACGTTGTCGTTGTTTAAATAATCCTCCACCTGACATTCAGATCAACTCCATATGCTGGCAGAGAAAGCTTACAGTCCAATCTAGCTACAGTGAATGGTCACCTCACCTGGGCCAAGTTCTGCAAGGAACATTTACCTGGTAATCATTTACCTTTTGGACATGGCTTGAAGCAATATTGGATCTAATTAAGAAACACATTTCTTCCCCCTTTGGATTGATGGGTATGTCATGGGCTTTGTTAGCAAGAGAAAGGACGGCTGTGCTAAGGATATAAATGCGCTGGCACCTTTTATTAAGATTTCAGTGAAGCCATCTCGGAGGAATAACTTTCACTGGGTGGACCATTTCTGAAAGTGGGAAGTGAGATTCCACTCTGTAGAAACCTTACAAATAAGGCCGGTTGTCTGCTCTGCCATTCCG
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		TGACATCCTGCGAGACTACAAAGTTATTATGGCTGAAAACATTCCTGAAAACCCCTCTGAAGTACCTATAT CCTGACATTCCCAAAGACAAAGCCTTCGGTAACACTACAGCTCTCAGCCTTGCGAAGTTTCAAGACCAA CAGAAAGGGGTGACAAAGGTTATGTTCTTCTGTTTTTATCCCATCTCAACAATCCGAAGTGATTC AAC AGAGCCACATTTCTCCATCAGACCTTTCTTCCCATGTCTCCAAGTGTGATGCGGTGTTGAGAGAAAACCTTG AGTCCCAACAATTGAAACTGCAATGAAGTCTCCTTATTTCTGCTGAATGACAGGATAAACTCTGACGCA CCAAGAAAGGAAGCAAAATGAAAAGTTTAAAGACTGTTCTTTGGCCCAATAACACATTTTATTCTTCAG CTTTGTAAATACCAGGTTCTAGGAAATGTTTGACATCTGAAGCTCTCTTCACACTCCCGTGGCACTCCTC AATTGGGAGTGTGTGACTGAAAATGCTTGAAACCAAGCTTCAGATAAACTTGCAAGATAAGACAACCTTT AAGAAACCAGTGTTAATAACAATATTAAACAG
8	granzyme K (granzyme 3; tryptase II) /// granzyme K (granzyme 3; tryptase II)	>gi 73747815 ref NM_002104.2 Homo sapiens granzyme K (granzyme 3; tryptase II) (GZMK), mRNA GATCAACACATTTTCATCTGGGCTTCTTAAATCTTAAATCTTAAATGACTAAGTTTCTTCTCTCTCT GTTTTCCTAATAGTTGGGCTTATATGACTCATGTGTGTTTCAATATGGAAATTTATTGGAGGGAAGAA GTGTACCTCATTTCCAGGCCATTTATGGCCCTCCATCCAGTATGGCGGACATCACGTTTGTGAGGTGTTT TGATTGATCCACAGTGGGTGCTGACAGCAGCCCACTGCCAATATCGGTTTACCAAAGGCCAGTCTCCAC TGTGGTTTTAGGCGCACACTCTCTCTCAAAGAAATGAGGCCCTCCAAACAACACTGGAGATCAAAAATTT ATACCATCTCAAGAGTTACATCAGATCCTCAATCAATGATATCATGTGTTAAGCTTCAAAACAGCCG CAAACTCAATAAACATGTCAAGATGCTCCACATAAGATCCAAAACCTCTCTTAGATCTGGAACCAAATG CAAGGTTACTGGCTGGGAGCCACCGATCCAGATTCATTAAAGACCTTCTGACACCTCTGCCGAGAAGTCACT GTTACTGTCTTAAGTCGAAAACCTTTGCAACAGCCAAAGTTACTACAAGGGGACCCCTTTTATACCAAAG ACATGGTCTGTGCAGGAGATGCCAAAGGCCAGAGGATTCCTGTAAAGGTGACTCAGGGGGCCCCCTTGAT CTGTAAAGGTGCTTCCACGCTATAGTCTCTGGAGGTCATGAATGTGGTGTGCCACAAGCCCTGGAATC TACACCCCTGTTAACCAAGAAATACCAAGACTTTGGATCAAAAGCAACCTTGTCCCGCTCATACAAATTAAG TTACAAATAAATTTTATTGGATGCACCTTGCTTCTTTTCTCTAATATGCTCGCAGGTTAGAGTTGGGTGTA AGTAAAGCAGAGCACATATGGGGTCCATTTTGGCACTTGTAAGTCATTTTATTAAAGGAATCAAGTTCTTT TTCACCTTGTATCACTGATGTAATTTCTACCATGCTGGTTTATTCTTAAATAAAATTTAGAAGACTCAAAAA AAAAA
9	CD3G antigen, gamma polypeptide (Tit3 complex)	>gi 4557428 ref NM_000073.1 Homo sapiens CD3g molecule, gamma (CD3 -TCR complex) (CD3G), mRNA GGGCTGCTCCACGCTTTTGCCGGAGACAGAGACTGACATGGAACAGGGGAGGCCCTGGCTGCTCATC CTGGCTATCATCTCTTCAAGGTACTTTGGCCCACTCAATCAAGGAAACCACTTGGTTAAGGTGTATG

		ACTATCAAGAAGATGGTTCGGTACTTCTGACTTGTGATGCAGAAGCCAAAATATCACATGGTTTAAAGA TGGGAAGATGATCGGCTTCCCTAACTGAAGATAAAAAAATGGAATCTGGGAAGTAATGCCAAGGACCCCT CGAGGATGTATCAGTGTAAAGGATACAGAACAAGTCAAAACCACTCCCAAGTGTATTACAGAATGTGTC AGAACTGCATTGAACTAAATGCAGCCACCATACTGGCTTCTCTTTGCTGAAATCGTCAGCATTTTTCGT CCTTGTCTGGGTCTACTTCACTGTGACAGGATGGAGTTCGCCAGTCGAGAGCTTCAGACAAGCAG ACTCTGTTGCCCAATGACCAAGCTCTACCAAGCCCTCAAGGATCGAGAAAGATGACCAAGTACAGCCACCTTC AAGGAAACCAAGTTGAGGAGGAATTGAATCAGGACTCAGAGTAGTCCAGGTGTTCTCCTATTCAAGTT CCAGAAATCAAGCAATGCAATTTTGGAAAAGCTCCTAGCAGAGAGACTTTCAGCCCTAAATCTAGACTCAA GGTTCCCAAGATGACAAATGGAGAAGAAAGCCCATCAGAGCAAAATTTGGGGGTTTCTCAAATAAAATAA AAATAAAACAATACTGTGTTCAGAAAGCGCCACCTATTGGGGAATTTGT
10	G protein-coupled receptor 171	>gi 31377771 ref NM_013308.2 Homo sapiens G protein-coupled receptor 171 (GPR171), mRNA GGTTGCTACTGCTGGGCTAACCAACAGCTCATGCTTCTGAAGACTTGCAGCAAGTTTGTGAGGC TCACAGAAGATAGCCCCAGTGTTTTGGAGTGGTTTGAATGTGATTTCTGAGATCAGACTGACTGAGCTGG AATCCTGGCTTTATATCTTACCAGCTACACAACCTTGGAGTCTTAGAAATTTTCTTTTCAATAAGCAG TCATCCTTACTTTCCCTCAAGATGACAAACAGTTCTGTTCTTCCCAAGTTTATAAAGATCTGGAGCCAT TCACGTATTTTCTTATTAGTTTCTTGTGGAATTTATGGAAGTTGTTTGCACCTGGGCTTTTAT ACAGAAGAATACGAATCACAGGTGTGAGCATCTACTTAATTAATTTGCTTACAGCCGATTTCTCTGCTT ACTCTGGCATTACCAGTGAAAATTTGTTGTGACTTGGGTGTCACCTTGGAAGCTGAAGATATTCCACT GCCAAGTAACAGCTGCTCATCTATATCAATATGATTTATCAATTAATCTTTAGCATTTGTGAGCAT TGACCGCTGTCTTCAGCTGACACACAGCTGCAAGATCTACCGAATACAGAACCCTGGATTTGCCAAAATG ATATCAACCGTTGTGTGGCTAATGCTCTCTTATAAATGGTGCCAAATATGATGATTTCCCATCAAAGACA TCAAGGAAAAGTCAAATGTGGGTGTATGGAGTTTAAAAAGGAATTTGGAAGAAATTTGGCATTTTGTGAC AAATTTCATATGTGTAGCAATATTTTAAATTTCTCAGCCATCATTTTAATATCCAATTCCTTGTAAAT CGACAGCTCTACAGAAACAAAGATAATGAAAATTAACCAATGTGAAAAGGCTCTCATCAACATACTTT TAGTGACCACGGGTACATCATATGCTTTGTTCTTACCACATTTGCCGAATCCCGTATACCTCAGCCA GACAGAAGTCATACTGATTGCTCAACCAAGGATTTCACTCTTCAAGCCAAAGAGGCTACACTGCTCCTG GCTGTGTCGAACCTGTGCTTTTGATCCTGTCTGTACTATCACCTCTCAAAAAGCATTTCCGCTCAAAGGTCA CTGAGACTTTTGGCTCACCTAAAGAGACCAAGGCTCAGAAAAGAAAATTAAGATGTGAAAATAATGCATA AAAGACAGGATTTTGTGCTACCAATTTCTGGCTTACTGGACCATAAAGTTAATTATAGCTTTGAAAAGAT AAAAAAAACAAAAACAAAAAACTCAGTATGAAAAAATACAGTTAGCTAGCAAAATATGGACAGGT TTACTTAGAAATCCTGTTTCTAAATGCAAGTCAAGCTTTATTGTTAGGCTTGTGCTACTCATTAACCCA AATATTTGTACAAAACAACTAAAGAGTCTCATTTGAACGAATGTAAAATCCTGCAATATCCTTGAAATCCAA

		AAGAGGTCATGACATAGACCCAAAGGTATTATGAGTTATTATTTAAATGCCTGGAACCTGACTTCTTG ATAAAAAATATAAAAAATAATTTCCATGTAAAGTTACCAGAAAGCCACAGCAACATAATTTTAAAGCCTT TCGGATTACTTTTAAAAAATGCAGCTTACATATAACAACTTGTGCCCTATTTTATTCTAATCTATCACTT CAAAAGATGGTAATCTTTCAACTCATTTATTCCTCCAATTTTAAATGTCGAATTTTCTTAACACAAATAA CCAAAAGCTTTTATTATATAAAAAAGGCTTGAAAAATATAAAAAAATAAAAAAATAAAAAAATAAAAAA AAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
11	Protein kinase C, beta 1	>gi 89353296 ref NM_001183.4 Homo sapiens ATPase, H+ transporting, lysosomal accessory protein 1 (ATP6AP1), mRNA GGGGCAACGGTCACCTGATCTGGGCTGTGAGCGCGCTGAGGCAGTGGAGCTGAGCTATGATGGCG GCCATGGCGACGGCTCGAGTCGGATGGGGCCGCGATGCGCCAGGCGCTCTGGCGCATGCCGTGGCTGC CGGTGTTTGTGCTGGCGCGCGGCGGCGGCGGAGCAGCGTCCCGCTGGTGTGTG GTCGAGTGACCGGACTTGTGGCTCTGCGGCCGACACTCATGAAGGCCACATCACAGCACTTGCAG CTCTTACCTACTTAGATCCCGCTGGAGCTGGGTCCAGGAATGTGCTGTCTCTGCAGGACAAGC TGAGCATTGAGGATTTCAACAGCATATGGCGGTGTGTTTGGAAACAAGCAGGACAGCGCTTTCTAACCT AGAGAATGCCCTGGACCTGGCCCCCTCTCACTGTGCTTCTGCGCTCGACTGGTATGAGTCAGCACT CTGAACCACTTACCTGCAGGAGAAAGCTCGGGGCCAGCCCTTGTCATGTGGACCTGGCCACCCCTGGGAGC TGAAGCTCAATGCCAGCTCCCTGCTGCTGCTCATTCGCTGCCCTACACAGCCAGCTCTGCTGTGAT GGACCCAGGGAAGTCTCACAGGCAACGATGAGTCACTGGGCGAGTCTCTGAGCACACTCAAGTCCGAA GATGTCCCATACACAGCGGCCCTCACAGCGGTCCGCCCTTCCAGGTGGCCCGTGTAGCCGTGGTGG CCGAGGGCTAGTGCAGCTGTCTACAAAACAGCCAGTATCACCTGTGATCCATCCTCCTGTGAGTTA CAATGACACCGCTCCCGGATCTGTCTGGGCCCAAACTTCTGTGGCGGTACAAAGCACAGTGGGAG GACCTGACTCCCTCACCTTTGGGTGCAGGAACCTCAACCTGACTGGCTCCTCTGGAATGACTCCTTG CCAGGCTCTCACTGACCTATGAACGACTCTTTGGTACCACAGTGACATTCAGTTTCACTTGGCCAAACG CCTTACCCAGTGTCTGCCCGCACTGGTTTACCATGGAGCGCTCGAAGTCCACAGCAATGGCTCCGTC GCCTACTTCAATGCTTCCAGGTACAGGGCCCGAGCATCTACTCCTTCCACTGCGAGTATGTCAGCAGCC TGAGCAAGAGGGTAGTCTCTCGTGGCCCGCACGCGCCCTCTCCCTGGCAGATGATGCTTCAGGACTT CCAGATCCAGGCTTTCAACGTAAATGGGGAGCAGTTCTCTACGCGAGCTGTGCCAGCTTCTTCTCC CCCGCATCTGGATGGGCTGCTCACCTCCCTGTTTCACTGCTCTTCACTTACCTATGGCCCTGCACATGA TCCTCAGCCTCAAGACCATGGATCGCTTTGATGACCAAGGCCCCCACTATTCTTTGACCCAGATTGT GTGACCCCTGTGCCAGTGGGGGGTTGAGGGTGGGACGGTGTCCGTGTTGTGCTTTCCACCCCTGCAGCG CACTGGACTGAAGAGCTTCCCTCTTCTACTGCAGCATGAACGTCAAGCTCCCTCAGCCCATCTTGCTC CCTCTTCAGCCCGCTGAGGAGCTTCTTGGGGTGGCCCCCATCTCTCCCAACAAGGTGTACATATTCTGCG TAGATGCTAGACCAACAGCTTCCAGGGTTCTGTCGCTGTGAGGCGTAAGGACATGAATTCTAGGGTCT

		CCTTTCCTTATTATTCTTGTGGCTACATCATCCCTGGCTGTGGATAGTCTTTTGTGTAGCAATGC TCCCTCCTTAAGGTTATAGGGCTCCCTGAGTTTGGAGTGTGGAAGTACTACTTAAGTGTCTGTCTGTCT TGGCTGTCGTTATCGTTTCTGCTGATGTTGTGCTAAACAATAAGAAAGTACACGGGTTTATTCTGTGGCC TGAGAAAGGAAGGACCTCCACGACAGGTGGCTGGTGCGATCGCCGGCTGTTTGGCATGTTCCACCCGG GAGTGCCGGCAGGAGCATGGGTGCTTGGTTGTTTCCCTTCCATAAATAAACAACGCGGTGCGCCATGCA AAAAAAA
12	major histocompatibility complex, class II, DR alpha /// major histocompatibility complex, class II, DR alpha	>gi 52426773 ref NM_019111.3 Homo sapiens major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA ACATTCTCTTTTCTTTTATTCTTGTCTGTTCTGCTCACTCCCGAGCTCTACTGACTCCCAACAGAGCGC CCAAGAAGAAAATGGCCATAAGTGGAGTCCCTGTGCTAGGATTTTTCATCATAGCTGTGCTGATGAGCGC TCAGGAATCATGGGCTATCAAGAAGAACATGTGATCATCCAGCGGAGTTCTATCTGAATCCTGACCAA TCAGGCGAGTTTATGTTTGAATTTGATGGTGATGAGATTTTCCATGTGGATATGGCAAAGAGGAGACGG TCTGGCGGCTTGAAGAATTGGACGATTTGCCAGCTTTGAGGCTCAAGGTGCATTTGGCCAAACATAGCTGT GGACAAAGCCAACTGGAAATCATGACAAAGCGCTCCAACTATACTCCGATCACCAATGTACCTCCAGAG GTAACGTGTCTCACGAACAGCCCTGTGGAACGTGAGAGAGCCCAACGTCCTCATCTGTTCATAGACAAGT TCACCCCAACGAGTGTCAATGTACGTGGCTTCGAAATGGAAACCTGTCAACACAGGAGTGTCAAGAGAC AGTCTTCCTGCCAGGAAGACCACTTTTCCGCAAGTTCCACTATCTCCCTTCTCCCTCAACTGAG GACGTTTACGACTGCAGGTGGAGCACTGGGCTTGGATGAGCCTTCTCAAGCACTGGGAGTTTGATG CTCCAAGCCCTCTCCAGAGACTACAGAGAACGTGTGTGTCCTGGGCTGACTGTGGTCTGGTGGG CATCATTAATTGGGACCATCTTCATCATCAAGGATTCGCAAAAGCAATGCAGCAGAACGAGGGGCTT CTGTAAGGCACATGGAGGTGATGGTGTCTTAGAGAGAAGATCACTGAAGAACTTCTGCTTTAATGGC TTTACAAAGCTGGCAATATTAACAATCCTTGACCTCAGTGAAGCAGTCACTTCAGCATTTTCCAGCCCT ATAGCCACCCCAAGTGTGGATATGCCCTCTTCGATTGCTCCGTACTCTAACATCTAGCTGGCTTCCCTGTC TATTGCCCTTTTCCCTGTATCTATTTCCTCTATTTTCCTATCATTTTATTATCACCATGCAATGCCTCTGGA ATAAAACATACAGGAGTCTGTCTCTGCTATGGAATGCCCATGGGCACTCTTGTGTACTTATTGTTTA AGGTTTCTCCTCAAACTGTGATTTTCTGAAACACAATAAACTATTTTGATGATCTTGGGTGGAAAAAAA AAAAAA
Sequence	Major histocompatibility complex, class II,	>gi 24797068 ref NM_002123.2 Homo sapiens major histocompatibility complex, class II, DQ beta 1 (HLA-DQB1), mRNA CAGATCCATCAGGTCCGAGCTGTGTGACTACCACTTTTCCCTTCGTCTCAATTATGTCTTGAAAAAGG CTTTGCGGATCCCCGGAGGCCCTTCGGGCAGCAACTGTGACCTTGATGCTGTCGATGCTGAGCACCCAGT

115

		TTACCTTTTGAAAAAATAAATGAAGGATTTGACCTGCTTCACTCTGGGAAAAAGTATCCGTACCGTCCCTGA CGTTTGTAGGCAATAGAGATGCCCTTCCCTGTAGCAGTCTTTCAGCCCTCCTCTACCCCTACAAGATCTGGAG CAACAGCTAGGAAATATCATTAATTCAGCTCTTCAGAGATGTATCAATAAATTAACATGCGGCTTTC CAAAGAAATGGAAATTGATGGGAAATTAATTTTCAGGAAATTTAAATTTCAAGTGAGAAAGTAAATAAAG TGTTGAACATCAGCTGGGAATTGAAGCCAAACAACCTTCCTTCTTAACCATTTCTACTGTGTACCTTTTG CCATTGAGGAAAAATATTCCTGTGACTTCTTGGCATTTTGGTATCTTTCATAAATCTTTAGTCATCGAATCC CAGTGGAGGGACCTTTTACTTGGCTGAACATACACATGCTGGGCCATTTGTGATTGAAGTCTTCTAAC TCTGTCTCAGTTTTCACCTGTCGACATTTTCCCTTTTCTAATAAATAATGTAACCAATCCCTGGGTAAAG CTAGGGTAAGGTAAAGGATAGACTCACATTTACAAGTAGTGAAGTCCAAGAGTTCTAAATACAGGAAAT TTCCTTAGGAACTCAAAATAAATGCCCCACATTTTACTACAGTAAATGCGAGTGTTTTATGACTTTTATA CTATTTCTTTATGGTCGATATACAAATTGATTTTAAATAAATAGCAGATTTCTTGCTTCATATGACAAA GCCTCAATTACTAATTGTAAAAAATGAACTATTTCCAGAAATCATGTTCAAAAAATCTGTAATTTTGTCTG ATGAAAGTGTCTTCAATTGACTAAACAGTATTAGTTTGTGGCTATAAATGATTAATTTAGATGATGACTGAAA ATGTGTATAAAGTAATTAAAGTAATAATGTTGGCTTTAAGTGTAGAGATGGGATGCAAAATGCTGTGAAT GCAGATGTAAAAATTGGTAACTAAGAAATGGCACAAAACCTTAAGCAATATAATTTTCTCTAGTAGATA TATATACACATACATATATACATATACAAATGTATATTTTGCAAAATGTTTTCAATCTAGAACTTT TCTATTAACTACCATGTCTTAAATCAAGTCTATAATCCTAGCATTAAGTTTAAATAATTTTGAATATGTAAA GACCTGTGTTAATGCTTTTGTAAATGCTTTTCCCACTCTCATTTGTTAATGCTTTCCCACTCTCAGGGGAA GGATTGTCATTTTGAGCTTTATCTCTAAATGTGACATGCAAAAGATTAATCTCTGTTAAAGGAGGTAGCTGT CTCCAAAAATGCTATTGTTGCAATATCTACATTTCTATTTTATGAAAGACCTTAGACATATAAGTAA AATAGTTTATCATTTACTGTGTGATCTTCAGTAAAGTCTCTCAGGCTCTCTGAGCTTGTTCATCTTTGTT TTGAAAAAATTACTCAACCAATCCATTACAGCTTAACCAAGATTAAATGGGATGATGTTAATGAAAGAGC TTCGCC
15	T cell receptor alpha constant /// T cell receptor alpha constant	>gi 36944 emb x02592.1 HSTCRAR Human mRNA for T-cell receptor alpha chain (TCR-alpha) TTTTGAAACCCTTCAAAGGCAGAGACTTGTCCAGCCTAACCTGCCTGCTCTAGCTCCTGAGGCTCA GGCCCTTGGCTTCTGTCCGCTCTGCTCAGGGCCCTCCAGCGTGGCCACTGCTCAGCCATGCTCCTGCTG CTCGTCCCAGTGTCTGAGGTGATTTTACCTTGGAGGAACCAAGAGCCCAAGTCCGTTGACCCAGCTTGGCA GCCACGTCTCTGTCTGTAAGGAGCCCTGTTCTGTGAGGTGCAACTACTCATCTGTCTGTCTCCACCAT TCTCTTCTGGTATGTGCAATACCCCAACCAAGACTCCAGCTTCTCTGAAGTACACATCAGCGGCCACC CTGGTTAAAGGCATCAACGGTTTGTAGGCTGAATTTAAGAAGAGTGAAACCTCTTCCACCTGACGAAAC CCTCAGCCCATATGAGCGACGGGCTGAGTACTTCTGTGTGTGTGATCTCGAAACCGAACAGCAGTGC TTCCAAGATAATCTTTGGATCAGGACCAAGTCTCAGCATCCGGCCAAATATCCAGAACCTGACCCCTGCC

117

		GTACATATTTCTTGCCTTTATAATCTTTTATACAGTGCTTTACAGAGAAAAAGACATAAAGCAAAAGACTAT GAGGAATATTTGCAAGACATAGAAATAGTGTGGAAAAATGTGCAATATATGTGATGTGGCAAAATCTCTATTAG GAAATATCTGTAAATCTTCAGACCTAGAAATAATACTAGTCTTATAATAGGTTTGTGACTTTCCTAAATCA ATCTATTTACGTGCAATACCTCAATACCTTCAATTTTAAATATTTTATGTGCAATAAAATGTATTTGTTTG TATTTTGTGTTCAGTACAATATATAAGCTGTTTATATATATGTGAAATAAAAGTAGAATAAACACACAAAAAA AAAAAAA
17	protein kinase C, theta	>gi 48255887 ref NM_006257.2 Homo sapiens protein kinase C, theta (PRKCQ), mRNA AGTCCCGCGCAGTCCCGCGCAGTCCAGCGCCACCGGGCAGCAGCGCGCGTCTCGCTCCAGGGG CAACCATGTCGCCATTCTTCGGATTGGCTTGTCCAACCTTGAACCTGCGGGTCTGCCAGTCTTGTGAGGG CGAGGCTGTTAACCCCTTACTGTGTGTCTGCTCGTCAAGAGTATGTGCAATCAGAGAACGGGCAGATGTAT ATCCAGAAAAAGCCTACCATGTACCCACCCTGGGACAGCACTTTTGATGCCCATATCAACAAGGGAAGAG TCATGCAGATCATTTGTGAAGGCAAAACGTGGACCTCATCTGAAAACCCACCGTGAGCTCTACTCGCT GGCTGAGAGGTGCAGGAAGAACACCGGAAGACAGAAATATGTTAGAGCTGAAACCTCAAGGCCGAATG CTAATGAATGCAAGATACCTTCTGGAAATGAGTGACACAAAGGACATGAATGAATTTGAGACGGAAGGCT TCTTTTGCTTTTGCAATCAGCGCGGGGTGCCATCAAGCAGGCAAGGTCCACACGTCAAGTGCCACGAGTT CACTGCCACCTTCTTCCACAGCCACATTTTGTCTGTCTGCCACGAGTTTGTCTGGGGCTGAACAAA CAGGGCTACCAGTCCGACAAATGCAGCAATTCACAGAGTGTATTGATAAAGTTATAGCAAAGT GCACAGGATCAGCTATCAATAGCCGAGAAACCATGTTCCACAGGAGAGATTCAAAATTGACATGCCACA CAGATTTAAAGTCTACAAATTACAAGAGCCCGACCTTCTGTGAACACTGTGGGACCCCTGTGTGGGACTG GCACGGCAAGGACTCAAGTGTGATGCAATGTGGCATGAATGTGCATCATAGATGCCAGACAAAGGTGGCCA ACCTTTGTGGCATAAACCCAGAGCTAATGGCTGAAGCGCTGGCCATGATTGAGAGCACTCAACAGGCTCG CTGCTTAAGAGATACCTGAACAGATCTTTCAGAGAAAGTCCGGTTGAAATTTGTTCTCCCATGCTCCATCAAA AATGAAGCAAGCGCCCATGTTTACCGACACCGGGAATAAGAGAGCCCTCAGGGCATTTTCTTGGGAGTCTC CGTTGGA TGAGGTGGATAAAATGTGCCATCTTCCAGAACCTGAACCTGAACAAAGAACCATCTCTGCA GATTAAACTAAAATTTGAGGATTTTATCTTGACAAATGTTGGGAAAGGAAAGTTTGGCAAGGTCTTC CTGGCAGAAATCAAGAAACCAATCAATTTTTCGCAATAAAGCCCTTAAAGAAAGATGTGTTGATGG ACGATGATGTTGAGTGCAACGATGTAGAGAAAGAGTCTTTCTTGGCCCTGGGAGCATCCGTTTCTGAC GCACATGTTTTGTACATTCAGACCAAGGAAACCTCTTTTGTGATGGAGTACCTCAACGGAGGGGAC TTAATGTACCACATCCAAGCTGCCACAAAGTTTCGACCTTTCCAGAGCGACGTTTATGCTGCTGAAATCA TTCCTTGGTCTGCAGTTCCTTCATTCCAAAGGAATAGTCTACAGGGACCTGAAGCTAGATAACATCCTGTT AGACAAAGATGGACATATCAAGATCGCGGATTTTGGAATGTGCAAGGAGAACATGTTAGGAGATGCCAAG ACGAATACCTTCTGTGGACACCTGACTACATCGCCCCAGAGATCTTGTGGTCAAGAAATACAACCACT

119

		GCCCTCAATGACTCCAGATACTGCCCTGAGCAGCCGCCCTGAGGGTCTCGGCCACCTTCTGGCAGAAACCCC GCAACCACTTCGGCTGTCAAGTCCAGTTCTACGGGCTCTCGGAGAATGACGAGTGGACCCAGGATAGGGC CAAACCCGTCAACCAGATCGTCAGCGCCGAGGCCCTGGGTAGAGCAGACTGTGGCTTTACCTCGGTGTCC TACCAGCAAGGGTCTGTCTGTCACCATCTCTATGAGATCCTGCTAGGAAAGGCCACCATGTATGCTG TGCTGTCAGCGCCCTTGTGTGATGGCCATGTTCAAGAGAAAGGATTTCTGAAGCAGCCCTGGAAGTG GAGTTAGGAGCTTCTAACCCGTGATGGTTTCAATACACATTTCTTTTGCCAGCGCTTCTGAAGAGCTG CTCTCACCTCTCTGCATCCCAATA
19	T cell receptor alpha locus /// T cell receptor delta variable 2 /// T cell receptor alpha variable 20 /// T cell receptor alpha joining 17 /// T cell receptor alpha constant	>gi 338765 gb M15565.1 HUMTCAYE Human T-cell receptor rearranged alpha- chain V-region (V-D-J) mRNA, complete cds TCCAAAATGAAGGTCTGTGGAAGGACATGAATAAAGCACAGGAGGTTGAAGTCAGATTTCAGCTTTCT AGCAGGAGACAAGACAAATCTGCATCTTCACAGGAGGATGGCCATGCTCTGGGGCATCAGTCTGAT TCTGTGGCTTCAGCCAGACTGGGTAACACAGTCAACAGAAAGATGATGACCAGCAAGTTAAGCAAAATTCA CCATCCCTGAGCGTCCAGGAAGGAAGAAATTTCTATTCTGAACCTGTGACTATATAACAGCATGTTTGATT ATTTCCCTATGTACAAAATAACCTGCTGAAGGTCCTACATTCCTGATATCTATAGTTCCATTAAAGGA TAAAAATGAAGATGGAAGATTCACTGTCTTCTTAAACAAAGTGCCAAAGCACCTCTCTCTGCACATTGTG CCCTCCAGCCTGGAGACTCTGCAGTGTAATCTGTGCAGCAAAAGGGCCGGCAGTGCAGTAAACTCA CCTTTGGACTGGAACAAGACTTCAGGTCACGCTCGATATCCAGAACCTGACCCCTGCCGTGTACCACT GAGAGACTCTAAATCCAGTGACAAGTCTGTCTGCCCTATTCACCGATTTTGATTCTCAACAAATGTGTCA CAAAGTAAGGATTTCTGATGTATATACAGACAAAACCTGTCTAGACATGAGGTCTATGGACTTCAAGA GCAACAGTGTGTGGCTGGAGCAACAAATCTGACTTTTGCAATGTGCAACAGCCCTTCAACAAACAGCATAT TCCAGAAAGACACCTTCTTCCCAGCCAGAAAGTTCTCTGTGATGTCAAGCTGGTCGAGAAAAGCTTTGAA ACAGATACGAACCTAAACTTTCAAAACCTGTGAGTGAATGGTTCCGAATCCTCCTGAAAGTGGCCG GGTTTAAATCTGCTCATGACGCTGCGGCTGTGCTCCAGCTGAGATCTGCAAGATTGTAAGACAGCCTGTGC TCCCTCGCTCCTTCTCTGCTGCAATTCGCCCTCTCTCCCTCTCCAAACAGAGGGAACCTCTCCACCCCAAG GAGGTGAAAGCTGCTACCCACCTCTGTGCC
20	T cell receptor gamma constant 2	>gi 339406 gb M30894.1 HUMTCRGAD Human T-cell receptor Ti rearranged gamma-chain mRNA V-J-C region, complete cds GAATCAGGAAGACCAGCTCCTCCTACTGTCTTCTGTGTACGGGATCAGCGTTCCTTGTGAGTGGGACC TGAGTTTTCAGAGGGTCTTCTGCTCCTCTTGGTCTGGTCCCTTACTTCCAGAGCCCCCAGAGGGAAGGC ATGCTGTTGGCTCTAGCTCTGCTTCTAGCTTTCCCTGCTCCTGCTCCAGTCAAGAAATCTTCCAACTTGGAAG GGAGAACAAAGTCAGTCACCCAGGCCAACTGGGTATCAGCTGTAATCACTTGTGATCTTCTCTGTAGAAAA

		TGCCGTCTACACCCACTGGTACCTACACCAGGAGGGGAAGCCCCACAGCGTCTTCTGTACTATGACTCC TACAACCTCAGGGTTGTGTGGAAATCAGGAATCAGTCGAGAAAAGTATCATACTTATGCAAGCACAGGGA AGAGCCTTAAATTTATACTGGAATACTAATTGAACGTGACTCTGGGTCTATTACTGTGCCACCTGGAA GGATTATATAAGAAACTCTTTGGCAGTGGAAACAACACTTGTGTACACAGATAAAACAACCTTGATGCAGAT GTTTCCCCCAAGCCCACATATTTTCTTCTTCCATTGCTGAAACAAAACTCCAGAAGGCTGGAAACATATC TTTGTCTTCTTGAGAAATTTTCCAGATATTAAGATACATTGGCAAGAAAAGAAAGAGCAACACGAT TCTGGGATCCCAGGAGGGGAACACCATGAAGACTAACGCACACATACATGAAAATTTAGCTGTTAACGGTG CCAGAAGAGTCACTGGACAAAAGAACACAGATGTATCGTCAGACATGAGAAATAATAAAACGGAATTGATC AAGAAATTATCTTCTCCTCAATAAAGACAGATGTCAACACAGTGGATCCCAAGACAGTTATTCAAAAAGA TGCAAAATGATGTCAACACAGTGGATCCCAATAACAATTATTCAAAAGGATGCAAAATGATCATCACAATG GATCCCAAGACAAATTGGTCAAAAGATGCAAAATGATACACTACTGTGCTGAGCTCAAAACACCTCTGCAT ATTACATGTACCTCTCTCTCAAGAGTGGTCTATTTTGCCATCATCACCTGCTGTCTGCTTGG AAGAACGGCTTTCTGCTGCAATGGAGAGAAATCAATAACAGACGGTGGCACAAAGAGGCCATCTTTTCCTC ATCGGTTATTGTCCCTAGAAAGCGTCTTCTGAGGATCTAGTTGGGCTTTCTTTCTGGGTTTGGGCCATTTC AGTTCATCATGTGTACTATCTATCATATTATGTATAATGGTTTCAAAACAGTGGGCACACAGAGAAACC TCAGTCTGTAATAACAATGAGGAATAGCCATGGCGATCTCCAGCACCAATCTCTCCATGTTTTCACACAGC TCCTCCAGCCAAACCAATAGCGCTGCTATAGTGTAGACAGCCTGCGGCTTCTAGCCTTGTCCCTCTCT TAGTGTTCTTTAATCAGATAAAGTGCCTGGAAGCCTTTTCATTTTACACGCCCTGAAGCAGTCTTCTTTGCT AGTTGAATTATGTGGTGTGTTTTTCCGTAATAAGCAAAATAAATTT
21	T cell receptor beta variable 21-1 /// T cell receptor beta variable 19 /// T cell receptor beta variable 5-4 /// T cell receptor beta variable 3-1 /// T cell receptor beta constant 1	>gi 3002924 gb AF043179.1 AF043179 Homo sapiens T cell receptor beta chain (TCRBV13S1-TCRBJ2S1) mRNA, complete cds ATGAGCATCGGCCTCCTGTGCTGTGCAGCCTTGTCTCTCTGTGGGCAGGTCCAGTGAATGCTGGTGTCA CTCAGACCCCAAAATTCAGGTCTGAAGACAGGACAGAGCATGACACTGCAGTGTGCCAGGATATGAA CCATGAATACATGTCTGTGATCGACAAGACCCAGGCATGGGCTGAGGCTGATTCTACTCAGTTGGT GCTGGTATCACTGACCAAGGAGAGTCCCAATGGCTACAATGTCTCCAGATCAACCACAGAGGATTTCC CGCTCAGGCTGTGTCGGCTGCTCCCTCCAGACATCTGTGTACTTTCTGTGCCAGCAGTTTCCCCCGGCA GCCGTCTACAATGAGCAGTTCTTCGGGCCAGGGACACGGCTCACCGTCTAGAGGACCTGAAAAACGTG TTCCACCCGAGTCTGTTTGTAGCCCATCAGAAAGCAGAGATCTCCACACCCAAAGGCCACACTGG TGTGCTTGCCACAGGTTTCTACCCCGACCACTGGAGCTGAGCTGGTGGTGAATGGGAAGGAGGTGCA CAGTGGGTGACACAGACCCGACCCCTCAAGGAGCAGCCCGCTCAATGACTCCAGATACTGCCCTG AGCAGCCGCTGAGGTCTCGGCCACCTTCTGGCAGAACCCCGCAACCACTTCCGCTGTCAAGTCCAGT TCTACGGGCTCTCGGAGATGACGAGTGGACCCAGGATAGGGCCAAACCTGTACCCAGATCGTCAGCGC CGAGGCTGGGTAGAGCAGACTGTGGCTTCCACCTCCGAGTCTTACCAGCAAGGGTCTGTGTGCCCACC ATCCTCTATGAGATCTTGCTAGGGAAGGCCACCTTGTATGTCTGTGCTCAGTGCCTCGTGTGATGG

		CCATGGTCAAGAGAAAGGATTCCAGAGGCTGA
22	T cell receptor alpha locus	>gi 1100165 gb L34703.1 HUMTCRAZ Homo sapiens T-cell receptor alpha chain (TCRA) mRNA (HLA-A1, 24; B7, 8; DR 1, 3), complete cds ATGGCATGCCCTGGCTTCCTGTGGGCACCTTGATATCCACCTGTCTTGAATTTAGCATGGCTCAGACAG TCACTCAGTCTCAACCAGAGATGTCTGTGAGGAGGAGACCCCTGACCCCTGAGCTGCACATATGACAC CAGTGAGAGTGATTATTATTATTTCTGTTACAAAGCAGCCTCCAGCAGGAGATGATTCTCGTTATTTCGC CAAGAAGCTTATAAGCAACAGAAATGCAACAGAGAAATCGTTTCTCTGTGAATTCAGAAAGCAGCCAAAT CCTTCAGTCTCAAGATCTCAGACTCAGAGCTGGGGATGCCGATGATTTCTGTGCTTATAGGAGTGC ATACTCTGGGCTGGGAGTTACCAACTCACTTTCGGGAAGGGACCAAACTCTCGTCTATACCAATATC CAGAAACCCTGACCCCTGCCGTGTACCACTGAGAGACTCTAAATCCAGTGACAAGTCTGTCTGCCTATTCA CCGATTTTGATTCTCAAAACAAATGTGTCAAAAGTAAGGATTCTGATGTATATCAGACACAAAACCTGT GCTAGACATGAGTCTATGGACTTCAAGAGCAACAGTGTGTGGCTGGAGCAACAAATCTGACTTTGCA TGTGCAAAACGCTTCAACAAACAGCATTTATCCAGAAAGACACCTTCTTCCAGCCAGAAAGTTCTCTGTG ATGTCAAGCTGGTCGAGAAAAGCTTTGAAACAGATACGAACCTAAACTTTCAAAACCTGTGAGTGTGG GTTCCGAATCCTCCTCTGAAAGTGGCCGGTTTAAATCTGCTCATGACGCTGCGGTTGTGTCCAGCTGA
23	T cell receptor beta variable 19 /// T cell receptor beta variable 19 /// T cell receptor beta constant 1 /// T cell receptor beta constant 1	>gi 46184507 gb AL559122.3 AL559122 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED Homo sapiens cDNA clone CS0DJ014YE01 5-PRIME, mRNA sequence TGCCTGGCCACAGGCTTCTTCCCGACCACTGGAGCTGAGCTGGTGAATGGGAAGGAGTGCACA ATGGGGTCAACACAGACCCCGAGCCCTCAAGAACAGCCCGCCCTCAATGACTCCAAATAMTGCCCTGAG CAGCCGCTGAGGCTCTCGGCCACCTTCTGGCAGAACCCCGCAACCACTTCGGTGTCAAAGTCCAGTTT TACGGGCTCTCGGAGAAATGACGAGTGGACCCAGGATAGGGCCAAACCCGTCAACCAATCGTCAGCGCG AGCCCTGGGTARAGCARAMTGTGGCTTTACCTCGGTGCTCTACCAACAAAGGGTCTCTGTCTGCCACCAT CCTCTATGARATCCTGTAGGGAAGGCCACCCCTGTATGTGTGTGTCAGCGCCCTTGTGTGTGATGGCC ATGGTCAAGAGAAAGGATTTCTGAAGGCAGCCCTGGAAAGTGAATTAAGAACTTCTAACCCGTCATGGTT TCAATACACATTCTTCTTTTGGCCAGCGCTTCTGAAGAGCTGCTCTCACCTCTCTGCATCCCAATAGATAT CCCCCTATGTGCATGCACACCTGCACACTCACGGCTGAAATCTCCCTAACCCAGGGGACCTTAGCATGC CTAAGTGACTAAACCAATAAAATGTTCTGGTCTGGCCCTGA
24	CD3D antigen, delta polypeptide (TiT3 complex)	>gi 98985799 ref NM_000732.4 Homo sapiens CD3d molecule, delta (CD3-TCR complex) (CD3D), transcript variant 1, mRNA AGAGAAGCAGACATCTTCTAGTTCCCTCCCACTCTCTCTTTCGGTACCTGTGAGTCAGCTAGGGGAG GGCAGCTCTCACCCAGGCTGATAGTTTCGGTGACCTGGCTTTATCTACTGGATGAGTTCCGCTGGGAGATG GAACATAGCACGTTTCTCTCTGGCTGGTACTGGCTACCCCTTCTCTCGCAAGTGAGCCCTTCAAGATAC

		CTATAGAGGAAC TTGAGGACAGAGTGT TTGTGAATTGCAATACCAGCATCACATGGGTAGAGGAAACGGT GGGAACACTGCTCTCAGACATTACAAGACTGGACCTGGGAAACGCACTCTGGACCCACGAGGAATATAT AGGTGTAATGGGACAGATATATACAAGGACAAAGAAATCTACCGTGCAAGTTCATTATCGAATGTGCCAGA GCTGTGTGAGCTGGATCCAGCCACCGGTGGCTGGCATCATTTGTCACTGATGTCTATGGCACCTCTGCTCCT TGCTTTGGGAGTCTTCTGTCTTGTCTGGACATGAGACTGGAAGCTGTCTGGGGCTGCCGACACACAAGCT CTGTTGAGGAATGACCAGTCTATCAGCCCTCCGAGATCGAGATGATGCTCAGTACAGCCACCTTGGAG GAAACTGGGCTCGGAACAAGTGAACCTGAGACTGGTGGCTTCTAGAAGCAGCCATTACCAA CTGTACCTT CCCTTCTTGCTCAGCCAATAAATATATATCCTCTTTCACCTCAGAAAAA AAAAAA AAAAAA AAAAAA A
25	T cell receptor gamma constant 2 /// T cell receptor gamma variable 9 /// similar to T- cell receptor gamma chain C region PT- gamma-1/2 /// similar to T-cell receptor gamma chain V region PT- gamma-1/2 precursor /// TCR gamma alternate reading frame protein	>gi 339168 gb M13231.1 HUMTCGXH Human T-cell receptor aberrantly rearranged gamma-chain mRNA from cell line HPB-MLT GGCATGGGTGGGCCCTACTGGTGTCTTAGCTTTCTCTGTCTCTGCTGCCAGTCAGAAATCTTCCAAC TTGG AAGGAGAACGAAGTCAGTCACCGAGGAGACTGGGTCTCTGTGAAATCACTTGCATCTTACTGTAAC AAATACCTTCTACATCCACTGGTACCTACACAGAGGGGAAAGGCCACAGCGCTTCTGTACTATGAC GTCTCCACTGCAAGGATGTGTTGGAATCAGGACTCAGTCCAGGAAAGTATATATCTCATACACCCAGGA GGTGAGCTGGATATTGAGACTGCAAAATCTAATTGAAAATGATCTGGGTCTATTACTGTGCCACCTG GGACAGGCAAAAATTTATTAAGAAAATCTTTTGGCAGTGGAACAACACTTTGTGTACAGATAAACAACT TGATGCAGATGTTTCCCCCAAGCCCACTAATTTCTTCTTCAATTGCTGAAAACAAAACTCCAGAAAGGCT GGAACATACCTTTGTCTTTTGAGAAATTTTCCAGATATTATTAAAGATACATTTGGCAAGAAAAGAGA GCAACACGATCTGGGATCCAGAGGGGAAACACCATGAAGACTAACGACACATACATGAAATTTAGCTG GTTAACGGTGCCAGAGAGTCACTGGACAAAGAACACAGATGTATCGTCAGACATGAGAAATAATAAAAC GGAATTGATCAAGAAATTTATCTTCTCCTCAATAAAGACAGATGTCAACACAGTGGATCCCAAGACAGTT ATTCAAAAGATGCAAAATGATGTCTATCAATGGATCCCAAGACAAATTTGGTCAAAAGATGCAAAATGATAC ACTACTGCTGCAGCTCACAAACACCTCTGCATATTACATGTACCTCCTCTGCTCCTCAAGAGTGTGGTC TATTTTGCCATCATCACTGCTGTCTGTGCTTGGAAGAACGGCTTTCTGCTGCAATGGAGAGAAATCATAAAC AGACGGTGGCACAAGGAGGCCATCTTTTCCTCATCGGTTATTGTCCCTAGAAAGCTCTTCTGAGGATCTA GTTGGGCTTTCTTCTGGGTTTGGGCCATTTTCAGTTCTCATGTGTGTACTATTCTATCATATTGTATATAA TGTTTTCAAACCAAGTGGGCACACAGAGAACCTCAGTCTGTAATAACAATGAGGAATAGCCATGGCGATC TCCAGCACCAATCTCTCCATGTTTTCACAGCTCCTCCAGCCAAACCAATAGCGCTGCTATAGTGTAG ACAGCCTGGGCTTCTAGCCTTGTCCCTCTCTTAGTGTCTTTAATCAGATAACTGCCCTGGAAGCCCTTTC ATTTTACACGCCCTGAAGCAGTCTTCTTGTGCTAGTTGAATTAATGTGGTGTGTTTTCCTCGTAATAAGCAAA ATAAAATTTAAAAAAATGAAAA

26	pyrin and HIN domain family, member 1	>gi 10437303 dbj AK024890.1 Homo sapiens cDNA: FLJ21237 fis, clone COL01114 GTCAAAGGAATAATCCCATCTAAAGACGAAACAGAAAGTGTATCCTGTACACCTGCATGCACCC CAAGCAACCGTCTCACAGCTAAAGGAGCAGAGGAGACTCTTGACCTCAGGTAAGCTTCAGGAAGAGGAG CAGGCTTCAAGTCTCACAGTGAAGCTCTGCTGTGGCTGTTCCACTCAATCTGTCCAGCAGGCAGTTATT TCTTCATATGTTTCCCATCAAGTTTCAGATTATCAAAATTACATAAATAATGATCATCTTTCTGCAAGGC AACAAAGTTAAACGCTTTTAGTAAACATAATGTAAATATACATAAAATAATAATATTTTCATCTCCAAT AGAGAAGGATGTTAACTTGAGAGTCAGATAAAAAACGTTTGCCATATGTTTACAAAAGCCTAGTTTCTTA ACTGCAAGTCAGCATATCCCCAAAACACAAGTAATTAAGGAATGATGTGTGTTACTTTCTCTGCTCCCTTT TTAAAAATGAACCATCTATGCCATGTTCTTTCAATTGGCCTGGGATGTAATAAGTTTCCAAGAAAAA CAATTTATATACAAATAATATATTACCTTGTAATGAATAATGTGCTCTGCTTCAATTGACACTGAAAAGTAA TTAACAAAGAAAAATAAACTACTTTGTAGAAAAGAAAAAACCATCTGAAGAAGAGACTGGAAACCAAAAGGA GTAAGATGTCCAAAGAGCAGACTCGGCTTCTGCTCTGAGAGCCAGCACGTCACAGCCATGGGCG TTCCCCACCTCCCCAGACCTCATCATCAGCTCCACCCAAACACTTCCCTCAACTGAGGTACACTTTCCTGG TCCCCCTTTTGATTCAATTTCTTCAACCCAAATGTAGGAATCTGATTTTCATCTTCTACTGAAAAAATGACA TCAATCATCAGCCAGTAAATCAAATGTATAGACTGAGAAATTAACGTGATTTTAATCTTTTGCTTCCACAG GCATAATTGATGAACCTTGACATTATCTCTGACTGCAGGAAGTTTCTGTCTCTGTCTGTTTGGGAAGAG ACAGAGAACTGCGGAATCTGGAATTTTCAAGCTTCTGACATAACCATGCTCTCTTTTCCCTTTAGGATTT CATTCCTTTTGCTCACTAATTTGTTCAAGTTTCTGACATAACCATGCTCTCTTTTCCCTTTAGGATTT TCACACACCATATTTCTTTTCACTTTTAACTCTTACCTGGCCAACTTATCCACCTCTGGATCCCAATA TTGAGATCTTATCTCAGGGAATCTCCTACTTAGACCTTGTACAGGTTAAATCTTCATGGTGTCTGTGTT TCCTAGGAACCTTTCTTTTCTACTGTTTATGACAACTGAAGTTAATAAGTGTGTTTATCTTTCCACCTA CTCAAAGTAGTTCCAAGATTAGGCTAGTTTGTAAATCTGTGACCACTGTAAACGAGGCCCTAGTTTCAG TGCTGCTCATGGGAAGCTTCCAAATAAATACCTTTGCTCAACGAAAAAATGAACCCAGTGGCTCAG CCTGTAATCCCAGCACTTTGGGAGGCCGAGGTGGATTGCTTGAACCAAGGTGAGGTTTGAGACTAGTCT GGCCAACATGTTGAACACTATCTCTACTATAAAATAACAAAAAATTAGCTGGTATGGTGGCTTACGCCT ATAATCCCAGCTACTCAGGAGGCTGAGGCAGGGGAATTGCTTGAACCAAGGAGGTGGAGTTGCAGTGAG CTGAGATCGCACCACTGCACCTCCAGCTGGGTGACAGAGCGAGACTCCATCTCAAAATAAAAAAGTAAAA AAAAAAA
27	T cell receptor associated transmembrane adaptor 1	>gi 54607136 ref NM_016388.2 Homo sapiens T cell receptor associated transmembrane adaptor 1 (TRAF1), mRNA GAGGCACAGATAAAGATAAGTTTACTGTGTCATGCTGCTTTTAAACATAACAGAGCAACATCACCTAGGAAA AAAGTTTGTAGGAGGATTTTAAATCCATATATTTGTCTTTATGGCTAGATAAAGATTTCTCTGAAAAAAG AAGCATGTCAGGAATCTCTGGGTGCCCTTTTCTCTGCGGACTTCTAGCATTGTGGGCTTGGCTTTG

		GTATATCACGTGATCTTCAATATTTCCCACTATGTGGAAGCAACGACAAGATAAAATGTACAGCTACT CCAGTGACCACACAGGGTTGATGAGTATTATATTGAAGACACACCAATTTATGGTAACTTAGATGATAT GATTTCAGAAACCAATGGATGAAAATTTGCTATGAACAAATGAAAGCCGACGAGAGAAATCTGTAAATAAG ATGCAGGAAGCCACCCCATCTGCACAGGCAACCAATGAAACACAGATGTGCTACGCCCTCACTTGATCACA GCGTTAAGGGGAAGCGTAGAAAGCCAGGAACAGAACTACTCATTTCTCAGACAAGGATGGAGATGAGCA ACTACATGCAATAGATGCCAGCGTTTCTAAGACCACCTTAGTAGACAGTTTCTCCCGAGAAAGCCAGGCA GTAGAGGAAAACATTTCATGATGATGCCCATCAGACTGTTTGGAATTGATCCGTCTAAGAGAGAAACCTATAA ACTAGCTGGACCATGATCTAGTTCAATGATTTGGCTCCTATTGAAGATGGCTTCTAAGAAAACAAAGATGC ACAGAGGACACAGAAGGACTTTGGCAGCAGGGTGATGACCTGATCATTTTGTGATGGGATGGTGGCTTACC TCTTATTCACAGCTTACACTTATGCATGCCAAATGTAAGGCCATGAAAATCAGTATTTCAAATAACTTAA AAAATGCTTTACTACTAAAATGTAAAAAATTAATGTGCTCACCTCGGCAGCACATATACTAAAAAATTAAT AAGACCCAGCTTGAAAAATTGAGCCTGATAACAAGATTACAAATTCACAATACCTAATACTTAGGGAAAA TAAAAAATTAAAGCATGAATGCGTTCTGTGAACACAGTTAGAAAGAAAATAAAGCCCAATGAGTTTTTTAA ATTCTCCTTTCTCACCAATGGGCAATAGCCCAATAATTGAAATAAATTTCTGATTGAAAGGTATAGGAAAC ATTAAAAATGCATTAAGAGAGAAAGTAATAAATTTCTTACAAGATATTTTCCCAAAGATAGCTTTTACT ATTTCAAAAAATTTGTCAAAATTAATGCATGCTCCTTACAACAAAACAATAATCAAAAAGAGTTTAGGAATTTCT ACTAGCCAGAGATAGTCACCTTGGAGAAACTTTCTATATATATCCTTCTAAATATTTTCTGGCATGCTTAT GTATGTACATCAGTTGTTTCTTTTATTTTGAAACCAAAATGTGGTTTCTTTGTACACATTACTTTAAAC TTTCTTTCCAGTCAACAATATATTTGTGATTTTATTTTCACTGTTATATTAACTATATAATAAATACGCAT ATATTGTAATTTTAATGTTCTGCTTAGCACCCCACTGATAACCAAAATCACAGTTTATTTTAAATAATTTTAA TGACTTTTCAAAAAACAATTTATTTGATGCAAAAAGCAAGGTTGAGATGACAATGTTTCTTTCAATAATTA AAAATACTGCTTCAC
28	SLAM family member 7	>gi 19923571 ref NM_021181.3 Homo sapiens SLAM family member 7 (SLAMF7) , mRNA CTTCCAGAGAGCAATATGGCTGGTTCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAG GGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAA GTCCAAAGTAAGCAAGTTGACTCTATTTGCTGTGACCTTCAACACACACCCCTCTTGTCAACATACAGCCA GAAGGGGGCACTATCATAGTGACCCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACT CCCTGAAGCTCAGCAAACTGAAGAAGAAATGACTCAGGGATCTACTATGTTGGGATATACAGCTCATCACT CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCTACGAGCACCTGTCAAAGCCTAAAGTCAACCATG GGTCTGCAGAGCAATAAGAAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAG ATGTGATTTTATACCTGGAAGGCCCTGGGGCAAGCAGCCCAATGAGTCCCATAATGGGTCCATCCTCCCCAT CTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCTGTGTCAGCAGAAACTTC

		TCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATGGTCTCTCC TGTTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGCTATTTCTTTGGTTCTGAAAGAG AGAGAGACAAGAAGAGTACATTGAAGAGAGAAGAGAGTGGACATTTGTCTGGGAAACTCCTAACATATGC CCCCATTCTGGAGAGAAACACAGAGTACGACACAATCCCTCACACTAATAGAACAAATCCTAAAGGAAGATC CAGCAAAATACGGTTTACTCCACTGTGGAATACCGAAAAGATGGAAAATCCCCACTCACTGCTCACGAT GCCAGACACACCAAGGCTATTGCTTATGAGAAATGTTATCTAGACAGCAGTGCACCTCCCTAAGTCTCTG CTCAAAAAAACAATTCTCGGCCCCAAAGAAAACAATCAGAAGAATTCACTGATTTGACTAGAAAACATC AAGGAAGAATGAAGAACGTTGACTTTTTCAGGATAAATATCTCTGATGCTTCTTTAGATTTAAGAGT TCATAATTCCATCCACTGCTGAGAAATCTCCTCAAAACCAGAGGTTTAAATCACTTCATCCCAAAAATGG GATTGTGAATGTCAGCAAACCATAAAAAAGTGTCTTAGAAGTATTCTTATAGAAAATGTAAATGCAAGGTC ACACATAATTAATGACAGCCTGTTGTATTAAATGATGGCTCCAGTCTGAGTCTGGAGTTTCAATCCATCCC AGGGCTTGATGTAAGGATTATACCAAGAGTCTTGCTACCAGAGGGCAAGAACCAAAAACAGACAGAC AAGTCCAGCAGAAAGCAGATGCACCTGACAAAAATGGATGTATTAATTGGCTCTATAAACTATGTGCCAG CACTATGCTGAGCTTACACTAATTGGTCAGACGTGCTGTCTGCCCCCTCATGAAAATTGGCTCCAAATGAATG AACTACTTTCATGAGCAGTTGTAGCAGGCTGACCACAGATTCCAGAGGGCCAGGTGTGGATCCACAGG ACTTGAAGGTCAAAGTTCACAAAGATGAAGAATCAGGGTAGCTGACCATGTTTGGCAGATACTATAATGG AGACACAGAAAGTGTGCTATGGCCCAAGGACAAGGACCTCCAGCCAGGCTTCATTTATGCACTTGTGCTGCA AAAGAAAAGTCTAGGTTTAAAGGCTGTGCCAGAACCCATCCCAATAAAGAGACCGAGTCTGAAGTCACAT TGTAATCTAGTGTAGGAGACTTGGAGTCAGGCAGTGAGACTGGTGGGCACGGGGGCAGTGGGTACTT GTAAACCTTTAAAGATGGTTAATTCAATTCATAGATAATTTATTAAGAACCTATGCGGCCCGGCATGGTGG CTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGGTGGGTGCTCATCTGAGGTCAGGAGTTCAAGAC CAGCCTGGCCAAACATGGTGAAACCCCATCTCTACTAAAGATACAAAAATTTGCTGAGCGTGGTGGTGTGC ACCTGTAATCCAGCTACTCGAGAGGCCAAGGCATGAGAAATCGCTTGAACCTGGGAGGTGGAGGTTGCGAG TGAGCTGAGATGGCACCACTGCACTCCGGCCTAGGCAACGAGAGCAAAACTCCAATACAAAACAAAC AAACACCTGTGCTAGTCACTGTCGACGTAAGATGAACATCCCTACCACACAGAGCTCACCATCTCTTT ATACTTAAGTGAAAAACATGGGGAAGGGGAAATGGCTGCTTTTGATAATGTTCCCTGACACATAT CTTGAATGGAGACCTCCCTACCAAGTGATGAAAGTGTGAAAAAATTAATAACAAATGCTTTGTTGGGCAA GAATGGGATTGAGGATTATCTTCTCTCAGAAAAGGCATTGTGAAGGAATTGAGCCAGATCTCTCTCCCTAC TGCAAAACCCCTATTGTAGTAAAAAAGTCTTCTTTTACTATCTTAATAAAACAGATATTGTGAGATTCAAAA AAAAA
29	chromosome 4 open reading frame 7	>gi 50428928 ref NM_152997.2 Homo sapiens chromosome 4 open reading frame 7 (C4orf7), mRNA TAAACAGCTACAATATTCAGGGCCAGTCACCTTGCCATTTCTCATAACAGCGTCAGAGAGAAAGAACTG

		ACTGAAACGTTTGAGATGAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCAGTGGCTGTTGGTTTCC CAGTCTCTCAAGACCAGGAACGAGAAAGAAAGATATCAGTGACAGCGATGAATTAGCTTCAGGGTTTTT TGTGTTCCCTTACCCATATCCATTTCGCCCACTTCCACCAATTCCATTCCAAAGATTTCCATGGTTTAGA CGTAAATTTTCTATTCCAATACCTGAATCTGCCCCCTACAACTCCCTTCCCTAGCGAAAGTAAACAAGAA GGAAAAGTCACGATAAACCTGGTCACCTGAAATTGAAATTGAGCCACTTCTTGAAGAATCAAAATTCCT GTTAATAAAGAAACAAATGTAATTGAAATAGCACACAGCATTTCTCTAGTCAATATCTTTAGTGATCT TCTTTAATAAACTTGAAAGCAAGATTTTGGTTTCTTAATTTCCACAAA
30	Major histocompatibility complex, class II, DQ alpha 1	>gi 52426772 ref NM_002122.3 Homo sapiens major histocompatibility complex, class II, DQ alpha 1 (HLA-DQA1), mRNA ACAATTACTCTACAGCTCAGAACACCAACTGCTGAGGCTGCCCTTGGGAAGAGGATGATCCTAAACAAAGC TCTGCTGCTGGGGCCCTCGCTCTGACCACCGTGATGAGCCCCCTGTGGAGGTGAAGACATTTGTGGCTGAC CACGTTGCCCTTTGTGTTAAACTTGTACCAGTTTACCGTCCCTCTGGCCAGTACACCCCATGAATTTG ATGGAGATGAGCAGTTCTACGTGGACCTGGAGAGGAAGGAGACTGCCCTGGCGGTGGCTGAGTTTCAGCAA ATTTGGAGGTTTGGACCCGAGGGTGCACTGAGAAACATGGCTGTGGCAAAACACAACTTGAAACATCATG ATTAAACGCTACAACTTACCGCTGCTACCAATGAGGTTCTGAGGTACACAGTGTTCCTCAAGTCTCCCG TGACACTGGGTCAGCCCAACACCTCATTTGTCTTGTGGACAACATCTTTCCTCCTGTGGTCAACATCAC ATGGCTGAGCAATGGGCAGTCAGTCACAGAAAGGTGTTTCTGAGACCAGCTTCTCTCCAAGAGTGATCAT TCCTTCTTCAAGATCAGTTACCTCACCTTCTCCCTTCTGCTGATGAGATTTATGACTGCAAGGTGGAGC ACTGGGCCCTGGACCAGCCTCTTCTGAAACACTGGGAGCCTGAGATTCCAGCCCCCTATGTCAAGACTCAC AGAGACTGTGTTCTGTGCCCTGGGGTTGTCTGTGGGCTCATGGGCATTTGTGGTGGCCTGTCTTCATC ATCCAAGGCTGCGTTTCAAGTGGTGCTTCCAGACACCAAGGCCATTTGTGAATCCCATCTCTGGAAGGAA GGTGCAATCGCCATCTACAGGAGCAGAAAGATGGACTTGCTAAATGACCTAGCACTATTCTCTGGCCCCGAT TTATCATAATCCCTTTTCTCCTCCAAATATTTCTCCTCTCACCTTTTCTCTGGGACTTAAGCTGCTATATC CCCTCAGAGCTCACAAATGCCCTTTACATTTCTTCCCTGACCTCCTGATTTTTTTTTTCTCTCAAATG TTACCTACAAAGACATGCTGGGGTAAGCCACCGGCTACCTAATTCCTCAGTAACCTCCATCTFAAAATC TCCAAGGAAGCAATAAATTCCCTTTTATGAGATCTATGTCAAATTTTTCATCTTTCATCCAGGGCTGACT GAACATAATGGCTAATAATTTGGGGTACTCTTATGTTTCAATCCAAATTTAACCCTCATTTCCAGATCATTT TCATGTCCAGTAACACAGAGAGCCACCAAGTACAGTATAGCTGATAAATATGTTGATTTTCTTAGCTGACAT TAATAATTTCTTGTCTTGTGTTTCCACCTTGGCACTGCCACCCCTCAATTCAGGCAACAAATGA AATTAATGGATACCGTCTGCCCTTGGCCCGAGAAATTTTATAGCAAAAATTTTAGAACCAAAAATAAGTC TGTAATAATTTCAATGTGGCTTTTAAAGTATGACAGAGAAAATAAGTTAGGATAAAGGAAATTTTGAATCT CA

31	Transcribed locus	>gi 3807951 gb AI225238.1 AI225238 qx12c04.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2001126 3', mRNA sequence AGCGCCGCCCTTTTCTTTTGAATGTTTATATATTTTCTCTCTCACCACATTAGA GATTCACATGTCAAAAAAGTTCAAAGATTCACCTTAAATGGTAGTCAAAATTAAAGCATGTTGTTT AATTGCCAACTATCCATAAATCCTGTGCTTGAAGCACTACCTTTTATCAACCACCTTGAAAGGAAGGAA TATGAAGTGTGACTCTTGAGGATTGCAGTTCATTTCTCCACAGACATAGCAGGGTGTAGTTCCTCCAAAT GGTTTCTTCCAAAGTCATCTCCTCAGAGTAGGACTGTCTGAGTAGTCATTCTGATAATGTTGCCATTAA CTACAAGCACATCTGAGAACCTCGTAAGGAAGTGCCATTAGATTTCAGA
32	Amphiphysin (Stiff- Man syndrome with breast cancer 128kDa autoantigen)	>gi 51466133 ref XM_499518.1 PREDICTED: Homo sapiens LOC442534 (LOC442534), mRNA GGCCAGCCCTAGGAGGGGCGAGTCCACAGCAGGCTCACACCCCTGCCCTTCAGAGTTGCAGCAGCTAAT GCTGATGCCAGGACCTTGTCTCTGCCAGGAAGCCTCTGATTAGGGCTGTGAACCAACTTCTCTTTCACATC TGCAAGGACTCTGCTCTAAGCTCAAAATTTTGCAGTTTCTGCTGTCAATCACAGCTGGGAATGAGAAAGGGA AGGGCTCCAGTTGGTCTCCCTCTGCTCTGAGCACACGTTGAGGACATGAGGCTTCCGCGAGGAACAGC TCTGAAAGCTGAGTTCTCGGGTCCCTGTGAAGGAGGGAAGCTTGCTGCTGCTGAGCGTGAAAAAGTCTT GCTGGACAGAGTCTCACGGTTTAAAACTGGGAAGGAGAGGATTGAGATCACACTAGAAATGCACAGAAA ATTCTT
33	dendritic cell- associated lectin-1	>gi 40548404 ref NM_172004.2 Homo sapiens dendritic cell-associated lectin-1 (DCAL1), mRNA ATGGTTAGTAATTTCTTCCATGTATACAAAGTATTCGAGAAATCTGTACCTTGATTAGTAAGACTGAAC ACATTGGTTTGTGTCATTTATTCATGGAGGAAGTCCACCACCACTTGGGAGCAGAGGAAATTTGCCAT CTCAATTTACTTATCAGAAAGTTTCTTTGCAGAAATATGATTGTCCCTTCAGTGGGACATCATTTGTGGTC TTCTCTCTCTTTTGTATCTGTGCAATGGCTGGAGATGTAGTCTACGCTGACATCAAAACTGTTTCGGACTT CCCCGTTAGAACTCGCGTTTCCACTTCAGAGATCTGTTTCTTTTCAACTTTTCTACTGTCCATAAATCATG TCCTGCCAAAGACTGGAAGGTGCATAAGGGAATGTTACTGGATTGCTGAAACTAAGAAATCTTGGAAC AAAAGTCAAAATGACTGTGCCATAAACAATTCATATCTCATGTGATTCAAGACATTTACTGCTATGTTGA GATTTAAACATTTAGAGGTGACAGCATCCCCACACTGGCAGTGAATTTTGTGTGTACAAACTTGGCAAA AGTCTGTGAAAAGAGTTTCAACTTCAATGTGTATTAATACTATACAAATATTAGTTGAATGAATGTTGAA TTACAAAAAATAAAAAA

Table 1B Probes for identifying genes of Table 1 (and their fold upregulation in Mage cancer patients)

Probe set ID	Gene name	Probeset sequence	Full gene sequence	Fold change
155897 2_s_at	chromosome 6 open reading frame 190	ttctaagaccacacatttggttatt gaaggccacagcgaatcttaacct aacagccttgac aaactgcaccataggtgttttag actcataataatttggtatttttca aacaatagtga taattaatattntgttttgaatt tgagnacaattaaatttgtacttt tagtaactacca ttctttgattagaaaaattagaga atgcataatcttactttggttgtaa attatcaagggc tttctaatagaatcatatataac atttctaataataagtcctttcac atactgtgttc cagttgtcttgataattgaaaagtg taataaacttcacgtcacctat [Seq ID No 49]	>gi 58218985 ref NM_001010923.1 Homo sapiens chromosome 6 open reading frame 190 (C6orf190), mRNA ATACTTACAATTACGAGATTATATTGTCATTAGTCTCTTTGGCTGG TGGGTAGGGGTGAGAGGCTCTTC CTGGATCCCTTATTTTCTACAGGAGAGGAGGAAAAACACCTGGGATGC TCCAGTGTCTTTACGCAGATAAT GATCATTAAATCAGCCCTCTCTGATCAAAAGAGCTACTCCACCCCACT CTGGCTGTAGTGTGACATTCCTG CCTGCCCTGAGGAAGAAATGGTGAGCAGGGGCTGCAATTGCAGACAAG TGTCACCCAGAACCCACAAGTTT CTGTGAGCACCCAGGTCTACAAACTACCCAAAGGCATAGCAATGGCATT ATCACTGGAAGAAATCGTCCACT CCCTTGACCTCAGGACCTTACCCAGGGTCTAGAAATCCAGGCAGGC ATCTATCTTTGAAGGCTCTATTTA TGAATGTTTTGGAAATGAATGCTGTTTTTCAACAGGAGAGTGATTA AAATTACTGTGCTCAAAAGTTAAG AAGATCATAGCTGAAATTTGTGAGCAGATTGAAGGTTGTGAGTCTCT ACAGCCATTTGAACTGCCTATGA ATTTTCCAGGTCTTTTAAAGATTGTGGCTGATAAACTCCATACCTT ACTATGGAAGAAATCACAAGGAC CATTTCATATTGGACCAAGTAGACTAGGGCATCCTTGCTTCTATCATC AGAAAGGATATAAAACTAGAGAAC CTCATCATAAAGCAGGGTGAGCAAAATCATGCTCAACTCAGTTGAAGA GATTGATGGAGAAATAATGGTGA GCTGTGCAGTAGCAAGGAATCATCAAACTCACTCATTTAATTGTCCT TTGTCACAAGAGGAGAAATTTA CGAGTGTGAAGATGAACGTATTTTACACTCTAAAGGAGATTGTTGAAT	44.93

		GGAAGATTCCCTAAGAACAGAACAA AGAACTGTAAACCTTACAGATTTTTCAAATAAGTGGGACTCAACGAA TCCATTTCCCTAAAGACTTTTATG GTACCCCTGATTCTCAAGCCTGTTTATGAAATTCAAGGTGTGATGAAA TTTCGAAAAAGATATAATCCGCAT CCTCCCAGTCTAGATGTCGAAGTCAAAGACATCACTGATTCTTACG ATGCTAACTGGTTTCTTCAGCTG TTATCAACAGAAAGATCTTTTGAATGACTAGTAAAGAGTTCCCCAT AGTGACTGAAGTCATAGAAGCAC CTGAAGGAAACCACTGCCCAAGCATTTTACAGCCTGGGAAAACC ATTGTGATCCACAAAAGTACCA GGCATCAAGAACTTTAGCTTCAGAAATTAGAAGCAATTTTCTCTAAAA GACACTTCTTGATCCCCACTAGC TATAAAGGCCAAGTTCAAGCGCGACCGAGGGAGTTCCCCAACGGCCTA TGACCTAGAGATCGCTAAGAGTG AAAAGGAGCCTCTTTCACGTGGTGGCCACCACCAAGCGTTTCATTCCCCCT CATGACAAGCTGTCAATCCGTATC TGTTGGGGACCAAGTTTCTGGTGTCATCAGTCAGAGACGACTGAAGTCC TCTGTGAGGGAATAAAAAAAGTG GTGAATGTTCTGGCCTGTGAAAAAATCCTCAAAAAGTCTCTATGAGGC TGCGCTGCTCCCTTTGTACATGG AAGGAGGTTTTGTAGAGGTGATTTCATGATAAGAAACAGTACCCGATT TCTGAGCTCTGTAAACAGTTCCG TTTGCCCTTCAATGTGAAGGTGCTGTCTCAGGGATCTTTCCATTGAAG AGGACGTGTTGGCTGCCACACCA GGACTGCAGTTGGAGGAGGACATTACAGACTCTTACCTACTCATAAG TGACTTTGCCAACCCACGGAGT GCTGGGAAATTCTGTGGCGCGCTTGAAATATGACTGTTCACTTAGTT AGTAATTTCTCTAGGGATGCCAGA ACCATTTCTAGTCAGGACTCTGGTAGAAGAGATCACTGAAGAGCAAT ATTACATGATGCGGAGATATGAA AGCTCAGCCTCACATCCCCCACCTCGCCCTCCGAAACACCCCTCAGT AGAGGAAACAAAGTTAACCCCTGC TAAACCTTAGCAGAAAGAAAGGACGGTAGACCTGCCCAAGTCTCCCCAAG

		CGTCATCACGTAGACATAACCAA GAAACTTCACCCAAATCAAGCTGGCTGGATTCAAAGTACTGATTG GTAGTCAGAATGATTTGGTGGAT GAAGAGAAAGAAAGGAGCAACCGTGGGGCCACAGCAATAGCAGAAAC ATTCAAAAATGAAAAACATCAAA AATAACAAGATGTGACAGAAAGCCACTTAGGCAGCAACATAAATGTT GCAGTGAAAAAAGAGCTAGCCT TCTAGCTGAAAAACGAGTATTCCCAATGGACTCCAGAAAGAACTTG ATTCAATCGCTGCAAGGAAAGAA CAACCTTAAACTTTTACAGATAAACTTACAGAAACCTATGATAT AGAAATTCATATAGTCTATTCTGT TGTGTCTAAATCTGTAGGCATTGTGTGTGTTGTTCTTTAGGACGTATT TATTTAACTTGCACATTTTTC GATTCTTATTTCTACTACCAACAATAAGTAATTGGGAAATAATTCT GTATTTCAAGTTTCTGAGTAAAC CAGTCTGAAATAGGATAAAAGCCACCACCAATAATTTCTTTTTTTTCCA GAATTTGTTTGGCATTTTTC TGCTATCATCATTCCTAACAGACTAACTTACAGAAAAATAATTATA TCTGACTGATTTAAAAATGTTTCAG GTTTCTTATCCAAATCCCTTGGAACTATGGAAAGGAGTTTGATTTC CATTCACAGTGTATTTACAAAAT ACGCTGTGTCATAAATATGTTTGAATTCCAACAGCCAAAGCCATTGA GAGTCATAGGAGTTTTCATAAC CTTCTCTTCTATGACCCCAACAACAGCTCATGACTGAAAATTTCCACCA GATTTCTGAGACGATGTCCTTAAT ATTCTATGTGCTATGTACCAGATAAATCTTTAGATGAATGTTTCTTA GGATTGTAGGAAAAATTTCTAGT TAATCATAAATATTTGATGGAAGAAAAAGACAATAAATGTAAATAT AATAAATTTGGCTGACAAAGAAC CAAAGTGATTCCTTAATTAGTATACATCAGAATGATGCTCTTATAGTT GTACCATCTATAAAAAATTACTTT AAGGGCTCTCACATTTTAAATAATTTATCTTATTATGTATTAAGTATA CAGGAACAATATTTTTCCTT TAACAAAATGAAGAGACAGGCTATCTGGTTAATGTTACATAGGAATT
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202957 _at			TAATAGTAATGCTTGAACTTCAT CCATAGATCATACTCTGTACAAAATTGTTAGCTAACATCCTATCTC ATAATTATTTTATGTTTGTGGA GAAATTGTTGATTTTGTACCAAAAGTGTCTCTGAAGACAATAAATTG TGAGTCAACTTTAGAACAAAAA AATTAGAGTTTTTTCAATGTTTATATTCTGATTAAAGCTTACTTTACC TTACATTTTTTTCTAAGTAACAAT GAATCCTGATTTCTAGTGTCTTAAATAATTGCTTAGTGATTGATTGT GGTAATATCATTTCTTATCTACA ATGTCATAAAGTTTTATGGGACAGTTTTTCTTTTATTATTATTGCGCTG TTTGTGCAGATAAGAACAGAAAC TTTTTCTAAGACCCACATTTGGTTATTGAAGGCCACAGCGAATCTTAA CCTAACAGCCTTGACAAACTGCA CCATAGGTGTTTTTTAGACTCATATAATTGTTATTTTTTCAAACAATA GTGAATAATAATTTTGT GGAATTTGAGAACAAATTAAATTTGTACTTTTAGTAACCTACCATTCTT TGATTAGAAAATTAAAGAGAAATG ATATCTTACTTTGGTTGTAATAATTATCAAGGGCTTTCTAATAGAAATC ATATAAACATTTCTAAATATAA GTCCTTTCACATACCTGTGTTTCCAGTTGTCTTGATATTGAAAAGTGT AATAAATTCATGCTCACCTATT GGAGATTTGGGAAGTTGAAAATAAACTTCCTAATTTTTTAAAAAAA AA	19.09
	hematopoie tic cell- specific Lyn substrate 1	ttgctggcttctcttataactaacc cagagtttgatcatatgtgtagg tgaatgcaaac ccatcgttgagccctgggtgtaag acttcaagccaagcgatgtatca attctagcttc caggattcacgggtgcacatgctgg cattcaacatgtggaaagcttgct ttagagggcctt ctgtatgtgtagcttgctagttt	>gi 37059786 ref NM_005335.3 Homo sapiens hematopoietic cell-specific Lyn substrate 1 (HCLS1), mRNA GTGGACGCGAGGAGCCGGCGCTTAGAACAGAGGCTTGCACAGGTGG AGATGTGGAAGTCTGTAGTGGC CATGATGTGCTGTTTCCGTGGAGACCCAGGCTGATGATTGGGACAC AGATCCTGACTTTGTGAATGACA TCTCTGAAAAGGAGCAACGATGGGGAGCCAAGACCATCGAGGGGTCT GGACGCACAGAACACATCAACAT CCACCAGCTGAGGAACAAGTATCAGAGGAGCATGATGTTCTCAGGA	

		gttttctacatttgaaaaatgttta gtttagaataag cgcatatccaattatagaggtac aatttccaacttccagaaactc atcaaatgaaca gacaatgtcaaaactactgtgtct gataccaaaatgcttcagtatattg taatttttcaag tcagaaagctgatgttcctggtaaa agtt [Seq ID No 50]	AGAAAGAGATGGAGTCAGGGCCC AAAGCATCCCATGGCTATGAGGTCGGTTTGGAGTAGAAAGAGACCG AATGGACAAGAGTGCAGTGGGCC ATGAGTATGTTGCCGAGGTGGAGAACCACTCTTCTCAGACGGATGCT GCCAAAGGCTTTGGGGGCAAGTA CGGAGTTGAGAGGACAGGGCAGACAAGTCAGCAGTCGGCTTTGATT ATAAAGGAGAAAGTGGAGAAGCAT ACATCTCAGAAAGATTACTCTCGTGGCTTTTGGTGGCCGGTACGGGGT GGAGAAAGGATAAATGGGACAAAG CAGCTCTGGGATATGACTACAAGGGAGAGACGGAGAAAACACGAGTCC CAGAGAGATTATGCCAAGGGCTT TGGTGGCCAGTATGGAATCCAGAAGGACCGAGTGGATAAGAGCGCTG TCGGCTTCAATGAAATGGAGGCC CCGACCCACAGCTTATAAGAAGACGCGCCCATAGAAAGCCGCTTCTAG TGGTGCCCGTGGGCTGAAGGCCA AATTTGAGTCCATGGCTGAGGAGAAAGAGAACCGAGAGGAAGAGGAG AAGGCACAGCAGGTGGCCAGGAG GCAACAGGAGCGAAAGGCTGTGACAAAGAGAGGCCCTGAGGCTCCAC AGCCAGTGATAGCTATGGAAGAG CCAGCAGTACCGGCCCCACTGCCCAAGAAAATCTCCTCAGAGGCCCTG GCCTCCAGTTGGGACTCCTCCAT CATCAGAGTCTGAGCCTGTGAGAACCCAGCAGGGAACACCCAGTGCCC TTGCTGCCCATTAGGCAGACTCT CCCGAGGACAATGAGGAGCCCCCAGCTCTGCCCCCTAGGACTCTGG AAGGCCTCCAGGTGGAGGAAGAG CCAGTGTACGAAGCAGAGCCTGAGCCTGAGCCCAGCCTGAGCCCCGA GCCTGAGAAATGACTATGAGGACG TTGAGGAGATGGACAGGCATGAGCAGGAGGATGAACAGAGGGGAC TATGAGGAGGTGCTCGAGCCTGA AGATTCTTCTTTTCTTCTGCTCTGGCTGGATCATCAGGCTGCCCGG CTGGGGCTGGGGCTGGGGCTGTG GCTCTGGGGATCTCAGCTGTGGCTCTATATGATTACCAAGGAGAGGG AAGTGATGAGCTTTCCTTIGATC CGGACGACGTAATCACTGACATTGAGATGGTGGACGAGGGCTGGTGG
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			CGGGACGTTGCCATGGCCACTT TGGACTCTTCCCTGCAAAATTATGTCAAGCTTCTGGAGTGA TAGAGC TCACTGTCTACTGCAACTGTGAT TTCCCATGTCCAAAGTGGCTCTGCCCTCCACCCCTCCCTATTCTCTGA TGCAAAATGTCTAACCCAGATGAGT TTCTGACACAGACTTCCCTCTCTCTGCTTCATTAAGGGCTTGGGCAGA GACAGCATGGGGAAGGAGGTCCC CTTCCCAAGAGTCTCTCTATCTCTGGATGAGCTCATGAACATTTCT CTTGTGTTCTCTGACTCCTTCCCA ATGAACACCTCTCTGCCCACCCCAAGCTCTGCTCTCCTCCTCTGTGAG CTCTGGGCTTCCAGTTTGTTA CCCGGAAAGTACGTCTAGATTGTGTGGTTTGCCTCATTTGTGCTATT TGCCCACTTTCCTTCCCTGAAGA AATATCTGTGAACCTTCTTTCTGTTTCAGTCTTAAATTCGAAATAAA GTGAGACTATGTTTCACTGTAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAA	
204116 _at	interleukin 2 receptor, gamma (severe combined immunodeficiency)	ttctgggtggaacggacgatgccc cgaattccccaccctgaaagaacctta gaggatcttgtt actgaataccacgggaactttctg gcctggagtgggtgtgtctaaggga ctggctgagagtctgcagccagac tacagtgaacgactctgcctcgtc agtgagattcccccaaaaggaggg gcccttggggaggggcctggggcc tccccatgcaaccagcatagcccc tactgggcccccccatgttacacc ctaaagcctgaaacctgaacccca atcctctgacagaagaacccagg gtcctgtagccctaagtggtaacta acttccttcattcaaccacactg cgtctcactacacctcacccac tgtggctgatttggaattttgtgc	>gi 4557881 ref NM_000206.1 Homo sapiens interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG), mRNA GAAGAGCAAGCGCCATGTTGAAGCCATCATACCATTCACATCCCTC TTATTCTCTGCAGCTGCCCTGCT GGGAGTGGGCTGAACACGACAATCTGACGCCCAATGGGAATGAAG ACACCACAGCTGATTTCTTCCTG ACCACTATGCCCACTGACTCCCTCAGTGTTCACACTCTGCCCTCCC AGAGGTTCAAGTGTTTTGTGTTCA ATGTCGAGTACATGAATTGCACCTTGGAACAGCAGCTCTGAGCCCCAG CCTACCAACCTCACTCTGCATTA TTGGTACAAGAAGTCCGATAATGATAAAGTCCAGAAGTGCAGCCACT ATCTATTCTCTGAAGAAATCACT TCTGGCTGTCAAGTTCGAAAAAAGAGATCCACCTCTACCAACATT TGTGTTTCAGCTCCAGGACCCAC GGGAACCCAGGAGACAGGCCACAGATGCTAAAACTGCAGAACTCTG GTGATCCCCTGGGCTCCAGAGAA	61.98

		ccccatgtaagcacc [Seq ID No 51]	CCTAACACTTCACAAACTGAGTGAATCCCAGCTAGAACTGAACTGGA ACAACAGATTCTTGAAACCACTGT TTGGAGCACTTGGTGCAGTACCGGACTGACTGGGACCAACAGCTGGAC TGAACAAATCAGTGGATTATAGAC ATAAGTTCTCCTTGCCTAGTGTGGATGGGCAGAAACGCTACACGTTT CGTGTTCGGAGCCGCTTTAACC ACTCTGTGGAAGTGTCTCAGCATTTGGAGTGAATGGAGCCACCAATCC ACTGGGGAGCAATACTTCAAAA GAGAAATCCTTTCCCTGTTTGCATTGGAAGCCGTGTTATCTCTGTTGG CTCCATGGGATTGATTATCAGCC TTCTCTGTGTGTAATTTCTGGCTGGAAACGGACGATGCCCCGAAATTC ACCTGAAGAAACCTAGAGGATCT TGTTACTGAATACCAACGGAACTTTTCGGCCTGGAGTGGTGTCTA AGGACTGGCTGAGAGTCTGCAG CCAGACTACAGTGAACGACTCTGCCTCGTCACTGAGATTCCTCCCAA AGGAGGGCCCTTGGGGAGGGC CTGGGGCTCCCATGCAACCAAGCATAGCCCTACTGGGCCCCC TGTTACACCCCTAAAGCCTGAAAC CTGAACCCCAATCCTCTGACAGAAGAACCCAGGGTCTCTGTAGCCCT AAGTGGTACTAACTTTCCCTTCAT TCAACCCACCTGCGTCTCATACTCACCCTCACCCTGCTGGCTGATT TGGAAATTTTGTGCCCCCATGTAA GCACCCCTTCATTTGGCATTTCCCACTTGAGAAATTACCCCTTTTGCCC CGAACATGTTTTTCTCTCCCTC AGTCTGGCCCTTCCTTTTCGAGGATTCTTCTCCCTCCCTCTTTCC CTCCCTTCCCTCTTTCCATCTACC CTCCGATTGTTCTCTGAACCGATGAGAAATAAAGTTTCTGTGATAAT CATC	
204661 _at	CD52 antigen (CAMPATH-1 antigen)	acagccacgaagatcctaccacaaa tgaagcgcttcctcttcctcctac tcaccatcagcc tcctgggtatggtagagatacaaa ctggactctcaggacaaaacgaca	>gi 68342029 ref NM_001803.2 Homo sapiens CD52 molecule (CD52), mRNA CTCCTGGTTCAAAAGCAGCTAAACCAAAAGAACCTCCAGACAGCCC TGAGATCACCTAAAAGCTGCTA CCAAGACAGCCACGAAGATCCTACCAAAATGAAGCGCTTCCTCTTCC	30.71

	/// CD52 antigen (CAMPATH-1 antigen)	ccagccaaaccagcagccccctcag catccagcagcatgagcggaggca ttttcctttctctcgtggccaatg ccataatccacctcttctgcttca gttgaggtgacacgtctcagcctt agccctgtgccc cctgaaacagctgccaccatcact cgcaagagaatcccctccatcttt gggaggggttgatgccagacatca ccaggttgtagaagttgacaggca gtgccatgggggcaacagccaaaa taggggggtaatatgatgtaggggccc aagc	TCCTACTCACCATCAGCCTCCTG GTTATGGTACAGATACAAACTGGA CTCTCAGGACAAACGACACCAG CCAAACCAGCAGCCCCCAGCAT CCAGCAACATAAGCGGAGGCATTTT TCCTTTTCTTCGTGGCCAAATGCC ATAATCCACCTCTTCTGCTTCAG TTGAGGTGACACGCTCTCAGCCTTA GCCCCCTGTGCCCTTGAACAGCT GCCACCATCACTCGCAAGAGAAAT CCCCCTCATCTTTGGAGGGTTGATG CCAGACATCACCAGGTTGTA GAAGTTGACAGGCAGTGCCATGG GGCAACAGCCAAATAGGGGGTAATG ATGATGTAGGGCCCAAGCAGTG CCCAGCTGGGGTCAATAAAGTT ACCCTTGTACTTGCAAAAAAAAAAA AAAAA	
205831 _at	CD2 antigen (p50), sheep red blood cell receptor /// CD2 antigen (p50), sheep red blood cell receptor	agacctcgagttcagccaaaacct ccccatgggagcagaaaaactca ttgtccccttccctcaattaaaaa agatagaaactgtctttttcaata aaaagcactgtggatttctgcct cctgatgtgcataatccgtacttcc atgaggtgttttctgtgtgcagaa cattgtcacctc ctgaggtgtgggcccacagccacc tctgcatcttcgaaactcagccatg tggtcaacatct ggagtttttggtctcctcagagag ctccatcacaccagtaaggagaag caatataagtg gattgcaagaatggtagaggaccg agcacagaaatcttagagatttct tgtcccctctca ggtcatgtgtagatgcgataaatc	>gi 31542293 ref NM_001767.2 Homo sapiens CD2 molecule (CD2), mRNA ACCAACCCCTAAGATGAGCTTTCCATGTA AATTTGTAGCCAGCTTCC TTCTGATTTTCAATGTTTCTTCC AAAGGTGCAGTCTCCAAGAGATTACGAATGCCTTGGAAACCTGGGG TGCCTTGGGTCAGGACATCAACT TGGACATTCCCTAGTTTTCAAATGAGTGATGATATTTGACGATATAAAA TGGGAAAAAATTTTCAAGACAAAG AAAGATTGCACAAATTCAGAAAAAGAGAAAGAGACTTTTCAAGGAAAAAG ATACATATAAGCTATTTAAAAAT GGAACCTCTGAAAAATTAAGCATCTGAAGACCGATGATCAGGATATCTA CAAGGTATCAATATATGATACAA AAGGAAAAAATGTGTTGGAAAAAATATTTGATTTGAAGATTCAAGAG AGGGTCTCAAAACCAAGATCTC CTGGAATTTGTATCAACACACACCCTGACCTGTGAGGTAATGAATGGAA CTGACCCCCGAATTTAAACCTGTAT CAAGATGGGAAACATCTAAACCTTTTCTCAGAGGGTCTATCACACACAA GTGGACCAACCGCTGAGTGCAA	22.66

137

		aggtgatgagggcaagagggcacct cctccaggtgcgaaggtccagctc agtggcacaagtgaagcaatgat cgagactaagacgggtataatccc tgagaccagattgtgacttgcaa tggaagagactggaagatgggaa gatgatggcagattacggcatcag aaagggcaacttactctcctggc atcttattgtattggagggtgacc accctgggatggggtgtggcag gggtcaaaaagcttatttctttta atctctactcaacgaacacatct tctgatgatttcccaaaattaatg agaatgagatgagtagagtaagat ttgggtgggatgggtaggatgaag tatattgccccaaactctatgttct ttga [Seq ID No 54]	GGACAAACACAGCAATCCAGGCA GGGGATTTCCAACTCAACTCTGGTATGTAAAGCTGCATGCAAAGTCCT TTTTCTGTCTCTGTGTTTCTGGCC CCTTGTCTGCAGAGATGGCTCCCAATGCTTCTGCTCTGTGTGCAT GTCCGTTCCGAGGAATGGGATTT AATGACCTTTGATGCCAACCCATATGACAGCGTGAAAAAATCAAAG AACATGTCCGGTCTAAGACCAAG GTTCCCTGTGCAGGACCAGGTTCTTTTGTCTGGCTCCAAGATCTTAAA GCCACGGAGAACCTCTCATCTT ACGGCATTTGACAAAGAGAAAGACCATCCACCTTACCCTGAAAAGTGGTG AAGCCCAGTGATGAGGAGCTGCC CTTGTCTTCTTGTGTGAGTCAGGTGATGAGGCAAGAGGCACCTCCTCC AGGTGCGAAGGTCCAGCTCAGTG GCACAAAGTGAAAGCAATGATCGAGACTAAGACGGGTATAATCCCCTGA GACCCAGATTGTGACTTGCAATG GAAAGAGACTGGAAGATGGGAAGATGATGGCAGATTACGGCATCAGA AAGGGCAACTTACTCTTCTCTGGC ATCTTATTGTATTGGAGGGTGACCCCTGGGCATGGGGTGTGGCA GGGGTCAAAAAGCTTATTCTTT TAATCTCTTACTCAACGAACACACATCTTCTGATGATTTCCTCCAAAATTA ATGAGAAATGAGATGAGTAGAGTA AGATTGGGTGGGTGGTAGGATGAAGTATATTGCCCAACTCTATG TTTCTTTGATTCTAACACAATTA ATTAAGTGACATGATTTTCTACTAATGTATTACTGAGACTAGTAAATA AATTTTAAAGCCAA	13.56
206118 _at	signal transducer and activator of transcript ion 4	gctgacatcctgcgagactacaaa gttattatggctgaaaacattcct gaaaaccctctg aagtacatatcctgacattccc aaagacaaaagccttcggtaaacac tacagctctcag ccttgcaagtttcaagaccaaca gaaaggggtgacaaaaggttatgtt ccttctgttttt	>gi 21618332 ref NM_003151.2 Homo sapiens signal transducer and activator of transcription 4 (STAT4), mRNA AGAGGACGCCCGGTGAAGGGCTCCAGCCTGGCAGTTTCTGCGTGT AGCATTTCTAGAAATAGAGTGGGT GGGAACTGACCCAAAGTAAAGTCCAGAGACTCGAACACTGACGCACA GGAAAGCCTCAAGTGGGAGGAGA AATGCAAAATCCCCTACTGATGATGCGGTGCGGCTTCTCTCCTAGGG ACTGTGAGGGCGCTTCTGACTT	

		atccccatctcaacaatccgaagt gattcaacagagccacattctcca tcagaccttctt cccatgtctccaagtgtgtatgcg gtgttgagagaaaaacctgagtc acaacaattgaa actgcaatgaagtctccttattct gctgaatgacaggataaactctga cgaccaagaaa ggaagcaaatgaaaaagttaaag actgttcttbgcccaataaaccaca ttttatttcttc agctttgtaaataccaggttctag gaaatgtttgacatctgaagctct cttcacactccc gtggcactcctcaattgggag [Seq ID No 55]	TGGACTTGAGCACTGCCTGGGACCTGTGTGAGAGAGCGCTAGCATG TCTCAGTGGAAATCAAGTCCAACA GTTAGAAATCAAGTTTTTGGAGCAGGTGGATCAATTCTATGATGACA ACTTTCCCATGGAAATTCGGCAT CTGTTGGCCCAATGGATTGAAAATCAAGACTGGGAGGCAGCTTCTAA CAATGAAACCATGCAACGATTCT TTCTTCAAAACTTTGTTAATACAACTGGATGAACAGTTAGGTCGTGTT TCCAAAGAGAAAACCTACTCTT GATACACAATCTAAAAAGAAATTAGGAAGGTCCTTCAGGGAAAAATTC ATGGAATCCAATGCATGTAGCT GTGGTTATTTCAAACCTGTTTAAAGGAAGAGAGAGAGAAATATTGGCTGC AGCCAACATGCCTGTCCAGGGGC CTCTAGAGAAAATCCTTACAAAGTTCTTCAGTTTCAGAAAGACAGAGG AATGTGGAGCACAAAGTGGCTGC CATTAATAACAGTGTGCAGATGACAGAACAGATACCAAATACTTAG AAGATCTGCAAGACGAATTTGAC TACAGGTATAAAACAATTACAGACAATGGATCAGAGTGACAAGAATAG TGCCATGGTGAATCAGGAAGTTT TGACACTGCAGGAAATGCTTAAACAGCCTCGATTTCAAGAGAAAAGGAG GCTCTCAGTAAATGACCCAAAT CATCCATGAGACAGACCTGTTAATGAACACCATGCTCATAGAAGAGC TGCAAGACTGGAAGCGCGGCAG CAAATCGCCTGCATCGGGGTCCACTCCACAATGGGCTCGACCAGCT TCAGAACTGCTTTACACTATTGG CAGAAAGTCTTTTCCAACTGAGAAAGGCAATTGGAGAAACTAGAGGAG CAATCTACCAAAATGACATATGA AGGTGATCCCAATCCCAATGCAAAAGAACTCACATGCTAGAAAGAGTCA CCTTCCTTGATCTACAACCTTTTC AAGAACTCATTTGTGGTTGAGCGCAGCCATGTATGCCAACCCACCC TCAGAGGCCGTTGGTACTTAAAA CCCTAATTTCAGTTCACTGTAAAACCTAAGGCTACTAATAAAATTGCCA GAACTAAACTATCAGGTAAAGGT TAAGGCATCAATTGACAAGAAATGTTTCAACTCTAAGCAACCGAAGAT TTGTACTTTGTGGAACATAATGTC
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		AAAGCCATGTCATTTGAAGAATCTTCCAATGGGAGTCTCTCAGTAGA ATTTCCGACATTTGCAACCAAAGG AAATGAAGTCCAGTCTGGAGGTAAAGAAATGAGGGCTGTCCATG GTGACTGAAGAACTTTCATTCAT AACGTTTGAAAACACAGATCTGCCTCTATGGCCCTGACCATAGATTGG AGACCAGCTCATTTGCCCTGTGGTG ATGATTTCCAAATGTCAGTCAGTTACCTAATGCTTGGGCATCCATCAT TTGTTACAACGTTGTCACCAACG ATTCCCAGAACTTTGGTTTTCCTTAATAATCCTCCACCCTGCCACATTG AGTCAACTACTGGAGGTGATGAG CTGGCAGTTTTCATCGTACGTTGGTCTGCTTAACTCAGATCAAC TCCATATGCTGGCAGAGAAGCTT ACAGTCCAATCTAGCTACAGTGTGTCACCTCACCTGGGCCAAGTT CTGCAAGGAACATTTACCTGGTA AATCATTTACCTTTTGGACATGGCTTGAAGCAATATTGGATCTAATT AAGAAACACATTTCTTCCCCCTTTG GATTGATGGGTATGTCATGGGCTTTGTAGCAAGAGAGGAACGGC TGTGCTAAAGGATAAAATGCCT GGCACCTTTTATTAAGATTCAAGTAAAGCCATCTCGGAGGAATAAC TTTCACCTGGGTGGACCATTTCTG AAAGTGGGAAGTGAATTCACCTCTGTAGAACCCTACAATAAAGGC CGGTTGTCTGCTCTGCCATTCGC TGACATCCTGCGAGACTACAAAGTTATTATGGCTGAAAACATTCCTG AAAACCTCTGAAGTACCTATAT CCTGACATTTCCCAAAGACAAAGCCTTCGGTAAACACTACAGCTCTCA GCCTTGCGAAGTTTCAAGACCAA CAGAAAGGGGTGACAAAGGTTATGTTCCCTTCTGTTTTTATCCCCATC TCAACAATCCGAAGTGATTCAC AGAGCCACATTTCTCCATCAGACCTTCTTCCCCTGTCTCCAAGTGTGT ATGCGGTGTGAGAGAAAACCTG AGTCCCACAACAATTGAAACTGCAATGAAGTCTCCTTATTCTGCTGA ATGACAGGATAAACTCTGACGCA CCAAGAAAGGAAGCAAAATGAAAAGTTTAAAGACTGTTCTTTTGCCCA ATAACCCACATTTTATTCTTCAG

206666_at	granzyme K (granzyme 3; tryptase II) /// granzyme K (granzyme 3; tryptase II)	aaacctctcttagatctggaacca aatgcaagggttactggctggggag ccaccgatccagattcattaagac cttctgacacccctgcgagaagtca ctgttactgtcctaagtcgaaaac tttgcaacagccaaaagttactaca acggcgacccttttatcaccaaaag acatgggtctgtg caggagatgccaaaaggccagaagg attcctgtaagggtgactcagggg gccccttgatctgtaaaagggtgtct tccacgctatagtctctggagggtc atgaatgtggtgttgccacaaaagc ctggaatctacaccctgttaacca agaaataccagacttggatcaaaa gcaaaccttggtccgcctcatacaa attaagttacaaaataattttattg gatgcacttgcttcttttttccta atatgctcgagggttagagttggg tgtaagtaagcagagcacatatg gggtccattttt gcacttgta	CTTTGTAATAACCAAGTTCTAGGAAATGTTTGACATCTGAAGCTCTC TTCACACTCCCGTGGCACTCCTC AATTGGGAGTGTGTGACTGAAATGCTTGAAACCAAGCTTCAGATA AACTTGCAAGATAAGACAACCTT AAGAAACCAGTGTTAATAACAATATTAACAG	18.25
		>gi 73747815 ref NM_002104.2 Homo sapiens granzyme K (granzyme 3; tryptase II) (GZMK), mRNA GATCAACACATTTTCATCTGGGCTTCTTAAATCTAAATCTTTAAATG ACTAAGTTTTCCTTCTCTTCTCT GTTTTCCTAATAGTTGGGCTTATATGACTCATGTGTGTTTCAATA TGGAAATTAATTGGAGGGAAAGAA GTGTCACCTCATTCAGGCCATTTATGGCCTCCATCCAGTATGGCGG ACATCACGTTTGTGGAGGTGTTT TGATTGATCCACAGTGGGTGCTGACAGCAGCCCACTGCCAATATCGG TTTACCAAAGGCCAGTCTCCAC TGTGGTTTTAGCGGCACACTCTCTCTCAAAGAATGAGGCCCTCCAAAC AAACACTGGAGATCAAAAATTT ATACCATTTCTCAAGAGTTACATCAGATCCTCAATCAAAATGATATCAT GCTGGTTAAGCTTCAAACAGCCG CAAAACTCAATAAACAATGTCAAGATGCTCCACATAAGATCCAAAACC TCTCTTAGATCTGGAACCAAAATG CAAGGTTACTGGCTGGGAGCCACCGATCCAGATTCATTAAGACCTT CTGACACCCCTGCGAGAAGTCACT GTTACTGTCTTAAGTCGAAAACCTTTTGCAACAGCCAAAGTTACTACAA CGGCGACCCCTTTTATCACCAAAG ACATGGTCTGTGCAGGAGATGCCAAAGGCCAGAGGATTCCTCTGTAAAG GGTGACTCAGGGGGCCCTTGAT CTGTAAAGGTGTCTTCCACGCTATAGTCTCTGGAGGTCAATGAATGTG GTGTTGCCACAAAGCCTGGAATC TACACCTGTGTTAACCAAGAAATACAGACTTGGATCAAAAGCAACCT TGTCCTCCGCTCATACAAATTAAG TTACAAATAAATTTTATTTGGATGCACTTGCTTCTTTTCTTCTAATATG		

206804 _at	CD3G antigen, gamma polypeptide e (TiT3 complex)	gtaatgccaaaggaccctcgagggg tgtatcagtgtaaaggatcacaga acaagtcaaaaccactccaagtgt attacagaaatgtgtcagaactgca ttgaactaaatgcagccaccatat ctggctttctcttctgtgaaatcg tcagcattttcgtccttgctgttg gggtctacttca ttgctggacaggatggagttcgcc agtcgagagcttcagacaagcaga ctctgttgcccaatgaccagctct accagccctcaaggatcgagaag atgaccagtacagccaccttcaag gaaaccagttgaggaaggaaattgaa ctcaggactcagagtagtccaggt gttctcctctatctcagttcccag aatcaaaagcaatgcatttttgga gctcctagcagagagacttttcagc cctaaatctagactcaagggtccc agagatgac [Seq ID No 57]	CTCGAGGTTAGAGTTGGGTGTA AGTAAAGCAGAGCACATATGGGGTCCATTTTTCACACTTGTAAATCAT TTTATTAAGGAATCAAGTTCTTT TTCACCTTGTATCACTGATGTATTTCTACCATGCTGCTTTTATTCTTAA ATAAAATTTAGAAAGACTCAAAAA AAAAAAAAAAAAAAAAAAAAAA	23.86
		>gi 4557428 ref NM_000073.1 Homo sapiens CD3g molecule, gamma (CD3-TCR complex) (CD3G), mRNA GGGCTGCTCCACGCTTTTGCCGGAGACAGAGACTGACATGGAACAGG GGAAGGGCCTGGCTGTCCTCATC CTGGCTATCATCTCTTCAAGGTACTTTGGCCAGTCAATCAAAGG AAACCACTTGGTTAAGGTGTATG ACTATCAAGAAAGATGGTTCGGTACTTCTGACTTGTGATGCAGAAGCC AAAAATATCACATGGTTTAAAGA TGGGAAGATGATCGGCTTCCTAACTGAAGATAAAAAAATGGAATC TGGGAAGTAATGCCAAGGACCCCT CGAGGGATGTATCAGTGTAAAGGATCACAGAACAAGTCAAAACCACT CCAAGTGATTTACAGAAATGTGTC AGAACTGCATTGAACTAAATGCAGGCCACCATATCTGGCTTTCTCTTT GCTGAAATCGTCAGCATTTTTCGT CCTTGCTGTTGGGGTCTACTTCAATTCGTCGACAGGATGGAGTTCGCC AGTCGAGAGCTTCAGACAAGCAG ACTCTGTTGCCCAATGACCAGCTCTACCAGCCCCCTCAAGGATCGAGA AGATGACCAAGTACAGCCACCTTC AAGGAAACCAGTTGAGGAGGAATTTGAACTCAGGACTCAGAGTAGTCC AGGTGTTCTCCTCCTATTCAGTT CCCAGAAATCAAAGCAATGCAATTTTGGAAGCTCCTAGCAGAGAGACT TTCAGCCCTAAATCTAGACTCAA GGTTCCCAGAGATGACAAATGGAGAAAGGCCATCAGAGCAAATT TGGGGGTTTCTCAAATAAATAA AAATAAAACAAATACTGTGTTTCAGAAAGGCCACCTATTTGGGGA ATTGT		

207651 _at	G protein-coupled receptor 171	ttgccttgtaattcgacagctcta cagaaacaaagataaatgaaaatta cccaaatgtgaa aaaggctctcatcaacatactttt agtgaccacgggctacatcatatg cttgttcctta ccacattgtccgaatcccgtatac cctcagccagacagaagtcataaac tgattgctcaac caggatttcactcttcaaagccaa agaggctacactgctcctggctgt gtcgaaacctgtg ctttgatcctatcctgtactatca cctctcaaaagcattccgctcaaa ggtaactgagac ttttgcctcacctaaagagaccaa ggctcagaaagaaaaattaagatg tgaaaaaatatgc ataaaaagacaggattttttgtgct accaattctggccttactgga	>gi 31377771 ref NM_013308.2 Homo sapiens G protein-coupled receptor 171 (GPR171), mRNA GGTGTACTGCTGCGCTAACCAACAGCTCATGTCTCTCTGAAGA CTTGACGCAAGTTTGCTGAGGC TCACAGAAAGATAGCCCCAGTGTTTTGGAGTGGTTTGAATGTGATTC TGAGATCAGACTGACTGAGCTGG AATCCTGGCTTTATATCTTACCAGCTACACAAACCTTGGAGTCTTAGA AATTTTCTTTTCAATAAGCAG TCATCCTTACTTTCCCTCAAGATGACAAACAGTTCGTTCTTCTGCCCC AGTTTATAAAGATCTGGAGCCAT TCACGTATTTTTTTTATTTTAGTTCCTTGTGGAATTTATTGGAAGT TGTTTGCACCTGGGCTTTTAT ACAGAAAGATAACGAATCACAGGTGTGTGAGCATCTACTTAATTAATT TGCTTACAGCCGATTTCCCTGCTT ACTCTGGCATTACCAGTGAAAAATTTGTTGTTGACTTGGGTGGCACC TTTGAAGCTGAAGATATTCCTACT GCCAAGTAACAGCCTGCCCTCATCTATATCAATATGTATTTATCAATT ATCTTCTTAGCATTTGTGTCAGCAT TGACCGCTGTCTTCAGCTGACACACAGCTGCAAGATCTACCGAATAC AAGAACCCGGATTTGCCCAAAATG ATATCAACCGTTGTGTGGTAAATGGTCTTCTTATAATGTGTCCAA TATGATGATTCCCATCAAAGACA TCAAGGAAAAAGTCAAATGTGGTTGTATGGAGTTTAAAAAGGAATTT GGAAGAAATTGGCATTTTGCTGAC AAATTTTCATATGTGTAGCAATATTTTAAATTTCTCAGCCCATCATTT TAATATCCAATTGCCCTTGTAATT CGACAGCTCTACAGAAACAAAGATAATGAAAAATACCCAAATGTGAA AAAGGCTCTCATCAACATACATTT TAGTGACCAAGGCTACATCATATGCTTTGTTCTTACCACATTGTC CGAATCCCGTATACCCCTCAGCCA GACAGAGTCAATACTGATTGCTCAACCAGGATTTCACTCTTCAAAG CCAAAGAGGCTACACTGCTCCTG GCTGTGTCGAAACCTGTGCTTTGATCCTGTCTGTACTATCACCTCTC AAAAGCATTCGCGCTCAAAGGTCA	46.65
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[Seq ID No 58]

207957	Protein kinase C, beta 1	tgatgagctttcccttgatccgga cgacgtaatcactgacattgagat ggtggacgaggg ctggtggcgggacgttgccatgg ccactttggactcttccctgcaaa ttatgtcaagct tctggagtactagagctcactgt ctactgcaactgtgatttcccatg tccaaagtggct ctgctccacccctccctattcct gatgcaaatgtctaaccagatgag ttctctqqacaga	CTGAGACTTTTGGCCTCACCTAAAGAGAGACCAAGGCTCAGAAAGAAAA TTAAGATGTGAAAAATAATGCATA AAAGACAGGATTTTGTGTCTACCAATTCTGGCCCTTACTGGACCATAA AGTTAATTATAGCTTTGAAAGAT AAAAAAAAAAAAAAAAAAAAAACTCAGTATGAAAAAATACAG TTAGCTAGCAAATATGGACAGGT TTACTTAGAAAAATCCTGTTTCTAAATGCAAGTCAAGCTTTATTGTTAG GCTTGCTGCTACTCATTAACCCA AATATTGTACAAAAAACTAAAGAGTCTCATTTGAACGAATGTAAAAAT CCTGCAATATCCTTGAAATCCAA AAGAGGTCATGACATAGACCCAAAGGTATTCATGAGTTATTCATTT AAATGCCTGGAACCTGACTTCTTG ATAAAAAATATAAAAAAATAATTCCATGTAAGTTACCAGAAAGCCAC CAGCAACATAAATTTTAAAGCCTT TCGGATTACTTTTAAAAAATGCAGCTTACATATAACAACCTTGTGCCT ATTTTATTTCTAATCTATCACTT CAAAAGATGGTAATCTTTCAACTCATTTATTCCTCCAATTTTAAATGT CGAATTTTCTTAACACAAATAA CCAAAAGCTTTTATTTATAAAAAGGCTTGAAAAATATAAAAAA AAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAA	34.17
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		cttccctctcctgcttcatatgaagg gcttgggagagagacagcatgggg aaggaggccccctccccaaagagt cctctctatcctggatgagctcat gaacattctcttgtgtccctgac tccttcccaatgaacacctctctg ccaccccaagctctgctctccctcc tctgtgagctct gggcttcccagtttgtttaccggg gaaagtaagctctagattgtgtggt ttgcctcattgt gctatttgcccactttcccttccct gaagaaatatctgtgaaccttctt tctgttcagtcc ta [Seq Id No 59]	GCTGCTGTTCTCGCAGGACAAGC TGAGCATTGAGGATTTACAGCATATGGCGGTGTGTTTGAAAAACAAG CAGACAGCGCTTTTCTAACCT AGAGAAATGCCCTGGACCTGGCCCCCTCCTCACTGGTGCTTCTCTGCCG TCGACTGGTATGCAGTCAGCACT CTGACCACTTACCTGCAGGAGAAGCTCGGGGCCAGCCCCCTTGCAATGT GGACCTGGCCACCCCTGCGGGAGC TGAAGCTCAATGCCAGCCTCCCTGCTCTGTGCTGCTCATTCGCCCTGCC TACACAGCCAGCTCTGCTCTGAT GGACCCAGGGAAGTCTCAACAGGCAACGATGAGGTCAATCGGGCAGG TCCTGAGCACACTCAAGTCCGAA GATGTCCATACACAGCGGCCCTCACAGCGGTCCGCCCTTCCAGGGT GGCCCCGTGATGTAGCCGTGTTG CCGAGGGCTAGGTGCCAGCTGCTACAAAACAGCCAGTATCACCT GTGATCCATCCTCCTGTGAGTTA CAATGACACCGCTCCCCGATCCTGTTCTGGGCCCAAAACTTCTCTG TGGCGTACAAGACCAAGTGGGAG GACCTGACTCCCCCTCACCTTTGGGGTGCAGGAACTCAACCTGACTGG CTCCTTCTGGAATGACTCCTTTG CCAGGCTCTCACTGACCTATGAACGACTCTTTGGTACCACAGTGACA TTCAAGTTCAATCTGGCCAAACCG CCTCTACCCAGTGTCTGCCCGGCACTGGTTTACCATGGAGCGCCTCG AAGTCCACAGCAATGGCTCCGTC GCCTACTTCAATGCTTCCCAGGTCAACAGGGCCCAGCATCTACTCCTT CCACTGCGAGTATGTCAGCAGCC TGAGCAAGAAAGGTAGTCTCTCGTGGCCCCGACGACGCCCTCTCTCC TGGCAGATGATGCTTCAGGACTT CCAGATCCAGGCTTTCAACGTAATGGGGGAGCAGTTCTCCTACGCCA GGGACTGTGCCAGCTTCTTCTCC CCCGCATCTGGATGGGGCTGCTCACCTCCCTGTTTCATGCTCTTCAT CTTCACCTATGGCCTGCACATGA TCCTCAGCCTCAAGACCATGGATCGCTTTGATGACCACAAGGGCCCC ACTATTCTTTGACCCAGATTGT GTGACCCCTGTGCCAGTGGGGGGTTGAGGGTGGGACGGTGTCCGTGT
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			TGTTGCTTTCCACCCCTGCAGCG CACTGGAAGAGCTTCCCTCTTCCCTACTGCAGCATGAACTGCAA GCTCCCTCAGCCCATCTTGCTC CCTCTTCAGCCCGCTGAGGAGCTTTCTTGGGCTGCCCCCATCTCTCC CAACAAGGTGTACATATTCTGCG TAGATGCTAGACCAACCAGCTTCCCAGGGTTCGTCGCTGTGAGGCGT AAGGACATGAATTCTAGGGTCT CCTTTCTCCTTATTATTCTTGTGGCTACATCATCCCTGGCTGTGGA TAGTGCTTTTGTGTAGCAAAATGC TCCCTCCTTAAGGTTATAGGGCTCCCTGAGTTTGGGAGTGTGGAAGT ACTACTTAACTGTCTGTCTGCT TGGCTGTCGTTATCGTTTCTTGTGTGATGTTGTGCTAAACAATAAGAAG TACACGGGTTTATTCTGTGGCC TGAGAAGGAAGGACCTCCACGACAGGTGGCTGGGTCCGATCGCCG GCTGTTTGGCATGTTCCACCCG GAGTGCCGGCAGGAGCATGGGTGCTTGGTTGTTTCTTCTCCTAATA AAATAAACGCGGTCCGCATGCA AAAAAAA	
208894 _at	major histocompa tibility complex, class II, DR alpha /// major histocompa tibility complex, class II, DR alpha	cgatcaccaatgtacctccagagg taactgtgtcacgaacagccctg tggaactgagagagcccaacgtcc tcattgtttcatagacaagtcca cccca [Seq Id No 60]	>gi 52426773 ref NM_019111.3 Homo sapiens major histocompatibility complex, class II, DR alpha (HLA-DRA), mRNA ACATTCTCTTTTCTTTTATTCTTGTCTGTCTGCTCCTCACTCCCGAGC TCTACTGACTCCCAACAGAGCGC CCAAGAAGAAATGCCATAAGTGGAGTCCCTGTGCTAGGATTTTTC ATCATAGCTGTGCTGATGAGCGC TCAGGAATCATGGGCTATCAAGAAGAACAATGTGATCATCCAGGCCG AGTTCTATCTGAATCCTGACCAA TCAGGCGAGTTTATGTTTGAATTTGATGTTGATGATGAGATTTTCCATGT GGATATGGCAAAAGAGGAGACGG TCTGGCGGCTTGAAGAATTGGACGATTGCGCAGCTTTGAGGCTCAA GGTGCAATTGGCCCAACATAGCTGT GGACAAAGCCCAACCTGGAAATCATGACAAAGCGCTCCAACTATACTC CGATCACCAATGTACCTCCAGAG	6.11

			GTAACGTGCTCAGAACAGCCCTGTGGAACTGAGAGAGCCCCAACGT CCTCATCTGTGTTTCATAGACAAGT TCACCCACACAGTGGTCAATGTCAAGTGGCTTCGAAATGGAAAAACCT GTCACCCACAGGAGTGTGAGAGAC AGTCTTCCTGCCAGGGAAGACCACTTTTCCGCAAGTTCACACTATC TCCCCTTCCTGCCCTCAACTGAG GACGTTTACGACTGCAGGGTGGAGCACTGGGGCTTGGATGAGCCTCT TCTCAAGCACTGGGAGTTTGATG CTCCAAGCCCTCTCCAGAGACTACAGAGAAACGTGGTGTGTGCCCTG GGCTGACTGTGGTCTGGTGGG CATCATTATTGGGACCATCTTCATCATCAAGGGATTGCGCAAAAGCA ATGCAGCAGAACGAGGGGCT CTGTAAGGCACATGGAGGTGATGGTGTTCCTTAGAGAGAAGATCACT GAAGAACTTCTGCTTTAATGGC TTTACAAAGCTGGCAATATTACAATCCTTGACCTCAGTGAAAGCAGT CATCTTCAGCATTTTCCAGCCCT ATAGCCACCCCAAGTGTGGATAAGCCTCTTCGATTGCTCCGTACTCT AACATCTAGCTGGCTTCCCTGTC TATTGCCCTTTTCTGTATCTATTTTCTCTATTTCTCTATCATTTTAT TATCACCATGCAATGCCCTCTGGA ATAAAACATACAGGAGTCTGCTCTCTGCTATGGAATGCCCATGGGC ATCTCTTGTGTACTTATTGTTTA AGGTTTCTCCTCAAACTGTGATTTTCTGAACACAAATAAACTATTTTGA TGATCTTGGGTGGAAAAA AAAAAA	12.55
209480 _at	Major histocompa tibility complex, class II, DQ beta 1	aaaaaggaaatcgctgcagaatg aaggaatatcccttgaggtagacc agccaaacctgtggccagaaggagg gtgtaccttgaaaagaccactga aagcattttggggtgtcaagtaag ggtggcagaggaggtagaaaatc aattcaattgtcgcatcattcatg gttctttaattattgatgctcagtg	>gi 24797068 ref NM_002123.2 Homo sapiens major histocompatibility complex, class II, DQ beta 1 (HLA-DQB1), mRNA CAGATCCATCAGGTCCGAGCTGTGTGACTACCACTTTTCCCTTCGT CTCAATTATGTCTTGGAAAAAGG CTTTGGGATCCCGGAGGCTTCGGGCAGCAACTGTGACCTTGATG CTGTGATGTGAGCACCCAGT GGCTGAGGCGAGAGACTCTCCGAGGATTCGTGTACCAGTTTAAGG	

	/// Major histocompa tibility complex, class II, DQ beta 1	cattggccttagaataatcccagcc tctcttctggttggtagtgctg tgtaagtaagcatggtagaattgt ttggagacatatatagtgatcctt ggtcactggtgt ttcaaacattctggaaagtcacat cgatcaagaatatattttt [Seq Id No 61]	GCAATGTGCTACTTCACCAACGGG ACAGAGCGCGTGGCTCTTGTGAGCAGAAGCATCTATAACCGAGAAGA GATCGTGGCTTCGACAGCGACG TGGGGAGTTCCGGCGGTGACGCTGCTGGGGCTGCCTGCCCGCGAG TACTGGAACAGCCAGAAGGACAT CCTGGAGAGGAACGGGCGCGGTGGACAGGGTGTGCAGACACAACCT ACCAAGTTGGAGCTCCGCACGACC TTGCAGCGCGAGTGGAGCCCAAGTGAACCATCTCCCATCCAGGAC AGAGGCCCTCAACCAACCAAC TGCTGGTCTGCTCGGTGACAGATTCTATCCAGCCAGATCAAAGTC CGGTGGTTTCGGAATGACCAGGA GGAGACAGCTGGCGTTGTGCCACCCCTTATTAGGAATGGTGACT GGACCTTCCAGATCCTGGTGATG CTGGAATAGTCCCGAGCGTGAGACGCTACACCTGCCACGTGGA GCACCCAGCCTCCAGAGCCCCA TCACCGTGGAGTGGCGGCTCAATCTGAATCTGCCAGAGCAAGATG CTGAGTGGCATTGGAGGCTTCGT GCTGGGCTGATCTTCTCGGGCTGGCCCTTATCATCCATCACAGGA GTCAGAAAGGCTCCTGCACTGA CTCCTGAGACTATTTAACTGGGATTGGTTATCACTTTTCTGTAACG CCTGCTTGTCCCTGCCAGAAAT CCCAGCTGTCTGTGTCAGCCTGTCCCCCTGAGATCAGAGTCTTACAG TGGCTGTACGCAGCCACCAAGGT CATCTCCTTTTCATCCCCACCTTGAGGGGATGGCTGTGACCCCTACTT CCTGCACTGACCCACAGCCTCTG CCTGTGCACGGCCAGCTGCATCTACTCAGGCCCCCAAGGGTTTCTGT TTCATATTCTCTCTCAGACTGCT CAAGAGAAGCACATGAAACCATTTACCTGACTTTTAGAGCTTTTAC ATAATTAAACATGATCCTGAGTT	58.89
209613 _s_at	alcohol dehydrogen ase IB	gcagatttcttgcttcatatgaca aagcctcaattactaattgtaaaa actgaactattc ccagaatcatgttcaaaaaaatctg	>gi 34577060 ref NM_000668.3 Homo sapiens alcohol dehydrogenase IB (class I), beta polypeptide (ADH1B), mRNA ATGCACTCAAGCAGAGAGAAGAAATCCACAAGACTCACAGTCTGCTGG	

	(class I), beta polypeptide	taatttttgctgatacgaaagtgcct tcattgactaaa cagtagttagttgtggctataaat gattatttagatgactgaaaa tgtgtataaagt aattaaaagtaatatggtggcttt aagtgtagagatgggatggcaaat gctgtgaatgca gaatgtaaaattggtaactaagaa atggcacaaaacaccttaagcaata tattttcctagt agatatatatatacacatacatat atacacatatatacaaatgtatat ttgcaaaaattgt tttcaatctagaacttttctatta actaccatgtcttaaaaatcaagtc tataatcctagc attagtttaatattttgaatatgt aaacacctgtgttaatgctttgtt aatgcttttccc actctcatttgttaatgctttccc actctcgggaaggatttgcatttt gagctttatctc taaagtgtgacatgca [Seq Id No 62]	TGGCAGAGAAACAGAAACGAC ATGAGCACAGCAGGAAAGTAATCAAAATGCAAAGCAGCTGTGCTATG GGAGGTAAAGAAACCTTTTCCA TTGAGGATGTGAGGTTGCACCTCCTAAGGCTTATGAAGTTGCGCATT AAGATGGTGGCTGTAGGAATCTG TCACACAGATGACCACTGTGTTAGTGGCAACCTGGTGACCCCCCTTC CTGTGATTTTAGGCCCATGAGGCA GCCGGCATCGTGAGAGTGTGGAGAAGGGTGACTACAGTCAAAACC AGGTGATAAAGTCATCCCCCTCT TTACTCCTCAGTGTGGAATAATGCAGAGTTTGTAAAAACCCGGAGAGC AACTACTGCTTGAAAAATGATCT AGGCAATCCTCGGGGACCCCTGCAGGATGGCACCCAGGAGGTTACACCT GCAGGGGAAGCCCATTCACAC TTCCTTTGGCACAGCACCTTCTCCAGTACACGGTGGTGGATGAGAA TGCAGTGGCCAAAATTGATGCAG CCTCGCCCCCTGGAGAAAAGTCTGCCCTCATTTGGCTGTGGATTCTCGACT GGTTATGGGTCTGCAGTTAACGT TGCCAAGGTCAACCCAGGCTCTACCTGTGCTGTGTTTGGCCTGGGAG GGGTCGGCCTATCTGCTGTTATG GGCTGTAAAGCAGCTGGAGCAGCCAGAAATCATTTGCGGTGGACATCAA CAAGGACAAATTGCAAGGCCA AAGAGTTGGTGCCACTGAATGCATCAACCTCAAGACTACAAGAAA CCCATCCAGGAAGTGCTAAAGGA AATGACTGATGGAGGTGTGGATTTTTCGTTTGAAGTCATCGGTGCGC TTGACACCATGATGGCTTCCCCTG TTATGTTGTGATGAGGCAATGTGGCACAAGCGTCATCGTAGGGTACC TCCTGCTTCCCAGAACCTCTCAA TAAACCCCTATGCTGCTACTGACTGGACGCACCTGGAAGGGGCTGTT TATGGTGGCTTTAAGAGTAAAGA AGGTATCCCAAACTTGTGGCTGATTTTATGGCTAAGAAGTTTTCAC TGGATGCGTTAATAACCCATGTT TTACCTTTTGAATAAAATAAATGAAGGATTTGACCTGCTTCACTCTGG GAAAAGTATCCGTACCGTCCCTGA CGTTTGTAGGCAATAGAGATGCCCTTCCCCTGTAGCAGTCTTCAGCCT
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			CCTCTACCCCTACAAGATCTGGAG CAACAGCTAGGAAATATCATTAATTCAGCTCTTCAGAGATGTTATCA ATAAATTACACATGGGGCTTTC CAAAGAAATGGAAATTGATGGGAAATTATTTTCAGGAAAAATTTAAA ATTCAAGTGAGAAGTAAATAAAG TGTGAAACATCAGCTGGGGAATTGAAGCCAACAACCTTCCTTCTTA ACCATTCCTACTGTGTACCTTTG CCATTGAGGAAATAATTCCTGTGACTTCTTGCATTTTGTGTATCTT CATAATCTTTAGTCATCGAATCC CAGTGGAGGGACCCCTTTTACTTGCCCTGAACATACACATGCTGGGC CATTGTGATTGAAGTCTTCTAAC TCTGTCTCAGTTTTCACCTGTCGACATTTTCCCTTTTCTAATAAAAAAT GTACCAAAATCCCTGGGGTAAAG CTAGGGTAAGGTAAGGATAGACTCACATTTACAAGTAGTGAAGGTC CAAGAGTTCTAAATACAGGAAAT TTCCTTAGGAACTCAAAATAAAATGCCCCACATTTTACTACAGTAAATG GCAGTGTTTTATGACTTTTATA CTATTCTTTATGGTCGATATACAATTGATTTTTTTAAATAATAGCA GATTTCTTGCTTCATATGACAAA GCCTCAATTACTAATTGTAAAAACTGAACTATTCCCAGAAATCATGTT CAAAAAATCTGTAATTTTGTCTG ATGAAAGTGCTTCATTGACTAAACAGTATTAGTTTGTGGCTATAAAT GATTATTTAGATGACTGAAA ATGTGTATAAAGTAATTAAAAGTAATATGGTGGCTTTAAGTGTAGAG ATGGGATGGCAAAATGCTGTGAAT GCAGAAATGTAAAAATTGGTAACTAAGAAATGGCACAACACCTTAAGC AATATATTTTCTAGTAGATATA TATATACACATACATATATACACATATACAATGTATATTTTGTCAA AATTGTTTTCAATCTAGAACTTT TCTATTAACTACCATGTCTTAAATCAAGTCTATAATCCTAGCATTA GTTTAAATATTTTGAATATGTAAA GACCTGTGTAAATGCTTTGTAAATGCTTTTCCCACCTCTCATTTGTTA ATGCTTTCCCACCTCTCAGGGGAA GGATTTCATTTTGAGCTTTTATCTCTAAATGTGACATGCAAGATTA

209670 _at	T receptor alpha constant /// T cell receptor alpha constant	caactggatcctaccggaatttat gattaagattgctgaagagctgccc aaacactgctgc caccctctctgttcccttattgct gcttgctcactgcctgacattcacg gcagaggcaagg ctgctgcagcctccccctggctgtg cacattccctcctgctccccagag actgcctccgcc atccacagatgatggatcttcag tggttctctcttggtctctaggtcc tgagagaatgtg tgaggggttttattttttttaata gtgttcataaagaaatacatagta ttcttcttctca agacgtggggggaattatctcat tatcgaggccctgctatgctgtgt gtctggggcgtgt tgtatgtccctgc [Seq Id No 63]	TTCCTGGTAAAGGAGGTAGCTGT CTCCTCAAAATGCTATTGTTGCAATATCTACATTCTATTTCATATTAT GAAAGACCTTAGACATAAAGTAA AATAGTTTATCATTTACTGTGTGATCTTTCAGTAAGTCTCTCAGGCTC TCTGAGCTTGTTCATCCTTTGTT TTGAAAAAATTACTCAACCAATCCATTACAGCTTAACCAAGATTAAA TGGGATGATGTTAATGAAAGAGC TTCGCC	>gi 36944 emb x02592.1 HSTCRAR Human mRNA for T-cell receptor alpha chain (TCR-alpha) TTTTGAAACCCCTTCAAAGGCAGAGACTTGTCCAGCCTAACCTGCCTG CTGCTCCTAGCTCCTGAGGCTCA GGGCCCTTGGCTTCTGTCCGCTCTGCTCAGGGGCCCTCCAGCGTGGCC ACTGCTCAGCCATGCTCCTGCTG CTCGTCCCAGTGTCTCGAGGTGATTTTACCCTGGGAGGAACACAGAGC CCAGTCGGTGACCCAGCTTGCA GCCACGTCTCTGTCTCTGAAGGAGCCCTGGTTCTGTGAGGTGCAAC TACTCATCGTCTGTCTCCACCAT TCTCTTCTGTTATGTGCAATACCCCAACCAAGGACTCCAGCTTCTCC TGAAGTACACATCAGCGGCCACC CTGTTTAAAGGCATCAACGGTTTGTAGGCTGAATTTAAGAAGAGTGA AACCTCCTTCCACCTGACGAAAC CCTCAGCCCATATGAGCGACGCGGCTGAGTACTTCTGTGTGTGAGT GATCTCGAACCCGAACAGCAGTGC TTCCAAAGATAATCTTTGGATCAGGGACCAGACTCAGCATCCGGCCAA ATATCCAGAACCCCTGACCCCTGCC GTGTACCAGCTGAGAGACTCTAAATCCAGTGACAAGTCTGTCTGCCT ATTCAACCGATTTTGATTCTCAAA CAAATGTGTCAAAAGTAAGGATTCTGTATGTATATCACAGACAAA ACTGTGCTAGACATGAGGTCTAT GGACTTCAAGAGCAACAGTGTGTGGCCTGGAGCAACAAATCTGACT TTGCATGTGCAACGCCCTTCAAC AACAGCATTATTCCAGAAGACACCTTCTTCCCCAGCCCGAAGTTC	24.26
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			CTGTGATGTCAAGCTGGTCGAGA AAAGCTTTTGAAACAGATACGAACCTAACTTTTCAAAACCTGTCAGTG ATTGGGTTCCGAATCCTCCTCCT GAAAGTGGCCGGGTTTAACTCTGCTCATGACGCTGCGGCTGTGGTCCA GCTGAGATCTGCAAGATTGTAAG ACAGCCTGTGCTCCCTCGCTCCTTCCCTCTGCAATTGCCCTCTTCTCC CTCTCCAAACAGAGGGAACTCTC CTACCCCAAGAGAGTGAAAGCTGTACCACTCTGTGCCCCCCCCGG TAATGCCACCAACTGGATCCTAC CCGAATTTATGATTAAAGATTGCTGAAGAGCTGCCAAACACTGCTGCC ACCCCTCTGTTCCTTATTGCT GCTTGTCACCTGCCCTGACATTCACGGCAGAGGCAAGGCTGCTGCAGCC TCCCCTGGCTGTGCACATTCCCT CCTGCTCCCCAGAGACTGCCCTCCGCCATCCACAGATGATGGATCTT CAGTGGGTTCTCTGGGCTCTAG GTCCTGGAGAAATGTTGTGAGGGGTTTATTTTTTTTAAATAGTTTCA TAAAGAAATACATAGTATTCTTC TTCTCAAGACGTGGGGGAAATTATCTCATTATCGAGGCCCTGCTAT GCTGTGTCTCTGGGCGTGTGTA TGTCCTGCTGCCGATGCTTTCATTTAAATGATTTTGAA	
209795 _at	CD69 antigen (p60, early T- cell activation antigen)	tagtctaattgaatcccttaaaact caggagcattttataaaatggcaaa tgcttatgaaac taagatttgtaatatattctctctt tttagagaaaatttgccaatttact ttggtatttttc cccaaaaagaatgggatgatcgtg tatttattttttacttcctcagc tgtagacaggtc cttttcgatggtacatatattcttt gcctttataatctttttatacagtg tcttacagagaa aagacataagcaaaagactatgagg aatatttgcaagacatagaatagt	>gi 4502680 ref NM_001781.1 Homo sapiens CD69 molecule (CD69), mRNA AGACTCAACAAGAGCTCCAGCAAGACTTTCAGTGTAGCTTGACTTG ACCTGAGATTAACTAGGGAATCT TGAGAAATAAGATGAGCTCTGAAAATTTGTTTCGTAGCAGAGAAACAGC TCTTTGCATCCGGAGAGTGGACA AGAAAATGATGCCACCAGTCCCCATTTCTCAACACGTCATGAAGGGT CCTTCCAAGTTCCCTGTCTGTGT GCTGTAATGAATGTGGTCTTCATCACCATTTTAATCATAGCTCTCAT TGCCTTATCAGTGGGCCAATACA ATTGTCCAGGCCAATACACATTCTCAATGCCATCAGACAGCCATGTT TCTTCATGCTCTGAGGACTGGGT TGGCTACCAGAGGAAATGCTACTTTTATTCTACTGTGAAGAGGAGCT GGACTTCAGCCCCAAATGCTTGT	30.48

		gttggaatgt gcaatatgtgatgtggcaaatctc tattaggaaatatctgtaatctt cagacctagaat aatactagtcttataataggtttg tgactttccataaatcaattctatt acgtgcaatact tcaatacttcat [Seq Id No 64]	TCTGAACATGGTGCTACTCTTGCTGTCAATTGATTCTGAAAAGGACAT GAACTTCTAAACGATACGCAG GTAGAGAGGAACACTGGGTTGGACTGAAAAAGAACCTGGTCACCCA TGGAAGTGGTCAAATGGCAAGA ATTTAACAACTGGTTCAACGTTACAGGCTCTGACAAGTGTGTTTTTC TGAAAAACACAGAGGTCAGCAGC ATGGAATGTGAGAAAGAAATTTATACCTGGATAATGTAACAAACCTTACAA ATAATAAGGAAACATGTTCACTT ATTGACTATTATAGAAATGGAACCTCAAGGAAATCTGTGTCAGTGGATG CTGCTCTGTGGTCCGAAAGTCCTC CATAGAGACTTTGTGAAAAAAAATTTATAGTGTCTTGGGAATTTTC TTCCAAACACAGAACTATGGAAAAA AAGGAAGAAATTCAGGAAATCTGCACGTGGGCTTTTATTTGCCAT GAGTAGAAGCATCACAGGTTGA CCAATAACCATGCCCAAGAATGAGAAGAAATGACTATGCAACCTTTGG ATGCACTTTATATTTTGAAT CCAGAAATAATGAAATAACTAGGCGGTGACTTACTATTTATTTGCTGA ATGACTACCAACAGTGAGAGCCC TTCATGCATTTGCACCTACTGGAAGGAGTTAGATGTTGGTACTAGATA CTGAAATGTAAACAAAGGAATTAT GGCTGGTAAACATAGGTTTTTAGTCTAATTGAATCCCTTAAACTCAGG GAGCATTTATAAATGGACAAATG CTTATGAAACTAAGATTTGTAATATTTCTCTCTTTTGTAGAGAAATTT GCCAATTTACTTTGTATTTTC CCCAAAAAGAAATGGGATGATCGTGTATTTATTTTACTTCCCTCAG CTGTAGACACAGGTCCTTTTCGATG GTACATATTTCTTTGCTTTTATAATCTTTTATACAGTGTCTTACAGA GAAAAGACATAAGCAAAAGACTAT GAGGAATATTTGCAAGACATAGAAATAGTGTGGAAAAATGTGCAATAT GTGATGTGGCAAAATCTCTATTAG GAAATATTTCTGTAATCTTCAGACCTAGATAATACTAGTCTTATAAT AGGTTTGTGACTTTCCCTAAATCA ATTCTATTACGTGCAATACCTCAATACCTTCAATTTAAATATTTTAT GTGCAATAAAAATGTATTTGTTTG
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			TATTTTGTGTT CAGTACAAT TATAAGCTGTT TTTTATATATGTGAAAT AAAAGTAGAATAAACACAAAAA AAAAAAA	
210038 _at	protein kinase C, theta	aatccattcatcctgattgggcat gaaatccatggtcaagaggacaag tggaagtgaaggggaggtttgc tagacaccttcgcttggttatcttg tcaagatagaaaagatagtatcat ttcaccttgccagtaaaaacctt tccatccacccattctcagcagac tccagtattggc acagtcactcactgccattctcac actataacaagaaaagaatgaag tgcataagtctc ctgggaaaagaaccttaacctt ctcgtgccatgactggtgatttca tgactcataagc ccctccgtaggcatcattcaagat caatggcccatgcatgctgtttgc agca [Seq Id No 65]	>gi 48255887 ref NM_006257.2 Homo sapiens protein kinase C, theta (PRKCQ), mRNA AGTCCCGCGAGTCCCGCGAGTCCAGCGCCACCGGCAGCAGC GGCGCCGTGCTCGCTCCAGGGCG CAACCATGTCGCCATTCTTCGGATTGGCTTGTCCTTGTGACTGC GGTCTCTGCCAGTCTTGTCAAGG CGAGGCTGTTAACCTTACTGTGCTGTGCTCGTCAAAGAGTATGTCTG AATCAGAGAACGGGCAGATGTAT ATCCAGAAAAAGCCTACCATGTACCCACCCCTGGGACAGCACCTTTTGA TGCCCATATCAACAAGGAAGAG TCATGCAGATCATTTGTGAAAGGCAAAAAACGTGGACCTCATCTCTGAA ACCACTGTGAGCTCTACTCGCT GGCTGAGAGGTGCAGGAAGAACAACGGGAAGACAGAAAAATATGGTTAG AGCTGAAACCTCAAGGCCGAATG CTAATGAATGCAAGATACTTTCTGGAAATGAGTGACACAAAGGACAT GAATGAATTTGAGACGGAAGCT TCTTTGCTTTGTCATCAGCGCCGGGTGCCATCAAGCAGGCAAGGTC CACCACTCAAGTCCACGAGTT CACTGCCACCTTCTTCCACAGCCCAATTTTGTCTGTCTGCCACG AGTTTGTCTGGGGCTGAACAA CAGGGCTACCAAGTCCGACAATGCAATGCAGCAATTCACAAGAAAGTG TATTGATAAAGTTATAGCAAAGT GCACAGGATCAGCTATCAATAGCCGAGAAACCATGTTCACAAGGAG AGATTCAAAATTGACATGCCACA CAGATTAAAGTCTACAATTACAAGAGCCCGACCTTCTGTGAACACT GTGGGACCTCTGTGGGGACTG GCACGGCAAGGACTCAAGTGTGATGTCATGTGGCATGAATGTGCATCA TAGATGCCAGACAAAGGTGGCCA ACCTTTGTGGCATAAACCAGAAGCTAATGGCTGAAGCGCTGGCCATG ATTGAGAGCACTCAACAGGCTCG	19.42

		CTGCTTAAGAGATACTGAACAGATCTTTCAGAGAAAGTCCGGTTGAAA TTGGTCTCCCATGCTCCATCAAA AATGAAGCAAGCGCCCATGTTTACCGACACCGGGAAAAAGAGAGCC TCAGGGCATTTCCCTGGGAGTCTC CGTTGGATGAGGTGGATAAAAATGTGCCATCTTCCAGAACCTGAACTG AACAAAGAAAGACCATCTCTGCA GATTAAACTAAAAATTGAGGATTTTATCTTGCACAAAATGTGTGGGA AAGGAAGTTTGGCAAGTCTTC CTGGCAGAAATTCAGAAAACCAATCAATTTTCGCAATAAAGGCCTT AAAGAAAGATGTGGTCTTGATGG ACGATGATGTTGAGTGACCGATGGTAGAGAAAGAGAGTTCTTTCCTTG GCCTGGGAGCATCCGTTTCTGAC GCACATGTTTGTACATTCAGACCAGGAAACCTCTTTTGTGTA TGGAGTACCTCAACGGAGGGAC TTAATGTACCACATCCAAAGCTGCCACAAGTTCGACCTTTCAGAGC GACGTTTATGCTGCTGAAATCA TTCTTGGTCTGCAGTTCCTTCATTCCAAAGGAATAGTCTACAGGGAC CTGAAGCTAGATAACATCCTGTT AGACAAAAGATGGACATATCAAGATCGCGGATTTTGGAATGTGCAAGG AGAACATGTTAGGAGATGCCAAG ACGAATACCTTCTGTGGACACCTGACTACATCGCCCCAGAGATCTT GCTGGGTCAGAAATACAACT CTGTGGA CTGGTGGTCTTCGGGGTCTCCTTTATGAAAATGCTGATT GGTCAGTCGCCTTTCCACGGGCA GGATGAGGAGGAGCTCTTCCACTCCATCCGCATGGACAAATCCCCTTTT ACCCACGGTGGCTGGAGAAGAA GCAAAGGACCTTCTGTGAAGCTCTTCGTGCGAGAACCTGAGAAGAG GCTGGCGGTGAGGGGAGACATCC GCCAGCACCTTTGTTCGGGAGATCAACTGGGAGGAACTTGAACGG AAGGAGATTGACCCACCGTTCCG GCCGAAAGTGAAATCACCATTTGACTGCAGCAATTTTCGACAAAGAAT TCTTAAACGAGAGAGCCCGGCTG TCATTTGCCGACAGAGCACTGATCAACAGCATGGACCAGAAATATGTT CAGGAACTTTTCCTTCATGAACC
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		CCGGATGGAGCGGCTGATATCCTGAATCTTGCCCCCTCCAGAGACAG GAAAGAAATTGCCCTTCTCCCTGG GAACTGGTTCAAGAGACACTGCTTGGGTTCCCTTTTTCAACTTGGAAA AAGAAAGAAACACTCAACAATAA AGACTGAGACCCGTTCCGCCCCCATGTGACTTTTATCTGTAGCAGAAA CCAAGTCTACTTCACTAATGACG ATGCCGTGTGTCTCGTCTCCTGACATGTCTCACAGACGCTCCTGAAG TTAGGTCATTACTAACCATAGTT ATTTACTTTGAAAGATGGGTCTCCGCACCTTGGAAGGTTTCAAGACTT GATACTGCAATAAATTATGGCTC TTCACTCTGGGCCCAACTGCTGATCAATGAATGCTTGTGTGAATCAG GGGCAAAACGGAGTACAGACGTCT CAAGACTGAAACGGCCCCCATTGCCCTGGTCTAGTAGCGGATCTCACTC AGCCGCAGACAAGTAATCACTAA CCCCGTTTATTCTATTCCCTATCTGTGGATGTGTAATGGCTGGGGG CCAGCCCTGGATAGGTTTATTATG GGAATTCTTTACAATAAACATAGCTTGTAACCTTGAGATCTACAAATC CATTCACTCCTGATTGGGCATGAA ATCCATGGTCAAGAGGACAAAGTGGAAGTGAGAGGGAAGGTTTGCTA GACACCTTCGCTTGTTATCTTGT CAAGATAGAAAAGATAGTATCATTTCAACCCCTTGCCAGTAAAAACCTT TCCATCCACCCATTCTCAGCAGA CTCCAGTATTGGCACAGTCACTCACTGCCATTCTCACACTATAACAA GAAAAGAAAATGAAGTGCATAAGT CTCCTGGGAAAAGAACCTTAACCCCTTCTCGTGCCATGACTGGTGAT TTCATGACTCATAAGCCCCCTCCG TAGGCATCATTTCAAGATCAATGGGCCCATGCATGCTGTTTGCAGCAGT CAATTGAGTTGAATTAGAATTCC AACCATACATTTTAAAGGTATTGTGCTGTGTATATTGTGATAAA ATGTTGTGACTTTCATGGCAACA GGTGGATGTGTAAAAATGGAATAAAAAAAGAGTCAAAAAA AAAAA

210915 _x_at	T cell receptor beta variable 19 /// T cell receptor beta constant 1	Aaagggccacactgggtgtgcctggc cacaggtatcttccctgaccacgt ggagctgagctggtgggtgaatgg gaaggaggtgcacagtgggtcag cacggacccgcagccctcaagga gcagcccgccctcaatgactccag atactgcctgagcagccgcctgag ggtctcgccaccttctggcagaa ccccgcaaccacttccgctgtca agtccagttctacgggctctcgga gaatgacgagtggaccaggatag ggccaaaaccgctacccagatcgt cagcgcgagggcctgggtagagc agactgtggctttacctcgggtgc ctaccagcaagggtcctgtctgc caccatcctctatgagatcctgct aggaaggccaccatgtatgctgt gctggtcagcgcccttggttgat ggccatggtcaagagaaaggattt ctgaaggcagccctggaagtggag ttaggagcttctaaccctcatggt tttcaatacacattcttcttttgc cagc [Seq Id No 66]	>gi 339011 gb M15564.1 HUMTCBYZ Human T-cell receptor rearranged beta-chain V-region (V-D-J) mRNA, complete cds GTAAAGCTCCCATCTGCCCTGACCTGCCATGGGCACCAGCCTCCT CTGCTGGATGGCCCTGTGTCTCC TGGGGCAGATCACGCAGATACTGGAGTCTCCAGAACCCACAGACAC AACATCACAAAGAGGGGACAGAA TGTAACCTTTCAGGTGTGATCCAATTTCTGAACACAAACCGCCTTTATT GGTACCGACAGACCCCTGGGGCAG GGCCAGAGTTTCTGACTTACTTCCAGAATGAAGCTCAACTAGAAAA ATCAAGGCTGCTCAGTGATCGGT TCTCTGCAGAGAGGCCCTAAGGGATCTTTCTCCACCTTGGAGATCCAG CGCACAGAGCAGGGGACTCGGC CATGTATCTCTGTGCCAGCAGCTTAGCAGGGTTGAATCAGCCCCAGC ATTTTGGTGATGGGACTCGACTC TCCATCTAGAGGACCTGAACAAGTGTTCCACCCGAGGTGCGTGT GTTTGAGCCATCAGAAAGCAGAGA TCTCCACACCCAAAGGCCACACTGGTGTGCTGGCCACAGGTATC TTCCCTGACCACGTGGAGCTGAG CTGTTGGTGAATGGGAAGGAGGTGCACAGTGGGTACACCGGACC CGCAGCCCCCTCAAGGAGCAGCCC GCCCTCAATGACTCCAGATACTGCTGAGCAGCCGCTGAGGGTCTC GGCCACCTTCTGGCAGAACCCCC GCAACCACTTCCGCTGTCAAGTCCAGTTCTACGGGCTCTCGGAGAAT GACGAGTGGACCCAGGATAGGGC CAAACCCGTCAACCAGATCGTCAGCGCCGAGGCCCTGGGGTAGAGCAG ACTGTGGCTTTACCTCGGTGTCC TACCAGCAAGGGGTCTGTCTGCCACCATCCTCTATGAGATCCTGTCT AGGGAAGGCCACCATGTATGCTG TGCTGGTCAGCGCCCTTGTGTTGATGGCCATGGTCAAGAGAAAGGAT TTCTGAAGGCAGCCCTGGAAGTG GAGTTAGGAGCTTCTAACCCGTGATGGTTTCAATACACATTCTTCTT TTGCCAGCGCTTCTGAAGAGCTG CTCTCACCTCTCTGTCATCCCAATA	48.45
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210972 _x_at	T cell receptor alpha locus /// T cell receptor delta variable 2 /// T cell receptor alpha variable 20 /// T cell receptor alpha joining 17 /// T cell receptor alpha constant	ggaacaagacttcagggtcacgctc gataccagaacctgacccctgcc gtgtaccagctgagagactctaaa tcagtgacaagtctgtctgccta ttcacggattttgattctcaaaaca aatgtgtcacaaagtaaggattct gatgtatatcacagacaaaaact gtgctagacatg aggtctatggacttcaagagcaac agtgtgtggcctggagcaacaaa tctgactttgcatgtgcaaacgcc ttcaacaacagcattattccagaa gacaccttctccccagcccagaa agttcctgtgatgtcaagctggtc gagaaaagccttgaaacagatacg aacctaaaacttt caaaacctgtcagtgattgggttc cgaatcctcctcctgaaagtggcc gggtttaatctg ctcatgacgtgcggctgtggtcc agctgagatctgcaagattgtaag acagcctgtgct ccct [Seq Id No 67]	>gi 338765 gb M15565.1 HUMTCAYE Human T-cell receptor rearranged alpha-chain V-region (V-D- J) mRNA, complete cds TCCAAATGAAGGGTCTGTGGAAGGACATGAATAAAGCACAGGAGGT TGAAGTCAGATTTCAGAGCTTTCT AGGCAGAGACAAAGACAATCTGCATCTTCACAGGAGGGATGGCCATG CTCCTGGGGGCATCAGTGTGAT TCTGTGGCTTCAGCCAGACTGGGTAAACAGTCAACAGAGAATGATG ACCAGCAAGTTAAGCAAAATTCA CCATCCCTGAGCGTCCAGGAAGGAATTTCTATTCTGAACTGTGA CTATACTAACAGCATGTTTGAT ATTTCCCTATGGTACAAAAAATACCCCTGCTGAAGGTCTTACATTCCCTG ATATCTATAAGTTCATTAAAGGA TAAAAATGAAGATGGAAGATTCACTGTCTTCTTAAACAAAAGTGCCA AGCACCTCTCTCTGCACATTGTG CCCTCCAGCCTGGAGACTCTGCAGTGTACTTCTGTGCAGCAAGGG GGCCGGCAGTCCAGTAACTCA CCTTTGGGACTGGAAACAAGACTTCAGGTCAAGCTCGATATCCAGAAC CCTGACCCCTGCCGTGTACCAGCT GAGAGACTCTAAATCCAGTGACAAAGTCTGTCTGCCTATTACCCGATT TTGATTCTCAAAACAAATGTGTCA CAAAGTAAGGATTCTGAIGTGTATATACACAGACAAAACCTGTGCTAGA CATGAGGTCTATGGACTTCAAGA GCAACAGTGTGTGGCCTGGAGCAACAAATCTGACTTTGCAATGTGCA AACGCCCTTCAACAACAGCATTA TCCAGAAGACACCTTCTTCCCCAGCCAGAAAGTTCCCTGTGATGTCA AGCTGGTCGAGAAAAGCTTTGAA ACAGATACGAACCTAAACTTCAAAAACCTGTCAAGTGTGGGTCCCG AATCCTCCTCCTGAAAGTGGCCG GGTTTAATCTGCTCATGACGCTGGGCTGTGGTCCAGCTGAGATCTG CAAGATTGTAAGACAGCCTGTGC TCCCTCGCTCCTTCTCTGCAATTGCCCTCTTCTCCCTCTCCAAACA GAGGGAACCTCTCCACCCCCAAG GAGGTGAAAGCTGCTACCAACCTCTCTGTGCC	26.45
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211144 _x_at	T cell receptor gamma constant 2	aatgatacactactgctgcagct cacaacacacctctgcataattacat gtacctcctcct gctcctcaagagtgtggtctatatt tgccatcatcacctgctgtctgct tggaagaacggc tttctgctgcaatggagagaaatc ataacagacggtggcacaaggagg ccatcttttccct catcgggttatgtccctagaagcg tcttctgaggatctagttgggctt tcttctcgggt tgggccatttcagttctcatgtgt gtactattctatcatattgtata atggttttcaaa ccagtgggcacacagagaaacctca gtctgtaataacaaatgaggaatag ccatggcgatctccagcaccatc tctccatgttttccacagctcctc cagccaaacccaaatagcgctgct atagtgtagacagcctgcggctc tagccttgctccctctcttagtggt ctttaatcagat aactgcctggaagcctttcatctt acacgccc [Seq Id No 68]	>gi 339406 gb M30894.1 HUMTCRGAD Human T-cell receptor Ti rearranged gamma-chain mRNA V-J-C region, complete cds GAATCAGGAAGACCAGCTCCTACTGTCTTCTGTGTACGGGATC AGCGTTCCTTGTGAGTGGGACC TGAGTTTGTAGAGGGTCTTCTGTCTCCTTGGTCTGGTCCCCTTACTT CCAAGAGCCCCAGAGAGGAAGGC ATGCTGTTGGCTCTAGCTCTGTCTTCTAGCTTTCCTGCTCCTGCCCAG TCAGAAATCTTCCAACTTGGAAG GGAGAAACAAAGTCAGTCAACAGGCCAACTGGGTCAATCAGCTGTAATC ACTTGTGATCTTCTCTGTAGAAAA TGCCGTCTACACCCACTGGTACCTACACCAGGAGGGGAAGGCCCCAC AGCGTCTTCTGTACTATGACTCC TACAACCTCCAGGTTGTGTGGAATCAGGAATCAGTCGAGAAAAAGTA TCATACTTATGCAAGCACAGGGA AGAGCCTTAAATTTATATACTGGAAAAATCTAATTGAACGTGACTCTGGG GTCTATTACTGTGCCACCTGGAA GGATTATTATAAGAAACTCTTTGGCAGTGGAAACAACACTTGTGTGTCA CAGATAAACAACTTGATGCAGAT GTTTCCCCCAAGCCCACTATTTTCTTCTCCTTCGATTGCTGAAACAAA ACTCCAGAAAGGCTGGAACATATC TTTGTCTTCTTGAGAAATTTTCCCAGATATTATTAAGATACATTGG CAAGAAAAGAAAGAGCAACACGAT TCTGGGATCCCAGGAGGGGAACACCATGAAGACTAACGACACATACA TGAAATTTAGCTGGTTAACGGTG CCAGAAAGAGTCACTGGACAAAGAACACAGATGTATCGTCAGACATGA GAATAATAAAAAACGGAATTGATC AAGAAATTATCTTTCTCCTCCAATAAAGACAGATGTCACCAAGTGGAT CCCCAAAGACAGTTATTCAAAAGA TGCAAAATGATGTCACCAAGTGGATCCCAATAACAATTATTCAAAGG ATGCAAAATGATGTCAATCAATG GATCCCAAAGACAATTTGGTCAAAAGATGCAATGATACACTACTGCT GCAGCTCACAAACACCTCTGCAT ATTACATGTACCTCCTCCTGCTCCTCAAGAGTGTGCTATTTTGCC	17.38
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			ATCATCACCTGCTGCTGCTTGG AAGAACGGCTTCTGCTGCAATGGAGAGAAATCATAACAGACGGTGG CACAAAGGAGGCCATCTTTTCCTC ATCGGTTATTGTCCCTAGAAAGCGTCTTCTGAGGATCTAGTTGGGCTT TCTTTCTGGGTTTGGGCCATTTC AGTTCTCATGTGTGTAATACTATCTATCATTTATGTAATGTTTCA AACAGTGGGCACACAGAGAACC TCAGTCTGTAATAACAATGAGGAATAGCCATGGCGATCTCCAGCACC AATCTCTCCATGTTTTCACAGC TCCCTCAGCCAAACCAATAGCGCTGCTATAGTGTAGACAGCCTGC GGCTTCTAGCCTTGTCCCTCTCT TAGTGTCTTTAATCAGATAACTGCCCTGGAAGCCCTTTCATTTTACAC GCCCTGAAGCAGTCTTCTTTGCT AGTTGAATTATGTGGTGTGTTTTCGGTAATAAGCAAAATAAATTT	63.34
211796 _s_at	T cell receptor beta variable 21-1 /// T cell receptor beta variable 19 /// T cell receptor beta variable 5-4 /// T cell	gccatcagaagcagagatctccca caccctaaaggccacactggtgtg cctggccacaggtttctaccccca ccacgtggagctgagctggtgggt gaatgggaaggagtgacacagtgg ggtcagcacagacccgcagccct caaggagcagccgcctcaatga ctccagatactgcctgagcagccg cctgagggctctcgccaccttctg gcagaaccccgcaaccacttccg ctgtcaagtccagttctacgggct ctcggagaaatgacgagtggaacca ggatagggccaaacctgtcaccca gatcgtcagcgcagagccctgggg tagagcagactgtggcttcacctc cgagctctaccagcaagggtcct gtctgccaccatcctctatgagat cttgctagggaaggccaccttga tgctgtgctggtcagtgccctcgt gctgatggccatggtcaagagaaa	>gi 3002924 gb AF043179.1 AF043179 Homo sapiens T cell receptor beta chain (TCRBV13S1-TCRBV2S1) mRNA, complete cds ATGAGCATCGGCCTCCTGTGTGTGCAGCCCTTGTCTCTCCTGTGGGC AGGTCCAGTGAATGCTGGTGCA CTCAGACCCCAAAATTCAGGTCTCTGAAGACAGGACAGAGCATGACA CTGCAGTGTGCCAGGATATGAA CCATGAATACATGTCCTGCTATCGACAAGACCCAGGCATGGGGCTGA GGCTGATTCAATTAATCAGTTGGT GCTGGTATCACTGACCAAGGAGAAAGTCCCCAATGGCTACAATGTCTC CAGATCAACCAACAGAGGATTTC CGCTCAGGCTGCTGTGGCTGCTCCTCCAGACATCTGTGTACTTC TGTGCCAGCAGTTTCCCCCGGCA GCCGTCTTACAATGAGCAGTTCTTCGGGCCAGGACACGGCTCACCG TGCTAGAGGACCTGAAAAACGTG TTCCCAACCCGAGGTCGCTGTGTTTGAGCCATCAGAAGCAGAGATCTC CCACACCCCAAAAGGCCACACTGG TGTGCTGGCCACAGGTTTCTACCCCGACCACTGGAGCTGAGCTGG TGGGTGAATGGGAAGGAGGTGCA CAGTGGGGTTCAGCACAGACCCCGAGCCCTCAAGGAGCAGCCCCCCC	

	receptor beta variable 3-1 /// T cell receptor beta constant 1	gga [Seq Id No 69]	TCAATGACTCCAGATACTGCCTG AGCAGCCGCTGAGGGTCTCGGCCACCTTCTGGCAGAACCCCGCAA CCACTTCCGCTGTCAAGTCCAGT TCTACGGGCTCTCGGAGAATGACGAGTGGACCCAGGATAGGGCCAAA CCTGTACCCAGATCGTCAGCGC CGAGGCCCTGGGTAGAGCAGACTGTGGCTTCACTCCGAGTCTTACC AGCAAGGGTCTCTGTGCCACC ATCCTCTATGAGATCTTGTAGGGAAGGCCACCTTGTATGCTGTGCT GGTCAGTGCCCTCGTGTGATGG CCATGGTCAAGAGAAAGGATTCCAGAGGCTGA	
211902 _x_at	T cell receptor alpha locus	gaatcgtttctctgtgaacttcca gaaagcagccaaatccttcagtct caagatctcaga ctcacagctggggatgcccgat gtatttctgtgcttataggagtgc atactctgggc tgggagttaccaactcactttcgg gaagggaccacaaactctcggtcat accacatataccagaaacctgaccc tgccgtgtaccagctgagagactc taaatccagtgacaaagtctgtctg cctattccagattttgattctca aacaaatgtgtcacaaagtaagga ttctgatgtga tatcacagacaaaactgtgctaga catgaggtctatggacttcaagag caacagtgtgt ggcctggagcaacaaatctgactt tgcatgtgcaaacgccttcaacaa cagcattattcc agaagacaccttcttccccagccc agaaagtctctgtgatgtcaagct ggtcgagaaaagctttgaaacaga tacgaacctaaacttcaaaacct	>gi 1100165 gb L34703.1 HUMTCRAZ Homo sapiens T-cell receptor alpha chain (TCRA) mRNA (HLA-A1, 24; B7, 8; DR 1, 3), complete cds ATGCAATGCCCTGGCTTCTGTGGCACTTGTGATCTCCACCTGTCT TGAATTTAGCATGGCTCAGACAG TCACTCAGTCTCAACAGAGATGTCTGTGAGGAGCAGAGACCCTG ACCCTGAGCTGCACATATGACAC CAGTGAGAGTGATTATTATTATTCTGTGTAACAAGCAGCCTCCCAGCA GGCAGATGATTCTCGTTATTGCG CAAGAAGCTTATAAGCAACAGAATGCAACAGAGAATCGTTTCTCTGT GAACTTCCAGAAAGCAGCCAAAT CCTTCAGTCTCAAGATCTCAGACTCAGCTGGGGATGCCGCGATG TATTTCTGTGCTTATAGGAGTGC ATACTCTGGGGCTGGAGTTACCAACTCACTTTCGGGAAGGGGACCA AACTCTCGGTCAATACCAATATC CAGAACCTTGACCTGCCGTGTACCAGCTGAGAGACTCTAAATCCAG TGACAAGTCTGTCTGCCTATTCA CCGATTTTGATTCTCAACAATAATGTGTCAACAAGTAAGGATTCTGAT GTGTATATCACAGACAAACTGT GCTAGACATGAGGTCTATGGACTTCAAGAGCAACAGTGTGTGGCCT GGAGCAACAAATCTGACTTTGCA TGTGCAACAGCCTTCAACAACAGCATTAATCCAGAAAGACACCTTCTT CCCCAGCCCCAGAAAGTTCCCTGTG ATGTCAAGCTGGTCGAGAAAAGCTTTTGAAACAGATACGAACCTAAAC	20.68

		gtcagt gattgggttccgaatcct cctcctgaaagtggcgggttttaa tctgctcatgacgctgcgggttg gtcc		TTC AAAACCTGT CAGTATTGG GTTCCGAATCCTCTCTCTGAAAGTGGCCGGTTTAAATCTGCTCATGA CGCTGCGGTTGTGTGTCCAGCTGA	
212999 _x_at	Major histocompa tibility complex, class II, DQ beta 1 /// Major histocompa tibility complex, class II, DQ beta 1	[Seq Id No 70] cactgcagaatgaaggaaacatccc ttgaggtgacccagccaacctgtg gccagaaggagnttgtaacctga aaagacactgaaagcattttggng tgtnaagtaagggtgggcagagga ggtagaaaaatcaattcaattgtcg catcattcatgggttctttaatat gatgctcagtgcantggcctnaga atatccagcctctcttctggttt gntgagtgctntntaagtaagcat ggtngaattgtttgggncanata tagtganccttggtcactgggtgt tcaaacattctg gnaagtcacatcnatcaagaatan ttttanttttaagaaagcataaac cagcaataaa	>gi 24797068 ref NM_002123.2 Homo sapiens major histocompatibility complex, class II, DQ beta 1 (HLA-DQB1), mRNA CAGATCCATCAGGTCGAGCTGTGTGACTACCACCTTTTCCCTTCGT CTCAATTATGTCTTGGAAAAAGG CTTTGCGGATCCCCGGAGGCCCTTCGGGCAGCAACTGTGACCTTGATG CTGTGATGTGTGACACCCAGT GGCTGAGGGCAGAGACTCTCCCGAGGATTTCTGTGTACCAGTTTAAGG GCATGTGCTACTTCAACCAACGGG ACAGAGCGCGTGCGTCTTTGTGAGCAGAGAAGCATCTATAACCGAGAAGA GATCGTGGCTTCGACAGCGACG TGGGGAGTTCCGGGCGGTGACGCTGTCTGGGGCTGCCTGCCGCCGAG TACTGGAACAGCCAGAAAGGACAT CCTGGAGAGGAAACGGGCGCGGTGGACAGGGTGTGCAGACACAACACT ACCAAGTTGAGCTCCGCACGACC TTGCAGCGCGAGTGGAGCCCCACAGTGACCATCTCCCCATCCAGGAC AGAGGCCCTCAACCAACCAACC TGCTGGTCTGCTCGGTGACAGATTCTATCCAGCCCCAGATCAAAGTC CGGTGGTTTCGGAATGACCAAGG GGAGACAGCTGGCGTTGTGTCCACCCCCCTTATTAGGAATGGTGACT GGACCTTCCAGATCCTGGTGATG CTGGAATGACTCCCCAGCGTGGAGACGCTTACACCTGCCACGTGGA GCACCCAGCCCTCCAGAGCCCCA TCACCGTGGAGTGGCGGCTCAATCTGAATCTGCCAGAGCAAGATG CTGAGTGGCATTTGGAGGCTTCGT GCTGGGCTGATCTTCTCGGGCTGGGCCCTTATCATCCATCACAGGA GTCAGAAAGGCTCCTGCACTGA	15.79	
		[Seq Id No 71] cactgcagaatgaaggaaacatccc ttgaggtgacccagccaacctgtg gccagaaggagnttgtaacctga aaagacactgaaagcattttggng tgtnaagtaagggtgggcagagga ggtagaaaaatcaattcaattgtcg catcattcatgggttctttaatat gatgctcagtgcantggcctnaga atatccagcctctcttctggttt gntgagtgctntntaagtaagcat ggtngaattgtttgggncanata tagtganccttggtcactgggtgt tcaaacattctg gnaagtcacatcnatcaagaatan ttttanttttaagaaagcataaac cagcaataaa			

			CCTGCTTGTCCTGCCAGAAAT CCCAGCTGTCTGTGTCAAGCCTGTCCCCCTGAGATCAGAGTCCTACAG TGGCTGTCAAGCAGCCACACAGGT CATCTCCTTTTCATCCCCACCTTGAGGGGATGGCTGTGACCCCTACTT CCTGCACTGACCCACAGCCTCTG CCTGTGCACGGCCAGCTGCATCTACTCAGGCCCCCAAGGGTTTCTGT TTCTATTCTCTCTCAGACTGCT CAAGAGAAGCACATGAAAACCATTACCTGACTTTAGAGCTTTTTTAC ATAATTAAACATGATCCTGAGTT	44.75
213193 _x_at	T cell receptor beta variable 19 /// T cell receptor beta variable 19 /// T cell receptor beta constant 1 /// T cell receptor beta constant 1	Tgactccagataactgcctgagcag ccgcctgagggtctctcgccacctt ctggcagaacccccgcaaccactt ccgctgtcaagtcagttctacgg gctctcggaatgacgagtggac ccaggatagggccaaacccgtcac ccagatcgtcagcgccgagggcctg gggtagagcagactgtggctttac ctcgggtgctctaccagcaagggt cctgtctgccaccatcctctatga gatcctgctagggaaaggccacct gtatgctgtgctggtcagcncct tgtgttgatggccatggtcaagag aaaggatttctgaaggcagccctg gaagtggagttaggagcttctaac ccgtcatgggttcaatacacattc ttcttttgccagcgcttctgaaga gctgctctcacctctctgcatccc aatagatatccccctatgtgcatg cacacctgcacactcacggctgaa atctccctaaccagggggacctt agcatgcctaagtga	>gi 46184507 gb AL559122.3 AL559122 AL559122 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10- NORMALIZED Homo sapiens cDNA clone CS0DJ014YE01 5-PRIME, mRNA sequence TGCCTGGCCACAGGCTTCTTCCCGACACGTGGAGCTGAGCTGGTG GGTGAATGGGAAGGAGTGCACA ATGGGTCAACACAGACCCGAGCCCTCAAAGAACAGCCCCCCTC AATGACTCCAAATAMTGCTGAG CAGCCGCTGAGGGTCTCGGCCACCTTCTGGCAGAACCCCGCAACC ACTTCCGCTGTCAAGTCCAGTTC TACGGGCTCTCGGAGAAATGACGAGTGGACCCAGGATAGGGCCAAACC CGTCACCCAAATCGTCAGCGCCG AGGCC TGGGTARAGCARAMTGTGGCTTTACCTCGGTGTCTACCAA CAAGGGGTCTGTGTGCCACCAT CCTCTATGARATCCTGTAGGAAAGGCCACCTGTATGTGTGTGCTGG TCAGCGCCCTTGTGTGATGGCC ATGCTCAAGAGAAAGGATTTCTGAAGGCAGCCCTGGAAGTGAATTA AGAACTTCTAACCCGTCATGGTT TCAATACACATTCTTCTTTTGGCAGCGCTTCTGAAGAGCTGCTCTCA CCTCTCTGCATCCCAATAGATA CCCCCTATGTGCATGCACACCTGCACACTCACGGCTGAAATCTCCCT AACCCAGGGGACCTTAGCATGC CTAAGTGACTAAACCAATAAAATGTTCTGTGTGGCCTGA	

213539 _at	CD3D antigen, delta polypeptid e (TiT3 complex)	gggaacactgctctcagacattac aagactggaccctgggaaaaacgcat cctggacccacgaggaatatatag gtgtaatgggacagatatatacaa ggacaaaagaatctaccgtgcaagt tcattatcgaatgtgccagagctg tgtggagctggatccagccaccgt ggctggcatcattgtcactgatgt cattgccactctgctccttgcttt gggagtcttctgcttctgctggaca tgagactggaaggctgtctggggc tgccgacacacaagctctgttgag gaatgaccaggctctatcagccct ccgagatcgagatgatgctcagta cagccaccttgagggaactgggc tcggaaacaagtgaacctgagactg gtggcttctagaagcagccattac caactgtacct [Seq Id No 73]	>gi 98985799 ref NM_000732.4 Homo sapiens CD3d molecule, delta (CD3-TCR complex) (CD3D), transcript variant 1, mRNA AGAGAAGCAGACATCTTCTAGTTCTCTCCCCCACTCTCTCTTTCCGG TACCTGTGAGTCAGCTAGGGGAG GGCAGCTCTCACCCAGGCTGATAGTTCCGGTGACCTGGCTTTATCTAC TGGATGAGTTCCGCTGGGAGATG GAAACATAGCACGTTTCTCTCTGCGCTGGTACTGGCTACCCCTTCTCTC GCAAGTGAGCCCCCTTCAAGATAC CTATAGAGGAACTTGAGGACAGAGTGTTTGTGAATTGCAATACCAGC ATCACATGGGTAGAGGGAACGGT GGGAACACTGCTCTCAGACATTACAAGACTGGACCTGGGAAAAACGCA TCCTGGACCCACGAGGAATATAT AGGTGTAATGGGACAGATATATACAAGGACAAAGAATCTACCGTGCA AGTTCATTATCGAATGTGCCAGA GCTGTGTGGAGCTGGATCCAGCCACCGTGGCTGGCATCATTTGTCACT GATGTCAATTGCCACTCTGCTCCT TGCTTTGGGAGTCTTCTGCTTTGCTGGACATGAGACTGGAAGGCTGT CTGGGCTGCCGACACACAAGCT CTGTTGAGGAATGACCAGGCTATCAGCCCCCTCCGAGATCGAGATGA TGCTCAGTACAGCCACCTTGGAG GAAACTGGGCTCGGAACAAGTGAACCTGAGACTGGTGGCTTCTAGAA GCAGCCATTACCAACTGTACCTT CCCTTCTTGCTCAGCCCAATAAATATATCCTCTTTCACTCAGAAAAAA AAAAAA A	34.66
215806 _x_at	T cell receptor gamma constant 2 /// T cell	aatgatacactactgctgcagct cacaacacacctctgcataattacat gtacctctcct gctcctcaagagtgtggtctattt tgccatcatcacctgctgtctgcn tgnaagaacggc nnnctgctgcaatggagagaantc	>gi 339168 gb M13231.1 HUMTCGXH Human T-cell receptor aberrantly rearranged gamma-chain mRNA from cell line HPB-MLT GGCATGCGGTGGGCCCTACTGGTGCTTCTAGCTTTCTGCTCTCCTGC CAGTCAGAAATCTTCCAACCTGG AAGGGAGAACGAAGTCAGTCACCAAGCAGGACACTGGGTCACTCTGCTGAA ATCACTTGGGATCTTACTGTAAAC	19.96

receptor gamma variable 9 /// similar to T-cell receptor gamma chain C region PT- gamma-1/2 /// similar to T-cell receptor gamma chain V region PT- gamma-1/2 precursor /// TCR gamma alternate reading frame protein	ataacagacggtggcacaagagg ccnncntntcctcatcggnnatg tccctagaagcgtcttctgaggat ctagttgggcttcttcttctgggtt tgggccatttcagttctcatgtgt gtactattctatcattattgtata atggtttttcaaa ccagtgggcacacagagaacctca gtctgtaataaacaatgaggaatag ccatggcgatctccagcaccaatc tctccatgttttccacagctcctc cagccaaacccaatagcgctgct atagtgtaganannctgcggcttc tagccttgtccctctcttagtggt ctttaatcagat aaactgcctggaagcctttcatttt acacgcccctgaagcagtcctcttt gcta [Seq Id No 74]	AAATACCTTCTACATCCACTGGTACCTACACAGGAGGGAAGGCCC CACAGCGTCTTCTGTACTATGAC GTCTCCACTGCAAGGGATGTGTGGAATCAGGACTCAGTCCAGGAAA GTATTATACTCATACACCCAGGA GGTGGAGCTGGATATTGAGACTGC AAAATCTAATTGAAAAATGATTCT GGGTCTATTACTGTGCCACCTG GGACAGGC AAAAATTATTATAAGAAACTCTTTGGCAGTGGAAACAACA CTTGTGTACAGATAAACAAC TGATGCAGATGTTTCCCCCAAGCCCACTATTTTCTTCTTCAATTG CTGAACAACA AACTCCAGAAGGCT GGAACATACCTTTGTCTTCTTGAGAAATTTTCCAGATATTATTAA GATACATTGGCAAGAAAAGA GCAACACGATTTCTGGATCCAGAGGGGAACACCATGAAGACTAAC GACACATACATGAAATTTAGCTG GTTAACGGTGCCAGAAGAGTCACTGGACAAAAGAACACAGATGTATCG TCAGACATGAGAAATAATAAAC GGAATTGATCAAGAAATTTATCTTCTCCAATAAAGACAGATGTCAC CACAGTGGATCCCAAGACAGTT ATTC AAAAGATGCAAAATGATGTCATCACAAATGGATCCCAAGACAAT TGGTCAAAAGATGCAAAATGATAC ACTACTGCTGCAGCTCACAACACACCTCTGCATATTACATGTACCTCC TCCTGCTCCTCAAGAGTGTGTC TATTTTGCCATCATCACCTGCTGCTGCTTGGGAAGAACGGCTTTCTG CTGCAATGGAGAGAAATCATAAC AGACGGTGGCACAAGGAGGCCATCTTTTCCATCGGTATTGTGTC TAGAAGCGTCTTCTGAGGATCTA GTTGGGCTTTCTTTCTGGGTTTGGGCCATTTCAGTTCTCATGTGTGT ACTATTCTATCATTTATTGTATAA TGGTTTTCAAACCAAGTGGGCACACAGAGAACCTCAGTCTGTAATAAC AATGAGGAATAGCCATGGCGATC TCCAGCACCAATCTCTCCATGTTTTCACAGCTCCTCCAGCCAACCC AAATAGCGCCTGCTATAGTGTAG ACAGCCTGCGGCTTCTAGCCCTTGTCCCTCTCTTAGTGTCTTTAATC AGATAACTGCGCTGGAAAGCCTTTC
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			ATTTACACGCCCTGAAGCAGTCTTCTTTGCTAGTTGAATTATGTGG TGTGTTTTTCCGTAATAAGCAAA ATAAATTTAAAAAATGAAAA	
216748 _at	pyrin and HIN domain family, member 1	ccaccctctggatcccaatatga gatcttatcctcaggggaatcctca cttagaccctg taacagggttaaatcttcatggtgt tctggttcctaggaacttcttctt tttctactgttt atgacaaactgaagttaataagtgt ttatctttccacctaactcaagt agttccaagatt agggctagtgtgtaattctgtgga ccactgtaaacgagggcctagttc agtgtctgcctc atgggaagccttccaataaacctt ttg [Seq Id No 75]	>gi 10437303 dbj AK024890.1 Homo sapiens cDNA: FLJ21237 fis, clone COL01114 GTCAAAGGAATAATCCCATCTAAAGACGAAACAGAAAGAGTGTA TCCTGCTACACCTGCATGCACCC CAAGCAACCGTCTCACAGCTAAAGGAGCAGAGGAGACTCTTGGACCT CAGGTAAGCTTCAGGAAGAGGAG CAGGCTTCAAGTCTCACAGTGGAGCTCTGTGTGGCTGTTCCACTC AATCTGTCCAGCAGGCAGTTAT TCTTCATATGTTTCCCATCAAGTTTCAGATTTATCAAAATTACATAAT AATTGATCATCTTTCTGCAAGGC AACAAAGTTAAACGCTTTTAGTAAACATAATGTAAATATACATAAAATA AATAAATAATTTTCATCTCCAAT AGAGAAGGATGTTAACTTGAGAGTCAGATAAAAAACGTTTGCCTAT GTTTACAAAAGCCTAGTTTCTTA ACTGCAAGTCAGCATATCCCCAAACACAAGTAATTAAGGAATGATGT GTGTTACTTTCTGCTCCCTTT TTAAAAATGAAACCATCTATGCCATGTTCTTTCAATTGGCCTGGGGA TGTACTTAAGTTTCCAAGAAAA CAATTTATATACAATAAATATATTACCTTGTAATGAAAAATGTGCTCT GCTTCATTTGACACTGAAAGTAA TTAAACAAGAAAAATAAACTACTTTGTAGAAAAAGAAAAACCATCTGA AGAAAGAGACTGGAACCAAAAGGA GTAAGATGTCCAAGAGCAGACTCGGCCCTTCCTGCTCTGCAGGAGCC AGCACGTCCACAGCCATGGGCCG TTCCCCACCTCCCAGACCTCATCATCAGCTCCACCCAACTTCCT CAACTGAGGTACACTCTTCCCTGG TCCCCCTTTTGATTCTATTTTCTTCAACCCCAAATGTAGGAATCTGATT TCATCTTCTACTGAAAAAATGACA TCAATCATCAGCCAGTAAATCAAATGTATAGACTGAGAAATTAACCTGC ATTTTAATCTTTTGTCTTCCACAG	10.74

			GCATATTTGATGAACCTGACATTATCTCTGACTGCAGGAAGTTTCT GTCCTGTGCTGTTTGGGAAGAG ACAGAGAACTGCGGAATCTGGAACCTTTCAGCAACAGACTCACTGTCT ACTGCCCCCATCTATTATACACC CATTCCTTTTGCTCACTAATTGTTCAAGTTTCTCTGACATACACCA TGCTCCTTTTCCCTTTAGGATT TCACACACCATATTCTTTTCACCTTTAAACTCTTACCTGGCCCAACCC TATCCACCTCTGGATCCCAATA TTGAGATCTTATCCTCAGGGAATCCTCACTTAGACCCCTGTAAACAGG TTAAATCTTCATGGTGTCTGTT TCCTAGGAACTTCTTTTCTTCTACTGTTTATGACAACTGAAGTTAA TAAGTGTATTATCTTTCCACCTA CTCAAAGTAGTTCCAAGATTAGGGCTAGTTTGTAATTCTGTGGACCA CTGTAACGAGGGCCTAGTTCAG TGTCTGCCCTCATGGGAAGCTTCCAATAAATACCTTTGCTCAACGAAA AAATGAAAAACCCAGTGGCTCAG CCTGTAATCCAGCACTTTGGAGGCCGAGGAGGTGGATTGCCCTGA GGTCAGGAGTTTGAGACTAGTCT GGCCAACATGGTGAAACACTATCTCTACTAAAAATACAAAAAATTA GCTGGGTATGGTGGCTTACGCCCT ATAATCCAGCTACTCAGGAGGCTGAGCAGGGGAATTGCTTGAACC AGGAGGTGGAGGTTGCAGTGAG CTGAGATCGCACCACTGCACCTCAGCCTGGGTGACAGAGCGAGACTC CATCTCAAAATAAAAAAGTAAAA AAAAAAATAAAAAA	
217147 _s_at	T cell receptor associated transmembr ane adaptor 1	tctccttctcaccaatgggcaat agccataattgaaataaatttct gattgaaaggta taggaaacattaaatgcattact aagagaagtaataattttctta caaagtattttt cccaaagatagctttactatttca aaaattgtcaaatatgaatgcattgct cctacaacaaa	>gi 54607136 ref NM_016388.2 Homo sapiens T cell receptor associated transmembrane adaptor 1 (TRAT1), mRNA GAGGCACAGATAAAGATAAGTTTACTGTCTCATGCTGCTTTTAAACATA ACAGAGCAACATCACCTAGGAAA AAAGTTTGTAGGAGGATTTTAAATCCATATATTGTCTTATGGCTAG ATAAAGATTCTCTGAAAAAAG AAGCATGTCAGGAATCTCTGGTGCCCTTTTCTCTGGGGACTTC TAGCATTTGTTGGCTTGGCTTTG	24.16

	caaatacaaaaagagtttaggaa ttctactagccagagatagtcact tgagaaaacttt ctatatccttctctaaatatattt ctgggcatgctcatgtatgtacat cagttgtttctt tttattttgaacccaaaatgtggt ttcttttgtacacattacttaaac tttctttccagt caacaatatatgtggatttat tcaactgttatatttaactatat aaatacgcata attgtaattttaatgtctgcttag caccctgataacccaaatcaca g	GTTATATCACTGATCTTCAATATTTCCCACTATGTGGAAAAGCAACG ACAAGATAAAATGTACAGCTACT CCAGTGACCAACACAGGTTGATGAGTATTATATTGAAGACACACCA ATTTATGGTAACTTAGATGATAT GATTTCAGAAACCAATGGATGAAAATTGCTATGAACAAATGAAAGCCC GACCAGAGAAATCTGTAAATAAG ATGCAGGAAGCCACCCCATCTGCACAGGCAACCAATGAAACACAGAT GTGCTACGCTCACTTGATCACA GCGTTAAGGGGAGCGTAGAAAGCCAGGAAACAGAATACTCATTTC TCAGACAAGGATGGAGATGAGCA ACTACATGCAATAGATGCCAGCGTTTCTAAGACCACCTTAGTAGACA GTTTCTCCCCAGAAAAGCCAGGCA GTAGAGGAAAACATTCAATGATGATCCCATCAGACTGTTTGGATTGAT CCGTGCTAAGAGAGAACCTATAA ACTAGCTGGACCATGATCTAGTTCAATGATTTGGCTCCTATTTGAAGA TGGCTTCTAAGAAAAACAAGATGC ACAGAGGACACAGAAAGGACTTGGCAGCAGGGTGATGACCTGATCAT TGTTGATGGGATGGTGGCTTACC TCTTATTCACAGCTTACACTATGCAATGCCAAATGTAAAGGCCATGAA AATCAGTATTTCAAAATAACTTAA AAAATGCTTTTACTACTAAAATGTAAAAAATTAATGTGCTCACCTCGG CAGCACATA TACTAAAAATTAAT AAGACCCAGCTTGAAAATTGAGCCTGATAACAAGATTACAAAATTCAC AATACCTAATACTTAGGGAAATA TAAAAATTTAAGCATGAATGCGTTCTTGGAACACACGTTAGAAAGAAAAAT AAAAGCCCAATGAGTTTTTTAA ATTCTCCTTTTCTCACCAATGGGCAATAGCCCATAATTGAAAATAAATT TCTGATTGAAAGGTATAGGAAAC ATTAAAATGCATTACTAAGAGAAAGTAATAATTTTCTTACAAAGTA TTTTTCCCAAAGATAGCTTTACT ATTTCAAAAAATTTGTCAAAATTAATGCATGCTCTTACAAACAAAT ATCAAAAAGAGTTTAGGAATTCT ACTAGCCAGAGATAGTCACCTTGGAGAACTTTCTATATATATCCTTCTA AATATTTTCTGGGCATGCTTAT	
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[Seq Id No 76]

219159 _s_at	SLAM family member 7	Gagagtggaacatttgcgcgggaaac tcctaacaatatgcccccatctcgg agagaacacagagtagcacacaat ccctcacactaatagaacaatcct a [Seq Id No 77]	GTATGTACATCAGTTGTTCTTTTATTTTGAACCAAAAATGTGGTT TCTTTTGTACACATTACTTAAAC TTTCTTCCAGTCAACAATATATTGTGGATTATTTTCACTGTTATA TTTAACTATATATAAATACGCAT ATATTGTAATTTTAAATGCTGCTTAGCACCCCACTGATAACCAAAATC ACAGTTTATTTAAATAATTTTAA TGACTTTTCAAAAACAATTTATTTGATGCAAAAAGCAAGGTTGAGATG ACAATGTTTCTTCAATAATTAA AAAATACTGCTTCAC	15.84
		>gi 19923571 ref NM_021181.3 Homo sapiens SLAM family member 7 (SLAMF7), mRNA CTTCCAGAGAGCAATATGGCTGGTTCCCAACATGCCTCACCCCTCAT CTATATCCTTTGGCAGCTCACAG GGTCAGCAGCCTCTGGACCCCGTGAAGAGCTGGTCCGTTCCGTTGGT GGGGCCGTGACTTTTCCCCCTGAA GTCCAAGTAAGCAAGTTGACTCTATTTGTCTGGACCTTCAACACAA CCCCTCTTGTCAACCATAACAGCCA GAAGGGGCACATATCATAGTGACCCCAAAATCGTAATAGGAGAGAGT AGACTTCCCAGATGGAGGCTACT CCCTGAAGCTCAGCAAACTGAAGAAGAAATGACTCAGGGATCTACTAT GTGGGGATATACAGCTCATCACT CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACC TGTCAAAGCCTAAAGTCACCATG GGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATG CTGCATGGAACATGGGGAAGAGG ATGTGATTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCC CATAATGGGTCCATCCTCCCCAT CTCCTGGAGATGGGAGAAAGTGATATGACCTTCATCTGCGTTGCCA GGAACCCCTGTCAGCAGAAACTTC TCAAGCCCCATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGA CCCAGATTCCCTCCATGGTCCCTCC TGTGTCCTCCTGTTGGTGCCCCCTCCTGCTCAGTCTCTTTGTACTGGGG CTATTTCTTTGGTTTCTGAAGAG		

		AGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGAGACATT GTCCGGAAACTCCTAACATATGC CCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA TAGAACAAATCCTAAAGGAAGATC CAGCAAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGATGGAA AATCCCACTCACTGCTCACGAT GCCAGACACACCAAGGCTATTTCCTATGAGAAATGTTATCTAGACAG CAGTGCACTCCCCTAAGTCTCTG CTCAAAAAAACAATTTCTCGGCCCAAGAAAAACAATCAGAAGAAT TCACTGATTGACTAGAAACATC AAGGAAGAAATGAAGAACGTTGACTTTTTCAGGATAAATTATCTCT GATGCTTCTTTAGATTTAAGAGT TCATAAATTCATCCACTGCTGAGAAATCTCTCAAAACCAGAAAGGTT TAATCACTTCATCCCCAAAATGG GATTGTGAATGTCAGCAAAACCATAAAAAAGTGCTTAGAAGTATTCC TATAGAAATGTAAATGCAAGGTC ACACATATTAAATGACAGCCTGTGTATTAATGATGGCTCCAGGTCAG TGTCTGGAGTTTCATTCATCCC AGGCTTGGATGTAAAGGATTATACCAAGAGTCTTGCTACCAGGAGGG CAAGAAGACCAAAACAGACAGAC AAGTCCAGCAGAAGCAGATGCACCTGACAAAAATGGATGTATTAAATT GGCTCTATAAACTATGTGCCCAG CACTATGCTGAGCTTACACTAATTGGTCAGACGCTGTCTGTGCCCTC ATGAAATTGGCTCCAAAATGAATG AACTACTTTTCATGAGCAGTTGTAGCAGGCTTGACCCACAGATTCCCAG AGGCCAGGTGTGGATCCACAGG ACTTGAAGGTCAAAGTTCACAAAGATGAAGAATCAGGGTAGCTGACC ATGTTTGGCAGATACTATAATGG AGACACAGAAGTGTGCATGGCCCCAAGGACAAGGACCTCCAGCCAGGC TTCATTTATGCACTTGTGCTGCA AAAGAAAAGTCTAGGTTTAAAGGCTGTGCCAGAACCCATCCCAATAA AGAGACCGAGTCTGAAGTCACAT TGTAATCTAGTGTAGGAGACTTGGAGTCAGGCAGTGAGACTGGTGG GGCACGGGGGCAGTGGGTACTT

			GTAAACCTTTAAAGATGGTTAATTCAATTCATAGATAATTATTAAAGA ACCTATGCGGCCCGGCATGGTGG CTCACACCTGTAAATCCAGCACTTTGGGAGGCCAAGGTGGTGGGTC ATCTGAGGTCAGGAGTTCAAGAC CAGCCTGGCCAAACATGTGTAAACCCCATCTCTACTAAAGATACAAAA ATTTGCTGAGCGTGGTGTGTC ACCTGTAATCCAGCTACTCGAGAGGCCAAGGCATGAGAATCGCTTG AACCTGGGAGGTGGAGTTGCCAG TGAGCTGAGATGGCACCACCTGCACTCCGGCCTAGGCAACGAGAGCAA AACTCCAATACAAACAACAAC AAACACCTGTGCTAGGTCACTCTGGCACGTAAGATGAACATCCCTAC CAACACAGAGCTCACCATCTCTT ATACTTAAGTGAATAACATGGGGAAGGGGAAAGGGAATGGCTGCTT TTGATATGTTCCCTGACACATAT CTTGAATGGAGACCTCCCTACCAAGTGATGAAAGTGTGAAAAACTT AATAACAAATGCTTGTGGGCAA GAATGGGATTGAGGATTATCTTCTCTCAGAAAGGCATTTGTGAAGGAA TTGAGCCAGATCTCTCTCCCTAC TGCAAAACCCCTATTGTAGTAAAAAAGTCTTCTTTACTATCTTAATAA AACAGATATTGTGAGATTCAAAA AAAAAATAAAAA	
222838 _at	SLAM family member 7	aacacctgtgctaggtcagtcctgg cacgtaagatgaacatccctacca acacagagctcaccatctcttata cttaagtgaataacatggggaagg ggaagggaatggctgcttttga tatgttccctgacacatatcttga atggagacctccctaccctaatgat gaaagtgttga aaacttaataacaaatgcttgttg ggcaagaatgggattgaggattat cttctctcagaa aggcattgtgaagggaattgagcca	>gi 19923571 ref NM_021181.3 Homo sapiens SLAM family member 7 (SLAMF7), mRNA CTTCCAGAGAGCAATATGGCTGGTTCCCAACATGCCCTCACCTCAT CTATATCCTTTGGCAGCTCACAG GGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGCTCGGTTCCGTTGGT GGGGCCGTGACTTTCCCTCCCTGAA GTCCAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAA CCCCTCTTGTCAACCATACAGCCA GAAGGGGGCACTATCATAGTGACCCCAAAATCGTAATAGGGAGAGAGT AGACTTCCCAGATGGAGGCTACT CCCTGAAGCTCAGCAAACTGAAGAAGAAATGACTCAGGGATCTACTAT GTGGGGATATACAGCTCATCACT	22.54

SUBSTITUTE SHEET (RULE 26)

			CACTATGCTGAGCTTACACTAAATTGGTCAGACGTGTGTCTGCCCCCTC ATGAAATTTGGCTCCAAATGAATG AACTACTTTTCATGAGCAGTTGTAGCAGGCCCTGACCACAGATTCCCAG AGGCCAGGTGTGGATCCACAGG ACTTGAAGGTCAAAAGTTACAAAAGATGAAGAAATCAGGGTAGCTGACC ATGTTTGGCAGATACTATAATGG AGACACAGAAGTGTGCATGGCCCAAGGACAAAGGACCTCCAGCCAGGC TTCATTTATGCACCTTGTGCTGCA AAAGAAAAGTCTAGGTTTAAAGGCTGTGCCAGAACCATCCCAATAA AGAGACCGAGTCTGAAGTCACAT TGTAATCTAGTGTAGGAGACTTGGAGTCAGGCAGTGAGACTGGTGG GGCACGGGGGCAGTGGGTACTT GTAAACCTTTAAAGATGGTTAATTCAATTCAATAGATATTTATTAAAGA ACCTATGCGGCCCGGCATGGTGG CTCACACCTGTAAATCCCAGCACTTTGGGAGGCCAAGGTGGGTGGTGC ATCTGAGGTCAGGAGTTCAAGAC CAGCCTGGCCAAACATGGTGAAACCCCATCTCTACTAAAGATACAAAA ATTTGCTGAGCGTGGTGGTGC ACCTGTAAATCCCAGCTACTCGAGAGGCCAAGGCATGAGAAATCGCTTG AACCTGGGAGGTGGAGTTGCAG TGAGCTGAGATGGCACCACTGCACCTCCGGCCCTAGGCCAACGAGAGCAA AACTCCAATACAAACAAACAAAC AAACACCTGTGTAGGTGAGTCTGGCACGTAAGATGAACATCCCTAC CAACACAGAGCTCACCATCTCTT ATACTTAAGTGAAAAACATGGGGAAGGGGAAAGGGGAATGGCTGCTT TTGATATGTTCCCTGACACATAT CTTGAATGGAGACCTCCCTACCAAGTGAAGTGTGAAAAAATCTT AATAACAAAATGCTTGTGGGCAA GAATGGGATGAGGATTAATCTTCTCTCAGAAAGGCATTTGTGAAGGAA TTGAGCCAGATCTCTCTCCCTAC TGCAAAACCCCTATTGTAGTAAAAAAGTCTTCTTACTATCTTAATAA AACAGATATTGTGAGATTCAAAA AAAAAAA

229152 _at	chromosome 4 open reading frame 7	tgaagaaagttctcctcctgatca cagccatctggcagtggtgttg gtttcccagtcct ctcaagaccaggaacgagaaaaa gaagtatcagtgacagcgaatgaat tagcttcagggttttttgtgttcc cttaccatatccatttcgcccac ttccaccaattccatttccaagat ttccatggttttagacgtaatttc ctattccaataacctgaatctgccc ctacaactcccc ttcctagcgaaaagtaaaagaa ggaagtcacgataaaacctggtc acctgaaattgaaattgagccact tccttgaagaatcaaaattcctgt taataaaagaaaacaaatgtaat tgaaatagcacacagcatctcta gtcaatatccttagtgatccttctt taata [Seq Id No 79]	>gi 50428928 ref NM_152997.2 Homo sapiens chromosome 4 open reading frame 7 (C4orf7), mRNA TAAACAGCTACAATATTCAGGGCCAGTCACCTTGCCATTCTCATATA ACAGCGTCAGAGAGAAAGAACTG ACTGAAACGTTTGAGATGAAGAAAGTTCTCTCTCTGATCACAGCCCAT CTTGGCAGTGGCTGTTGGTTTCC CAGTCTCTCAAGACCAGGAACGAGAAAAAGAAAGTATCAGTGACAGC GATGAATTAGCTTCAGGGTTT TGTGTTCCCTTACCCATATCCATTTCGCCCACTTCCACCAATTCCCAT TTCCAAGATTTCCATGGTTTAGA CGTAATTTTCTTATTCCAATACCTGAATCTGCCCTACAACCTCCCT TCCTAGCGAAAAGTAAACAAGAA GGAAAGTACGATAAAACCTGGTCACCTGAAATTGAAATTGAGCCAC TTCCTTGAAAGAAATCAAAATTCCT GTTAATAAAAGAAAAACAAATGTAATTGAAATAGCACACAGCATTTCT CTAGTCAATATCTTTAGTGATCT TCTTTAATAAACTTGAAAGCAAGATTTTGGTTTCTTAATTTCACACA AA	154.0 5
236203 _at	Major histocompa tibility complex, class II, DQ alpha 1	atgtcagggtttgtacctaaccacat ttaaaatagggaacttgaagaatta aacatthttatta caaatgaagcacttcatgacacaga ctggcacatagtaagtagtcgata gggtgtaacaat ttgtgttattgtttattttctggag tccaactaacaatcccacagtgga atgacatcacag ggatgcaaccaacaagatccagaa tatggaaacttctactagataaac aactccatttct tcagcaacaattcaagagagagag agaagagaagctatacatatttaaa	>gi 52426772 ref NM_002122.3 Homo sapiens major histocompatibility complex, class II, DQ alpha 1 (HLA-DQA1), mRNA ACAATTACTCTACAGCTCAGAAACCAACTGCTGAGGCTGCCTTGGG AAGAGGATGATCCTAAACAAGC TCTGCTGCTGGGGCCCTCGCTCTGACCACCGTGATGAGCCCCCTGTG GAGGTGAAGACATTTGGCTGAC CACGTTGCCCTCTTGTGGTGTAACCTTGTAACAGTTTACGGTCCCTC TGGCCAGTACACCCATGAATTG ATGGAGATGAGCAGTTCTACGTGGACCTGGAGAGGAAGAGACTGCC TGGCGGTGGCCCTGAGTTCAGCAA ATTGTGGAGGTTTTCACCCGCGAGGTGCACTGAGAAACATGGCTGTGG CAAAACACAACTTGAAACATCATG ATTAAACGCTACAACTCTACCGCTGCTACCAATGAGGTTCTCTGAGGT	38.77

		aggctgaagaaatatatgaaccaa at ttgtatgaggcaatcagaaaaa ctgacaccgactgtattaaggaat tatctaatttttagtggtggaatga gattgctgttatgttttcttaa [Seq Id No 80]	CACAGTGTTTTCCAAGTCTCCCG TGACACTGGGTAGCCCCAACACCTCATTTGTCTTTGTGGACAAACATC TTTCCTCCTGTGTCAACATCAC ATGGCTGAGCAATGGGCCAGTCAGTCACAGAAAGGTGTTTCTGAGACCA GCTTCCTCTCCAAGAGTGATCAT TCCTTTCTCAAGATCAGTTACCTCACCTTCCTCCCTTCTGCTGATGA GATTATGACTGCAAGGTGGAGC ACTGGGGCCTGGACCAAGCCTCTTCTGAAACACTGGGAGCCTGAGATT CCAGCCCCTATGTCAGAGCTCAC AGAGACTGTGGTCTGTGCCCTGGGGTTGTCTGTGGGCCCTCATGGGCA TTGTGGTGGGCACGTCTTCATC ATCCAAGGCTGCGTTCAAGTTGGTGCTTCCAGACACCAAGGCCATT GTGAATCCCCATCCTGGAAGGAA GGTGCATCGCCATCTACAGGAGCAGAGAAGAAATGGACTTGCTAAATGAC CTAGCACTATTCTCTGGCCCCGAT TTATCATATCCCTTTTCTCCTCCAAATAATTTCTCCTCTCACCTTTTC TCTGGGACTTAAGCTGCTATATC CCCTCAGAGCTACAAATGCCCTTTACATTCTTTCCCTGACCTCCTGA TTTTTTTTTCTCTCAAATG TTACCTACAAGACATGCCCTGGGGTAAGCCACCCGGCTACCTAATTC CTCAGTAACCTCCATCTAAATC TCCAAGGAAGCAATAAATTCCTTTTATGAGATCTATGTCAAATTTT CCAATCTTTCATCCAGGGCTGACT GAAACTATGGCTAATAATTTGGGGTACTCTTATGTTTCAATCCAATT AACCTCAATTTCCAGATCATTT TCATGTCCAGTAACACAGAAAGCCACCAAGTACAGTATAGCCTGATAA TATGTTGATTTCTTAGCTGACAT TAATAATTTCTTGTCTTCTTGTGTTCCCACTTGGCACTGCCACCCA CCCCTCAATTCAGGCAACAATGA AATTAAATGGATACCGTCTGCCCTTGGCCAGAAATTGTTATAGCAAAA ATTTTAGAACCAAAAATAAGTC TGTAATAATTTCAATGTGGCTTTTAAAGTATGACAGAGAAATAAGT TAGGATAAAGGAAATTTGAATCT CA
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236280 _at	Transcribe d locus	aaaagatctctcactgggaaaaaga aaaagtatgcatttataaaagtaa ttaaactggttt tccttgtaactttattaatctgaat ctaattggcacttccttacgaggg tttcagatgtgc ttgtagttaatggcaacattatca gaatgactacacagacagtcctac tctgaggagatg actttggaagaaccattttggaa ctacacaccctgctatgtctgtgg agaaatggaact gcaatcctcaagagtcacacttca tattccttcctttcaagtggttga taaaaggtagtg cttcaagcacaggatttatggaat agttggcaaattaacaacatgct ttttattttgac tacca [Seq Id No 81]	>gi 3807951 gb AI225238.1 AI225238 qx12c04.xl NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2001126 3', mRNA sequence AGCGCCGCCCTTTTCTTTTGAATGTTTATATTTTATG TTTTTCTCTCACCACATTAGA GATTCACATGTCAAAAAAAGTTCAAGATTCCACTTAAATGGTAG TCAAAATTAAAGCATGTTGTTT AATTGCCCAACTATTCATAAATCCTGTGCTTGAAGCACTACCTTTT ATCAACCACCTTGAAAGGAGGAA TATGAAGTGTGACTCTTGAGGATTGCAGTTCCATTCTCCACAGACA TAGCAGGGTGTAGTTCCAAAT GGTTTCTTCCAAAGTCACTCCTCAGAGTAGGACTGTCTGAGTAGT CATTCTGATAATGTTGCCATTAA CTACAAGCACATCTGAGAAACCTCGTAAGGAAGTGCCATTAGATTCA GA	77.63
239237 _at	Amphiphysi n (Stiff- Man syndrome with breast cancer 128kDa autoantige	ttatcaccatttaattccatgccagt tatgtacagttttgcatgtttgtt ttttattttact cttttctctccttcattccctatt cctgttcccccataggtgccccagt ctaatgtatttg atatctgtccttagagcctccgta tctgtgaagactagagtcatgcac ttcatcacattt cagtaaacgatgggcccgcgtgtacc acagtccccatgagatgatagaggt gcagaaaaattcctgtcatctagt	>gi 51466133 ref XM_499518.1 PREDICTED: Homo sapiens LOC442534 (LOC442534), mRNA GGCCCAGCCCTAGGAGGGGCGAGTCCCACAGCAGGCTCACACCCCTGC CCTTCAGAGTTGCAGCAGCTAAT GCTGATGCCAGGACCTTGTCCTGCCAGGAAGCCTCTGATTAGGGCTG TGAACCAACTTCCTTTTCACATC TGCAAGGACTCTGCTCTAAGCTCAAATTTGCAGTTTCTGCTGTCTCAT CACAGCTGGGAATGAGAAAGGGA AGGGCTCCAGTTGGTCTCCCTCTGCCTCTGGAGCACACGTGGAGGA CATGAGGCTTCCGCAGGAACAGC TCTGAAAGCTGAGTTCTCGGTCCTGTGAGGAGGGAAGCTTGCCT GCCTTGGAGCGTGAAAAAAGTCTT	25.87

	n)	gacatcgtagccatcataaacatnn caacacgactctcatattgtggtga ccctgggtgtacacaaacctac	GCTGGACAGAAGTCTCACGGTTTAAACTGGGAAGGGAGAGGATTGA GATCACACTAGAAATGCACAGAAA ATTCTT	
244413 _at	dendritic cell- associated lectin-1	[Seq Id No 82] atggctggagatgtagtctacgct gacatcaaaactgttcggacttcc ccgttagaactc gcgtttccacttcagagatctgtt tctttcaacttttctactgtccat aaatcatgtcct gccaaagactggaagggtgcataag ggaaaatgttactggattgctgaa actaagaaaatcttggaacaaaagt caaaatgactgtgccataaaacaat tcatactcatgggtgattcaagac attactgctatggtgagatttaac atttagagggtgacagcatccccca cactggcagtga atthttgtgctacaaaacttggca aaagtctgtgaaaagaagtthtcaa cttcatgtgtta ttaact [Seq Id No 83]	>gi 40548404 ref NM_172004.2 Homo sapiens dendritic cell-associated lectin-1 (DCAL1), mRNA ATGGTTAGTAATTTCTTCCATGTCATACAAAGTATTCGAGAAATCTGC TACCTTGATTAGTAAGACTGAAC ACATTGGTTTGTGCATTTATTCATGGAGGAAGTCCACCACCCTTG GGAGCAGAGGAAATTTGCCAT CTCAATTTACTTATCAGAAGTTTCTTTGCAGAAATATGATTGTCCCT TCAGTGGGACATCATTTGTGGTC TTCTCTCTCTTTTGTGATCTGTGCAATGGCTGGAGATGTAGTCTACGC TGACATCAAAACTGTTTCGGACTT CCCCGTTAGAACTCGCGTTTCCACTTCAGAGATCTGTTCTTTCAAC TTTTCTACTGTCCATAAATCATG TCCTGCCAAAGACTGGAAGGTGCATAAAGGAAAATGTTACTGGATTG CTGAAACTAAGAAATCTTTGGAAC AAAAGTCAAAATGACTGTGCCATAAACAATTCATATCTCATGGTGAT TCAAGACATTAATGCTATGGTGA GATTTAACATTTAGAGGTGACAGCATCCCCCACACTGGCAGTGAATT TTTTGTGCTACAAACTTGGCAA AGTCTGTGAAAAGAAAGTTTCAACTTCATGTGTTATTAACTATACAAA TATTAGTTGAATGAATTGTTGAA TTACAAAAAATAAAAAA	12.75
34210_ at	CD52 antigen (CAMPATH-1 antigen)	Taatcgggtcactataggaatttg cntcgaggccaagattcgnacgag nnngttcaaaagcagctaaaccaa aagaagcctccagacagccctgag atcacctaaaaagctgctaccaag acagccacgaagatcctaccacaaa	>gi 68342029 ref NM_001803.2 Homo sapiens CD52 molecule (CD52), mRNA CTCCTGGTTCAAAAGCAGCTAAACCAAAAGAGCCTCCAGACAGCCC TGAGATCACCTAAAAGCTGCTA CCAAGACAGCCACGAAGATCTACCAAAATGAAGCGCTTCTCTTCC TCCCTACTCACCATCAGCCTCCTG	31.41

		tgaagcgcttcctcttcctcctac tcaccatcagcctcctggttatgg tacagatacaaaactggactctcag gacaaaacgacacacagccaaccaa gcagcccctcagcatccagcagca tgagcgaggcatcttccttttct tcgtggccaatgccataatccacc tcttctgcttcagttgaggtgaca cgtctcagccttagccctgtgccc cctgaaacannnnnnnnnnnn nnnnagagaatcccctccatcttt gggaggggttgatgccagacatca ccaggttgtagaagtgacaggca gtgccatggggncaacagccaaaa taggggggtaatgatgtaggggcc aagcagtgcccagctgggggtcaa taaaagttacccttgacttg [Seq Id No 84]	GTATGGTACAGATACAAACTGGACTCTCAGGACAAAACGACACCAG CCAAACCAGCAGCCCTCAGCAT CCAGCAACATAAGCGGAGGCATTTTCCTTTTCTTCGTGGCCAAATGCC ATAATCCACCTCTCTGCTTCAG TTGAGGTGACACGTCTCAGCCTTAGCCCTGTGCCCTTGAACACAGCT GCCACCATCACTCGCAAGAGAAT CCCCTCCATCTTTGGGAGGGTTGATGCCAGACATCACCAGGTTGTA GAAGTTGACAGGCAGTGCCATGG GGGCAACAGCCAAAATAGGGGGTAATGATGTAGGGGCCAAGCAGTG CCCAGCTGGGGTCAATAAAGTT ACCCTTGTA CTGCAAAAAA AAAAAA AAAAAA	
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TABLE 3A List of 13 probe sets suitable for identify the genes listed in Table 3

Probe Set ID	Gene Symbol	Gene Title	Gene Sequences
204661_at	CD52	CD52 molecule /// CD52 molecule	Acagccacgaagatcctaccaaaatgaagcgcttcctctctcctactcaccatcagcctcctgggttatggtac agatacaaaactggactctcaggaacaaacgacacacagccaaacagcagccctcagcatccagcagcatgagcg gaggcatcttcctctctcgtggccaatgccataatccacctctctgcttcagttgaggtgacacgtctcagc cttagccctgtgccccctgaaacagctgccaccatcactcgcaagagaatccccctccatctttgggagggggttga tgccagacatcacccagggtgtagaagttagacaggcagtgccatgggggcaacagcccaaaataggggggtaatgat gtaggggccaagc [Seq Id No 85]
205890_s_at	UBD	gamma- aminobutyric acid (GABA) B receptor, 1 /// ubiquitin D	Gatctaaagccacggagaagcctctcatcttatggcattgacaaaagagaaccatccaccttacccctgaaagt ggtgaagcccaagtgatgaggagctgccccttgcttcttgaggatcaggtgatgaggcaaaagagccacctctcca ggtgcgaaggtccagctcagtggcacaaagtgaagcaatgatcgagactaagacgggtataatccctgagaccca gattgtgacttgcattgaaagagactgggaagatgggaagatgagtcagattacggcatcagaaaaggcaactt actctccctggcatcttattgtattggagggtgaccacctggggatgggtgttggcaggggtcaaaaagctta ttctcttttaatctcttactcaacgaacacacatcttctgatgatttccccaaaattaatgagaatgagatgagtagag taagatttgggtgggatgggtaggatgaagtatattgccccaaactctatgtttcttctga [Seq Id No 86]
206118_at	STAT4	signal transducer and activator of transcription 4	Gctgacatcctgcgagactacaaagtattatggctgaaaacattcctgaaaaaccctctgaagtacacctatcct gacattcccaaagacaaagccttcggtaaacactacagctctcagccttgcgaaagtttcaagaccacagaaaagg ggtgacaaaaggttatgttcctctgttttatccccatctcaacaatccgaaagtgttcaacagagccacattct ccatcagacacctcttccccatgtctccaaagtgtgatcggtgttgagagaaaaacctgagtcaccaacaattgaa actgcaatgaagtctccttattctgtctgaatgacaggataaaactctgacgcaccaagaaaggaaatgaaaa agtttaaagactgttcttggcccaataaccacattttattcttcagctttgtaaaataccaggttcttaggaaatg tttgacatctgaagctctcttccacactcccgtaggcactccctcaattggggag [Seq Id No 87]

206666 _at	GZMK	granzyme K (granzyme 3; tryptase II) /// granzyme K (granzyme 3; tryptase II)	aaacctcttagatctggaaccaaatgcaagggtactggctggggagccaccgatccagattcattaaagacctt ctgacaccctgcgagaagtcactgttactgtcctaaagtcgaaaactttgcaacagccaaagttactacaaggcg acccttttatcaccaaaagacatggtctgtgcaggagatgccaaaggccagaaggattcctgtaagggtgactcag ggggcccttgatctgtaaagggtgtcttccacgctatagtctctggaggatcatgaatgtggtgttggccaaaagc ctggaatctacaccctgttaaccaagaataccagacttggatcaaaagcaaccttgtcccgctcatatacaaat aagttacaaaataattttattggatgcacttgccttttttccctaataatgctcgcagggttagagttgggtgtaag taaagcagagcacatatgggggtccatttttgcacttgta
			[Seq Id No 88]
207651 _at	GPR171	G protein-coupled receptor 171	Ttgccttgtaattcgacagctctacagaacaagaataatgaaaaatgcccaaatgtgaaaaaggctctcatcaa catacttttagtgaccacgggctacatcatatgctttgttcccttaccacattgtccgaatcccgatataccctcag ccagacagaagtataaactgattgctcaaccaggatttcaacttcaaaagccaaagaggctacactgctcctggc tgtgtcgaaacctgtgctttgatcctatcctgtactatcacctctcaaaagcatccgctcaaaaggctcactgagac ttttgcctcacctaaagagaccaaggctcagaaagaaaaattaaagatgtgaaaaataatgcataaaaagacaggatt ttttgtgctaccaattctggccttacttgga
			[Seq Id No 89]
210038 _at	PRKCQ	protein kinase C, theta	Aatccattcatcctgattgggcatgaaatccatgggtcaagaggacaagtggaaagtgaagggtttgctag acaccttcgcttggttatcttgtcaagatagaaaagatagtatcatttccaccttgccagtaaaacctttccatc caccattctcagcagactccagtatgtggcacagtcaactcactgccaattctcacactataacaagaaaagaaatg aagtgcataaagtcctcctgggaaaagaaaccttaaccttctcgtgccatgactggtgatttcatgactcataagc ccctccgtaggcatcatcaagatcaatggcccatgcatgctgtttgcagca
			[Seq Id No 90]
210972 _x_at	TRA@ /// TRDV2 /// TRAV20 /// TRAC	T cell receptor alpha locus /// T cell receptor delta variable 2 /// T cell receptor alpha variable 20 /// T cell receptor alpha constant	Ggaacaagacttcagggtcacgctcgatatccagaaccctgacccctgcccgtgtaccagctgagagactctaaatcc agtgaacaagtctgtctgcctattcaccgattttgattctcaaaacaaatgtgtcacaaaagtaaggattctgatgtg tatatcacagacaaaactgtgctagacatgaggtctatggacttcaagagcaacagtgctgtggcctggagcaac aaatctgactttgcatgtgcaaacgcttcaacaacagcatatttccagaagacaccttcttcccagcccagaa agttcctgtgatgtcaagctggtcgagaaaagctttgaaacagatacgaaacctaaactttcaaaacctgtcagtg attgggttccgaatcctcctcctgaaagtggccgggtttaatctgctcatgacgctgcggctgtggtccagctga gatctgcaagattgtaagacagcctgtgctcct
			[Seq Id No 91]

211144 _x_at	TRGC2 /// TRGV2 /// TRGV9 /// TARP /// LOC642 083	T cell receptor gamma constant 2 /// T cell receptor gamma variable 2 /// T cell receptor gamma variable 9 /// TCR gamma alternate reading frame protein /// hypothetical protein LOC642083	Aaatgatacacactactgctgcagctcacaacacacctctgcatattacatgtacacctcctcctgctcctcaagagtgtggtctatattggccatcatcacctgctgtctgttggaagacggcttctgtgcaatggagagaaaatcataaca gacggtggcacaaaggagccatcttctcctcatcggttatgtccctagaagcgtcttctgaggatctagttagg cttctcttctgggttggccatttcagttctcatgtgtgtactattctatcattatgtataatggttttcaaa ccagtgggcacacagagaaacctcagttctgtaataacaatgaggaatagccatggcgatctccagcaccaatctct ccatgttttccacagctcctccagccaaacccaaatagcgcctgctatagtgtagacagcctgcggcttcttagcct tgtccctctcttagtgttctttaaataacagataactgcctggaagccttctcattttacacgccc
211796 _s_at	TRBV21 -1 /// TRBV19 /// TRBV5- 4 /// TRBV3- 1 /// TRBC1	T cell receptor beta variable 21- 1 /// T cell receptor beta variable 19 /// T cell receptor beta variable 5-4 /// T cell receptor beta variable 3-1 /// T cell receptor beta constant 1 /// similar to T- cell receptor beta chain V region CTL-L17 precursor	gccatcagaagcagagatctccacaccccaaaaggccacactgggtgctgggccacaggttctacccccgacca cgtggagctgagctggtgggtgaatgggaaggaggtgcacagtggggtcagcacagacccgcagccccccaaggga gcagcccgccctcaatgactccagataactgctgagcagcgcctgagggtctcgggccaccttctggcagaacccc ccgcaaccacttccgctgtcaagtccagttctacgggtctctcggaagatgacgagtggaaccaggatagggccaa acctgtcaccagatcgtcagcgcgagcctgggttagagcagactgtggcttcacctccgagctctaccagca aggggtcctgtctgccaccatcctctatgagatcttgcctagggaaggccacctgtgtatgctgtgtggtcagtgcc cctcgtgctgatggccatgggtcaagagaaaagga
213193 _x_at	TRBV19 /// TRBC1	T cell receptor beta variable 19 /// T cell receptor beta variable 19 /// T cell receptor beta constant 1 /// T cell receptor beta	Tgactccagatactgcctgagcagccgcctgaggggtctcggccaccttctggcagaacccccgcaaccacttccg ctgtcaagtccagttctacgggctctcggagaatgacgagtggaacccaggataggggccaaaacccgtcacccagat cgtcagcgcggagcctggggtagagcagactgtggctttacctcggtgtcctaccagcaagggtcctgtctgc caccatcctctatgagatcctgctagggaaaggccacctgtatgctgtgctggtcagcnccttgtgttgatggc catgggtcaagagaaaaggattcttgaaggcagccctggaagtggagttaggagcttctaaccggtcatgggttcaa tacacattcttcttggccagcgttctgaagagctgctctcacctctctgcatcccaatagatatccccctatg tgcatgcacacctgcacactcacgggtgaaatctccctaaccacgggggaccttagcatgcctaaagtga

	constant 1	[Seq Id No 94]	
213539_at	CD3D CD3d molecule, delta (CD3-TCR complex)	gggaacactgctctcagacattacaagactggacctgggaaacgcgcatcctggaccacgaggaatatataggtgtaatgggacagatatatacaaggacaaagaattctaccgtgcaagttcattatcgaaatgtgccagagctgtgtgga gctggatccagccaccgtggctggcatcattgtcactgatgtcattgccactctgctccttgggagtcttctgctttgctggacatgagactggaaggctgtctggggctgccgacacacaagctctgttgaggaatgaccagggtctatcagccccctccgagatcgagatgatgctcagtacagccaccttggaggaaactgggctcgggaacaagtgaacctgagactgggtggcttcttagaagcagccattaccaactgtacct	
		[Seq Id No 95]	
217147_s_at	T cell receptor associated transmembrane adaptor 1	Tctcctttctcaccaatgggcaatagcccataattgaaataaaatttctgattgaaagggtataggaacatatataaa tgcatctactaagagaagtaataataatttcttacaaaagtatttcccaaaagatagcttactatttcaaaaattgtcaaattaatgcctgctccttacaacaaacaaatatcaaaaagagtttaggaattctactagccagagatagtc acttgagaaacttctatatatactctctaaatatcttctgggcagctcatgtatgtacatcagttgtttcttctttatttgaaacaaaatgtggttcttctgtacacattacttaaaacttcttccagtcacaatatatgtg gatttatttccactgttatatttaactatatataataacgcgcatatatgttaatttctaattgtctgcttagcaccctt actgataaccaaatacacag	
		[Seq Id No 96]	
34210_at	CD52 CD52 molecule	Taatcggctcactataggaatttgcntcggagcccaagattcgna cgagnnngttcaaaagcagctaaacccaaaag aagcctccagacagccctgagatcacctaaaaagctgctaccaagacagccacgaagatcctaccaaaatgaagc gcttcctcttccctcctactcaccatcagcctcctgggtatgggtacagatacaaaactggactctcaggacaaaacg acaccagccaaaaccagcagccccctcagcagcagcatgagcggaggcatcttcccttctcgtggccaatg ccataatccacctcttctgcttcagttgaggtgacacgtctcagccttagccctgtgccccctgaaacannnnnn nnnnnnnnnnnnagagaatccccctccatcttggggaggggttgatgccagacatcacagggtttagaagttga caggcagtgccatggggncacagccaaaataggggggtaatatgatgtaggggccaagcagtgcccagctgggggt caataaagttacccttgacttg	
		[Seq Id No 97]	

Table 4A: Table linking probe set id and the gene list of Table 4.

Probe Set ID	Gene Symbol	Gene Name
218802_at	FLJ20647	NA (not applicable)
224774_s_at	NAV1	neuron navigator 1
207651_at	GPR171	G protein-coupled receptor 171
205392_s_at	CCL14	chemokine (C-C motif) ligand 14
1555229_a_at	C1S	complement component 1, s subcomponent
209774_x_at	CXCL2	chemokine (C-X-C motif) ligand 2
211796_s_at	TRBV3-1	T cell receptor beta variable 3-1
210972_x_at	TRDV2	T cell receptor delta variable 2
210251_s_at	RUFY3	RUN and FYVE domain containing 3
225502_at	DOCK8	dedicator of cytokinesis 8
204224_s_at	GCH1	GTP cyclohydrolase 1 (dopa-responsive dystonia)
218950_at	CENTD3	centaurin, delta 3
218322_s_at	ACSL5	acyl-CoA synthetase long-chain family member 5
228094_at	AMICA1	adhesion molecule, interacts with CXADR antigen 1
204116_at	IL2RG	interleukin 2 receptor, gamma (severe combined immunodeficiency)
202643_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3
209606_at	PSCDBP	pleckstrin homology, Sec7 and coiled-coil domains, binding protein
205225_at	ESR1	estrogen receptor 1
213193_x_at	TRBC1	T cell receptor beta constant 1
204661_at	CD52	CD52 antigen (CAMPATH-1 antigen)
216920_s_at	LOC442535	NA
210915_x_at	TRBV19	T cell receptor beta variable 19
226218_at	IL7R	interleukin 7 receptor
209670_at	TRAC	T cell receptor alpha constant
209949_at	NCF2	neutrophil cytosolic factor 2 (65kDa, chronic granulomatous

		disease, autosomal 2)
226697_at	LOC92689	NA
206666_at	GZMK	c("granzyme K (granzyme 3", " tryptase II)")
235831_at	NA	NA
1555630_a_at	RAB34	RAB34, member RAS oncogene family
207977_s_at	DPT	dermatopontin
1558290_a_at	PVT1	Pvt1 oncogene homolog, MYC activator (mouse)
215806_x_at	TRGC2	T cell receptor gamma constant 2
64064_at	GIMAP5	GTPase, IMAP family member 5
34210_at	CD52	CD52 antigen (CAMPATH-1 antigen)
213539_at	CD3D	CD3d antigen, delta polypeptide (TiT3 complex)
232313_at	TMEM132C	transmembrane protein 132C
201502_s_at	NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha
211902_x_at	TRA@	T cell receptor alpha locus
217147_s_at	TRAT1	T cell receptor associated transmembrane adaptor 1
211144_x_at	LOC442535	NA
224710_at	RAB34	RAB34, member RAS oncogene family
209795_at	CD69	CD69 antigen (p60, early T-cell activation antigen)
232843_s_at	DOCK8	dedicator of cytokinesis 8
218805_at	GIMAP5	GTPase, IMAP family member 5
204057_at	IRF8	interferon regulatory factor 8
214470_at	KLRB1	killer cell lectin-like receptor subfamily B, member 1
236280_at	NA	NA
201474_s_at	ITGA3	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)
235421_at	MAP3K8	mitogen-activated protein kinase kinase kinase 8
228532_at	C1orf162	chromosome 1 open reading frame 162
205890_s_at	UBD	ubiquitin D
209813_x_at	TRGV9	T cell receptor gamma variable 9

224772_at	NAV1	neuron navigator 1
224451_x_at	ARHGAP9	Rho GTPase activating protein 9
226117_at	TIFA	NA
213068_at	DPT	dermatopontin
1569942_at	NA	NA
219243_at	GIMAP4	GTPase, IMAP family member 4
202957_at	HCLS1	hematopoietic cell-specific Lyn substrate 1
218764_at	PRKCH	protein kinase C, eta
206118_at	STAT4	signal transducer and activator of transcription 4
236203_at	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1
206170_at	ADRB2	adrenergic, beta-2-, receptor, surface
239237_at	NA	NA
214450_at	CTSW	cathepsin W (lymphopain)
201497_x_at	MYH11	myosin, heavy polypeptide 11, smooth muscle
219777_at	GIMAP6	GTPase, IMAP family member 6
211654_x_at	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1
205758_at	CD8A	CD8 antigen, alpha polypeptide (p32)
202644_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3
1558034_s_at	CP	ceruloplasmin (ferroxidase)
223235_s_at	SMOC2	SPARC related modular calcium binding 2
232234_at	C20orf24	chromosome 20 open reading frame 24
1559584_a_at	C16orf54	chromosome 16 open reading frame 54
205831_at	CD2	CD2 antigen (p50), sheep red blood cell receptor
203812_at	SLIT3	slit homolog 3 (Drosophila)
222780_s_at	BAALC	brain and acute leukemia, cytoplasmic
218145_at	TRIB3	tribbles homolog 3 (Drosophila)
242881_x_at	LOC440160	NA
1558972_s_at	C6orf190	chromosome 6 open reading frame 190
229723_at	TAGAP	T-cell activation GTPase activating protein
235391_at	FAM92A1	family with sequence similarity 92, member A1

219938_s_at	PSTPIP2	proline-serine-threonine phosphatase interacting protein 2
212587_s_at	PTPRC	protein tyrosine phosphatase, receptor type, C
210982_s_at	HLA-DRA	major histocompatibility complex, class II, DR alpha
211200_s_at	EFCAB2	EF-hand calcium binding domain 2
210260_s_at	TNFAIP8	tumor necrosis factor, alpha-induced protein 8
228869_at	SLIC1	NA
205987_at	CD1C	CD1c antigen
213888_s_at	TRAF3IP3	TRAF3 interacting protein 3
212671_s_at	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1
242986_at	NAV1	neuron navigator 1
212999_x_at	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1
212588_at	PTPRC	protein tyrosine phosphatase, receptor type, C
212592_at	IGJ	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides
203471_s_at	PLEK	pleckstrin
209671_x_at	TRA@	T cell receptor alpha locus
228054_at	TMEM44	transmembrane protein 44
216191_s_at	TRA@	T cell receptor alpha locus
205419_at	EBI2	Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor)
220330_s_at	SAMSN1	SAM domain, SH3 domain and nuclear localisation signals, 1
213008_at	KIAA1794	KIAA1794
201425_at	ALDH2	aldehyde dehydrogenase 2 family (mitochondrial)
1552613_s_at	CDC42SE2	CDC42 small effector 2
205696_s_at	GFRA1	GNDF family receptor alpha 1
211339_s_at	ITK	IL2-inducible T-cell kinase
208894_at	HLA-DRA	major histocompatibility complex, class II, DR alpha
228071_at	GIMAP7	GTPase, IMAP family member 7
222496_s_at	FLJ20273	NA
206687_s_at	PTPN6	protein tyrosine phosphatase, non-receptor type 6

210375_at	PTGER3	prostaglandin E receptor 3 (subtype EP3)
219440_at	RAI2	retinoic acid induced 2
208450_at	LGALS2	lectin, galactoside-binding, soluble, 2 (galectin 2)
203665_at	HMOX1	heme oxygenase (decycling) 1
227995_at	NA	NA
227346_at	ZNFN1A1	zinc finger protein, subfamily 1A, 1 (Ikaros)
205159_at	CSF2RB	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)
205559_s_at	PCSK5	proprotein convertase subtilisin/kexin type 5
212886_at	CCDC69	coiled-coil domain containing 69
1552612_at	CDC42SE2	CDC42 small effector 2
205488_at	GZMA	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)
217767_at	C3	complement component 3
208296_x_at	TNFAIP8	tumor necrosis factor, alpha-induced protein 8
223484_at	C15orf48	chromosome 15 open reading frame 48
204070_at	RARRES3	retinoic acid receptor responder (tazarotene induced) 3
214719_at	LOC283537	NA
209687_at	CXCL12	chemokine (C-X-C motif) ligand 12 (stromal cell-derived factor 1)
224773_at	NAV1	neuron navigator 1
231882_at	NA	NA
215223_s_at	SOD2	superoxide dismutase 2, mitochondrial
232617_at	CTSS	cathepsin S
210554_s_at	CTBP2	C-terminal binding protein 2
219528_s_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)
207861_at	CCL22	chemokine (C-C motif) ligand 22
222592_s_at	ACSL5	acyl-CoA synthetase long-chain family member 5
1554966_a_at	DOC1	NA
204204_at	SLC31A2	solute carrier family 31 (copper transporters), member 2

219926_at	POPDC3	popeye domain containing 3
204135_at	DOC1	NA
217995_at	SQRDL	sulfide quinone reductase-like (yeast)
230233_at	RASGEF1B	RasGEF domain family, member 1B
227265_at	FGL2	fibrinogen-like 2
228372_at	C10orf128	chromosome 10 open reading frame 128
204912_at	IL10RA	interleukin 10 receptor, alpha
219454_at	EGFL6	EGF-like-domain, multiple 6
206295_at	IL18	interleukin 18 (interferon-gamma-inducing factor)
226219_at	ARHGAP30	Rho GTPase activating protein 30
218736_s_at	PALMD	palmelphin
223322_at	RASSF5	Ras association (RalGDS/AF-6) domain family 5
209603_at	GATA3	GATA binding protein 3
204687_at	DKFZP564O 0823	NA
222895_s_at	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)
201010_s_at	TXNIP	thioredoxin interacting protein
226818_at	DTX4	deltex 4 homolog (Drosophila)
208335_s_at	DARC	Duffy blood group, chemokine receptor
213566_at	RNASE6	ribonuclease, RNase A family, k6
205685_at	CD86	CD86 antigen (CD28 antigen ligand 2, B7-2 antigen)
201531_at	ZFP36	zinc finger protein 36, C3H type, homolog (mouse)
202391_at	BASP1	brain abundant, membrane attached signal protein 1
201804_x_at	CKAP1	cytoskeleton associated protein 1
206082_at	HCP5	HLA complex P5
206204_at	GRB14	growth factor receptor-bound protein 14
228563_at	GJA7	gap junction protein, alpha 7, 45kDa (connexin 45)
219054_at	FLJ14054	NA
205844_at	VNN1	vanin 1
203741_s_at	ADCY7	adenylate cyclase 7

223280_x_at	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A
205624_at	CPA3	carboxypeptidase A3 (mast cell)
209193_at	PIM1	pim-1 oncogene
210072_at	CCL19	chemokine (C-C motif) ligand 19
226068_at	SYK	spleen tyrosine kinase
216155_at	NAV1	neuron navigator 1
205484_at	SIT1	signaling threshold regulating transmembrane adaptor 1
228812_at	NA	NA
219368_at	NAP1L2	nucleosome assembly protein 1-like 2
206407_s_at	CCL13	chemokine (C-C motif) ligand 13
203761_at	SLA	Src-like-adaptor
236295_s_at	NOD3	NA
206099_at	PRKCH	protein kinase C, eta
217143_s_at	TRD@	T cell receptor delta locus
218899_s_at	BAALC	brain and acute leukemia, cytoplasmic
229391_s_at	RP1-93H18.5	NA
219093_at	FLJ20701	NA
219710_at	SH3TC2	SH3 domain and tetratricopeptide repeats 2
206978_at	CCR2	chemokine (C-C motif) receptor 2
204655_at	CCL5	chemokine (C-C motif) ligand 5
211991_s_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1
223922_x_at	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A
208983_s_at	PECAM1	platelet/endothelial cell adhesion molecule (CD31 antigen)
222108_at	AMIGO2	adhesion molecule with Ig-like domain 2
1553102_a_at	CCDC69	coiled-coil domain containing 69
221698_s_at	CLEC7A	C-type lectin domain family 7, member A
206637_at	P2RY14	purinergic receptor P2Y, G-protein coupled, 14
226459_at	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1
209613_s_at	ADH1B	alcohol dehydrogenase IB (class I), beta polypeptide
225802_at	TOP1MT	topoisomerase (DNA) I, mitochondrial

224859_at	CD276	CD276 antigen
209480_at	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1
219213_at	JAM2	junctional adhesion molecule 2
208747_s_at	C1S	complement component 1, s subcomponent
224356_x_at	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A
226625_at	TGFR3	transforming growth factor, beta receptor III (betaglycan, 300kDa)
1554240_a_at	ITGAL	c("integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1", " alpha polypeptide"))
202948_at	IL1R1	interleukin 1 receptor, type I
219666_at	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A
215193_x_at	HLA-DRB1	major histocompatibility complex, class II, DR beta 1
232024_at	GIMAP2	GTPase, IMAF family member 2
1559263_s_at	ZC3H12D	zinc finger CCCH-type containing 12D
219737_s_at	PCDH9	protocadherin 9
222838_at	SLAMF7	SLAM family member 7
227983_at	MGC7036	NA
223809_at	RGS18	regulator of G-protein signalling 18
213831_at	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1
203416_at	CD53	CD53 antigen
226841_at	MPEG1	NA
228552_s_at	SSBP4	single stranded DNA binding protein 4
231262_at	NA	NA
206898_at	CDH19	cadherin 19, type 2
210835_s_at	CTBP2	C-terminal binding protein 2
227584_at	NAV1	neuron navigator 1
223059_s_at	FAM107B	family with sequence similarity 107, member B
221671_x_at	IGKC	immunoglobulin kappa constant
205786_s_at	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)

216194_s_at	CKAP1	cytoskeleton associated protein 1
209312_x_at	HLA-DRB1	major histocompatibility complex, class II, DR beta 1
235639_at	CDH19	cadherin 19, type 2
233562_at	MGC16291	NA
232476_at	DDEF2	development and differentiation enhancing factor 2
202510_s_at	TNFAIP2	tumor necrosis factor, alpha-induced protein 2
222484_s_at	CXCL14	chemokine (C-X-C motif) ligand 14
207277_at	CD209	CD209 antigen
204724_s_at	COL9A3	collagen, type IX, alpha 3
239196_at	ANKRD22	ankyrin repeat domain 22
209734_at	NCKAP1L	NCK-associated protein 1-like
212977_at	CMKOR1	chemokine orphan receptor 1
204670_x_at	HLA-DRB5	major histocompatibility complex, class II, DR beta 5
208885_at	LCP1	lymphocyte cytosolic protein 1 (L-plastin)
209612_s_at	ADH1B	alcohol dehydrogenase IB (class I), beta polypeptide
233955_x_at	CXXC5	CXXC finger 5
228776_at	GJA7	gap junction protein, alpha 7, 45kDa (connexin 45)
1553906_s_at	FGD2	FYVE, RhoGEF and PH domain containing 2
221760_at	MAN1A1	mannosidase, alpha, class 1A, member 1
223361_at	C6orf115	chromosome 6 open reading frame 115
229390_at	RP1-93H18.5	NA
203915_at	CXCL9	chemokine (C-X-C motif) ligand 9
223058_at	FAM107B	family with sequence similarity 107, member B
219789_at	NPR3	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)
205285_s_at	FYB	FYN binding protein (FYB-120/130)
203868_s_at	VCAM1	vascular cell adhesion molecule 1
204236_at	FLI1	Friend leukemia virus integration 1
224516_s_at	CXXC5	CXXC finger 5
202368_s_at	TRAM2	translocation associated membrane protein 2

224795_x_at	IGKC	immunoglobulin kappa constant
235238_at	SHC4	SHC (Src homology 2 domain containing) family, member 4
227791_at	SLC9A9	solute carrier family 9 (sodium/hydrogen exchanger), member 9
207238_s_at	PTPRC	protein tyrosine phosphatase, receptor type, C
204897_at	PTGER4	prostaglandin E receptor 4 (subtype EP4)
213975_s_at	LILRB1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1
228964_at	PRDM1	PR domain containing 1, with ZNF domain
228362_s_at	RP1-93H18.5	NA
244061_at	ARHGAP15	Rho GTPase activating protein 15
1553313_s_at	SLC5A3	solute carrier family 5 (inositol transporters), member 3
212538_at	DOCK9	dedicator of cytokinesis 9
226043_at	GPSM1	G-protein signalling modulator 1 (AGS3-like, C. elegans)
1405_i_at	CCL5	chemokine (C-C motif) ligand 5
204222_s_at	GLIPR1	GLI pathogenesis-related 1 (glioma)
221087_s_at	APOL3	apolipoprotein L, 3
203932_at	HLA-DMB	major histocompatibility complex, class II, DM beta
225895_at	SYNPO2	synaptopodin 2
221651_x_at	NA	NA
231929_at	NA	NA
229543_at	RP1-93H18.5	NA
211367_s_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
210038_at	PRKCQ	protein kinase C, theta
205403_at	IL1R2	interleukin 1 receptor, type II
220066_at	CARD15	caspase recruitment domain family, member 15
1555812_a_at	ARHGDIB	Rho GDP dissociation inhibitor (GDI) beta
208306_x_at	HLA-DRB4	major histocompatibility complex, class II, DR beta 4
218854_at	SART2	squamous cell carcinoma antigen recognized by T cells 2

203523_at	LSP1	lymphocyte-specific protein 1
207992_s_at	AMPD3	adenosine monophosphate deaminase (isoform E)
228660_x_at	SEMA4F	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F
218170_at	ISOC1	isochorismatase domain containing 1
1555759_a_at	CCL5	chemokine (C-C motif) ligand 5
227253_at	HPS3	Hermansky-Pudlak syndrome 3
211990_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1
212998_x_at	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1
204778_x_at	HOXB7	homeobox B7
204834_at	FGL2	fibrinogen-like 2
205039_s_at	ZNFN1A1	zinc finger protein, subfamily 1A, 1 (Ikaros)
232543_x_at	ARHGAP9	Rho GTPase activating protein 9
209710_at	GATA2	GATA binding protein 2
200612_s_at	AP2B1	adaptor-related protein complex 2, beta 1 subunit
201487_at	CTSC	cathepsin C
201939_at	PLK2	polo-like kinase 2 (Drosophila)
203547_at	CD4	CD4 antigen (p55)
228376_at	GGTA1	glycoprotein, alpha-galactosyltransferase 1
207574_s_at	GADD45B	growth arrest and DNA-damage-inducible, beta
213560_at	GADD45B	growth arrest and DNA-damage-inducible, beta
219525_at	FLJ10847	NA
204411_at	KIF21B	kinesin family member 21B
200953_s_at	CCND2	cyclin D2
201859_at	PRG1	proteoglycan 1, secretory granule
223044_at	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1
213537_at	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1
216841_s_at	SOD2	superoxide dismutase 2, mitochondrial
205081_at	CRIP1	cysteine-rich protein 1 (intestinal)
226382_at	LOC283070	NA

219519_s_at	SIGLEC1	sialic acid binding Ig-like lectin 1, sialoadhesin
1558586_at	ZNF11B	zinc finger protein 11B
217028_at	CXCR4	chemokine (C-X-C motif) receptor 4
217478_s_at	HLA-DMA	major histocompatibility complex, class II, DM alpha
204438_at	MRC1	mannose receptor, C type 1
211366_x_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
204249_s_at	LMO2	LIM domain only 2 (rhombotin-like 1)
221081_s_at	DENND2D	DENN/MADD domain containing 2D
32128_at	CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)
220005_at	P2RY13	purinergic receptor P2Y, G-protein coupled, 13
209924_at	CCL18	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)
242458_at	ANGPTL1	angiopoietin-like 1
230391_at	NA	NA
213475_s_at	ITGAL	c("integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1", " alpha polypeptide"))
207458_at	C8orf51	chromosome 8 open reading frame 51
235306_at	GIMAP8	GTPase, IMAP family member 8
227780_s_at	NA	NA
205841_at	JAK2	Janus kinase 2 (a protein tyrosine kinase)
202687_s_at	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10
212067_s_at	C1R	complement component 1, r subcomponent
236908_at	ACPL2	acid phosphatase-like 2
223827_at	TNFRSF19	tumor necrosis factor receptor superfamily, member 19
213652_at	PCSK5	proprotein convertase subtilisin/kexin type 5
219631_at	LRP12	low density lipoprotein-related protein 12
1557116_at	NA	NA
208981_at	PECAM1	platelet/endothelial cell adhesion molecule (CD31 antigen)

209685_s_at	PRKCB1	protein kinase C, beta 1
238488_at	IPO11	importin 11
1568736_s_at	DLGAP1	discs, large (Drosophila) homolog-associated protein 1
238439_at	PRKAR2B	protein kinase, cAMP-dependent, regulatory, type II, beta
205027_s_at	MAP3K8	mitogen-activated protein kinase kinase kinase 8
211742_s_at	EVI2B	ecotropic viral integration site 2B
202269_x_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa
204533_at	CXCL10	chemokine (C-X-C motif) ligand 10
229163_at	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1
1556579_s_at	MED12L	mediator of RNA polymerase II transcription, subunit 12 homolog (yeast)-like
201566_x_at	ID2	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
201220_x_at	CTBP2	C-terminal binding protein 2
214677_x_at	IGLJ3	immunoglobulin lambda joining 3
235175_at	GBP4	guanylate binding protein 4
232001_at	LOC439949	NA
228427_at	FBXO16	F-box protein 16
214617_at	PRF1	perforin 1 (pore forming protein)
202369_s_at	TRAM2	translocation associated membrane protein 2
202625_at	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog
213618_at	CENTD1	centaurin, delta 1
209970_x_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
218035_s_at	FLJ20273	NA
206715_at	TFEC	transcription factor EC
1563473_at	PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B
204118_at	CD48	CD48 antigen (B-cell membrane protein)
201137_s_at	HLA-DPB1	major histocompatibility complex, class II, DP beta 1
230538_at	SHC4	SHC (Src homology 2 domain containing) family, member 4

1568822_at	GTPBP5	GTP binding protein 5 (putative)
229625_at	GBP5	guanylate binding protein 5
212233_at	MAP1B	microtubule-associated protein 1B
209202_s_at	EXTL3	exostoses (multiple)-like 3
209083_at	CORO1A	coronin, actin binding protein, 1A
205226_at	PDGFRL	platelet-derived growth factor receptor-like
227640_s_at	RP9	retinitis pigmentosa 9 (autosomal dominant)
223168_at	RHOU	ras homolog gene family, member U
1553132_a_at	MTAC2D1	membrane targeting (tandem) C2 domain containing 1
214038_at	CCL8	chemokine (C-C motif) ligand 8
219505_at	CECR1	cat eye syndrome chromosome region, candidate 1
214669_x_at	IGKC	immunoglobulin kappa constant
233123_at	SLC40A1	solute carrier family 40 (iron-regulated transporter), member 1
209195_s_at	ADCY6	adenylate cyclase 6
204846_at	CP	ceruloplasmin (ferroxidase)
204642_at	EDG1	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
239744_at	RGS3	regulator of G-protein signalling 3
206545_at	CD28	CD28 antigen (Tp44)
228339_at	NA	NA
218739_at	ABHD5	abhydrolase domain containing 5
224358_s_at	MS4A7	membrane-spanning 4-domains, subfamily A, member 7
1559425_at	PRKCH	protein kinase C, eta
231577_s_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa
231032_at	LOC286071	NA
207655_s_at	BLNK	B-cell linker
242546_at	NA	NA
211066_x_at	PCDHGC3	protocadherin gamma subfamily C, 3
216714_at	CCL13	chemokine (C-C motif) ligand 13
1562031_at	JAK2	Janus kinase 2 (a protein tyrosine kinase)

212763_at	CAMSAP1L1	calmodulin regulated spectrin-associated protein 1-like 1
205440_s_at	NPY1R	neuropeptide Y receptor Y1
227458_at	CD274	CD274 antigen
226303_at	PGM5	phosphoglucomutase 5
204613_at	PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)
202688_at	TNFSF10	tumor necrosis factor (ligand) superfamily, member 10
221477_s_at	SOD2	superoxide dismutase 2, mitochondrial
201236_s_at	BTG2	BTG family, member 2
205569_at	LAMP3	lysosomal-associated membrane protein 3
215121_x_at	IGLC1	immunoglobulin lambda constant 1 (Mcg marker)
202255_s_at	SIPA1L1	signal-induced proliferation-associated 1 like 1
215051_x_at	AIF1	allograft inflammatory factor 1
209138_x_at	IGLC2	immunoglobulin lambda constant 2 (Kern-Oz- marker)
232311_at	B2M	beta-2-microglobulin
1555756_a_at	CLEC7A	C-type lectin domain family 7, member A
221756_at	MGC17330	NA
238544_at	IGF1R	insulin-like growth factor 1 receptor
204512_at	HIVEP1	human immunodeficiency virus type I enhancer binding protein 1
230728_at	FKBP14	FK506 binding protein 14, 22 kDa
201720_s_at	LAPTM5	lysosomal associated multispinning membrane protein 5
223395_at	ABI3BP	ABI gene family, member 3 (NESH) binding protein
200905_x_at	HLA-E	major histocompatibility complex, class I, E
202207_at	ARL4C	ADP-ribosylation factor-like 4C
207076_s_at	ASS	argininosuccinate synthetase
211368_s_at	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
204628_s_at	ITGB3	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)
207540_s_at	SYK	spleen tyrosine kinase
213603_s_at	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small

		GTP binding protein Rac2)
1557222_at	NA	NA
206804_at	CD3G	CD3g antigen, gamma polypeptide (TiT3 complex)
209542_x_at	IGF1	insulin-like growth factor 1 (somatomedin C)
228858_at	NA	NA
207843_x_at	CYB5A	cytochrome b5 type A (microsomal)
223924_at	TTC25	tetratricopeptide repeat domain 25
1552497_a_at	SLAMF6	SLAM family member 6
241701_at	ARHGAP21	Rho GTPase activating protein 21
213819_s_at	FLOT1	flotillin 1
213095_x_at	AIF1	allograft inflammatory factor 1
228153_at	IBRDC2	IBR domain containing 2
213007_at	KIAA1794	KIAA1794
217525_at	OLFML1	olfactomedin-like 1
204220_at	GMFG	glia maturation factor, gamma
203508_at	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B
217629_at	NA	NA
226659_at	DEF6	differentially expressed in FDCP 6 homolog (mouse)
200904_at	HLA-E	major histocompatibility complex, class I, E
206571_s_at	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4
232746_at	CMKOR1	chemokine orphan receptor 1
1563461_at	NA	NA
204233_s_at	CHKA	choline kinase alpha
226865_at	NA	NA
227361_at	HS3ST3B1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1
204923_at	CXorf9	chromosome X open reading frame 9
204774_at	EVI2A	ecotropic viral integration site 2A
202270_at	GBP1	guanylate binding protein 1, interferon-inducible, 67kDa
243099_at	NFAM1	NFAT activating protein with ITAM motif 1

242874_at	NA	NA
229127_at	ATP5J	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit F6
224771_at	NAV1	neuron navigator 1
215379_x_at	IGLC2	immunoglobulin lambda constant 2 (Kern-Oz- marker)
222142_at	CYLD	cylindromatosis (turban tumor syndrome)
229367_s_at	GIMAP6	GTPase, IMAP family member 6
212713_at	MFAP4	microfibrillar-associated protein 4
214023_x_at	TUBB2B	tubulin, beta 2B
203413_at	NELL2	NEL-like 2 (chicken)
236583_at	NA	NA
212657_s_at	IL1RN	interleukin 1 receptor antagonist
227231_at	KIAA1211	NA
244023_at	SYK	spleen tyrosine kinase
206134_at	ADAMDEC1	ADAM-like, decysin 1
204894_s_at	AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1)
204502_at	SAMHD1	SAM domain and HD domain 1
218002_s_at	CXCL14	chemokine (C-X-C motif) ligand 14
205421_at	SLC22A3	solute carrier family 22 (extraneuronal monoamine transporter), member 3
215561_s_at	IL1R1	interleukin 1 receptor, type I
217138_x_at	IGLV3-25	immunoglobulin lambda variable 3-25
1556185_a_at	NA	NA
219681_s_at	RAB11FIP1	RAB11 family interacting protein 1 (class I)
205251_at	PER2	period homolog 2 (Drosophila)
224896_s_at	TTL	tubulin tyrosine ligase
209899_s_at	SIAHBP1	NA
201721_s_at	LAPTM5	lysosomal associated multispinning membrane protein 5
241671_x_at	FLJ22536	NA

218499_at	RP6-213H19.1	NA
235804_at	NA	NA
207677_s_at	NCF4	neutrophil cytosolic factor 4, 40kDa
227609_at	EPSTI1	epithelial stromal interaction 1 (breast)
227035_x_at	LOC441212	NA
206385_s_at	ANK3	ankyrin 3, node of Ranvier (ankyrin G)
1565602_at	PCDH9	protocadherin 9
228908_s_at	C21orf86	chromosome 21 open reading frame 86
223952_x_at	DHRS9	dehydrogenase/reductase (SDR family) member 9
38149_at	ARHGAP25	Rho GTPase activating protein 25
235688_s_at	TRAF4	TNF receptor-associated factor 4
214181_x_at	LST1	leukocyte specific transcript 1
222725_s_at	PALMD	palmelphin
1555852_at	TAP1	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)
210319_x_at	MSX2	msh homeobox homolog 2 (Drosophila)
220485_s_at	SIRPG	signal-regulatory protein gamma

Table 5. Primers and probes used for Q-PCR in standard 96 well plates

Gene name	Forward primers	Reverse primers	TaqMan Probes
IL7R	TCC-TAC-CAG-CCT-TTG-CCT-CTT	CCA-TAC-TTG-GCT-TTT-CTG-AAG-CA	FAM-CTT-CAA-TGT-TGT-TTC-CAT-GGG-MGB
CD3D	GTT-GAG-GAA-TGA-CCA-GGT-CTA-TCA-G	AAG-GTG-GCT-GTA-CTG-AGC-ATC-A	FAM-CCT-CCG-AGA-TCG-AG-MGB
CD52	TCA-GCC-TCC-TGG-TTA-TGG-TAC-AG	TGG-TTT-GGC-TGG-TGT-OGT-T	FAM-CAA-ACT-GGA-CTC-TCA-GGA-C-MGB
UBD	TGA-GGA-GCT-GCC-CTT-GTT-TC	CTG-GAG-GAG-GTG-CCT-CTT-TG	FAM-CAT-CAC-CTG-ACT-CCA-CA-MGB
GPR171	GAA-GTC-ATA-ACT-GAT-TGC-TCA-ACC-A	GAC-ACA-GCC-AGG-AGC-AGT-GTA-G	FAM-TCA-CTC-TTC-AAA-GCC-AAA-GA-MGB
GMZK	GTC-TGT-GCA-GGA-GAT-GCC-AA	GGG-CGC-CCT-GAG-TCA-CC	FAM-TTA-CAG-GAA-TCC-TTC-TGG-C-MGB
PRKCQ	ATC-CAT-GGT-CAA-GAG-GAC-AAG-TGG-A	GAC-AAG-ATA-ACA-AGC-GAA-GGT-GTC	FAM_CAA-ACC-TTC-CCT-CTC-ACT_MGB
STAT4	GTC-CCA-CAA-CAA-TTG-AAA-CTG-C	GTG-OGT-CAG-AGT-TTA-TCC-TGT-CAT	FAM_TGA-AGT-CTC-CTT-ATT-CTG-CT_MGB
TRDV2	GGT-CGA-GAA-AAG-CTT-TGA-AAC-AG	GGA-ACC-CAA-TCA-CTG-ACA-GGT-T	FAM_ACG-AAC-CTA-AAC-TTT-C_MGB
TRAT1	AAG-CCA-CGC-CAT-CTG-CAC	CTG-TGA-TCA-AGT-GAG-GCG-TAG	FAM_CAA-CCA-ATG-AAA-CAC-AGA-TG_MGB
TRBV19	GAG-GCC-TGG-GGT-AGA-GCA-G	AGA-GGA-TGG-TGG-CAG-ACA-GG	FAM_TGT-CCT-ACC-AGC-AAG-GG_MGB
CD69	AAT-CAT-AGC-TCT-CAT-TGC-CTT-ATC-AG	TGT-CTG-ATG-GCA-TTG-AGA-ATG-TG	FAM_CCA-ATA-CAA-TTG-TCC-AGG-CC_MGB
INDO1	CCA-GCA-GAC-TGC-TGG-TGG-A	GGC-ATA-TAT-CTT-CTC-ATG-TCC-TGG-A	FAM_ACA-TGC-TGC-TCA-GTT-C_MGB
H3F3A	CAG-CTA-TCG-GTG-CTT-TGC-AG	GAT-AGC-ACA-CAG-GTT-GGT-GTC-TTC	FAM_CAA-GTG-AGG-CCT-ATC-T_MGB
CD45R	GAG-ATG-CCT-GAT-GGT-TCA-AGT-AGAG	TTC-TTC-AAA-CTG-ATT-GTA-TTC-CAC-C	FAM_CAG-TAC-ATC-TTG-ATC-CAT-C_MGB
CD45RO	GGC-AAA-GCC-CAA-CAC-CTT-C	CAG-AAG-GGC-TCA-GAG-TGG-TTG-T	FAM_TGC-CTA-CCT-TAA-TGC-C_MGB
FoxP3	CAC-CTG-GCT-GGG-AAA-ATG-G	GGAGCC-CTT-GTC-GGA-TGA-T	FAM_CAA-GGC-TTC-ATC-TGT-G_MGB
CD20	CAT-ACA-ATC-TCT-GTT-CTT-GGG-CAT-T	TCA-TTC-TCA-ACG-ATG-CCA-GCT-A	FAM_TCA-GTG-ATG-CTG-ATC-TT_MGB
TLR9	CGC-CAG-ACC-CTC-TGG-AGA-A	GCC-TGC-ACC-AGG-AGA-GAC-A	FAM_TTC-TGC-CGC-AGC-G_MGB
ITGB3	AAG-TCC-ATC-CTG-TATG-TGG-TAG-AAG-AG	GAG-CAG-GAC-CAC-CAG-GAT-GT	FAM_AGT-GTC-CCA-AGG-GC_MGB
TLR3	GGA-AAG-GCT-AGC-AGT-CAT-CCA	GTG-GAG-GAT-GCA-CAC-AGC-AT	FAM_ATG-AGA-CAG-ACT-TTG-CC_MGB
TLR4	CCA-GAA-CTG-CAG-GTG-CTG-G	GGT-GGC-TTA-GGC-TCT-GAT-ATG-C	FAM_CCA-GGT-GTG-AAA-TCC-AGA-CA_MGB
TLR7	Assay-on-demand Hs00152971_m1 (Applied Biosystems)		
TLR10 variant 1	Assay-on-demand Hs01675179_m1 (Applied Biosystems)		
IRF1	Assay-on-demand Hs00971965_m1 (Applied Biosystems)		

Table6. Gene included into the TaqMan® Immune Profiling Array

Assay ID	Gene Symbol	Target Exons	NCBI Gene Reference
Hs00174092_m1	IL1A	6	NM_000575,M15329,X02531,X02851,X56086,CR457414,BC035169,BC013142,BT007014
Hs00174097_m1	IL1B	5	NM_000576,K02770,M15330,M54933,X02532,X56087,AF043335,BC008678,CR407679,BT007213
Hs00174114_m1	IL2	2	NM_000586,U25676,V00564,X01586,S82692,S77835,S77834,AF228636,BC066255,BC066256,BC066257
Hs00174117_m1	IL3	2	C066254,AY523040,BC070338,A14844
Hs00174122_m1	IL4	3	NM_000588,M17115,M14743,M20137,BC066274,BC066276,BC066272,BC066273,BC069472
Hs00174200_m1	IL5	2	NM_172348,NM_000589,M13982,X81851,AF043336,BC066277,BC067514,BC067515,BC070123,AB1
Hs00174131_m1	IL6	3	NM_000879,X12705,X04688,BC066282
Hs00174202_m1	IL7	2	NM_000600,X04403,M14584,M18403,M29150,X04430,X04602,M54894,S56892,CR450296,BT019748
Hs00174103_m1	IL8	1	39749,A09363,BC015511
Hs00174125_m1	IL9	3	NM_000880,J04156,BC047698
Hs99999901_s1	18S	1	NM_000584,M17017,M26383,Z11686,Y00787,CR542151,AK131067,BC013615,BT007067
Hs00174086_m1	IL10	3	NM_000590,M30134,X17543,S63356,BC066284,BC066283,BC066285,BC066286
Hs00168405_m1	IL12A	2	1X03205
Hs00233688_m1	IL12B	3	NM_000572,M57627,AF043333,AY029171,CR541993
Hs00174379_m1	IL13	1	NM_000882,M65271,M65291,AF101062,AF180562,BG702253
Hs00174106_m1	IL15	1	NM_002187,M65272,M65290,AF180563,BC067501,BC067498,BC067499,BC067500,BC067502,BC07
Hs00174383_m1	IL17	2	NM_002188,L06801,X69079,BC096141,BC096139
Hs00155517_m1	IL18	4	NM_000585,U14407
Hs00234142_m1	CCL3	1	NM_002190,Z58820,U32659,BC066251,BC066252,BC066253,BC067504,BC067503,BC067505
Hs00171149_m1	CCL19	1	NM_001562,D49950,U90434,AF077611,AY266351,CR541973,CR542001,AY044641,BC015863,BC00
Hs00234140_m1	CCL2	1	NM_002983,M25315,D63785,M23452,D00044,X03754,BC071834
Hs00174575_m1	CCL5	2	NM_006274,AB000887,U77180,U88321,CR456868,BC027968
Hs00174150_m1	CCR2	1	NM_002982,M24545,M28226,X14768,S69738,S71513,AV733621,BC009716,BT007329
Hs99999919_m1	CCR4	N/A	NM_002985,M21121,AF043341,BC008600,AF266753
Hs00152917_m1	CCR5	2	NM_000647,U03882,BC074751
Hs00171054_m1	CCR7	1	NM_005508,BC069139,BC071751,BC074935
Hs00171041_m1	CXCR3	1	NM_000579,U54994,BC038398
Hs00171042_m1	CXCL10	1	NM_001838,L31581,L08176,BC035343,AK127810
Hs00171138_m1	CXCL11	1	NM_001504,X95876
Hs00174164_m1	CSF1	4	NM_001565,X02530,BC010954
Hs00171266_m1	CSF2	3	NM_005409,Y15220,U59286,AF030514,AF002985,U66096,BC005292,AF352781,BC012532,BT00678
Hs00357085_g1	CSF3	1	NM_172210,NM_172211,NM_172212,NM_000757,U22386,M37435,M76453,M64592,M27087,X05825,
Hs00234174_m1	STAT3	N/A	NM_000758,M10663,M11220,AY720441,AF510855
Hs00174517_m1	NFKB2	6	NM_172219,NM_000759,M17706,X03438,X03655,CR541891
Hs00395088_m1	IKKB	8	NM_139276,AJ012463,L29277,BC014482
			NM_002502,U09609,X61498,X61499,S76638,BC002844,BT009769
			NM_001556,AF029684,AF031416,AF080158,AB209090,BX648165

Hs00167894_m1	CD3E		1	NM_000733,X03884,BI910359
Hs00181217_m1	CD4		2	NM_000616,M12807,BT019791,BT019811,BC025782
Hs00233520_m1	CD8A		5	NM_171827,NM_001768,M12824,M12828,AY039664,AK124156,BC025715,AK097942
Hs00174333_m1	CD19		4	NM_001770,M21097,X13312,BC006338,AK130657,BC052294
Hs00166229_m1	IL2RA		1	NM_000417,X01057,K03122,AK223313
Hs00174796_m1	CD28		2	NM_006139,J02988,BC093698
Hs00233552_m1	CD38		1	NM_001775,D84276,M34461,BC007964,CD688069
Hs00374176_m1	CD40		1	NM_152854,NM_001250,AJ300189,BC064518,BC012419,BM761221,AK222896
Hs00365634_g1	PTPRC		1	NM_080921,NM_080922,NM_080923,NM_002838,Y00062,BC017863,BC014239
Hs00154355_m1	CD68		6	NM_001251,S57235,BC015557,BT009923,AK222492,AK222514
Hs00175478_m1	CD80		2	NM_005191,M27533,AY197777,AY197778,AY081815,BC042665
Hs00199349_m1	CD86		2	NM_175862,NM_006889,L25259,U04343,CR541844,BC040261
Hs00175480_m1	CTLA4		1	NM_005214,L15006,BC069566,BC070162,BC074842,BC074893,AY209009,AF414120,AF486806
Hs00163934_m1	CD40LG		4	NM_000074,L07414,X67878,Z15017,X68550,BC071754,BC074950
Hs00219575_m1	HLA-DRA		1	NM_019111,J00194,M60334,M35979,K01171,M60333,CR457013,BC071659,BC032350
Hs99999917_m1	HLA-DRB1	N/A		NM_002124,M11161,M33600,X03069,DQ002917
Hs00203436_m1	TBX21		1	NM_013351,AF093098,AF241243,BC039739,AK223634
Hs00188346_m1	TNFRSF18		2	NM_148901,NM_148902,NM_004195,AF117297,AF125304,AF241229,BT019531,BT019532,AY358877
Hs00359999_m1	ICOS		1	NM_012092,AB023135,AJ277832,BC028006,BC028210
Hs00167248_m1	NOS2A		11	NM_153292,NM_000625,AB022318,U05810,D26525,L24553,X73029,U20141,U31511,S75615
Hs00153350_m1	BCL2		1	NM_000633,M13994,M14745,X06487,BC027258
Hs00169141_m1	BCL2L1		1	NM_001191,Z23116
Hs00180269_m1	BAX			NM_138761,NM_138763,NM_004324,L22473,L22474,U19599,AF247393,AF250190,AJ586909,3 AJ586910,BM706954,BC014175,AJ417988
Hs00164932_m1	ICAM1		2	NM_000201,M24283,J03132,X06990,AF340038,AF340039,BC015969,AK130659,BT006854
Hs00174583_m1	SELP		1	NM_003005,M25322,BC068533
Hs00174057_m1	SELE		4	NM_000450,M24736,M30640
Hs00157965_m1	HMOX1		2	NM_002133,M23041,X06985,CR456505,CR541945,CR541968,BT019785,BC001491
Hs00153133_m1	PTGS2		5	NM_000963,M90100,L15326,AJ634912,AY462100,BC013734,AY151286
Hs00166915_m1	REN		1	NM_000537,CR536498,BC047752,BC033474
Hs00189742_m1	LRP2		17	NM_004525,U33837,AY265357,AY265358
Hs00411908_m1	MYH6		23	NM_002471,D00943
Hs00192564_m1	RPL3L		3	NM_005061,U65581,BC050413
Hs00167927_m1	CYP1A2		2	NM_000761,M55053,Z00036,AF182274,BC067425,BC067427,BC067429,BC067426,BC067428
Hs00167982_m1	CYP7A1		3	NM_000780,X56088,M93133
Hs00174143_m1	IFNG		1	NM_000619,X13274,V00543,X87308,BC070256,AY255837,AY255839,AY044154,AF506749
Hs00169473_m1	PRF1		1	NM_005041,M28393,X13224,BC063043,BC047695

Table 7A
Geomean ratio
between
responder and
non-responder
groups

Gene	Ratio	LL	UL
CCL5	7.83	3.09	19.84
FASLG	7.57	2.77	20.70
GNLY	8.82	3.61	21.56
GZMB	12.15	4.38	33.71
PRF1	11.07	4.85	25.28
IFNG	21.19	5.36	83.86
ICOS	13.44	3.44	52.51
TBX21	13.93	3.63	53.41
CD8A	11.60	4.22	31.90
CD3E	12.78	3.55	46.04
CXCL11	4.71	1.44	15.35
CXCL10	7.39	2.56	21.39
CXCR3	16.96	3.10	92.90
CD20	9.46	1.35	66.42
FOXP3	5.57	2.58	12.04
INDO	13.62	2.89	64.20
CD45Ro	4.02	1.84	8.79
CD45R	4.92	1.90	12.77
CD69	5.84	2.00	17.06
TRBV19	11.15	3.56	34.94
TRAT1	9.67	2.77	33.80
TRDV2	7.05	2.79	17.82
STAT4	3.41	1.75	6.65
PRKCQ	7.41	3.24	16.94
GMZK	9.20	2.60	32.49
GPR171	5.25	2.47	11.17
UBD	14.68	3.95	54.65
CD52	6.17	1.96	19.41
CD3D	10.03	3.07	32.77
IL7R	6.49	2.08	20.26
IRF1	5.54	2.83	10.83
TLR7	3.44	1.50	7.89

Table 8 (BELOW) . Correlation matrix between 30 genes

Variable	lg_LR	lg_CO3D	lg_CO32	lg_UBD	lg_GPR171	lg_GMZX	lg_PRCO0	lg_STAT4	lg_TPOV2	lg_TRA11	lg_TPB19	lg_CO38	lg_CO45R	lg_CO45FO	lg_INDO	lg_FOX23	lg_CO20	lg_CX283	lg_CXQ10	lg_CXQ11	lg_CO3E	lg_CO3A	lg_TB21	lg_ICOS	lg_IPNG	lg_PPF1	lg_G2MB	lg_GNLY	lg_FASLG	lg_CO35
lg_LR	1.00	0.90	0.91	0.79	0.60	0.80	0.83	0.84	0.88	0.92	0.92	0.95	0.90	0.84	0.76	0.78	0.87	0.84	0.85	0.54	0.86	0.77	0.91	0.85	0.75	0.76	0.80	0.74	0.69	0.77
lg_CO3D	0.90	1.00	0.94	0.93	0.89	0.93	0.88	0.88	0.96	0.96	0.99	0.92	0.91	0.91	0.89	0.80	0.82	0.88	0.94	0.74	0.94	0.93	0.97	0.94	0.91	0.92	0.92	0.87	0.87	0.93
lg_CO32	0.91	0.94	1.00	0.80	0.83	0.82	0.84	0.83	0.91	0.89	0.95	0.92	0.88	0.83	0.79	0.75	0.88	0.82	0.88	0.60	0.92	0.82	0.93	0.87	0.78	0.82	0.89	0.84	0.78	0.83
lg_UBD	0.79	0.93	0.80	1.00	0.82	0.91	0.80	0.82	0.86	0.89	0.91	0.80	0.80	0.83	0.91	0.74	0.69	0.85	0.92	0.81	0.81	0.89	0.90	0.89	0.92	0.89	0.86	0.77	0.65	0.91
lg_GPR171	0.80	0.89	0.83	0.82	1.00	0.81	0.94	0.92	0.94	0.95	0.90	0.80	0.83	0.86	0.81	0.83	0.67	0.74	0.76	0.75	0.85	0.88	0.83	0.78	0.74	0.88	0.90	0.85	0.82	0.83
lg_GMZX	0.80	0.93	0.82	0.91	0.81	1.00	0.83	0.85	0.87	0.95	0.92	0.88	0.88	0.90	0.87	0.78	0.74	0.86	0.83	0.74	0.87	0.91	0.87	0.87	0.92	0.91	0.84	0.83	0.85	0.92
lg_PRCO0	0.83	0.88	0.84	0.80	0.94	0.83	1.00	0.93	0.93	0.99	0.91	0.87	0.89	0.89	0.83	0.91	0.74	0.79	0.72	0.71	0.88	0.91	0.81	0.78	0.75	0.91	0.88	0.88	0.81	0.81
lg_STAT4	0.84	0.88	0.83	0.82	0.92	0.85	0.93	1.00	0.89	0.91	0.89	0.87	0.90	0.88	0.83	0.84	0.74	0.78	0.73	0.77	0.83	0.87	0.81	0.79	0.78	0.87	0.87	0.82	0.81	0.82
lg_TPOV2	0.88	0.96	0.91	0.86	0.94	0.87	0.93	0.89	1.00	0.92	0.97	0.88	0.91	0.91	0.83	0.85	0.76	0.84	0.79	0.72	0.94	0.92	0.92	0.89	0.82	0.91	0.91	0.86	0.65	0.88
lg_TRA11	0.92	0.96	0.89	0.89	0.85	0.95	0.89	0.91	0.92	1.00	0.96	0.92	0.95	0.93	0.87	0.82	0.83	0.88	0.77	0.68	0.91	0.89	0.92	0.90	0.88	0.89	0.87	0.83	0.83	0.88
lg_TPB19	0.92	0.99	0.95	0.91	0.90	0.92	0.91	0.89	0.97	0.96	1.00	0.93	0.92	0.91	0.87	0.83	0.83	0.89	0.91	0.70	0.95	0.93	0.97	0.93	0.89	0.92	0.93	0.87	0.87	0.92
lg_CO38	0.95	0.92	0.92	0.80	0.80	0.88	0.87	0.87	0.88	0.92	0.93	1.00	0.92	0.90	0.80	0.79	0.86	0.83	0.89	0.67	0.93	0.88	0.87	0.87	0.83	0.88	0.87	0.87	0.86	0.87
lg_CO45R	0.90	0.91	0.88	0.80	0.83	0.88	0.89	0.90	0.91	0.95	0.92	0.92	1.00	0.97	0.83	0.86	0.78	0.82	0.88	0.64	0.87	0.85	0.86	0.83	0.78	0.84	0.83	0.80	0.79	0.80
lg_CO45FO	0.94	0.91	0.83	0.83	0.86	0.90	0.89	0.88	0.91	0.93	0.91	0.90	0.97	1.00	0.86	0.83	0.69	0.82	0.75	0.70	0.86	0.87	0.87	0.84	0.82	0.88	0.85	0.82	0.85	0.84
lg_INDO	0.76	0.89	0.79	0.91	0.81	0.87	0.83	0.83	0.83	0.87	0.87	0.80	0.83	0.86	1.00	0.80	0.66	0.78	0.92	0.74	0.76	0.82	0.82	0.78	0.87	0.83	0.80	0.78	0.75	0.81
lg_FOX23	0.78	0.80	0.75	0.74	0.83	0.78	0.91	0.84	0.85	0.82	0.83	0.79	0.86	0.83	0.80	1.00	0.65	0.73	0.64	0.59	0.75	0.81	0.72	0.68	0.71	0.81	0.77	0.78	0.69	0.68
lg_CO20	0.87	0.82	0.88	0.69	0.67	0.74	0.74	0.74	0.76	0.83	0.83	0.86	0.78	0.69	0.66	0.65	1.00	0.73	0.51	0.47	0.82	0.68	0.79	0.74	0.67	0.68	0.71	0.68	0.63	0.68
lg_CX283	0.84	0.89	0.82	0.85	0.74	0.66	0.79	0.78	0.84	0.88	0.89	0.83	0.82	0.82	0.78	0.73	0.73	1.00	0.81	0.73	0.87	0.89	0.89	0.90	0.82	0.85	0.82	0.77	0.78	0.89
lg_CXQ11	0.85	0.84	0.88	0.92	0.76	0.83	0.72	0.73	0.79	0.77	0.81	0.89	0.88	0.75	0.82	0.64	0.51	0.81	1.00	0.90	0.73	0.87	0.81	0.84	0.89	0.86	0.80	0.74	0.83	0.91
lg_CXQ11	0.54	0.74	0.60	0.61	0.75	0.74	0.71	0.77	0.72	0.68	0.70	0.67	0.64	0.70	0.74	0.59	0.47	0.73	0.90	1.00	0.65	0.81	0.67	0.72	0.73	0.79	0.75	0.69	0.81	0.81
lg_CO3E	0.86	0.94	0.92	0.81	0.85	0.87	0.88	0.83	0.94	0.91	0.95	0.93	0.87	0.86	0.76	0.75	0.82	0.87	0.73	0.65	1.00	0.91	0.92	0.91	0.83	0.91	0.90	0.89	0.87	0.91
lg_CO3A	0.77	0.93	0.82	0.89	0.88	0.91	0.91	0.87	0.92	0.89	0.93	0.88	0.85	0.87	0.82	0.81	0.68	0.89	0.87	0.81	0.91	1.00	0.88	0.90	0.89	0.98	0.92	0.89	0.93	0.96
lg_TB21	0.91	0.97	0.93	0.90	0.83	0.87	0.81	0.81	0.92	0.92	0.97	0.87	0.86	0.87	0.82	0.72	0.79	0.89	0.91	0.67	0.92	0.88	1.00	0.95	0.87	0.87	0.89	0.80	0.85	0.91
lg_ICOS	0.95	0.94	0.87	0.89	0.78	0.87	0.78	0.79	0.89	0.90	0.93	0.87	0.83	0.84	0.78	0.68	0.74	0.90	0.84	0.72	0.91	0.90	0.95	1.00	0.90	0.88	0.90	0.83	0.88	0.94
lg_IPNG	0.75	0.91	0.78	0.92	0.74	0.92	0.75	0.78	0.82	0.88	0.89	0.83	0.78	0.82	0.87	0.71	0.67	0.82	0.89	0.73	0.83	0.89	0.87	0.90	1.00	0.90	0.85	0.82	0.84	0.93
lg_PPF1	0.76	0.92	0.82	0.89	0.88	0.91	0.91	0.87	0.91	0.89	0.92	0.88	0.84	0.88	0.83	0.81	0.68	0.85	0.79	0.91	0.98	0.87	0.88	0.90	1.00	1.00	0.94	0.92	0.93	0.95
lg_G2MB	0.80	0.92	0.89	0.86	0.90	0.84	0.88	0.87	0.91	0.87	0.93	0.87	0.83	0.85	0.80	0.77	0.71	0.82	0.80	0.75	0.90	0.92	0.89	0.90	0.85	0.94	1.00	0.92	0.91	0.92
lg_GNLY	0.74	0.87	0.84	0.77	0.85	0.83	0.88	0.82	0.86	0.83	0.87	0.87	0.80	0.82	0.78	0.78	0.68	0.77	0.74	0.69	0.89	0.89	0.80	0.83	0.82	0.92	0.92	1.00	0.86	0.88
lg_FASLG	0.88	0.87	0.78	0.85	0.82	0.85	0.81	0.81	0.86	0.83	0.87	0.86	0.79	0.85	0.75	0.68	0.63	0.78	0.83	0.81	0.87	0.93	0.85	0.88	0.84	0.93	0.91	0.86	1.00	0.93
lg_CO35	0.77	0.93	0.83	0.91	0.83	0.92	0.81	0.82	0.88	0.88	0.92	0.87	0.80	0.84	0.81	0.68	0.68	0.89	0.91	0.81	0.91	0.96	0.91	0.94	0.93	0.95	0.92	0.88	0.93	1.00

Table 9A 18 best models obtained by logistic regression.

Predictor	R2 (%)	Chi-square Score
PRF1	55	16
IRF1	50	14
GZMB	46	14
GNLY	45	14
CD8A	46	14
PRKCQ	45	14
FOXP3	42	13
IFNG	52	13
CCL5	45	13
GPR171	41	12
TRBV19	44	11
CD3E	39	11
TBX21	44	11
FASLG	39	11
CXCL10	35	10
ICOS	39	10
CXCR3	35	9
CXCL11	22	6

Table10 Percentage of correct classification calculated using the logistic regression model for some genes.

Model	Percentage of patients correctly classified
PRF1	86,6%
IRF1	89,7%
GZMB	82,8%
GNLY	82,8%
CD8A	82,8%
PRKCQ	89,7%
FOXP3	86,2%
IFNG	89,7%
CCL5	79,3%
GPR171	82,8%
TRBV19	86,2%
CDE3	75,9%
TBX21	82,8%
FASLG	75,9%
CXCL10	75,9%
ICOS	75,9%
CXR3	75,9%
CXCL11	72,4%

TABLE 11A			Patient Identity Number									
Probe Set	Gene Title	Gene Symbol	14	52	66	37	16	13	55	56	5	60
1555759_a_at	chemokine (C-C motif) ligand 5	CCL5	3.148	3.204	3.208	3.096	3.055	3.049	3.096	3.208	2.664	2.835
1555834_at	Ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	UCHL1	7.911	2.4	2.324	5.169	5.06	2.401	3.561	2.627	4.868	2.401
1558290_a_at	Pvt1 oncogene homolog, MYC activator (mouse) /// LOC441378	PVT1 /// LOC441378	10.849	10.579	11.312	10.154	9.815	10.752	11.192	9.514	10.132	8.752
1569942_at	CDNA clone IMAGE:4796388	---	5.295	3.843	4.837	5.187	3.748	5.656	3.518	6.042	6.463	4.378
204661_at	CD52 antigen (CAMPATH-1 antigen) /// CD52 antigen (CAMPATH-1 antigen)	CD52	5.673	5.506	8.56	5.104	5.814	5.755	4.087	4.785	3.839	4.29
205890_s_at	ubiquitin D	UBD	4.731	7.003	9.226	4.138	3.687	8.103	3.242	6.126	3.231	7.706
206118_at	signal transducer and activator of transcription 4	STAT4	4.336	3.291	4.142	2.396	3.235	3.291	2.382	2.439	2.663	2.948

206666_ at	granzyme K (granzyme 3; tryptase II) /// granzyme K (granzyme 3; tryptase II)	GZMK	6.187	5.357	7.079	2.659	2.571	5.033	2.225	3.383	2.567	3.104
207072_ at	interleukin 18 receptor accessory protein	IL18R AP	2.225	2.237	2.232	2.232	2.231	2.232	2.227	2.237	2.227	2.237
207651_ at	G protein-coupled receptor 171	GPR171	3.961	7.086	4.363	4.635	3.271	5.499	3.426	4.679	3.42	4.672
209606_ at	pleckstrin homology, Sec7 and coiled-coil domains, binding protein /// pleckstrin homology, Sec7 and coiled-coil domains, binding protein	PSCDB P	4.553	5.031	5.888	4.679	3.194	3.996	3.036	3.285	3.692	3.473
209949_ at	neutrophil cytosolic factor 2 (65kDa, chronic granulomatous disease, autosomal 2)	NCF2	6.058	6.184	3.286	6.305	4.585	3.866	4.672	3.294	4.457	3.802
210038_ at	protein kinase	PRKC	2.362	2.18	2.415	2.178	2.364	2.358	2.577	2.181	2.179	2.191

at	C, theta	Q																
210629_x_at	leukocyte specific transcript 1	LST1	5.649	6.559	6.72	5.368	5.367	3.893	3.484	6.134	4.775	5.283						
210972_x_at	T cell receptor alpha locus /// T cell receptor delta variable 2 /// T cell	TRA@ /// TRDV2 ///	4.292	6.159	7.116	3.791	4.059	6.091	5.234	5.057	4.291	4.842						
	receptor alpha variable 20 /// T cell receptor alpha joining 17 /// T cell	TRAV2 0 /// TRAJ1 7 ///																
	receptor alpha constant	TRAC																
	T cell receptor gamma constant 2	TRGC2																
211144_x_at	T cell receptor gamma constant 2	TRGC2	2.887	2.261	4.452	2.257	2.193	3.203	2.347	2.453	2.332	2.196						
211796_s_at	T cell receptor beta variable 21-1 /// T cell	TRBV2 1-1 ///	3.275	3.556	7.359	2.877	2.424	5.177	2.521	2.728	2.297	2.909						
	receptor beta variable 19 /// T cell receptor cell receptor beta variable 5-4 /// T cell	TRBV1 9 /// TRBV5 -4 ///																
	receptor beta variable 3-1 /// T cell receptor cell receptor beta constant 1	TRBV3 -1 /// TRBC1																

212671_ s_at	major histocompatibilit y complex, class II, DQ alpha 1 /// major histocompatibilit y complex, class II, DQ alpha 2	HLA- DQA1 /// HLA- DQA2	8.1	7.479	6.553	8.223	6.574	7.356	7.347	5.884	6.068	5.558
213193_ x_at	T cell receptor beta variable 19 /// T cell receptor beta variable 19 /// T cell receptor beta constant 1 /// T cell receptor beta constant 1	TRBV1 9 /// TRBC1	4.185	3.787	7.027	3.011	2.962	4.53	3.096	3.192	2.829	3.058
213539_ at	CD3D antigen, delta polypeptide (TiT3 complex)	CD3D	3.179	4.399	7.52	3.352	3.182	5.87	2.8	3.183	3.178	3.626
213560_ at	Growth arrest and DNA- damage- inducible, beta	GADD 45B	4.967	5.948	6.218	5.528	4.673	5.367	5.49	3.67	5.735	5.048
216261_ at	integrin, beta 3 (platelet glycoprotein IIla, antigen CD61)	ITGB3	8.21	2.588	4.394	3.536	6.237	4.486	3.088	6.729	6.77	2.606

217147_ s_at	T cell receptor associated transmembrane adaptor 1	TRAT1	3.914	4.251	5.453	2.871	2.292	4.283	2.327	2.887	2.277	2.308
217478_ s_at	major histocompatibility complex, class II, DM alpha	HLA- DMA	8.989	8.655	8.599	9.516	8.621	7.051	8.181	8.129	7.41	8.04
218950_ at	centaurin, delta 3	CENT D3	9.212	7.139	8.794	8.51	8.32	7.438	9.077	8.075	9.012	7.142
220330_ s_at	SAM domain, SH3 domain and nuclear localisation signals, 1	SAMS N1	4.712	4.228	5.117	4.641	4.804	3.557	2.702	4.246	3.492	3.828
222934_ s_at	C-type lectin domain family 4, member E	CLEC4 E	5.382	4.219	2.931	2.753	2.511	3.812	4.494	2.512	3.917	3.417
223827_ at	tumor necrosis factor receptor superfamily, member 19	TNFRS F19	4.16	3.985	5.98	2.86	5.91	3.239	4.301	6.268	5.029	4.931
224771_ at	neuron navigator 1	NAV1	7.893	6.773	7.352	7.998	8.385	7.571	7.077	7.277	6.956	7.304
224772_ at	neuron navigator 1	NAV1	10.827	9.319	9.458	9.799	10.771	10.304	9.47	9.943	9.752	9.998
224773_ at	neuron navigator 1	NAV1	8.959	7.241	7.742	9.332	9.582	8.051	8.427	8.479	7.795	7.564
224774_ s_at	neuron navigator 1	NAV1	7.288	6.204	7.292	8.109	7.683	6.486	7.056	5.947	6.406	6.181

227145_ at	lysyl oxidase- like 4	LOXL4	11.368	8.235	10.93	12.565	12.636	12.563	7.768	11.858	12.092	11.625
227584_ at	Neuron navigator 1	NAV1	11.735	10.222	10.601	10.533	11.778	11.041	10.121	11.247	10.732	11.005
227812_ at	tumor necrosis factor receptor superfamily, member 19	TNFRSF19	11.9	11.787	12.618	10.566	12.747	11.729	11.115	12.911	12.125	11.835
229723_ at	T-cell activation GTPase activating protein	TAGAP	5.224	4.874	5.527	5.091	2.501	3.01	4.398	2.891	3.472	3.425
232024_ at	GTPase, IMAP family member 2	GIMAP2	8.489	7.321	7.275	6.411	7.83	6.861	6.317	8.172	7.42	7.119
238544_ at	Insulin-like growth factor 1 receptor	IGF1R	6.79	8.031	9.43	5.969	7.331	7.827	8.887	6.322	9.011	7.444
242886_ at	Chromosome 17 open reading frame 63	C17orf63	10.066	10.766	9.654	8.976	9.813	9.864	10.039	9.839	8.819	9.808
242986_ at	Neuron navigator 1	NAV1	9.936	9.155	9.341	10.292	10.071	9.41	9.098	9.552	8.465	8.663
34210_at	CD52 antigen (CAMPATH-1 antigen)	CD52	6.58	6.581	9.446	5.799	6.518	6.798	4.246	6.008	3.469	5.289

TABLE 11B			Patient Identity Number											
Probe Set	Gene Title	Gene Symbol	75	2	65	20	10	19	23	26	27	38	8	67
155575 9_a_at	chemokine (C-C motif) ligand 5	CCL5	4.665	5.498	7.109	3.207	5.121	3.656	4.159	4.664	5.256	5.411	3.034	3.11
155583 4_at	Ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	UCHL1	2.329	2.36	2.4	2.399	2.358	2.398	2.463	2.401	2.4	2.4	5.041	2.40
155829 0_a_at	Pvt1 oncogene homolog, MYC activator (mouse) /// LOC441378	PVT1 /// LOC441378	8.59	7.403	8.63	8.588	9.536	8.46	9.384	9.409	8.504	8.57	10.616	9.90
156994 2_at	CDNA clone IMAGE:4796388	---	3.605	3.324	4.066	2.849	4.189	2.198	3.972	3.61	3.392	2.944	5.832	4.38
204661_at	CD52 antigen (CAMPATH-1 antigen) /// CD52 antigen (CAMPATH-1 antigen)	CD52	8.008	8.301	9.702	8.979	9.415	6.144	8.556	8.487	11.34	10.289	4.082	8.69
205890	ubiquitin D	UBD	11.687	10.159	11.582	7.52	9.692	8.088	9.801	12.384	10.657	10.131	3.178	9.54

[illegible]

	domains, binding protein																		
209949 _at	neutrophil cytosolic factor 2 (65kDa, chronic granulomatou s disease, autosomal 2)	NCF2	6.928	6.845	7.973	5.572	5.428	6.643	7.499	6.281	6.48	7.213	3.405	7.445					
210038 _at	protein kinase C, theta	PRKC Q	4.981	4.768	2.406	2.836	6.907	4.108	5.51	5.272	8.218	4.73	2.179	2.301					
210629 _x_at	leukocyte specific transcript 1	LST1	7.078	6.711	6.926	5.831	6.424	6.69	7.323	6.834	7.058	8.828	3.779	7.285					
210972 _x_at	T receptor alpha locus /// T cell receptor delta variable 2 /// T cell receptor alpha variable 20 /// T cell receptor alpha joining 17 /// T cell	TRA@ /// TRDV2 /// TRAV2 0 /// TRAJ1 7 /// TRAC	7.913	8.072	11.25	6.451	10.646	7.331	8.326	9.727	11.544	8.3	4.292	6.411					

	receptor alpha constant																			
211144 _x_at	T cell receptor gamma constant 2	TRGC2	6.096	4.892	6.456	2.624	6.163	2.689	6.279	7.941	7.365	6.31	2.189	2.641						
211796 _s_at	T cell receptor beta variable 21-1 /// T cell receptor beta variable 19 /// T cell receptor beta variable 5-4 /// T cell receptor beta variable 3-1 /// T cell receptor beta constant 1	TRBV2 1-1 /// TRBV1 9 /// TRBV5 -4 /// TRBV3 -1 /// TRBC1	7.924	8.11	10.708	6.84	9.737	6.456	8.211	9.022	11.111	8.316	2.293	5.741						
212671 _s_at	major histocompati bility complex, class II, DQ alpha 1 /// major histocompati	HLA- DQA1 /// HLA- DQA2	10.798	9.601	11.257	9.336	8.87	9.39	9.435	10.008	10.974	10.757	2.679	7.61						

	bility complex, class II, DQ alpha 2																			
213193 _x_at	T cell receptor beta variable 19 /// T cell receptor beta variable 19 /// T cell receptor beta constant 1 /// T cell receptor beta constant 1	TRBV1 9 /// TRBC1	7.553	7.871	10.191	6.704	9.248	5.828	7.936	8.266	11.152	7.722	2.83	5.47						
213539 _at	CD3D antigen, delta polypeptide (TiT3 complex)	CD3D	8.208	8.038	9.64	7.257	8.387	6.635	8.381	9.075	10.519	8.841	2.311	6.07						
213560 _at	Growth arrest and DNA- damage- inducible, beta	GADD 45B	7.243	5.936	6.794	7.57	6.389	7.236	7.105	6.776	7.114	6.774	3.402	7.12						
216261 _at	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	ITGB3	2.545	2.691	2.651	2.592	2.59	2.553	2.609	4.561	2.622	2.557	6.05	2.60						

217147 _s_at	T cell receptor associated transmembrane adaptor 1	TRAT1	6.748	6.139	8.028	5.044	7.377	7.56	6.512	7.612	9.246	8.077	2.281	3.00
217478 _s_at	major histocompatibility complex, DM class II, DM alpha	HLA-DMA	10.873	10.838	11.541	9.389	10.193	9.475	10.475	9.998	11.266	10.161	7.109	9.33
218950 _at	centaurin, delta 3	CENTD3	7.911	7.983	5.552	6.866	7.456	5.891	7.35	5.522	5.804	6.245	8.04	8.20
220330 _s_at	SAM domain, SH3 domain and nuclear localisation signals, 1	SAMS N1	7.494	6.244	4.271	5.243	7.151	6.458	7.429	8.583	8.421	7.405	2.325	6.71
222934 _s_at	C-type lectin domain family 4, member E	CLEC4E	6.912	6.523	6.984	5.384	4.588	6.678	6.941	4.589	4.731	5.877	3.019	7.66
223827 _at	tumor necrosis factor receptor superfamily, member 19	TNFRSF19	3.043	3.308	2.721	2.855	3.48	2.8	2.854	2.977	2.796	3.43	4.669	2.99
224771 _at	neuron navigator 1	NAV1	6.378	7.607	6.624	6.24	6.483	4.678	6.467	6.537	3.882	5.375	6.798	5.73

224772 _at	neuron navigator 1	NAV1	9.184	10.073	8.059	7.897	8.937	8.214	8.963	9.472	7.529	7.742	9.418	8.412
224773 _at	neuron navigator 1	NAV1	7.427	7.781	5.878	5.855	6.881	5.668	6.94	7.344	4.953	7.035	7.352	6.472
224774 s_at	neuron navigator 1	NAV1	5.706	7.087	5.432	5.724	5.939	3.907	6.432	6.166	5.262	5.989	6.48	5.912
227145 _at	lysyl oxidase- like 4	LOXL4	3.699	7.798	3.703	4.953	8.792	7.205	9.531	9.214	9.691	3.702	11.838	8.602
227584 _at	Neuron navigator 1	NAV1	10.236	10.828	8.45	9.758	9.512	8.8	10.254	10.798	8.769	9.367	10.568	9.562
227812 _at	tumor necrosis factor receptor superfamily, member 19	TNFRS F19	9.962	9.478	9.706	8.939	11.568	11.39	9.998	10.948	9.083	10.541	12.176	10.572
229723 _at	T-cell activation GTPase activating protein	TAGA P	6.398	6.009	9.043	7.032	8.532	5.424	7.084	6.786	10.798	7.081	3.21	5.292
232024 _at	GTPase, IMAP family member 2	GIMAP 2	9.137	9.127	8.794	7.948	9.093	9.673	10.09	9.763	10.696	9.891	6.523	8.292
238544 _at	Insulin-like growth factor 1 receptor	IGF1R	7.023	6.644	6.255	4.359	6.899	5.442	6.574	4.359	5.264	3.677	9.187	5.442
242886 _at	Chromosome 17 open reading frame	C17orf 63	9.338	10.004	7.65	7.978	8.744	5.974	8.959	9.284	6.208	7.589	9.344	7.332

	63																			
242986 at	Neuron navigator 1	NAV1	8.777	8.689	8.154	6.863	8.461	5.136	8.727	8.749	4.83	5.92	8.296							6.751
34210 at	CD52 antigen (CAMPATH- 1 antigen)	CD52	9.102	9.324	10.652	10.24	10.103	7.423	9.382	9.344	11.944	10.812	2.854							9.441

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39					

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SUBSTITUTE SHEET (RULE 26)

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[577]	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103
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[721]	6.430333e-02	-7.649410e-01	9.157078e-01	3.640731e-01	-1.306945e-02
[726]	9.203552e-02	-6.416202e-01	-6.434372e-01	-7.309035e-01	6.760630e-01
[731]	5.793554e-01	3.266417e-01	-5.467879e-01	1.875603e-02	6.823768e-01
[736]	6.605321e-01	-2.192790e-01	6.458484e-01	1.256230e-01	-3.446176e-01
[741]	-7.349580e-01	-3.794139e-01	-5.742886e-01	-7.069700e-01	2.605697e-01
[746]	-2.759157e+00	-3.153237e-01	6.614816e-01	-1.399808e+00	2.537040e-01
[751]	-2.566458e-01	-9.300803e-01	-3.258002e-01	1.847266e+00	-8.318504e-01
[756]	8.032399e-01	-7.391342e-02	-1.458280e-01	1.475066e-01	-2.016509e-01
[761]	-1.116992e+00	2.565951e-01	-1.417568e+00	-4.075312e-01	-4.624426e-01
[766]	-3.892320e-01	9.233114e-02	8.039994e-01	1.708351e-01	3.140843e-01
[771]	1.558756e-01	4.926293e-01	-1.257969e+00	-7.845624e-01	1.556651e-01
[776]	-1.152795e+00	-1.463677e+00	-8.108185e-01	-8.317870e-02	-1.456545e-01
[781]	6.954507e-01	-8.047871e-01	-8.898140e-01	-1.254371e+00	-6.563698e-01
[786]	3.967049e-01	9.335104e-01	1.299258e-02	-2.453240e-01	-5.841076e-01
[791]	-1.658272e-01	-1.326827e+00	8.844022e-01	-6.606743e-01	4.137678e-01
[796]	7.360620e-02	-1.241175e+00	1.066117e+00	-1.086576e-01	7.812635e-01
[801]	-5.793264e-01	3.664636e-02	5.461605e-01	-1.468411e-01	-1.200992e+00
[806]	7.664790e-02	-9.648972e-01	8.464096e-02	8.781079e-01	-1.329100e-01
[811]	-3.140853e-01	-3.603208e-01	5.330240e-01	9.776989e-01	1.754023e-01
[816]	-3.932540e-02	1.381857e+00	4.967358e-01	2.445305e-01	2.033007e-02
[821]	-1.660898e+00	-3.826148e-01	-1.350548e-01	2.055229e-01	-4.826541e-01
[826]	-3.437897e-02	-1.131522e+00	-2.924096e-01	1.078663e+00	-3.618922e-01
[831]	-3.795694e-01	7.062471e-01	1.818627e-01	3.360420e-02	-5.509515e-01
[836]	2.820342e-01	-5.169129e-01	-7.298595e-01	6.831575e-02	-4.718518e-01
[841]	-1.177961e-01	3.261549e-01	9.243626e-01	-9.539287e-01	-8.574709e-01
[846]	8.404623e-01	-1.477904e+00	7.161732e-01	-7.213226e-02	-1.072695e+00
[851]	1.099245e+00	3.907082e-02	4.707593e-01	-1.037259e+00	-6.337726e-01
[856]	-6.489972e-01	-8.105587e-01	-1.132535e-01	5.618367e-01	1.120736e+00

[861]	-1.589420e-01	-4.736779e-01	-3.492589e-01	-5.292510e-01	7.552729e-02
[866]	6.245302e-01	-1.599877e+00	1.961020e+00	-5.986310e-01	7.907619e-01
[871]	9.258619e-01	4.602164e-01	-4.456243e-01	2.256970e-01	1.180578e+00
[876]	-2.202471e-01	-1.595068e+00	-7.650998e-01	1.068712e-01	3.886734e-03
[881]	3.158598e-02	-7.733971e-01	1.905452e-01	-6.009153e-01	2.211837e-01
[886]	-5.134809e-02	-8.393086e-01	-1.087550e+00	-3.173469e-01	-1.101492e+00
[891]	4.972408e-01	1.799967e-01	-2.447001e-01	-8.741257e-01	2.992654e-01
[896]	-9.245988e-01	9.044085e-02	9.133224e-01	7.446155e-01	-7.193918e-01
[901]	9.205514e-02	-1.402019e+00	4.976776e-01	-6.959568e-01	4.945441e-01
[906]	1.286614e-01	-8.543565e-01	-3.603456e-02	4.664471e-01	-7.580873e-03
[911]	-3.060679e-01	-6.700308e-01	4.941296e-04	-8.978372e-01	-6.954622e-01
[916]	-3.736479e-01	1.754756e-02	1.567201e+00	8.573695e-01	3.966870e-01
[921]	-2.215584e-02	-1.169949e-01	4.257213e-01	-2.346597e-01	7.421774e-01
[926]	-5.966420e-01	5.751260e-02	-2.472787e-01	2.334021e-01	1.300946e+00
[931]	2.341594e-01	1.049020e+00	-3.269379e-01	-1.269805e-01	-6.880527e-01
[936]	-3.229197e-01	7.076868e-01	-3.403887e-01	1.676770e-01	-7.620830e-02
[941]	3.558033e-01	1.459493e-01	-6.244181e-01	1.770295e-01	-1.216517e-01
[946]	7.426668e-01	-1.385593e-01	-6.277839e-01	-1.879113e-01	9.488544e-02
[951]	2.351063e-01	1.073347e+00	-4.874189e-01	3.801474e-01	-6.690750e-01
[956]	-6.047573e-01	-3.134005e-01	-6.000130e-01	-3.197655e-01	6.631834e-01
[961]	-6.356578e-01	-5.904780e-01	1.097918e+00	6.007569e-01	-2.505695e+00
[966]	-5.697962e-01	5.674896e-01	4.245279e-01	-1.060281e-01	-1.130024e-01
[971]	1.595858e+00	1.516974e-01	-3.702457e-02	-1.700967e-01	-3.641777e-01
[976]	-1.604025e-01	-1.447675e+00	-1.008405e+00	3.365701e-01	2.348416e-01
[981]	-1.189562e+01	2.427842e+01	-2.275821e+01		

\$fitted.values
[,1]

1	9.999958e-01	17	4.189989e-06
2	0.000000e+00	18	-6.820198e-06
3	0.000000e+00	19	-6.825022e-06
4	0.000000e+00	20	-3.118923e-05
5	0.000000e+00	21	0.000000e+00
6	9.999958e-01	22	0.000000e+00
7	9.999958e-01	23	4.189989e-06
8	9.999958e-01	24	0.000000e+00
9	9.999958e-01	25	0.000000e+00
10	9.999958e-01	26	4.189989e-06
11	9.999958e-01	27	0.000000e+00
12	0.000000e+00	28	4.189989e-06
13	9.999958e-01	29	4.189989e-06
14	0.000000e+00	30	0.000000e+00
15	0.000000e+00	31	0.000000e+00
16	0.000000e+00		
17	9.999958e-01		\$lev
18	6.820198e-06		[1] "NR" "R"
19	6.825022e-06		
20	3.118923e-05		
21	0.000000e+00		\$call
22	0.000000e+00		nnet.formula(formula = f ~ .,
23	9.999958e-01		data = data, MaxNWts = 10000,
24	0.000000e+00		maxit = 250,
25	0.000000e+00		size = 2, skip = FALSE,
26	9.999958e-01		rang = 0.7, decay = 0, Hess =
27	0.000000e+00		FALSE,
28	9.999958e-01		trace = TRUE, abstol = 1e-
29	9.999958e-01		04, reltol = 1e-08, metric =
30	0.000000e+00		"euclidean",
31	0.000000e+00		subset = training)
	\$residuals		
	[,1]		
1	4.189989e-06		
2	0.000000e+00		
3	0.000000e+00		
4	0.000000e+00		
5	0.000000e+00		
6	4.189989e-06		
7	4.189989e-06		
8	4.189989e-06		
9	4.189989e-06		
10	4.189989e-06		
11	4.189989e-06		
12	0.000000e+00		
13	4.189989e-06		
14	0.000000e+00		
15	0.000000e+00		
16	0.000000e+00		

Appendix B: R object of class lda for linear discriminant analysis clinical outcome prediction of patients.

\$prior

NR R
0.5862069 0.4137931

\$counts

NR R

17 12

\$scaling

LD1

X1405_i_at	5.944209e-03
X1552497_a_at	-1.489159e-03
X1552612_at	1.928010e-03
X1552613_s_at	-3.948620e-03
X1553102_a_at	2.035336e-02
X1553132_a_at	-1.048751e-02
X1553313_s_at	-3.034153e-02
X1553906_s_at	-1.834813e-02
X1554240_a_at	1.365655e-02
X1554966_a_at	3.759930e-03
X1555229_a_at	8.797787e-02
X1555630_a_at	-2.791031e-02
X1555756_a_at	1.654466e-02
X1555759_a_at	1.036814e-03
X1555812_a_at	1.278876e-02
X1555852_at	-3.512472e-03
X1556185_a_at	3.025315e-02
X1556579_s_at	4.497852e-02
X1557116_at	4.611121e-03
X1557222_at	2.410949e-02
X1558034_s_at	2.790575e-02
X1558290_a_at	-1.523617e-02
X1558586_at	-4.151460e-02
X1558972_s_at	5.561221e-04
X1559263_s_at	7.463183e-03
X1559425_at	1.864440e-03
X1559584_a_at	-5.820026e-03
X1562031_at	9.246741e-03
X1563461_at	-2.064194e-02
X1563473_at	4.011858e-03
X1565602_at	-4.884858e-02
X1568736_s_at	-2.773483e-02
X1568822_at	2.099681e-03
X1569942_at	6.739294e-03
X200612_s_at	-6.365853e-02
X200904_at	6.387716e-03
X200905_x_at	5.294827e-03
X200953_s_at	-8.671791e-03
X201010_s_at	4.474642e-03

COLUMN 2

X213007_at	-3.352605e-02
X213008_at	-4.189798e-03
X213068_at	2.658290e-02
X213095_x_at	1.421934e-02
X213193_x_at	2.914348e-03
X213475_s_at	-4.914118e-04
X213537_at	-8.357035e-03
X213539_at	7.487953e-03
X213560_at	-4.020759e-03
X213566_at	5.845149e-03
X213603_s_at	-5.088264e-03
X213618_at	1.305106e-02
X213652_at	8.548287e-03
X213819_s_at	8.196495e-03
X213831_at	1.631173e-02
X213888_s_at	8.134177e-05
X213975_s_at	-2.095655e-02
X214023_x_at	-2.237865e-02
X214038_at	2.389479e-02
X214181_x_at	-8.976012e-03
X214450_at	1.788553e-02
X214470_at	2.213217e-02
X214617_at	1.563590e-02
X214669_x_at	1.972879e-03
X214677_x_at	3.809399e-03
X214719_at	1.439531e-03
X215051_x_at	1.072135e-02
X215121_x_at	4.118073e-03
X215193_x_at	2.105556e-04
X215223_s_at	1.530709e-02
X215379_x_at	7.064224e-03
X215561_s_at	-2.385977e-02
X215806_x_at	1.767858e-02
X216155_at	-3.705145e-02
X216191_s_at	4.747897e-02
X216194_s_at	-4.006836e-02
X216714_at	2.405266e-02
X216841_s_at	8.716417e-03
X216920_s_at	3.911396e-03
X217028_at	5.128469e-03
X217138_x_at	9.357220e-03

X201137_s_at	-1.506315e-02	X217143_s_at	7.546655e-03
X201220_x_at	-2.667959e-02	X217147_s_at	-1.958024e-02
X201236_s_at	1.404961e-02	X217478_s_at	-1.327997e-02
X201425_at	1.554231e-02	X217525_at	-1.717356e-02
X201474_s_at	-6.107372e-03	X217629_at	7.854937e-03
X201487_at	2.472156e-02	X217767_at	-5.238491e-03
X201497_x_at	7.254710e-04	X217995_at	-6.809023e-03
X201502_s_at	5.696526e-03	X218002_s_at	9.869321e-03
X201531_at	1.148431e-02	X218035_s_at	1.245016e-03
X201566_x_at	1.794849e-02	X218145_at	-3.291834e-02
X201720_s_at	1.570380e-03	X218170_at	-7.323517e-03
X201721_s_at	-9.613928e-03	X218322_s_at	-8.250237e-03
X201804_x_at	-2.053567e-02	X218499_at	5.140903e-04
X201859_at	-1.376084e-04	X218736_s_at	2.138520e-02
X201939_at	-3.369784e-02	X218739_at	2.714745e-03
X202207_at	-1.196899e-02	X218764_at	-9.158772e-03
X202255_s_at	-4.340999e-02	X218802_at	5.152377e-02
X202269_x_at	-1.833048e-02	X218805_at	-2.574003e-03
X202270_at	-8.686638e-03	X218854_at	3.989147e-03
X202368_s_at	-2.233262e-02	X218899_s_at	-3.411423e-02
X202369_s_at	-1.278489e-02	X218950_at	-4.336176e-02
X202391_at	-5.586253e-03	X219054_at	4.975575e-03
X202510_s_at	1.200980e-02	X219093_at	2.082412e-02
X202625_at	1.449689e-02	X219213_at	-4.341432e-03
X202643_s_at	2.057522e-02	X219243_at	2.233332e-03
X202644_s_at	2.044322e-02	X219368_at	-1.134073e-03
X202687_s_at	1.939420e-03	X219440_at	2.580567e-02
X202688_at	8.690145e-04	X219454_at	3.065280e-02
X202948_at	-1.822099e-02	X219505_at	5.933108e-03
X202957_at	-1.143226e-02	X219519_s_at	2.660637e-02
X203413_at	-3.803468e-02	X219525_at	4.320312e-03
X203416_at	-1.189864e-02	X219528_s_at	1.066797e-02
X203471_s_at	1.553784e-02	X219631_at	-2.616546e-02
X203508_at	9.486448e-03	X219666_at	1.182519e-02
X203523_at	5.575011e-03	X219681_s_at	8.705075e-03
X203547_at	9.218142e-03	X219710_at	-1.046131e-02
X203665_at	3.487226e-02	X219737_s_at	-6.473357e-02
X203741_s_at	2.161880e-02	X219777_at	-6.023843e-03
X203761_at	8.568780e-03	X219789_at	8.550214e-03
X203812_at	4.104549e-02	X219926_at	-8.456673e-03
X203868_s_at	-3.218808e-02	X219938_s_at	1.596546e-02
X203915_at	1.356669e-02	X220005_at	6.859902e-03
X203932_at	-1.767768e-03	X220066_at	7.525339e-03
X204057_at	1.199848e-02	X220330_s_at	3.751801e-03
X204070_at	-8.013273e-04	X220485_s_at	2.962480e-03
X204116_at	6.190984e-03	X221081_s_at	-4.394394e-03
X204118_at	1.625516e-02	X221087_s_at	8.161216e-03
X204135_at	4.612466e-03	X221477_s_at	1.240372e-02
X204204_at	3.177067e-02	X221651_x_at	1.118009e-02
X204220_at	-6.573462e-03	X221671_x_at	5.247343e-03
X204222_s_at	8.871953e-03	X221698_s_at	-1.058842e-02
X204224_s_at	-4.997460e-03	X221756_at	-1.209965e-02

X204233_s_at	-1.586361e-02	X221760_at	-1.764419e-02
X204236_at	5.467904e-03	X222108_at	4.026916e-02
X204249_s_at	-1.313280e-02	X222142_at	-3.508958e-02
X204411_at	6.579659e-03	X222484_s_at	-8.096999e-03
X204438_at	2.031749e-02	X222496_s_at	-4.133924e-03
X204502_at	6.392044e-03	X222592_s_at	1.511240e-02
X204512_at	-1.534429e-05	X222725_s_at	2.808005e-02
X204533_at	2.287973e-02	X222780_s_at	-2.679162e-02
X204613_at	5.458783e-03	X222838_at	4.550716e-03
X204628_s_at	-3.028829e-02	X222895_s_at	-2.841100e-02
X204642_at	-3.867430e-03	X223044_at	5.255602e-02
X204655_at	-5.765680e-03	X223058_at	9.381819e-03
X204661_at	2.636612e-02	X223059_s_at	8.539393e-03
X204670_x_at	-1.182992e-02	X223168_at	-4.973917e-03
X204687_at	3.953856e-02	X223235_s_at	4.953002e-04
X204724_s_at	-1.982230e-02	X223280_x_at	6.016285e-03
X204774_at	-1.596679e-02	X223322_at	-1.188607e-02
X204778_x_at	-2.436425e-02	X223361_at	-5.418802e-03
X204834_at	4.664052e-02	X223395_at	1.411881e-02
X204846_at	2.224653e-02	X223484_at	1.743558e-02
X204894_s_at	4.442071e-03	X223809_at	2.119400e-02
X204897_at	-2.250415e-02	X223827_at	-1.852331e-02
X204912_at	2.155492e-03	X223922_x_at	8.293530e-03
X204923_at	-9.860185e-03	X223924_at	-2.212120e-02
X205027_s_at	3.406286e-03	X223952_x_at	3.606709e-02
X205039_s_at	1.453129e-03	X224356_x_at	4.977366e-03
X205081_at	2.008363e-02	X224358_s_at	-9.225797e-04
X205159_at	4.374158e-03	X224451_x_at	-4.781080e-03
X205225_at	-8.687131e-03	X224516_s_at	-1.494258e-02
X205226_at	-4.151219e-02	X224710_at	-2.279989e-02
X205251_at	2.071759e-02	X224771_at	-1.243246e-02
X205285_s_at	9.469306e-03	X224772_at	-4.059490e-02
X205392_s_at	1.236199e-02	X224773_at	-7.626004e-03
X205403_at	1.344662e-02	X224774_s_at	-1.743111e-02
X205419_at	-6.256056e-03	X224795_x_at	5.385788e-03
X205421_at	1.955389e-02	X224859_at	-1.540871e-02
X205440_s_at	2.903482e-02	X224896_s_at	-4.228341e-03
X205484_at	-1.026029e-02	X225502_at	3.460051e-03
X205488_at	2.109358e-02	X225802_at	-2.887415e-02
X205559_s_at	-2.837597e-02	X225895_at	4.741893e-03
X205569_at	1.407987e-02	X226043_at	1.277772e-02
X205624_at	2.531892e-02	X226068_at	5.224876e-03
X205685_at	4.266186e-02	X226117_at	2.490399e-02
X205696_s_at	-7.143024e-03	X226218_at	-1.341873e-02
X205758_at	9.290501e-03	X226219_at	4.175131e-03
X205786_s_at	-7.188176e-03	X226303_at	4.358878e-02
X205831_at	8.970703e-03	X226382_at	6.264514e-04
X205841_at	-1.024458e-02	X226459_at	4.497883e-03
X205844_at	2.406034e-02	X226625_at	4.213244e-02
X205890_s_at	1.526584e-02	X226659_at	-4.064464e-03
X205987_at	5.099598e-03	X226697_at	-5.986636e-02
X206082_at	-2.365415e-02	X226818_at	2.581249e-02

X206099_at	4.205302e-02	X226841_at	1.092228e-02
X206118_at	1.153657e-02	X226865_at	-2.335927e-02
X206134_at	-4.474477e-03	X227035_x_at	8.655280e-03
X206170_at	-1.785743e-02	X227231_at	-1.692593e-02
X206204_at	1.969866e-02	X227253_at	1.018350e-02
X206295_at	1.528790e-02	X227265_at	1.360205e-02
X206385_s_at	-1.655446e-02	X227346_at	-1.295157e-02
X206407_s_at	3.592881e-02	X227361_at	-5.811243e-03
X206545_at	1.272019e-02	X227458_at	1.893847e-02
X206571_s_at	-3.009919e-02	X227584_at	-2.425646e-02
X206637_at	7.423640e-03	X227609_at	3.029790e-02
X206666_at	1.204182e-02	X227640_s_at	-5.262288e-03
X206687_s_at	-1.762981e-02	X227780_s_at	1.333635e-02
X206715_at	1.116688e-02	X227791_at	1.583168e-02
X206804_at	1.234660e-02	X227983_at	-1.027572e-02
X206898_at	-3.907050e-02	X227995_at	-1.414606e-02
X206978_at	-4.979548e-03	X228054_at	-1.428632e-03
X207076_s_at	1.863378e-02	X228071_at	-8.103128e-03
X207238_s_at	-5.780355e-03	X228094_at	9.305227e-03
X207277_at	2.125419e-02	X228153_at	1.840560e-02
X207458_at	2.748393e-02	X228339_at	1.115556e-02
X207540_s_at	-1.283397e-02	X228362_s_at	1.505306e-02
X207574_s_at	-2.431727e-03	X228372_at	-1.233323e-02
X207651_at	2.066787e-02	X228376_at	3.005129e-03
X207655_s_at	5.405012e-04	X228427_at	1.441232e-02
X207677_s_at	2.230816e-02	X228532_at	-1.984789e-02
X207843_x_at	3.315503e-02	X228552_s_at	1.488213e-02
X207861_at	4.377097e-02	X228563_at	5.478160e-03
X207977_s_at	1.145723e-02	X228660_x_at	-3.321971e-03
X207992_s_at	6.265461e-03	X228776_at	1.735059e-02
X208296_x_at	-2.224775e-03	X228812_at	2.966052e-02
X208306_x_at	-5.132684e-03	X228858_at	8.798795e-03
X208335_s_at	3.329359e-03	X228869_at	1.576960e-02
X208450_at	3.811124e-02	X228908_s_at	1.715903e-02
X208747_s_at	-7.912263e-03	X228964_at	1.578864e-02
X208885_at	-1.288364e-02	X229127_at	2.437139e-02
X208894_at	7.896947e-03	X229163_at	-1.306446e-03
X208981_at	-1.015968e-02	X229367_s_at	8.285081e-03
X208983_s_at	-3.056594e-02	X229390_at	9.455414e-03
X209083_at	4.483265e-04	X229391_s_at	2.152998e-02
X209138_x_at	7.183442e-03	X229543_at	1.337527e-02
X209193_at	1.740572e-02	X229625_at	1.390034e-02
X209195_s_at	-2.237887e-02	X229723_at	1.284379e-02
X209202_s_at	8.930806e-03	X230233_at	6.517225e-03
X209312_x_at	-5.814581e-03	X230391_at	-1.165179e-02
X209480_at	1.848455e-02	X230538_at	-4.922326e-02
X209542_x_at	4.971766e-03	X230728_at	-3.921071e-02
X209603_at	3.004576e-02	X231032_at	1.220460e-02
X209606_at	5.064024e-03	X231262_at	8.401904e-03
X209612_s_at	2.595736e-02	X231577_s_at	-4.352510e-03
X209613_s_at	1.417618e-02	X231882_at	-1.597680e-02
X209670_at	-1.636542e-02	X231929_at	-7.190517e-03

X209671_x_at	2.518135e-03	X232001_at	-2.527809e-02
X209685_s_at	-9.113030e-03	X232024_at	1.562502e-02
X209687_at	-1.842487e-02	X232234_at	1.979601e-02
X209710_at	5.230642e-03	X232311_at	-5.811767e-04
X209734_at	-5.196811e-03	X232313_at	3.438576e-02
X209774_x_at	2.951233e-02	X232476_at	-1.156007e-02
X209795_at	-6.624457e-03	X232543_x_at	-6.890048e-03
X209813_x_at	2.371992e-02	X232617_at	2.120826e-03
X209899_s_at	7.998200e-04	X232746_at	-1.032038e-02
X209924_at	3.375216e-02	X232843_s_at	-1.582714e-03
X209949_at	3.781916e-02	X233123_at	3.841746e-02
X209970_x_at	2.564418e-02	X233562_at	-6.149035e-02
X210038_at	6.929319e-03	X233955_x_at	-2.411061e-02
X210072_at	1.293525e-02	X235175_at	-8.822903e-03
X210251_s_at	1.756383e-02	X235238_at	-4.455537e-02
X210260_s_at	-1.082042e-03	X235306_at	-1.163963e-02
X210319_x_at	-1.726655e-02	X235391_at	9.692727e-03
X210375_at	2.483769e-03	X235421_at	-7.303012e-04
X210554_s_at	-2.077789e-02	X235639_at	-3.367098e-02
X210835_s_at	-7.455480e-03	X235688_s_at	-1.717805e-03
X210915_x_at	3.172003e-03	X235804_at	-1.564079e-03
X210972_x_at	6.080266e-03	X235831_at	2.675921e-03
X210982_s_at	9.635875e-03	X236203_at	-8.187551e-03
X211066_x_at	-1.164103e-02	X236280_at	6.197497e-03
X211144_x_at	4.992137e-02	X236295_s_at	4.606321e-03
X211200_s_at	-4.031722e-02	X236583_at	2.311931e-03
X211339_s_at	-8.002311e-03	X236908_at	-2.109408e-02
X211366_x_at	3.593000e-02	X238439_at	3.286334e-02
X211367_s_at	6.231728e-02	X238488_at	2.932061e-02
X211368_s_at	2.045696e-02	X238544_at	1.183049e-03
X211654_x_at	2.874123e-02	X239196_at	4.987304e-02
X211742_s_at	-1.282275e-02	X239237_at	3.319884e-02
X211796_s_at	6.744624e-03	X239744_at	-1.276710e-02
X211902_x_at	1.350420e-03	X241671_x_at	-6.586756e-03
X211990_at	-1.552756e-02	X241701_at	-8.761918e-03
X211991_s_at	-2.759634e-03	X242458_at	-1.194306e-02
X212067_s_at	-9.461685e-03	X242546_at	4.355118e-03
X212233_at	8.400376e-03	X242874_at	5.607680e-03
X212538_at	7.226797e-03	X242881_x_at	-6.062508e-03
X212587_s_at	-5.979921e-03	X242986_at	2.749620e-03
X212588_at	-7.824565e-04	X243099_at	1.186699e-02
X212592_at	3.516261e-03	X244023_at	-1.018460e-02
X212657_s_at	2.978857e-02	X244061_at	1.229564e-03
X212671_s_at	-2.602076e-02	X32128_at	2.935196e-02
X212713_at	3.233683e-02	X34210_at	3.776762e-03
X212763_at	-3.275778e-03	X38149_at	4.937711e-04
X212886_at	3.683799e-03	X64064_at	-3.336735e-03
X212977_at	9.877644e-03		
X212998_x_at	5.090511e-03		
X212999_x_at	3.695828e-02		

Continued in column 2

\$lev

```
[1] "NR" "R"
$svd
[1] 7.995862
$N
[1] 29
$call
lda(formula = f ~ ., data = datatr)
```

Appendix C: R object of class naiveBayes for naïve Bayes clinical outcome prediction of patients.

```
$apriori
Y
NR R
17 12
tablestable$X1405_i_at
X1405_i_at
Y [,1] [,2]
NR -0.1639258 0.5851902
R 0.6748740 0.6631486
tablestable$X1552497_a_at
X1552497_a_at
Y [,1] [,2]
NR -0.3029996 0.6800071
R 0.6607734 0.8223674
tablestable$X1552612_at
X1552612_at
Y [,1] [,2]
NR -0.2523340 0.5485271
R 0.4450904 0.5434438
tablestable$X1552613_s_at
X1552613_s_at
Y [,1] [,2]
NR -0.2165343 0.5894093
R 0.4800677 0.4432806
tablestable$X1553102_a_at
X1553102_a_at
Y [,1] [,2]
NR -0.2474064 0.5834113
R 0.7071397 0.7121750
tablestable$X1553132_a_at
X1553132_a_at
Y [,1] [,2]
NR -0.1377405 0.3946696
R 0.4961300 0.4509575
tablestable$X1553313_s_at
X1553313_s_at
Y [,1] [,2]
NR 0.2393526 0.6100254
R -0.3838373 0.3940848
tablestable$X1553906_s_at
X1553906_s_at
```

```
Column 2
Y [,1] [,2]
NR -0.3674984 0.5888660
R 0.3219144 0.5336377
tablestable$X213539_at
X213539_at
Y [,1] [,2]
NR -0.3813796 0.5040301
R 0.3415072 0.2577433
tablestable$X213560_at
X213560_at
Y [,1] [,2]
NR -0.5055000 0.7230271
R 0.2766383 0.2303920
tablestable$X213566_at
X213566_at
Y [,1] [,2]
NR -0.2311022 0.5691307
R 0.3719339 0.4376776
tablestable$X213603_s_at
X213603_s_at
Y [,1] [,2]
NR -0.3061774 0.6126919
R 0.3508772 0.5262723
tablestable$X213618_at
X213618_at
Y [,1] [,2]
NR -0.3695683 0.681454
R 0.4212985 0.554157
tablestable$X213652_at
X213652_at
Y [,1] [,2]
NR -0.2586966 0.4605599
R 0.3270410 0.8177604
tablestable$X213819_s_at
X213819_s_at
Y [,1] [,2]
NR 0.00122895 0.3972336
R -0.64986825 0.9085849
tablestable$X213831_at
X213831_at
```

Y [,1] [,2]
 NR -0.3915645 0.6474232
 R 0.2882052 0.3076821
 tables\$X1554240_a_at
 X1554240_a_at
 Y [,1] [,2]
 NR 0.01780307 0.4865912
 R 0.88377535 0.8029798
 tables\$X1554966_a_at
 X1554966_a_at
 Y [,1] [,2]
 NR -0.1357018 0.3678133
 R 0.6662706 0.6833596
 tables\$X1555229_a_at
 X1555229_a_at
 Y [,1] [,2]
 NR -0.2263265 0.3882668
 R 0.5467680 0.4361597
 tables\$X1555630_a_at
 X1555630_a_at
 Y [,1] [,2]
 NR 0.2005512 0.3578418
 R -0.6088957 0.7683101
 tables\$X1555756_a_at
 X1555756_a_at
 Y [,1] [,2]
 NR -0.2186897 0.5247142
 R 0.4061700 0.5187056
 tables\$X1555759_a_at
 X1555759_a_at
 Y [,1] [,2]
 NR 0.08037061 0.5249017
 R 0.85078348 0.7360755
 tables\$X1555812_a_at
 X1555812_a_at
 Y [,1] [,2]
 NR -0.4493812 0.8437685
 R 0.4087372 0.6145611
 tables\$X1555852_at
 X1555852_at
 Y [,1] [,2]
 NR -0.3431720 0.6409197
 R 0.3060830 0.4160286
 tables\$X1556185_a_at
 X1556185_a_at
 Y [,1] [,2]
 NR -0.3542416 0.4573215
 R 0.3876607 0.8113095
 tables\$X1556579_s_at
 X1556579_s_at
 Y [,1] [,2]
 NR -0.08046679 0.2880584

Y [,1] [,2]
 NR -0.3533186 0.4215363
 R 0.1563120 0.3886529
 tables\$X213888_s_at
 X213888_s_at
 Y [,1] [,2]
 NR -0.2086168 0.5349552
 R 0.4303498 0.4269851
 tables\$X213975_s_at
 X213975_s_at
 Y [,1] [,2]
 NR -0.4990363 0.6803409
 R 0.1878550 0.2710180
 tables\$X214023_x_at
 X214023_x_at
 Y [,1] [,2]
 NR 0.1848739 0.7174998
 R -0.4325008 0.4810479
 tables\$X214038_at
 X214038_at
 Y [,1] [,2]
 NR -0.3255701 0.6706608
 R 0.3599967 0.6048520
 tables\$X214181_x_at
 X214181_x_at
 Y [,1] [,2]
 NR -0.3415893 0.6522400
 R 0.2853699 0.2763122
 tables\$X214450_at
 X214450_at
 Y [,1] [,2]
 NR -0.1562932 0.2807857
 R 0.8434281 0.8613678
 tables\$X214470_at
 X214470_at
 Y [,1] [,2]
 NR -0.2839688 0.4885156
 R 0.4212807 0.3750679
 tables\$X214617_at
 X214617_at
 Y [,1] [,2]
 NR -0.3487562 0.4518071
 R 0.2125207 0.4242197
 tables\$X214669_x_at
 X214669_x_at
 Y [,1] [,2]
 NR -0.1915274 0.4981106
 R 0.3359622 0.4156267
 tables\$X214677_x_at
 X214677_x_at
 Y [,1] [,2]
 NR -0.2087490 0.4787112

R 0.58371780 0.7445854
 tables\$X1557116_at
 X1557116_at
 Y [,1] [,2]
 NR -0.4470538 0.6892889
 R 0.3267151 0.4124078
 tables\$X1557222_at
 X1557222_at
 Y [,1] [,2]
 NR -0.04818824 0.402835
 R 0.74360000 0.863980
 tables\$X1558034_s_at
 X1558034_s_at
 Y [,1] [,2]
 NR -0.2487822 0.4220782
 R 0.4252406 0.4675114
 tables\$X1558290_a_at
 X1558290_a_at
 Y [,1] [,2]
 NR 0.3179399 0.5555339
 R -0.4890204 0.4786095
 tables\$X1558586_at
 X1558586_at
 Y [,1] [,2]
 NR -0.2298781 0.4177707
 R 0.3950435 0.5416909
 tables\$X1558972_s_at
 X1558972_s_at
 Y [,1] [,2]
 NR -0.2797971 0.5418070
 R 0.4745703 0.5335784
 tables\$X1559263_s_at
 X1559263_s_at
 Y [,1] [,2]
 NR -0.3833393 0.5703645
 R 0.3494365 0.4676936
 tables\$X1559425_at
 X1559425_at
 Y [,1] [,2]
 NR -0.2287316 0.5560199
 R 0.4282525 0.4558128
 tables\$X1559584_a_at
 X1559584_a_at
 Y [,1] [,2]
 NR -0.4622881 0.5846900
 R 0.3021721 0.4028788
 tables\$X1562031_at
 X1562031_at
 Y [,1] [,2]
 NR -0.3551523 0.4862453
 R 0.1736934 0.4872335
 tables\$X1563461_at

R 0.3128333 0.3867513
 tables\$X214719_at
 X214719_at
 Y [,1] [,2]
 NR -0.4511937 0.6070570
 R 0.2711287 0.3505487
 tables\$X215051_x_at
 X215051_x_at
 Y [,1] [,2]
 NR -0.3597073 0.8514825
 R 0.4054302 0.3092948
 tables\$X215121_x_at
 X215121_x_at
 Y [,1] [,2]
 NR -0.1634545 0.4642640
 R 0.3410072 0.4014670
 tables\$X215193_x_at
 X215193_x_at
 Y [,1] [,2]
 NR -0.2667421 0.7134086
 R 0.4777644 0.4030902
 tables\$X215223_s_at
 X215223_s_at
 Y [,1] [,2]
 NR -0.3883071 0.4910665
 R 0.2565276 0.4364856
 tables\$X215379_x_at
 X215379_x_at
 Y [,1] [,2]
 NR -0.09709331 0.4452099
 R 0.39542823 0.4092484
 tables\$X215561_s_at
 X215561_s_at
 Y [,1] [,2]
 NR -0.2711632 0.4077480
 R 0.7072055 0.9320206
 tables\$X215806_x_at
 X215806_x_at
 Y [,1] [,2]
 NR -0.007773052 0.3665788
 R 0.661454102 0.4785205
 tables\$X216155_at
 X216155_at
 Y [,1] [,2]
 NR 0.5119447 0.6151164
 R -0.1726881 0.3347342
 tables\$X216191_s_at
 X216191_s_at
 Y [,1] [,2]
 NR -0.01479148 0.4433394
 R 0.67109688 0.5079869
 tables\$X216194_s_at

X1563461_at
 Y [,1] [,2]
 NR 0.3566529 0.5512415
 R -0.2706966 0.6822506
 tables\$X1563473_at
 X1563473_at
 Y [,1] [,2]
 NR -0.4074615 0.5896901
 R 0.2254661 0.4096997
 tables\$X1565602_at
 X1565602_at
 Y [,1] [,2]
 NR 0.4490349 0.6371381
 R -0.1986003 0.5670284
 tables\$X1568736_s_at
 X1568736_s_at
 Y [,1] [,2]
 NR 0.6111740 0.9655418
 R -0.1669456 0.3464934
 tables\$X1568822_at
 X1568822_at
 Y [,1] [,2]
 NR 0.4611639 0.6061123
 R -0.1089934 0.3960131
 tables\$X1569942_at
 X1569942_at
 Y [,1] [,2]
 NR 0.4441859 0.7007245
 R -0.2886340 0.3295043
 tables\$X200612_s_at
 X200612_s_at
 Y [,1] [,2]
 NR 0.2054340 0.4467337
 R -0.4553481 0.5048914
 tables\$X200904_at
 X200904_at
 Y [,1] [,2]
 NR -0.2660950 0.4738856
 R 0.3014091 0.4032104
 tables\$X200905_x_at
 X200905_x_at
 Y [,1] [,2]
 NR -0.1327891 0.5236164
 R 0.4735567 0.3948498
 tables\$X200953_s_at
 X200953_s_at
 Y [,1] [,2]
 NR -0.2814847 0.8261769
 R 0.5757425 0.6362976
 tables\$X201010_s_at
 X201010_s_at
 Y [,1] [,2]

X216194_s_at
 Y [,1] [,2]
 NR 0.1641682 0.3935104
 R -0.3667475 0.4613841
 tables\$X216714_at
 X216714_at
 Y [,1] [,2]
 NR -0.1657215 0.6600958
 R 0.5669961 0.9931878
 tables\$X216841_s_at
 X216841_s_at
 Y [,1] [,2]
 NR -0.2378813 0.7063683
 R 0.5838156 0.5499012
 tables\$X216920_s_at
 X216920_s_at
 Y [,1] [,2]
 NR -0.3626922 0.5129860
 R 0.4424685 0.4026252
 tables\$X217028_at
 X217028_at
 Y [,1] [,2]
 NR -0.3936253 0.7242766
 R 0.2813510 0.3842826
 tables\$X217138_x_at
 X217138_x_at
 Y [,1] [,2]
 NR 0.06341764 0.4690319
 R 0.61978484 0.5049407
 tables\$X217143_s_at
 X217143_s_at
 Y [,1] [,2]
 NR -0.1709594 0.6329777
 R 0.6395395 0.5675738
 tables\$X217147_s_at
 X217147_s_at
 Y [,1] [,2]
 NR -0.1919006 0.3907915
 R 0.4594408 0.3635919
 tables\$X217478_s_at
 X217478_s_at
 Y [,1] [,2]
 NR -0.3453566 0.7688595
 R 0.5037971 0.4475461
 tables\$X217525_at
 X217525_at
 Y [,1] [,2]
 NR -0.2639411 0.8866455
 R 0.6075298 0.5960824
 tables\$X217629_at
 X217629_at
 Y [,1] [,2]

NR -0.3613038 0.7929993
 R 0.4944130 0.2677128
 tables\$X201137_s_at
 X201137_s_at
 Y [,1] [,2]
 NR -0.3646008 0.7012958
 R 0.3957589 0.4949475
 tables\$X201220_x_at
 X201220_x_at
 Y [,1] [,2]
 NR 0.08672472 0.5177988
 R -0.48143253 0.5513205
 tables\$X201236_s_at
 X201236_s_at
 Y [,1] [,2]
 NR -0.1198028 0.5613972
 R 0.5331348 0.5322952
 tables\$X201425_at
 X201425_at
 Y [,1] [,2]
 NR -0.5116596 0.7193710
 R 0.4964073 0.5304284
 tables\$X201474_s_at
 X201474_s_at
 Y [,1] [,2]
 NR 0.6028068 0.6299064
 R -0.2457276 0.3007111
 tables\$X201487_at
 X201487_at
 Y [,1] [,2]
 NR -0.4225210 0.8252371
 R 0.3171429 0.4591150
 tables\$X201497_x_at
 X201497_x_at
 Y [,1] [,2]
 NR -0.3200855 0.4908815
 R 2.5010094 2.6712499
 tables\$X201502_s_at
 X201502_s_at
 Y [,1] [,2]
 NR -0.3308824 0.4722939
 R 0.5454167 0.3159327
 tables\$X201531_at
 X201531_at
 Y [,1] [,2]
 NR -0.1938551 0.3744374
 R 0.5269050 0.5074891
 tables\$X201566_x_at
 X201566_x_at
 Y [,1] [,2]
 NR -0.2981010 0.6780610
 R 0.3509438 0.5014504

NR -0.1348654 0.671148
 R 0.8011176 1.134701
 tables\$X217767_at
 X217767_at
 Y [,1] [,2]
 NR -0.4316702 0.6383017
 R 0.3296425 0.3962954
 tables\$X217995_at
 X217995_at
 Y [,1] [,2]
 NR -0.6500190 1.0622844
 R 0.3656452 0.3596701
 tables\$X218002_s_at
 X218002_s_at
 Y [,1] [,2]
 NR -0.2371548 0.4549764
 R 0.3590465 0.5928193
 tables\$X218035_s_at
 X218035_s_at
 Y [,1] [,2]
 NR -0.3792486 0.6876336
 R 0.3685478 0.4296116
 tables\$X218145_at
 X218145_at
 Y [,1] [,2]
 NR 0.5407030 0.7961511
 R -0.5330237 0.7914334
 tables\$X218170_at
 X218170_at
 Y [,1] [,2]
 NR -0.2778944 0.5053423
 R 0.5047588 0.6555875
 tables\$X218322_s_at
 X218322_s_at
 Y [,1] [,2]
 NR -0.4368137 0.5136086
 R 0.3249243 0.2575257
 tables\$X218499_at
 X218499_at
 Y [,1] [,2]
 NR -0.2574311 0.6676495
 R 0.4022312 0.4066238
 tables\$X218736_s_at
 X218736_s_at
 Y [,1] [,2]
 NR -0.03615144 0.4561428
 R 1.08677338 1.1597104
 tables\$X218739_at
 X218739_at
 Y [,1] [,2]
 NR -0.02247695 0.4787563
 R 0.98329866 1.2407971

```

tables$X201720_s_at
  X201720_s_at
Y      [,1]      [,2]
NR -0.1977420 0.6818082
R   0.5749931 0.7157990
tables$X201721_s_at
  X201721_s_at
Y      [,1]      [,2]
NR -0.1677046 0.5133205
R   0.4231327 0.5084300
tables$X201804_x_at
  X201804_x_at
Y      [,1]      [,2]
NR  0.1992091 0.4851767
R  -0.4765795 0.5915133
tables$X201859_at
  X201859_at
Y      [,1]      [,2]
NR -0.4216528 0.7283696
R   0.2486708 0.3163434
tables$X201939_at
  X201939_at
Y      [,1]      [,2]
NR  0.2953508 0.5226393
R  -0.3592031 0.5614863
tables$X202207_at
  X202207_at
Y      [,1]      [,2]
NR -0.4088858 0.6063797
R   0.2159392 0.2923256
tables$X202255_s_at
  X202255_s_at
Y      [,1]      [,2]
NR -0.5135289 0.8447912
R   0.3161547 0.6241535
tables$X202269_x_at
  X202269_x_at
Y      [,1]      [,2]
NR -0.4070967 0.6699657
R   0.3070278 0.3134680
tables$X202270_at
  X202270_at
Y      [,1]      [,2]
NR -0.3598381 0.7402801
R   0.4664866 0.4311290
tables$X202368_s_at
  X202368_s_at
Y      [,1]      [,2]
NR  0.4828523 0.6622996
R  -0.3498387 0.7337426
tables$X202369_s_at
  X202369_s_at

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```

tables$X218764_at
  X218764_at
Y      [,1]      [,2]
NR -0.4099779 0.4830029
R   0.3567869 0.4038910
tables$X218802_at
  X218802_at
Y      [,1]      [,2]
NR -0.3430126 0.4453773
R   0.5970457 0.3951568
tables$X218805_at
  X218805_at
Y      [,1]      [,2]
NR -0.3671355 0.5708859
R   0.4517210 0.2930704
tables$X218854_at
  X218854_at
Y      [,1]      [,2]
NR -0.3745559 0.7096822
R   0.4739352 0.5603528
tables$X218899_s_at
  X218899_s_at
Y      [,1]      [,2]
NR  0.3671446 0.5909345
R  -0.5393210 0.4381099
tables$X218950_at
  X218950_at
Y      [,1]      [,2]
NR  0.2691863 0.4573251
R  -0.6111111 0.6474936
tables$X219054_at
  X219054_at
Y      [,1]      [,2]
NR  0.01472793 0.584855
R   2.49050475 2.683467
tables$X219093_at
  X219093_at
Y      [,1]      [,2]
NR -0.2971580 0.4688604
R   0.5384298 0.6366817
tables$X219213_at
  X219213_at
Y      [,1]      [,2]
NR -0.1731958 0.4047427
R   0.6423430 0.7730134
tables$X219243_at
  X219243_at
Y      [,1]      [,2]
NR -0.5195758 0.7578959
R   0.4000750 0.3801539
tables$X219368_at
  X219368_at

```

Y [,1] [,2]
 NR 0.3894707 0.7051767
 R -0.4762401 0.5968765
 tables\$X202391_at
 X202391_at
 Y [,1] [,2]
 NR -0.5342313 1.0124766
 R 0.5933123 0.6491928
 tables\$X202510_s_at
 X202510_s_at
 Y [,1] [,2]
 NR -0.6015966 0.9255712
 R 0.4919973 0.6463912
 tables\$X202625_at
 X202625_at
 Y [,1] [,2]
 NR -0.2142036 0.7804199
 R 0.6620458 0.7148131
 tables\$X202643_s_at
 X202643_s_at
 Y [,1] [,2]
 NR -0.4832904 0.5361050
 R 0.3792320 0.4385239
 tables\$X202644_s_at
 X202644_s_at
 Y [,1] [,2]
 NR -0.3513719 0.5742499
 R 0.4307245 0.3838438
 tables\$X202687_s_at
 X202687_s_at
 Y [,1] [,2]
 NR -0.4279648 0.7540136
 R 0.3504315 0.4045005
 tables\$X202688_at
 X202688_at
 Y [,1] [,2]
 NR -0.4163941 0.8163225
 R 0.4027076 0.4386812
 tables\$X202948_at
 X202948_at
 Y [,1] [,2]
 NR -0.5154460 0.7699102
 R 0.4056092 0.4764355
 tables\$X202957_at
 X202957_at
 Y [,1] [,2]
 NR -0.3735948 0.5616205
 R 0.4472934 0.5131898
 tables\$X203413_at
 X203413_at
 Y [,1] [,2]
 NR -0.3383329 0.5941084

Y [,1] [,2]
 NR -0.1679820 0.3075502
 R 0.6324772 0.6637538
 tables\$X219440_at
 X219440_at
 Y [,1] [,2]
 NR 0.08196161 0.2856868
 R 0.87878388 0.7545222
 tables\$X219454_at
 X219454_at
 Y [,1] [,2]
 NR -0.1553019 0.3324367
 R 0.6028235 0.7768835
 tables\$X219505_at
 X219505_at
 Y [,1] [,2]
 NR -0.335471 0.5884701
 R 0.331203 0.4762600
 tables\$X219519_s_at
 X219519_s_at
 Y [,1] [,2]
 NR -0.3029785 0.6574268
 R 0.4245899 0.6733826
 tables\$X219525_at
 X219525_at
 Y [,1] [,2]
 NR -0.4849566 0.6164310
 R 0.2295082 0.3984913
 tables\$X219528_s_at
 X219528_s_at
 Y [,1] [,2]
 NR -0.2597881 0.4319096
 R 0.4928448 0.5142826
 tables\$X219631_at
 X219631_at
 Y [,1] [,2]
 NR 0.5705786 0.6831084
 R -0.2784402 0.3830630
 tables\$X219666_at
 X219666_at
 Y [,1] [,2]
 NR -0.5430705 0.7930909
 R 0.2839697 0.3631652
 tables\$X219681_s_at
 X219681_s_at
 Y [,1] [,2]
 NR -0.417274 0.7733850
 R 0.376309 0.5736019
 tables\$X219710_at
 X219710_at
 Y [,1] [,2]
 NR 0.2636804 0.4736957

R 0.3196087 0.6292591
 tables\$X203416_at
 X203416_at
 Y [,1] [,2]
 NR -0.3141917 0.6552882
 R 0.4391612 0.4251811
 tables\$X203471_s_at
 X203471_s_at
 Y [,1] [,2]
 NR -0.2041767 0.5987281
 R 0.6153344 0.5620431
 tables\$X203508_at
 X203508_at
 Y [,1] [,2]
 NR -0.2695595 0.5179795
 R 0.2812243 0.4853358
 tables\$X203523_at
 X203523_at
 Y [,1] [,2]
 NR -0.3791594 0.8958684
 R 0.8117565 0.9246945
 tables\$X203547_at
 X203547_at
 Y [,1] [,2]
 NR -0.008562598 0.4462166
 R 0.663436693 0.5733365
 tables\$X203665_at
 X203665_at
 Y [,1] [,2]
 NR -0.2522801 0.5533137
 R 0.6428083 0.7340506
 tables\$X203741_s_at
 X203741_s_at
 Y [,1] [,2]
 NR -0.1850309 0.5721364
 R 0.6581712 0.6185694
 tables\$X203761_at
 X203761_at
 Y [,1] [,2]
 NR -0.1852189 0.5956581
 R 0.5255720 0.4369002
 tables\$X203812_at
 X203812_at
 Y [,1] [,2]
 NR 0.0587172 0.3136796
 R 1.0676683 0.8555980
 tables\$X203868_s_at
 X203868_s_at
 Y [,1] [,2]
 NR -0.3688355 0.6726738
 R 0.2602381 0.3965858
 tables\$X203915_at

R -0.3241903 0.5279440
 tables\$X219737_s_at
 X219737_s_at
 Y [,1] [,2]
 NR 0.3596773 0.5146777
 R -0.2409581 0.4405703
 tables\$X219777_at
 X219777_at
 Y [,1] [,2]
 NR -0.3965677 0.5974954
 R 0.5026195 0.4178151
 tables\$X219789_at
 X219789_at
 Y [,1] [,2]
 NR 0.0625228 0.3929864
 R 1.5326986 1.6918348
 tables\$X219926_at
 X219926_at
 Y [,1] [,2]
 NR 0.2428123 0.5989463
 R -0.6869766 0.9798973
 tables\$X219938_s_at
 X219938_s_at
 Y [,1] [,2]
 NR -0.4681105 0.5841168
 R 0.3093149 0.2386032
 tables\$X220005_at
 X220005_at
 Y [,1] [,2]
 NR -0.09036238 0.5172305
 R 0.62083607 0.5403729
 tables\$X220066_at
 X220066_at
 Y [,1] [,2]
 NR -0.2813542 0.4958868
 R 0.2894245 0.2549095
 tables\$X220330_s_at
 X220330_s_at
 Y [,1] [,2]
 NR -0.1838030 0.5516329
 R 0.4155977 0.3566931
 tables\$X220485_s_at
 X220485_s_at
 Y [,1] [,2]
 NR -0.2516505 0.989380
 R 1.2092181 1.358517
 tables\$X221081_s_at
 X221081_s_at
 Y [,1] [,2]
 NR -0.3406222 0.5260212
 R 0.2204497 0.3080250
 tables\$X221087_s_at

X203915_at
 Y [1] [2]
 NR -0.4061025 0.5236050
 R 0.2301446 0.2415020
 tables\$X203932_at
 X203932_at
 Y [1] [2]
 NR -0.2494244 0.6622825
 R 0.4463418 0.3757829
 tables\$X204057_at
 X204057_at
 Y [1] [2]
 NR -0.3274287 0.5906957
 R 0.4847696 0.4283121
 tables\$X204070_at
 X204070_at
 Y [1] [2]
 NR -0.2719985 0.6097243
 R 0.4394442 0.3954333
 tables\$X204116_at
 X204116_at
 Y [1] [2]
 NR -0.2653059 0.4657288
 R 0.5320249 0.3827573
 tables\$X204118_at
 X204118_at
 Y [1] [2]
 NR -0.2188632 0.5465435
 R 0.4397206 0.4841528
 tables\$X204135_at
 X204135_at
 Y [1] [2]
 NR -0.2511983 0.3620796
 R 0.5582305 0.6587871
 tables\$X204204_at
 X204204_at
 Y [1] [2]
 NR -0.2476304 0.5677727
 R 0.5469376 0.5015591
 tables\$X204220_at
 X204220_at
 Y [1] [2]
 NR -0.4512334 0.9464671
 R 0.4470878 0.4911261
 tables\$X204222_s_at
 X204222_s_at
 Y [1] [2]
 NR -0.2858410 0.8009875
 R 0.4771543 0.4557632
 tables\$X204224_s_at
 X204224_s_at
 Y [1] [2]

X221087_s_at
 Y [1] [2]
 NR -0.3965314 0.6050086
 R 0.2956204 0.3544964
 tables\$X221477_s_at
 X221477_s_at
 Y [1] [2]
 NR -0.3833003 0.7680959
 R 0.4128233 0.5675033
 tables\$X221651_x_at
 X221651_x_at
 Y [1] [2]
 NR -0.3022085 0.4778491
 R 0.2004842 0.2922928
 tables\$X221671_x_at
 X221671_x_at
 Y [1] [2]
 NR -0.3000931 0.4932356
 R 0.2268629 0.2801547
 tables\$X221698_s_at
 X221698_s_at
 Y [1] [2]
 NR -0.6376038 0.9130990
 R 0.3423824 0.3837021
 tables\$X221756_at
 X221756_at
 Y [1] [2]
 NR -0.1597059 0.4810294
 R 0.7144792 0.8100807
 tables\$X221760_at
 X221760_at
 Y [1] [2]
 NR -0.3895238 0.6667009
 R 0.2589523 0.4120362
 tables\$X222108_at
 X222108_at
 Y [1] [2]
 NR -0.3578270 0.4644883
 R 0.3207759 0.3326270
 tables\$X222142_at
 X222142_at
 Y [1] [2]
 NR -0.1876780 0.4933581
 R 0.3824561 0.4368395
 tables\$X222484_s_at
 X222484_s_at
 Y [1] [2]
 NR -0.4729730 0.6937840
 R 0.3761529 0.5801888
 tables\$X222496_s_at
 X222496_s_at
 Y [1] [2]

NR -0.4034291 0.533261
 R 0.4591664 0.324186
 tables\$X204233_s_at
 X204233_s_at
 Y [,1] [,2]
 NR 0.1725203 0.526541
 R -0.4473613 0.498801
 tables\$X204236_at
 X204236_at
 Y [,1] [,2]
 NR -0.3405471 0.7438102
 R 0.4577420 0.4830432
 tables\$X204249_s_at
 X204249_s_at
 Y [,1] [,2]
 NR -0.2439368 0.6736956
 R 0.5798690 0.5938803
 tables\$X204411_at
 X204411_at
 Y [,1] [,2]
 NR -0.1561360 0.5046013
 R 0.5348875 0.6639757
 tables\$X204438_at
 X204438_at
 Y [,1] [,2]
 NR -0.2155729 0.8013524
 R 0.5238707 0.5465740
 tables\$X204502_at
 X204502_at
 Y [,1] [,2]
 NR -0.3163975 0.5660414
 R 0.3122723 0.3372872
 tables\$X204512_at
 X204512_at
 Y [,1] [,2]
 NR -0.3823994 0.7656201
 R 0.3405082 0.3302137
 tables\$X204533_at
 X204533_at
 Y [,1] [,2]
 NR -0.3432882 0.5411550
 R 0.2820025 0.3529044
 tables\$X204613_at
 X204613_at
 Y [,1] [,2]
 NR -0.2921141 0.5365989
 R 0.3433918 0.4634024
 tables\$X204628_s_at
 X204628_s_at
 Y [,1] [,2]
 NR 0.2412563 0.5057318
 R -0.4238494 0.4487938

NR -0.4144878 0.6266733
 R 0.2909259 0.2895369
 tables\$X222592_s_at
 X222592_s_at
 Y [,1] [,2]
 NR -0.2780972 0.5068942
 R 0.4106129 0.2951602
 tables\$X222725_s_at
 X222725_s_at
 Y [,1] [,2]
 NR -0.004398634 0.5694045
 R 1.150669643 1.2645302
 tables\$X222780_s_at
 X222780_s_at
 Y [,1] [,2]
 NR 0.4139560 0.5398394
 R -0.4224571 0.2983037
 tables\$X222838_at
 X222838_at
 Y [,1] [,2]
 NR -0.2978748 0.5457765
 R 0.2590990 0.2508078
 tables\$X222895_s_at
 X222895_s_at
 Y [,1] [,2]
 NR -0.4561043 0.5248071
 R 0.1985346 0.3539992
 tables\$X223044_at
 X223044_at
 Y [,1] [,2]
 NR -0.4249287 0.7273378
 R 0.3345815 0.5282742
 tables\$X223058_at
 X223058_at
 Y [,1] [,2]
 NR -0.5976291 0.7565737
 R 0.2836632 0.4557419
 tables\$X223059_s_at
 X223059_s_at
 Y [,1] [,2]
 NR -0.2707661 0.6996713
 R 0.5245500 0.4391394
 tables\$X223168_at
 X223168_at
 Y [,1] [,2]
 NR -0.3429218 0.5205996
 R 0.2543322 0.3823076
 tables\$X223235_s_at
 X223235_s_at
 Y [,1] [,2]
 NR -0.2858518 0.4718234
 R 0.6748075 0.7147878

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tables$X204642_at
  X204642_at
Y      [,1]      [,2]
NR -0.3125616 0.7411993
R   0.6952398 1.0691429
tables$X204655_at
  X204655_at
Y      [,1]      [,2]
NR -0.2716510 0.6208783
R   0.5579874 0.5183030
tables$X204661_at
  X204661_at
Y      [,1]      [,2]
NR -0.1558546 0.4835795
R   0.5868508 0.3065469
tables$X204670_x_at
  X204670_x_at
Y      [,1]      [,2]
NR -0.3190668 0.6529019
R   0.4161121 0.3104711
tables$X204687_at
  X204687_at
Y      [,1]      [,2]
NR  0.1167838 0.3453266
R   1.0001048 0.8753104
tables$X204724_s_at
  X204724_s_at
Y      [,1]      [,2]
NR  0.5223107 0.6822646
R  -0.1768374 0.3008967
tables$X204774_at
  X204774_at
Y      [,1]      [,2]
NR -0.3545849 0.6395887
R   0.1938959 0.3271488
tables$X204778_x_at
  X204778_x_at
Y      [,1]      [,2]
NR  0.3141006 0.5671928
R  -0.4937885 0.7083350
tables$X204834_at
  X204834_at
Y      [,1]      [,2]
NR -0.2829585 0.5026786
R   0.2222514 0.2582449
tables$X204846_at
  X204846_at
Y      [,1]      [,2]
NR  0.1129389 0.4384144
R   0.7672991 0.7249123
tables$X204894_s_at
  X204894_s_at

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tables$X223280_x_at
  X223280_x_at
Y      [,1]      [,2]
NR -0.5988057 0.8558921
R   0.2763766 0.4726699
tables$X223322_at
  X223322_at
Y      [,1]      [,2]
NR -0.5307109 0.7623257
R   0.4863893 0.5655322
tables$X223361_at
  X223361_at
Y      [,1]      [,2]
NR -0.2076597 0.5924435
R   0.3858025 0.5723073
tables$X223395_at
  X223395_at
Y      [,1]      [,2]
NR -0.2616053 0.5452143
R   0.4342364 0.5337485
tables$X223484_at
  X223484_at
Y      [,1]      [,2]
NR -0.2440592 0.3975480
R   0.4224246 0.4741438
tables$X223809_at
  X223809_at
Y      [,1]      [,2]
NR -0.2342077 0.5645847
R   0.3558237 0.3616038
tables$X223827_at
  X223827_at
Y      [,1]      [,2]
NR  0.60366334 0.8225446
R  -0.06966146 0.1454527
tables$X223922_x_at
  X223922_x_at
Y      [,1]      [,2]
NR -0.4981749 0.7014087
R   0.2234232 0.3896602
tables$X223924_at
  X223924_at
Y      [,1]      [,2]
NR  0.4849658 0.6301636
R  -0.1459645 0.4704890
tables$X223952_x_at
  X223952_x_at
Y      [,1]      [,2]
NR  0.1264371 0.4236437
R   0.8628858 0.9031651
tables$X224356_x_at
  X224356_x_at

```

Y [,1] [,2]
 NR -0.04169668 0.5285664
 R 0.90340136 1.0066307
 tables\$X204897_at
 X204897_at
 Y [,1] [,2]
 NR -0.5753379 0.7174762
 R 0.2097906 0.3253104
 tables\$X204912_at
 X204912_at
 Y [,1] [,2]
 NR -0.1581854 0.4616605
 R 0.4406020 0.3673491
 tables\$X204923_at
 X204923_at
 Y [,1] [,2]
 NR -0.1810564 0.5020173
 R 0.4762799 0.5956602
 tables\$X205027_s_at
 X205027_s_at
 Y [,1] [,2]
 NR -0.2115740 0.8053652
 R 0.9541627 0.9478824
 tables\$X205039_s_at
 X205039_s_at
 Y [,1] [,2]
 NR -0.07447284 0.6105666
 R 0.75225499 0.7306959
 tables\$X205081_at
 X205081_at
 Y [,1] [,2]
 NR -0.4320239 0.6844631
 R 0.4515831 0.6544651
 tables\$X205159_at
 X205159_at
 Y [,1] [,2]
 NR -0.3955032 0.7064307
 R 0.4559497 0.4821926
 tables\$X205225_at
 X205225_at
 Y [,1] [,2]
 NR -0.4166425 0.5776734
 R 0.4113626 0.4147703
 tables\$X205226_at
 X205226_at
 Y [,1] [,2]
 NR -0.07833695 0.4854712
 R 0.44132335 0.7107620
 tables\$X205251_at
 X205251_at
 Y [,1] [,2]
 NR -0.3110220 0.6899898

Y [,1] [,2]
 NR -0.5122008 0.7621637
 R 0.2604697 0.4291461
 tables\$X224358_s_at
 X224358_s_at
 Y [,1] [,2]
 NR -0.4371837 0.8408400
 R 0.3218548 0.5126749
 tables\$X224451_x_at
 X224451_x_at
 Y [,1] [,2]
 NR -0.2604966 0.5285926
 R 0.4760714 0.4279992
 tables\$X224516_s_at
 X224516_s_at
 Y [,1] [,2]
 NR 0.2968854 0.6541436
 R -0.5889220 0.9012319
 tables\$X224710_at
 X224710_at
 Y [,1] [,2]
 NR 0.2230392 0.3643719
 R -0.7978563 0.9064005
 tables\$X224771_at
 X224771_at
 Y [,1] [,2]
 NR 0.4329412 0.8903073
 R -0.4421469 0.6725526
 tables\$X224772_at
 X224772_at
 Y [,1] [,2]
 NR 0.1916542 0.4865887
 R -0.5224768 0.4540955
 tables\$X224773_at
 X224773_at
 Y [,1] [,2]
 NR 0.3157972 0.5857999
 R -0.4979135 0.4238849
 tables\$X224774_s_at
 X224774_s_at
 Y [,1] [,2]
 NR 0.5703417 0.6486541
 R -0.5030708 0.5503160
 tables\$X224795_x_at
 X224795_x_at
 Y [,1] [,2]
 NR -0.3054091 0.4872416
 R 0.2135411 0.2854565
 tables\$X224859_at
 X224859_at
 Y [,1] [,2]
 NR 0.4830222 0.7137397

R 0.5272399 0.6253671
 tables\$X205285_s_at
 X205285_s_at
 Y [,1] [,2]
 NR -0.04432586 0.5000114
 R 0.80925537 0.9021956
 tables\$X205392_s_at
 X205392_s_at
 Y [,1] [,2]
 NR -0.4220336 0.4956664
 R 0.4657780 0.3693635
 tables\$X205403_at
 X205403_at
 Y [,1] [,2]
 NR -0.2005647 0.4806835
 R 0.5966667 0.7091052
 tables\$X205419_at
 X205419_at
 Y [,1] [,2]
 NR -0.2813820 0.5751165
 R 0.5056242 0.4918400
 tables\$X205421_at
 X205421_at
 Y [,1] [,2]
 NR 0.07840435 0.3868954
 R 0.86698828 0.8643222
 tables\$X205440_s_at
 X205440_s_at
 Y [,1] [,2]
 NR -0.3108277 0.5223075
 R 0.3749281 0.5730182
 tables\$X205484_at
 X205484_at
 Y [,1] [,2]
 NR -0.2739962 0.5607660
 R 0.4613413 0.4462779
 tables\$X205488_at
 X205488_at
 Y [,1] [,2]
 NR -0.211302 0.5156343
 R 0.451222 0.3725271
 tables\$X205559_s_at
 X205559_s_at
 Y [,1] [,2]
 NR -0.1967785 0.4797350
 R 0.4925489 0.5104237
 tables\$X205569_at
 X205569_at
 Y [,1] [,2]
 NR -0.3112147 0.5708862
 R 0.3356277 0.4533386
 tables\$X205624_at

R -0.3679703 0.6853105
 tables\$X224896_s_at
 X224896_s_at
 Y [,1] [,2]
 NR 0.1816808 0.7977231
 R -0.6408326 0.5850013
 tables\$X225502_at
 X225502_at
 Y [,1] [,2]
 NR -0.3910820 0.6073778
 R 0.4852237 0.4201402
 tables\$X225802_at
 X225802_at
 Y [,1] [,2]
 NR 0.1344681 0.5702449
 R -0.4950925 0.5294767
 tables\$X225895_at
 X225895_at
 Y [,1] [,2]
 NR -0.3277170 0.7566241
 R 0.6412089 0.7479682
 tables\$X226043_at
 X226043_at
 Y [,1] [,2]
 NR 0.1973572 0.6004289
 R -0.3655970 0.4868833
 tables\$X226068_at
 X226068_at
 Y [,1] [,2]
 NR -0.3490564 0.6019387
 R 0.4335378 0.4792696
 tables\$X226117_at
 X226117_at
 Y [,1] [,2]
 NR -0.2837194 0.5233255
 R 0.4253069 0.3317653
 tables\$X226218_at
 X226218_at
 Y [,1] [,2]
 NR -0.3859418 0.6090051
 R 0.4404194 0.3778062
 tables\$X226219_at
 X226219_at
 Y [,1] [,2]
 NR -0.2943873 0.5216637
 R 0.4004941 0.4131372
 tables\$X226303_at
 X226303_at
 Y [,1] [,2]
 NR -0.04068867 0.4037450
 R 0.73077236 0.8465357
 tables\$X226382_at

X205624_at
 Y [,1] [,2]
 NR 0.005427652 0.4382683
 R 0.763112333 0.7396355
 tables\$X205685_at
 X205685_at
 Y [,1] [,2]
 NR -0.1946623 0.5288449
 R 0.4467601 0.4223863
 tables\$X205696_s_at
 X205696_s_at
 Y [,1] [,2]
 NR -0.01091462 0.3565887
 R 0.77207850 0.7974577
 tables\$X205758_at
 X205758_at
 Y [,1] [,2]
 NR -0.2386930 0.4171697
 R 0.4248193 0.3603297
 tables\$X205786_s_at
 X205786_s_at
 Y [,1] [,2]
 NR -0.4968271 0.8934640
 R 0.4149078 0.5488123
 tables\$X205831_at
 X205831_at
 Y [,1] [,2]
 NR 0.04447927 0.4259325
 R 0.69838627 0.4833483
 tables\$X205841_at
 X205841_at
 Y [,1] [,2]
 NR -0.5900546 0.7313311
 R 0.3136276 0.5142651
 tables\$X205844_at
 X205844_at
 Y [,1] [,2]
 NR -0.1423775 0.4883837
 R 0.4235432 0.4438472
 tables\$X205890_s_at
 X205890_s_at
 Y [,1] [,2]
 NR -0.3511421 0.4822404
 R 0.3120630 0.2244957
 tables\$X205987_at
 X205987_at
 Y [,1] [,2]
 NR -0.09413415 0.3978789
 R 0.59504052 0.5335613
 tables\$X206082_at
 X206082_at
 Y [,1] [,2]

X226382_at
 Y [,1] [,2]
 NR -0.3657410 0.4652645
 R 0.2469253 0.4366802
 tables\$X226459_at
 X226459_at
 Y [,1] [,2]
 NR -0.3680501 0.7660787
 R 0.5040254 0.5894990
 tables\$X226625_at
 X226625_at
 Y [,1] [,2]
 NR -0.3757333 0.7664846
 R 0.5166961 0.4684207
 tables\$X226659_at
 X226659_at
 Y [,1] [,2]
 NR -0.4911180 0.6832209
 R 0.2612643 0.5381065
 tables\$X226697_at
 X226697_at
 Y [,1] [,2]
 NR 0.1958473 0.3711059
 R -0.5652399 0.4049380
 tables\$X226818_at
 X226818_at
 Y [,1] [,2]
 NR -0.2318967 0.6119576
 R 0.4987669 0.3954684
 tables\$X226841_at
 X226841_at
 Y [,1] [,2]
 NR -0.2979441 0.7024396
 R 0.5392790 0.4413953
 tables\$X226865_at
 X226865_at
 Y [,1] [,2]
 NR -0.1559129 0.5471301
 R 0.5041605 0.5099762
 tables\$X227035_x_at
 X227035_x_at
 Y [,1] [,2]
 NR 0.2005227 0.4921465
 R -0.3809524 0.4152160
 tables\$X227231_at
 X227231_at
 Y [,1] [,2]
 NR 0.2353572 0.7279505
 R -0.6509830 0.8181286
 tables\$X227253_at
 X227253_at
 Y [,1] [,2]

NR -0.4540809 0.6785699
 R 0.4716106 0.5496119
 tables\$X206099_at
 X206099_at
 Y [,1] [,2]
 NR -0.0531401 0.3438675
 R 0.5295345 0.5201337
 tables\$X206118_at
 X206118_at
 Y [,1] [,2]
 NR -0.2013207 0.4883106
 R 0.5011802 0.4695632
 tables\$X206134_at
 X206134_at
 Y [,1] [,2]
 NR -0.2474317 0.6355258
 R 0.3651382 0.4198818
 tables\$X206170_at
 X206170_at
 Y [,1] [,2]
 NR -0.4274713 0.5078651
 R 0.3104491 0.3419569
 tables\$X206204_at
 X206204_at
 Y [,1] [,2]
 NR -0.02057820 0.2205198
 R 0.94769151 0.9338282
 tables\$X206295_at
 X206295_at
 Y [,1] [,2]
 NR -0.4222879 0.5539909
 R 0.2869025 0.3697476
 tables\$X206385_s_at
 X206385_s_at
 Y [,1] [,2]
 NR -0.1448051 0.4343064
 R 0.5421084 0.6951307
 tables\$X206407_s_at
 X206407_s_at
 Y [,1] [,2]
 NR -0.0965811 0.4714271
 R 0.5253937 0.6785424
 tables\$X206545_at
 X206545_at
 Y [,1] [,2]
 NR -0.2348002 0.6434845
 R 0.3898586 0.5979256
 tables\$X206571_s_at
 X206571_s_at
 Y [,1] [,2]
 NR 0.2964052 0.5266454
 R -0.5021825 0.7307312

NR 0.03671536 0.4958005
 R 1.03309945 1.0290932
 tables\$X227265_at
 X227265_at
 Y [,1] [,2]
 NR -0.3512747 0.6026026
 R 0.3283856 0.3401296
 tables\$X227346_at
 X227346_at
 Y [,1] [,2]
 NR -0.3365397 0.7439603
 R 0.6189716 0.5315020
 tables\$X227361_at
 X227361_at
 Y [,1] [,2]
 NR -0.2481734 0.4900125
 R 0.2745731 0.3724106
 tables\$X227458_at
 X227458_at
 Y [,1] [,2]
 NR -0.1210425 0.5832677
 R 0.5061539 0.5297024
 tables\$X227584_at
 X227584_at
 Y [,1] [,2]
 NR 0.1614340 0.6512560
 R -0.6792229 0.5867806
 tables\$X227609_at
 X227609_at
 Y [,1] [,2]
 NR -0.2162779 0.6215554
 R 0.4224651 0.4449701
 tables\$X227640_s_at
 X227640_s_at
 Y [,1] [,2]
 NR 0.2476183 0.5414889
 R -0.3764071 0.4938285
 tables\$X227780_s_at
 X227780_s_at
 Y [,1] [,2]
 NR -0.3434434 0.6237700
 R 0.4192693 0.6791114
 tables\$X227791_at
 X227791_at
 Y [,1] [,2]
 NR -0.2588648 0.5252067
 R 0.4328271 0.4393930
 tables\$X227983_at
 X227983_at
 Y [,1] [,2]
 NR -0.3232334 0.6182386
 R 0.3661930 0.5316841

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tables$X206637_at
  X206637_at
Y      [,1]      [,2]
NR -0.4929224 0.8293232
R   0.5561408 0.7415308
tables$X206666_at
  X206666_at
Y      [,1]      [,2]
NR -0.3815276 0.4518748
R   0.3020703 0.1922297
tables$X206687_s_at
  X206687_s_at
Y      [,1]      [,2]
NR -0.3592461 0.6018756
R   0.3975221 0.5022615
tables$X206715_at
  X206715_at
Y      [,1]      [,2]
NR -0.2541760 0.6982257
R   0.4082547 0.3259496
tables$X206804_at
  X206804_at
Y      [,1]      [,2]
NR  0.1482064 0.5068781
R   0.9166047 0.7147839
tables$X206898_at
  X206898_at
Y      [,1]      [,2]
NR  0.1056709 0.4682096
R  -0.5435822 0.5520821
tables$X206978_at
  X206978_at
Y      [,1]      [,2]
NR -0.3496069 0.5339659
R   0.2843234 0.3287630
tables$X207076_s_at
  X207076_s_at
Y      [,1]      [,2]
NR -0.02361779 0.5694192
R   1.31170006 1.6322450
tables$X207238_s_at
  X207238_s_at
Y      [,1]      [,2]
NR -0.2571791 0.6182402
R   0.5089045 0.4856678
tables$X207277_at
  X207277_at
Y      [,1]      [,2]
NR -0.3525872 0.7509863
R   0.4181711 0.4255746
tables$X207458_at
  X207458_at

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tables$X227995_at
  X227995_at
Y      [,1]      [,2]
NR -0.1696409 0.3982272
R   0.4873422 0.5629170
tables$X228054_at
  X228054_at
Y      [,1]      [,2]
NR  0.1996287 0.5784055
R  -0.4191671 0.4113732
tables$X228071_at
  X228071_at
Y      [,1]      [,2]
NR -0.5040346 0.7357555
R   0.4529897 0.4488694
tables$X228094_at
  X228094_at
Y      [,1]      [,2]
NR -0.5037012 0.7256858
R   0.5085461 0.4165603
tables$X228153_at
  X228153_at
Y      [,1]      [,2]
NR -0.3116782 0.6938566
R   0.3443284 0.3237526
tables$X228339_at
  X228339_at
Y      [,1]      [,2]
NR -0.2039593 0.7344429
R   0.5985043 0.7672987
tables$X228362_s_at
  X228362_s_at
Y      [,1]      [,2]
NR -0.3778104 0.5378346
R   0.2342191 0.2730511
tables$X228372_at
  X228372_at
Y      [,1]      [,2]
NR -0.4350057 0.7819102
R   0.4561920 0.3911495
tables$X228376_at
  X228376_at
Y      [,1]      [,2]
NR -0.3453361 0.7260925
R   0.5292299 0.5379290
tables$X228427_at
  X228427_at
Y      [,1]      [,2]
NR  0.1593717 0.7055373
R  -0.6106282 0.8316641
tables$X228532_at
  X228532_at

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Y          [,1]      [,2]
NR  0.2419331 0.5735746
R   -0.3710235 0.4350871
tables$X207540_s_at
X207540_s_at
Y          [,1]      [,2]
NR -0.2692932 0.5488522
R    0.3711915 0.4966252
tables$X207574_s_at
X207574_s_at
Y          [,1]      [,2]
NR -0.3958191 0.7713632
R    0.4298086 0.3017609
tables$X207651_at
X207651_at
Y          [,1]      [,2]
NR -0.3101854 0.4462963
R    0.5275557 0.2883934
tables$X207655_s_at
X207655_s_at
Y          [,1]      [,2]
NR -0.2656028 0.6249668
R    0.4038824 0.4984622
tables$X207677_s_at
X207677_s_at
Y          [,1]      [,2]
NR -0.1067724 0.6536107
R    0.6251422 0.4735116
tables$X207843_x_at
X207843_x_at
Y          [,1]      [,2]
NR -0.1980640 0.4840094
R    0.6923162 1.1190386
tables$X207861_at
X207861_at
Y          [,1]      [,2]
NR -0.1260775 0.3508021
R    0.6778354 0.7911460
tables$X207977_s_at
X207977_s_at
Y          [,1]      [,2]
NR -0.02630196 0.3452417
R    0.72601762 0.5798353
tables$X207992_s_at
X207992_s_at
Y          [,1]      [,2]
NR -0.2962782 0.6213732
R    0.4065298 0.3562586
tables$X208296_x_at
X208296_x_at
Y          [,1]      [,2]
NR -0.3202962 0.6726712

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Y          [,1]      [,2]
NR -0.3794859 0.6481241
R    0.5000793 0.4684207
tables$X228552_s_at
X228552_s_at
Y          [,1]      [,2]
NR  0.1167790 0.4798513
R   -0.5450925 0.7268180
tables$X228563_at
X228563_at
Y          [,1]      [,2]
NR  0.4236616 0.5619516
R   -0.3316479 0.5347978
tables$X228660_x_at
X228660_x_at
Y          [,1]      [,2]
NR  0.5804684 0.7378901
R   -0.1713584 0.4483440
tables$X228776_at
X228776_at
Y          [,1]      [,2]
NR  0.06752481 0.5251283
R   -0.80628566 0.8423271
tables$X228812_at
X228812_at
Y          [,1]      [,2]
NR -0.3127907 0.6313677
R    0.5074128 0.6516242
tables$X228858_at
X228858_at
Y          [,1]      [,2]
NR -0.2190644 0.7355751
R    0.8241261 0.8754638
tables$X228869_at
X228869_at
Y          [,1]      [,2]
NR -0.3255735 0.5223796
R    0.3751149 0.4806706
tables$X228908_s_at
X228908_s_at
Y          [,1]      [,2]
NR  0.3383439 0.4459491
R   -0.2935832 0.7121557
tables$X228964_at
X228964_at
Y          [,1]      [,2]
NR -0.3612173 0.5362295
R    0.2810782 0.4326503
tables$X229127_at
X229127_at
Y          [,1]      [,2]
NR -0.4082796 0.5831644

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R 0.4715979 0.3630417
 tables\$X208306_x_at
 X208306_x_at
 Y [,1] [,2]
 NR -0.3404445 0.6697022
 R 0.3560108 0.2684112
 tables\$X208335_s_at
 X208335_s_at
 Y [,1] [,2]
 NR -0.6832978 0.8622729
 R 0.3887120 0.6307942
 tables\$X208450_at
 X208450_at
 Y [,1] [,2]
 NR 0.05646932 0.6161496
 R 0.97349919 0.7211533
 tables\$X208747_s_at
 X208747_s_at
 Y [,1] [,2]
 NR -0.7269106 1.215719
 R 0.6146325 0.602124
 tables\$X208885_at
 X208885_at
 Y [,1] [,2]
 NR -0.4878552 0.6970401
 R 0.3000394 0.4132369
 tables\$X208894_at
 X208894_at
 Y [,1] [,2]
 NR -0.2782715 0.5325159
 R 0.3660963 0.3734728
 tables\$X208981_at
 X208981_at
 Y [,1] [,2]
 NR -0.3974853 0.7581136
 R 0.3901547 0.3829096
 tables\$X208983_s_at
 X208983_s_at
 Y [,1] [,2]
 NR -0.3682743 0.6238660
 R 0.3346874 0.3924348
 tables\$X209083_at
 X209083_at
 Y [,1] [,2]
 NR 0.1258308 0.6751235
 R 0.9235844 0.8069453
 tables\$X209138_x_at
 X209138_x_at
 Y [,1] [,2]
 NR -0.1402324 0.4308172
 R 0.3394879 0.3946554
 tables\$X209193_at

R 0.3339318 0.8204140
 tables\$X229163_at
 X229163_at
 Y [,1] [,2]
 NR 0.4273831 0.7589842
 R -0.2717283 0.5013583
 tables\$X229367_s_at
 X229367_s_at
 Y [,1] [,2]
 NR -0.05987742 0.3928434
 R 0.56349206 0.5126817
 tables\$X229390_at
 X229390_at
 Y [,1] [,2]
 NR -0.4894938 0.6210411
 R 0.1935497 0.2963602
 tables\$X229391_s_at
 X229391_s_at
 Y [,1] [,2]
 NR -0.4084651 0.5373347
 R 0.2172787 0.2684421
 tables\$X229543_at
 X229543_at
 Y [,1] [,2]
 NR -0.3788834 0.5874714
 R 0.2662277 0.2904183
 tables\$X229625_at
 X229625_at
 Y [,1] [,2]
 NR -0.3005955 0.6601697
 R 0.5530654 0.4811529
 tables\$X229723_at
 X229723_at
 Y [,1] [,2]
 NR -0.2920168 0.5053402
 R 0.4696342 0.4191172
 tables\$X230233_at
 X230233_at
 Y [,1] [,2]
 NR -0.4143786 0.5555824
 R 0.3424073 0.3923358
 tables\$X230391_at
 X230391_at
 Y [,1] [,2]
 NR -0.3501254 0.8265678
 R 0.4900276 0.4781532
 tables\$X230538_at
 X230538_at
 Y [,1] [,2]
 NR 0.1276822 0.3932100
 R -0.5735748 0.7224135
 tables\$X230728_at

X209193_at
 Y [1] [2]
 NR -0.2565556 0.5468921
 R 0.4873494 0.4649883
 tables\$X209195_s_at
 X209195_s_at
 Y [1] [2]
 NR 0.1800756 0.4677919
 R -0.4026223 0.3673557
 tables\$X209202_s_at
 X209202_s_at
 Y [1] [2]
 NR 0.1964649 0.7379767
 R -0.5653081 0.5741860
 tables\$X209312_x_at
 X209312_x_at
 Y [1] [2]
 NR -0.2928795 0.6652902
 R 0.4275265 0.3568548
 tables\$X209480_at
 X209480_at
 Y [1] [2]
 NR -0.2841051 0.4380402
 R 0.2693738 0.4024957
 tables\$X209542_x_at
 X209542_x_at
 Y [1] [2]
 NR -0.2363103 0.6011656
 R 0.4349808 0.5810748
 tables\$X209603_at
 X209603_at
 Y [1] [2]
 NR -0.4656699 0.4521237
 R 0.3621330 0.6118526
 tables\$X209606_at
 X209606_at
 Y [1] [2]
 NR -0.2611256 0.5441526
 R 0.5627781 0.3290949
 tables\$X209612_s_at
 X209612_s_at
 Y [1] [2]
 NR -0.2482860 0.4645433
 R 0.3891742 0.5803480
 tables\$X209613_s_at
 X209613_s_at
 Y [1] [2]
 NR -0.3246706 0.4195264
 R 0.2137530 0.4363348
 tables\$X209670_at
 X209670_at
 Y [1] [2]

X230728_at
 Y [1] [2]
 NR 0.3244249 0.4668566
 R -0.2743950 0.5139070
 tables\$X231032_at
 X231032_at
 Y [1] [2]
 NR 0.43019858 0.5207535
 R -0.04588641 0.3560523
 tables\$X231262_at
 X231262_at
 Y [1] [2]
 NR 0.05461486 0.2495836
 R 1.32806434 1.1081493
 tables\$X231577_s_at
 X231577_s_at
 Y [1] [2]
 NR -0.3279081 0.7462895
 R 0.4819051 0.4270797
 tables\$X231882_at
 X231882_at
 Y [1] [2]
 NR 0.1390358 0.4492620
 R -0.4280975 0.4211427
 tables\$X231929_at
 X231929_at
 Y [1] [2]
 NR -0.4149811 0.6028339
 R 0.3275499 0.4633949
 tables\$X232001_at
 X232001_at
 Y [1] [2]
 NR -0.4082551 0.5622408
 R 0.2120889 0.4452512
 tables\$X232024_at
 X232024_at
 Y [1] [2]
 NR -0.2767578 0.5975732
 R 0.4329087 0.3644723
 tables\$X232234_at
 X232234_at
 Y [1] [2]
 NR -0.2485230 0.5169943
 R 0.5378690 0.4919297
 tables\$X232311_at
 X232311_at
 Y [1] [2]
 NR -0.2207241 0.5017714
 R 0.4996502 0.4849287
 tables\$X232313_at
 X232313_at
 Y [1] [2]

NR -0.3904387 0.5757881
 R 0.4960604 0.4286288
 tables\$X209671_x_at
 X209671_x_at
 Y [,1] [,2]
 NR 0.005489902 0.4958616
 R 0.946682909 0.6669064
 tables\$X209685_s_at
 X209685_s_at
 Y [,1] [,2]
 NR -0.3380362 0.6105057
 R 0.3675781 0.4181149
 tables\$X209687_at
 X209687_at
 Y [,1] [,2]
 NR -0.5180091 0.5954837
 R 0.3297076 0.5807315
 tables\$X209710_at
 X209710_at
 Y [,1] [,2]
 NR -0.2868007 0.3941463
 R 0.4039716 0.7769142
 tables\$X209734_at
 X209734_at
 Y [,1] [,2]
 NR -0.2771824 0.5584141
 R 0.3480342 0.4269202
 tables\$X209774_x_at
 X209774_x_at
 Y [,1] [,2]
 NR -0.5154483 0.5084051
 R 0.3327482 0.2052511
 tables\$X209795_at
 X209795_at
 Y [,1] [,2]
 NR -0.5014384 0.5485146
 R 0.2126023 0.2563472
 tables\$X209813_x_at
 X209813_x_at
 Y [,1] [,2]
 NR -0.02446552 0.4178348
 R 0.66828816 0.5665816
 tables\$X209899_s_at
 X209899_s_at
 Y [,1] [,2]
 NR 0.2607015 0.6973904
 R -0.4270344 0.5920830
 tables\$X209924_at
 X209924_at
 Y [,1] [,2]
 NR -0.1412661 0.5234151
 R 0.3997205 0.5359769

NR 0.09690295 0.2976671
 R 0.96479280 0.7382041
 tables\$X232476_at
 X232476_at
 Y [,1] [,2]
 NR 0.1978897 0.4874151
 R -0.3000000 0.4272541
 tables\$X232543_x_at
 X232543_x_at
 Y [,1] [,2]
 NR -0.1276883 0.6158742
 R 0.5695534 0.5964269
 tables\$X232617_at
 X232617_at
 Y [,1] [,2]
 NR -0.2190263 0.6769132
 R 0.5988644 0.4031826
 tables\$X232746_at
 X232746_at
 Y [,1] [,2]
 NR -0.3742172 0.5931449
 R 0.3407643 0.5742058
 tables\$X232843_s_at
 X232843_s_at
 Y [,1] [,2]
 NR -0.3175189 0.5332408
 R 0.3950617 0.3666760
 tables\$X233123_at
 X233123_at
 Y [,1] [,2]
 NR -0.2015742 0.5531279
 R 0.4654343 0.7103440
 tables\$X233562_at
 X233562_at
 Y [,1] [,2]
 NR 0.2792368 0.4159995
 R -0.2877796 0.4229988
 tables\$X233955_x_at
 X233955_x_at
 Y [,1] [,2]
 NR 0.3290657 0.6359343
 R -0.3166667 0.5295163
 tables\$X235175_at
 X235175_at
 Y [,1] [,2]
 NR -0.1311223 0.4904278
 R 0.4533666 0.4676313
 tables\$X235238_at
 X235238_at
 Y [,1] [,2]
 NR 0.1248063 0.3770484
 R -0.5772758 0.7499223

```

tables$X209949_at
  X209949_at
Y      [,1]      [,2]
NR -0.2882600 0.4631077
R   0.4047160 0.3303257
tables$X209970_x_at
  X209970_x_at
Y      [,1]      [,2]
NR -0.4439942 0.6955252
R   0.1102440 0.2548926
tables$X210038_at
  X210038_at
Y      [,1]      [,2]
NR  0.1317110 0.4768708
R   0.8494560 0.7295487
tables$X210072_at
  X210072_at
Y      [,1]      [,2]
NR  0.01156063 0.3737049
R   0.57481931 0.4627490
tables$X210251_s_at
  X210251_s_at
Y      [,1]      [,2]
NR  0.2240660 0.4879510
R  -0.6597691 0.6547051
tables$X210260_s_at
  X210260_s_at
Y      [,1]      [,2]
NR -0.3640910 0.6337100
R   0.4487179 0.3720418
tables$X210319_x_at
  X210319_x_at
Y      [,1]      [,2]
NR -0.08072798 0.5440481
R   0.83296501 1.2085067
tables$X210375_at
  X210375_at
Y      [,1]      [,2]
NR -0.0859139 0.2736614
R   0.9924649 1.0291749
tables$X210554_s_at
  X210554_s_at
Y      [,1]      [,2]
NR  0.1522882 0.5489999
R  -0.5083098 0.6130962
tables$X210835_s_at
  X210835_s_at
Y      [,1]      [,2]
NR  0.2332468 0.5454729
R  -0.4438314 0.6253821
tables$X210915_x_at
  X210915_x_at

```

```

tables$X235306_at
  X235306_at
Y      [,1]      [,2]
NR -0.5666624 1.047734
R   0.4955309 0.534125
tables$X235391_at
  X235391_at
Y      [,1]      [,2]
NR  0.3239007 0.6545010
R  -0.5514259 0.6035657
tables$X235421_at
  X235421_at
Y      [,1]      [,2]
NR -0.2094653 0.4583538
R   0.4672043 0.4014682
tables$X235639_at
  X235639_at
Y      [,1]      [,2]
NR  0.3234035 0.5491068
R  -0.3795961 0.6104110
tables$X235688_s_at
  X235688_s_at
Y      [,1]      [,2]
NR  0.01982982 0.5208595
R  -0.55915444 0.5353062
tables$X235804_at
  X235804_at
Y      [,1]      [,2]
NR  0.2009344 0.5886169
R  -0.4162556 0.4684402
tables$X235831_at
  X235831_at
Y      [,1]      [,2]
NR -0.08120476 0.4915252
R   1.14904526 1.1198369
tables$X236203_at
  X236203_at
Y      [,1]      [,2]
NR  0.005259016 0.3895193
R   0.676842217 0.4524154
tables$X236280_at
  X236280_at
Y      [,1]      [,2]
NR -0.1220235 0.4998530
R   0.5788924 0.4002499
tables$X236295_s_at
  X236295_s_at
Y      [,1]      [,2]
NR -0.1165942 0.5645451
R   0.6163840 0.5662135
tables$X236583_at
  X236583_at

```

Y [,1] [,2]
 NR -0.2269420 0.466748
 R 0.5087007 0.360080
 tables\$X210972_x_at
 X210972_x_at
 Y [,1] [,2]
 NR -0.2866590 0.4272028
 R 0.5598691 0.4527992
 tables\$X210982_s_at
 X210982_s_at
 Y [,1] [,2]
 NR -0.3512586 0.5571462
 R 0.3419340 0.3732178
 tables\$X211066_x_at
 X211066_x_at
 Y [,1] [,2]
 NR 0.2422814 0.6284310
 R -0.5086901 0.7771297
 tables\$X211144_x_at
 X211144_x_at
 Y [,1] [,2]
 NR 0.05087736 0.3119915
 R 0.70598903 0.4822038
 tables\$X211200_s_at
 X211200_s_at
 Y [,1] [,2]
 NR 0.2580184 0.5530421
 R -0.4922700 0.5506593
 tables\$X211339_s_at
 X211339_s_at
 Y [,1] [,2]
 NR -0.2296132 0.5247178
 R 0.5767409 0.5988969
 tables\$X211366_x_at
 X211366_x_at
 Y [,1] [,2]
 NR -0.3681938 0.6327750
 R 0.1432735 0.2631491
 tables\$X211367_s_at
 X211367_s_at
 Y [,1] [,2]
 NR -0.1751026 0.5723239
 R 0.3320629 0.2562800
 tables\$X211368_s_at
 X211368_s_at
 Y [,1] [,2]
 NR -0.51886132 0.7515452
 R 0.07358956 0.2643141
 tables\$X211654_x_at
 X211654_x_at
 Y [,1] [,2]
 NR -0.3850022 0.5573621

Y [,1] [,2]
 NR 0.02541689 0.5675783
 R 0.82576116 0.7584443
 tables\$X236908_at
 X236908_at
 Y [,1] [,2]
 NR 0.5408046 0.8859905
 R -0.3849473 0.3825884
 tables\$X238439_at
 X238439_at
 Y [,1] [,2]
 NR -0.08639162 0.4532391
 R 0.64076976 0.7133665
 tables\$X238488_at
 X238488_at
 Y [,1] [,2]
 NR -0.2588720 0.5056425
 R 0.4974834 0.7836170
 tables\$X238544_at
 X238544_at
 Y [,1] [,2]
 NR 0.2824277 0.7145403
 R -0.4079449 0.4677199
 tables\$X239196_at
 X239196_at
 Y [,1] [,2]
 NR 0.04478165 0.456084
 R 0.92699218 0.784260
 tables\$X239237_at
 X239237_at
 Y [,1] [,2]
 NR -0.06887682 0.4538298
 R 0.56173192 0.5087772
 tables\$X239744_at
 X239744_at
 Y [,1] [,2]
 NR -0.1939947 0.4873477
 R 0.3861305 0.5051036
 tables\$X241671_x_at
 X241671_x_at
 Y [,1] [,2]
 NR 0.3853780 0.6714183
 R -0.2467927 0.4002054
 tables\$X241701_at
 X241701_at
 Y [,1] [,2]
 NR 0.3603183 0.8440397
 R -0.4068724 0.5295527
 tables\$X242458_at
 X242458_at
 Y [,1] [,2]
 NR -0.2312046 0.7607719

```

R    0.3719847 0.3143733
tables$X211742_s_at
  X211742_s_at
Y      [,1]      [,2]
NR -0.2540869 0.6521022
R    0.4880575 0.5506316
tables$X211796_s_at
  X211796_s_at
Y      [,1]      [,2]
NR -0.3093201 0.4536705
R    0.4624019 0.3008702
tables$X211902_x_at
  X211902_x_at
Y      [,1]      [,2]
NR -0.2792212 0.5535743
R    0.6836665 0.6034058
tables$X211990_at
  X211990_at
Y      [,1]      [,2]
NR -0.4590253 0.8582217
R    0.4251869 0.4814630
tables$X211991_s_at
  X211991_s_at
Y      [,1]      [,2]
NR -0.2092869 0.6666829
R    0.5537245 0.3967729
tables$X212067_s_at
  X212067_s_at
Y      [,1]      [,2]
NR -0.4803278 0.7242299
R    0.3558230 0.6889846
tables$X212233_at
  X212233_at
Y      [,1]      [,2]
NR  0.1442229 0.5131552
R   -0.4879059 0.7214358
tables$X212538_at
  X212538_at
Y      [,1]      [,2]
NR -0.3849016 0.7522011
R    0.6516464 0.6995619
tables$X212587_s_at
  X212587_s_at
Y      [,1]      [,2]
NR -0.3531934 0.5890246
R    0.3718118 0.3431055
tables$X212588_at
  X212588_at
Y      [,1]      [,2]
NR -0.5662804 0.8162279
R    0.4008046 0.4444447
tables$X212592_at

```

```

R    0.5057350 0.7076187
tables$X242546_at
  X242546_at
Y      [,1]      [,2]
NR  0.1097238 0.4715672
R   -0.4309505 0.5259991
tables$X242874_at
  X242874_at
Y      [,1]      [,2]
NR -0.2219024 0.3807166
R    0.5644292 0.7338815
tables$X242881_x_at
  X242881_x_at
Y      [,1]      [,2]
NR  0.08543868 0.3930728
R   -0.63018680 0.5655045
tables$X242986_at
  X242986_at
Y      [,1]      [,2]
NR  0.2371634 0.5409865
R   -0.6643602 0.7457416
tables$X243099_at
  X243099_at
Y      [,1]      [,2]
NR  0.01903757 0.6357632
R    0.80481642 0.8461258
tables$X244023_at
  X244023_at
Y      [,1]      [,2]
NR -0.3068381 0.6806949
R    0.4666732 0.5605710
tables$X244061_at
  X244061_at
Y      [,1]      [,2]
NR -0.2379335 0.5919363
R    0.5615362 0.6126814
tables$X32128_at
  X32128_at
Y      [,1]      [,2]
NR -0.04592188 0.6445335
R    0.60003775 0.6856519
tables$X34210_at
  X34210_at
Y      [,1]      [,2]
NR -0.3404304 0.6066166
R    0.4975685 0.2978426
tables$X38149_at
  X38149_at
Y      [,1]      [,2]
NR -0.4040241 0.6171240
R    0.2427490 0.4577025
tables$X64064_at

```

```

      X212592_at
Y      [,1]      [,2]
NR -0.3409693 0.4849486
R    0.2387676 0.2127384
tables$X212657_s_at
      X212657_s_at
Y      [,1]      [,2]
NR -0.3419394 0.6083771
R    0.2570024 0.4217927

tables$X212671_s_at
      X212671_s_at
Y      [,1]      [,2]
NR -0.5140866 0.8193929
R    0.5074176 0.3776582
tables$X212713_at
      X212713_at
Y      [,1]      [,2]
NR 0.03767197 0.3268940
R    0.74731430 0.8347694
tables$X212763_at
      X212763_at
Y      [,1]      [,2]
NR 0.2888164 0.8845972
R   -0.6529463 0.9707572
tables$X212886_at
      X212886_at
Y      [,1]      [,2]
NR -0.3765371 0.7892555
R    0.6201350 0.6611937
tables$X212977_at
      X212977_at
Y      [,1]      [,2]
NR -0.4688782 0.8767720
R    0.5293928 0.6187406
tables$X212998_x_at
      X212998_x_at
Y      [,1]      [,2]
NR -0.2035514 0.6457962
R    0.5296660 0.3118830
tables$X212999_x_at
      X212999_x_at
Y      [,1]      [,2]
NR -0.2290011 0.4910183
R    0.4331640 0.3718106
tables$X213007_at
      X213007_at
Y      [,1]      [,2]
NR 0.2632353 0.6401111
R   -0.3996142 0.4037179
tables$X213008_at
      X213008_at

```

```

      X64064_at
Y      [,1]      [,2]
NR -0.4613187 0.6447816
R    0.4548881 0.3392856

levels
[1] "NR" "R"
call
naiveBayes.default(x = X, y = Y,
laplace = laplace)

```

```
Y          [,1]      [,2]
NR  0.4761995 0.7015473
R   -0.4947303 0.8235263
tables$X213068_at
X213068_at
Y          [,1]      [,2]
NR -0.1758656 0.4044001
R    0.4193472 0.3911686
tables$X213095_x_at
X213095_x_at
Y          [,1]      [,2]
NR -0.3502315 0.8054069
R    0.3616843 0.3443190
tables$X213193_x_at
X213193_x_at
Y          [,1]      [,2]
NR -0.2370856 0.4636341
R    0.5058580 0.3505763
tables$X213475_s_at
X213475_s_at
Y          [,1]      [,2]
NR -0.2137215 0.4617051
R    0.4040370 0.4908631
tables$X213537_at
X213537_at
CONTINUED COLUMN 2
```

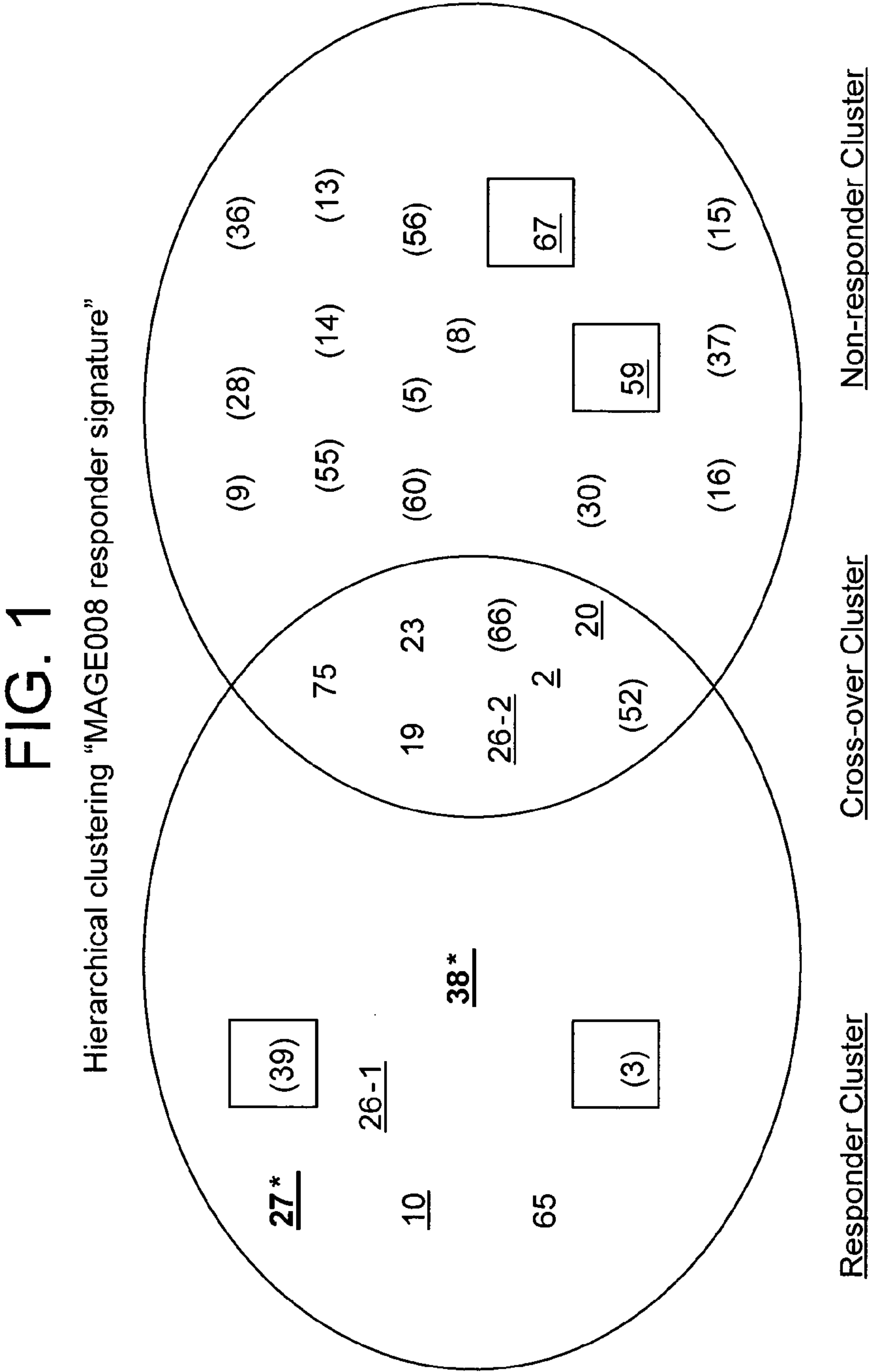
CLAIMS

1. A gene profile, from a patient derived sample, which is indicative of an increased likelihood that the patient will be a responder or a non-responder to an immunotherapy, wherein the profile comprises differential regulation of at least one immune activation gene.
2. A gene profile according to claim 1, wherein the immunotherapy is a cancer immunotherapy.
3. A gene profile according to claim 2, wherein the cancer immunotherapy is Mage antigen specific cancer immunotherapy.
4. A gene profile according to any one of claims 1 to 3, wherein the at least one immune activation gene is selected from the gene list in Table 1, 2, 3, 4, 7, 9, 11, 12 and/or 13.
5. A gene profile according to any one of claims 1 to 4, wherein the at least one immune gene is 5 or more genes.
6. A gene profile according to claim 4, wherein the at one gene is at least 10% of the genes listed (such as 40, 50, 60 or 70% of the genes listed) in Table 1, 2, 3, 4, 7, 9, 11, 12 and/or 13.
7. A gene profile according to claim 6, wherein the at least one gene is at least in Table 1, 2, 3, 4, 7, 9, 11, 12 and/or 13.
8. A gene profile according to claim 7, wherein the at least one gene is 80, 90 or 100% of the genes listed in Table 1, 2, 3, 4, 7, 9, 11, 12 and/or 13.
9. A gene profile according to any one of claims 1 to 8, wherein the at least one gene(s) is upregulated.
10. A gene profile according to claim 9, wherein the profile is indicative of a responder.
11. Use of a profile as defined in any one of claims 1 to 10 for the identification of a responder or a non-responder to immunotherapy.
12. A method of identifying a profile as claimed in any one of claims 1 to 10 comprising the steps:
 - a) analyzing a patient derived sample for differential expression of one or more immune response genes, and
 - b) characterizing the patient from which the sample was derived as a responder or a non-responder based on the results of step (a),

wherein the characterization is optionally performed by reference or comparison to a standard.

13. A method according to claim 12, wherein the standard is a sample with a known clinical outcome.
14. A method according to claim 12, wherein the comparison is performed using an algorithm.
15. Use of a probe for the identification of differential expression of at least one product of an immune activation gene for establishing if the profile of claims 1 to 10 is present in a patient derived sample.
16. Use according to claim 15, wherein the differential expression is upregulation.
17. Use of a microarray kit for the identification of differential expression of at least one product of an immune activation gene for establishing if the profile of claims 1 to 10 is present in a patient derived sample.
18. Use according to claim 17, wherein the differential expression is upregulation.
19. A microarray comprising one or more probes suitable for the detection of differential expression of one or more immune activation genes.
20. A microarray according to claim 19, wherein the immune activation genes are selected from the group comprising the list of genes in Table 1, 2, 3, 4, 7, 9, 11, 12 and/or 13.
21. A diagnostic kit comprising at least one component for performing an analysis on a patient derived sample to identify a profile according to any one of claims 1 to 11, the results of which may be used to designate a patient from which the sample was derived as a responder or non-responder to immunotherapy.
22. A method of treating a patient comprising administering a therapeutically effective amount of an appropriate immunotherapy, after first characterising the patient as responder thereto based on differential activation of at least one immune activation gene.
23. A method according to claim 22, wherein the therapy is cancer immunotherapy.
24. A method according to claim 23, wherein the therapy is MAGE cancer immunotherapy.
25. A method according to any one of claims 22 to 24, wherein the patient is characterised as a responder based on a profile as defined in any one of claims 1 to 10.

26. A method according to any one of claims 22 to 25, wherein the immunotherapy comprises an antigen and an appropriate adjuvant.
27. A method according to any one of claims 21 to 25 wherein the at least one immune activation gene is upregulated.
28. A method of inducing a responder gene profile in a patient characterised as a non-responder comprising the step of stimulating a systemic immune or inflammatory response in the patient.
29. A method according to claim 28, wherein the systemic response is induced by radiotherapy or administering an effective amount of interferon
30. A method according to claim 28 or 29, wherein after optionally analysing the patient to identify a gene profile as claimed in one of claims 1 to 10 and characterising the patient as a responder, administering an effective amount of an appropriate immunotherapy, for example an appropriate cancer immunotherapy, such as a Mage immunotherapy.



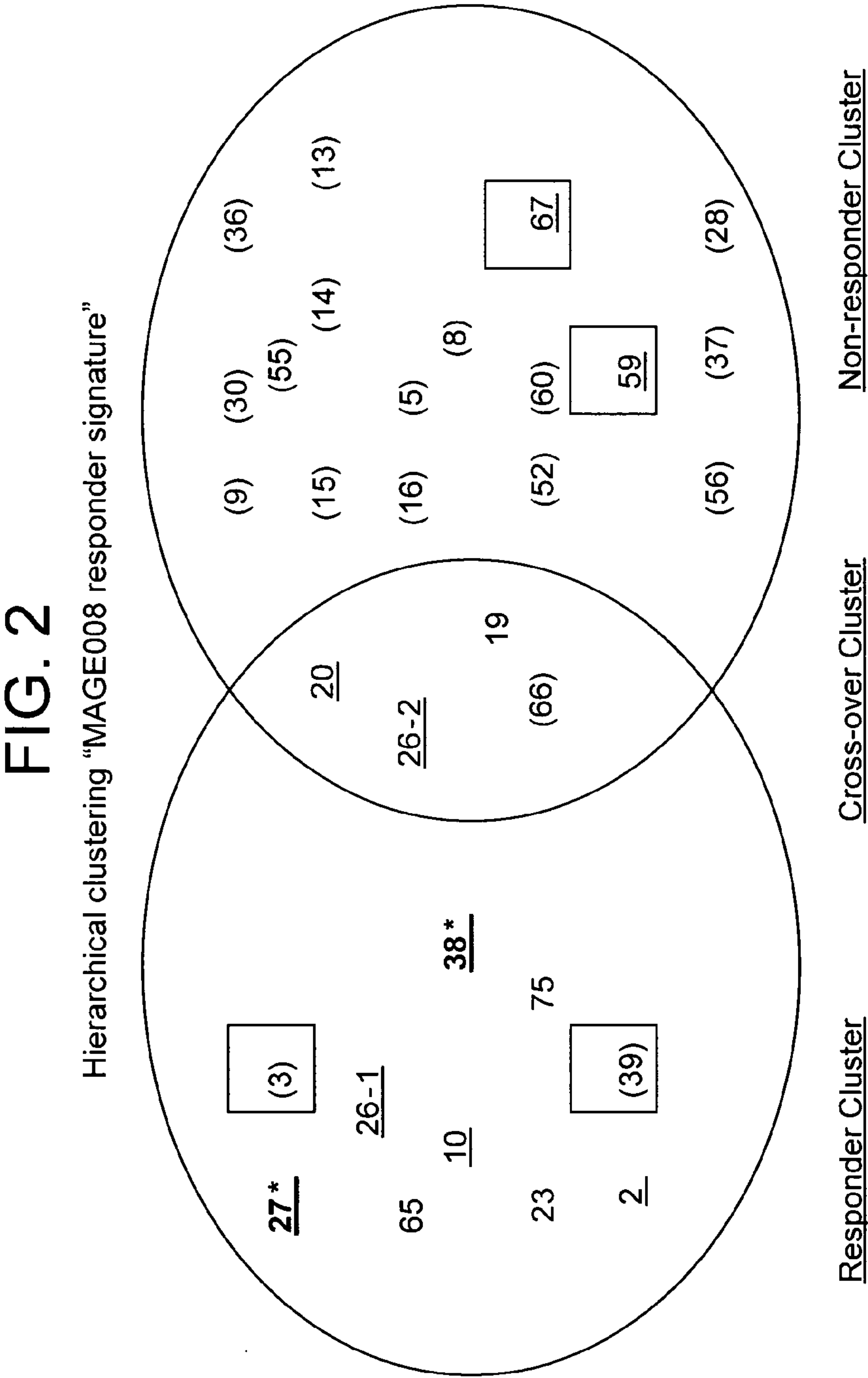
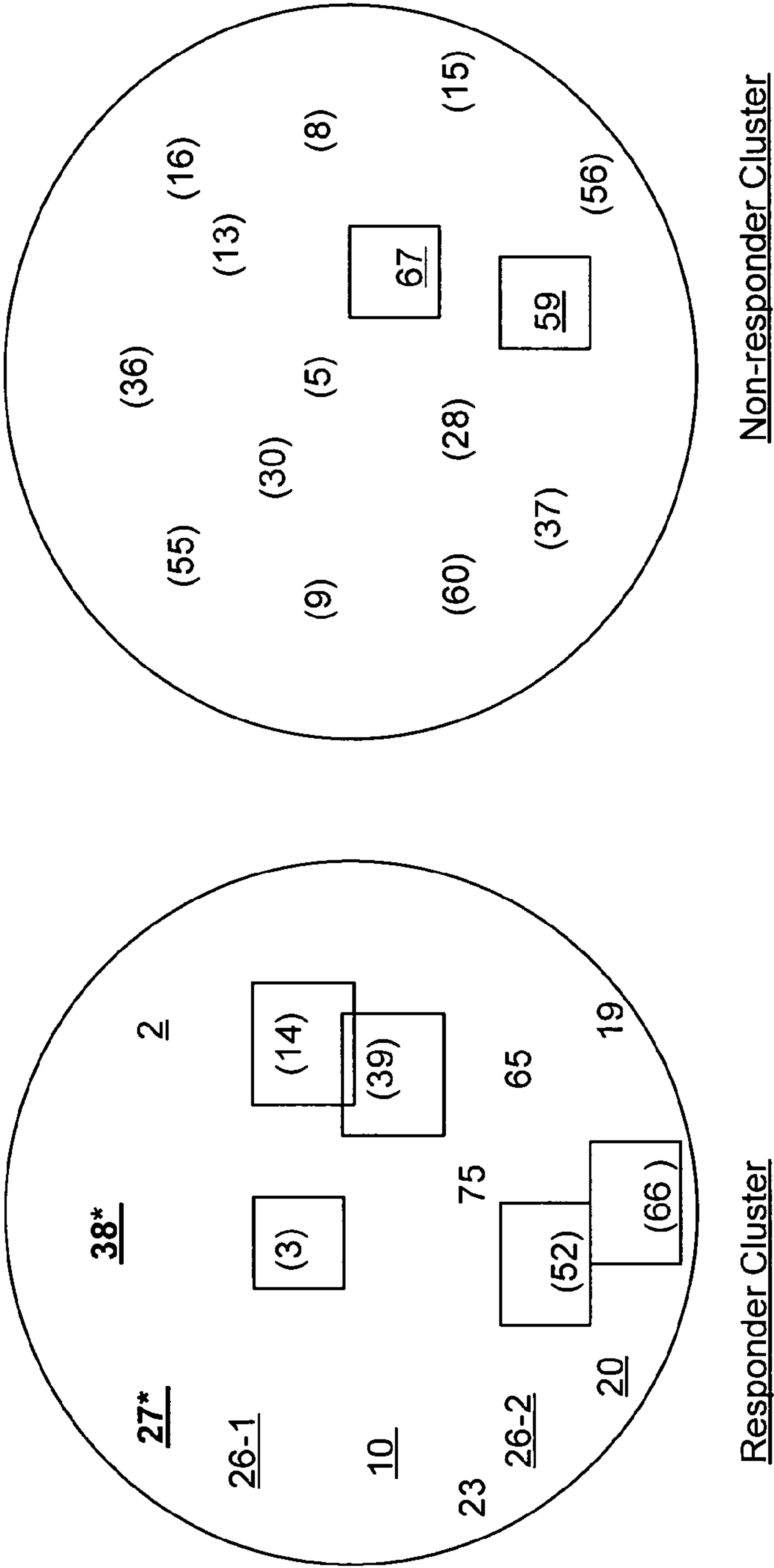
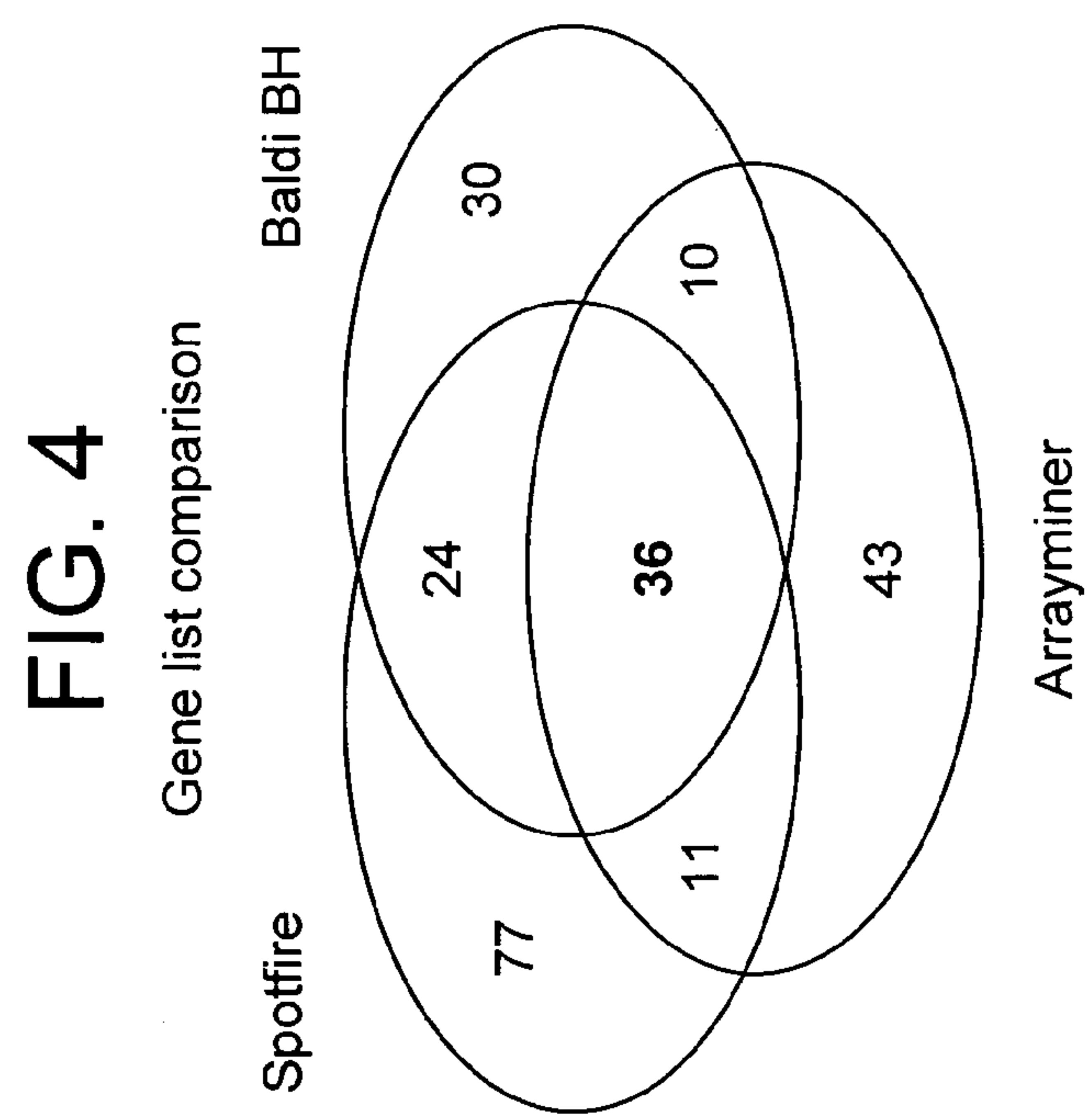


FIG. 3

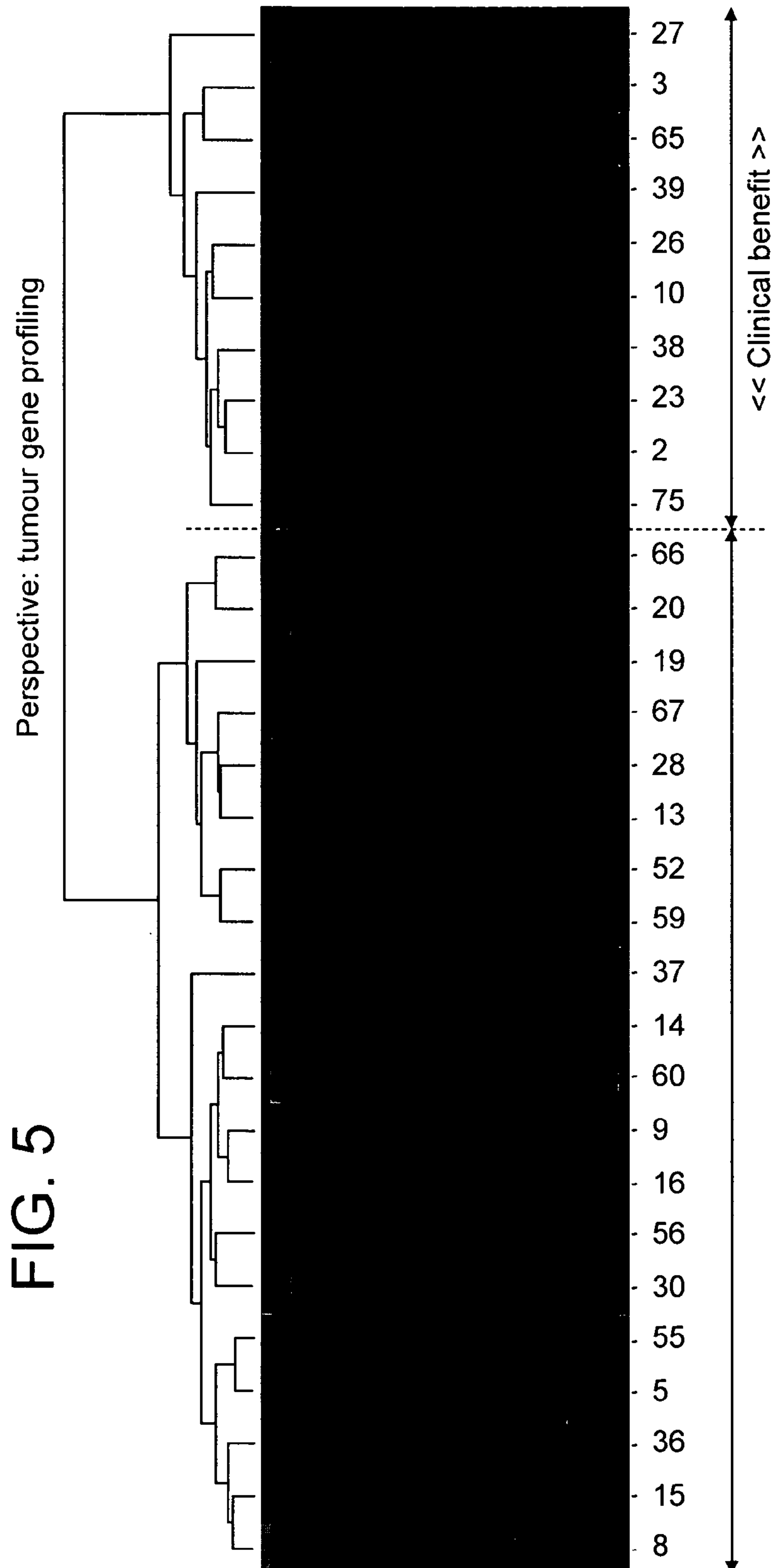
Arrayminer - ClassMaker Software (5 Responses/5 Non-responders)



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FIG. 5A

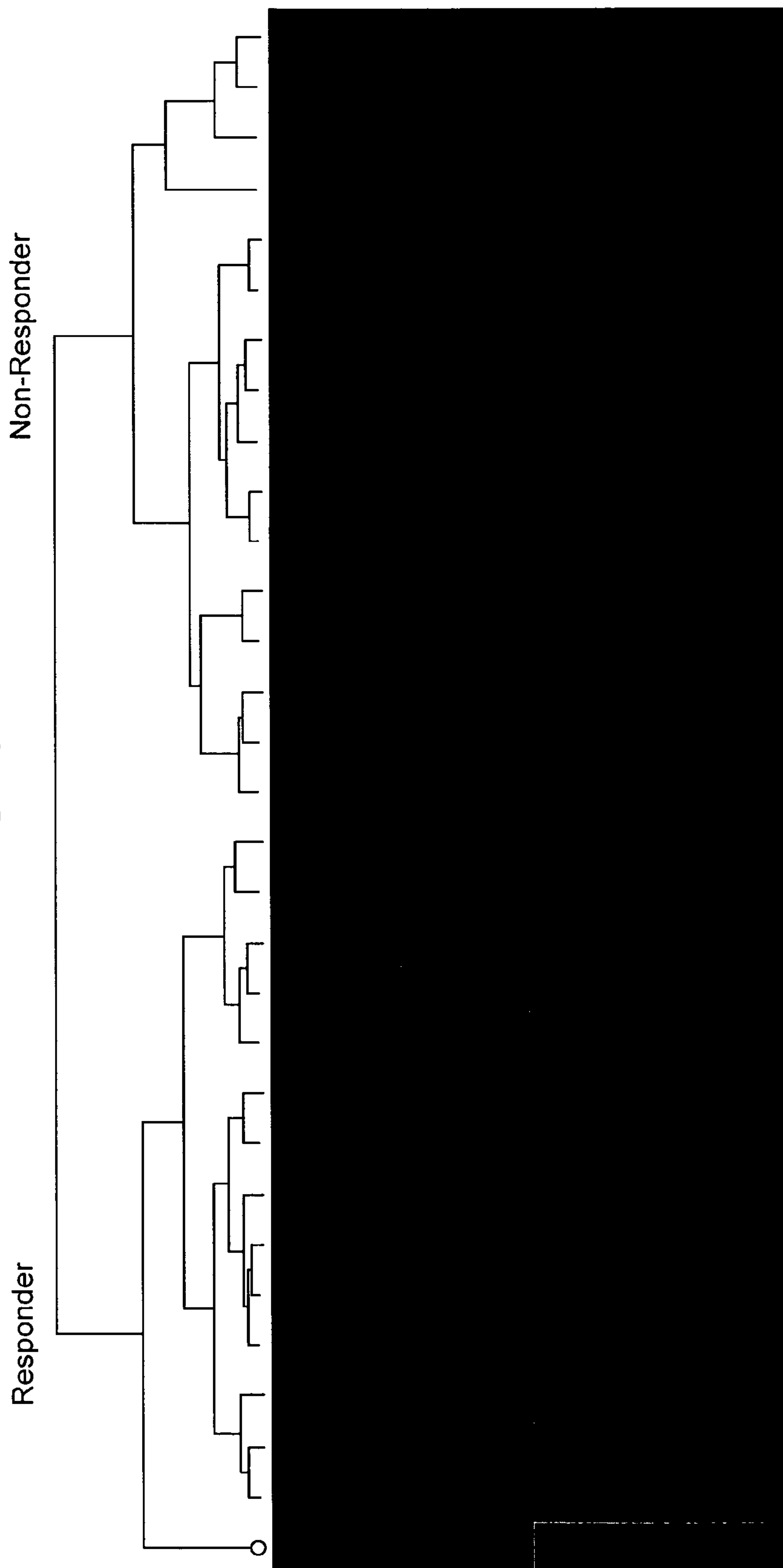
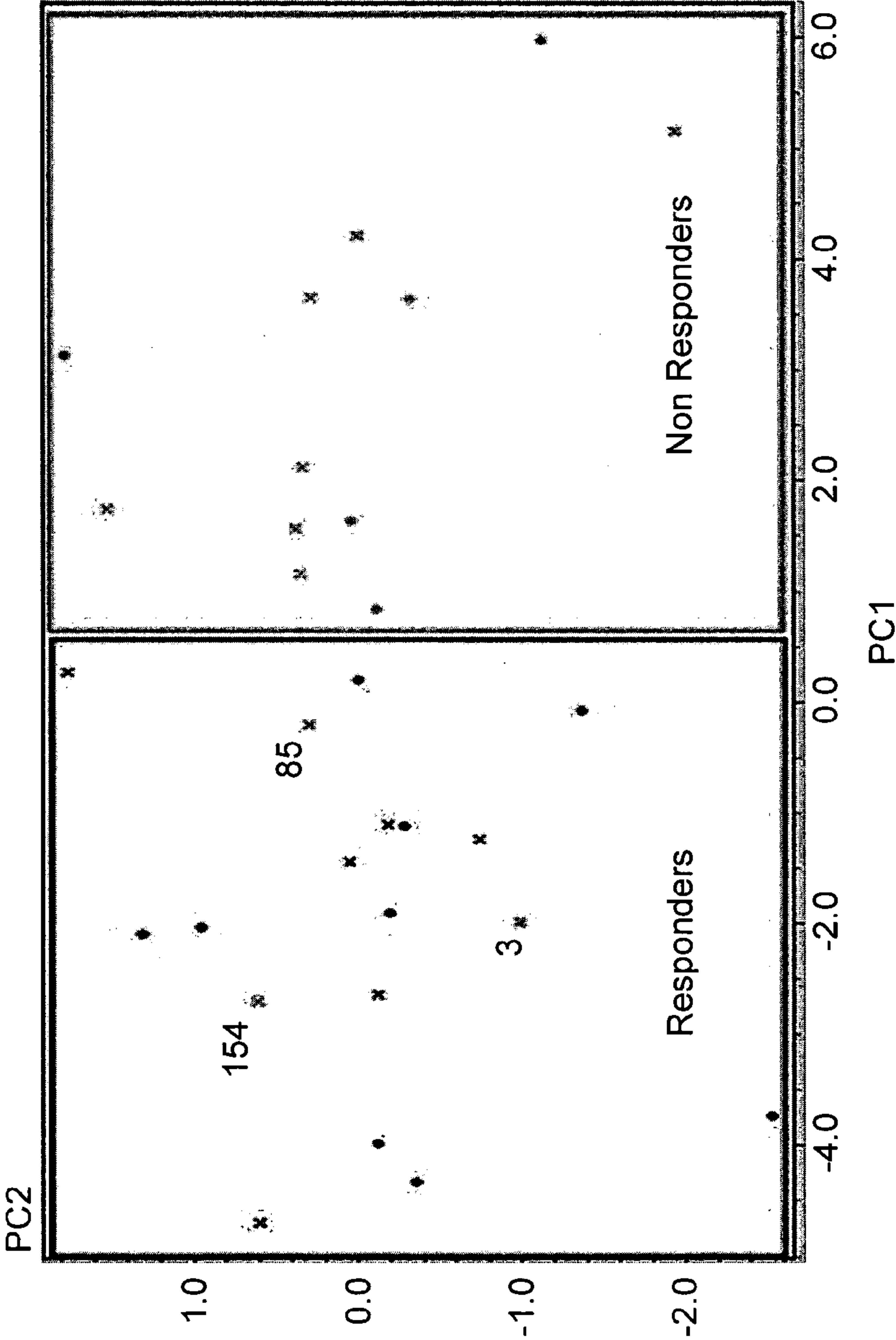


FIG. 6

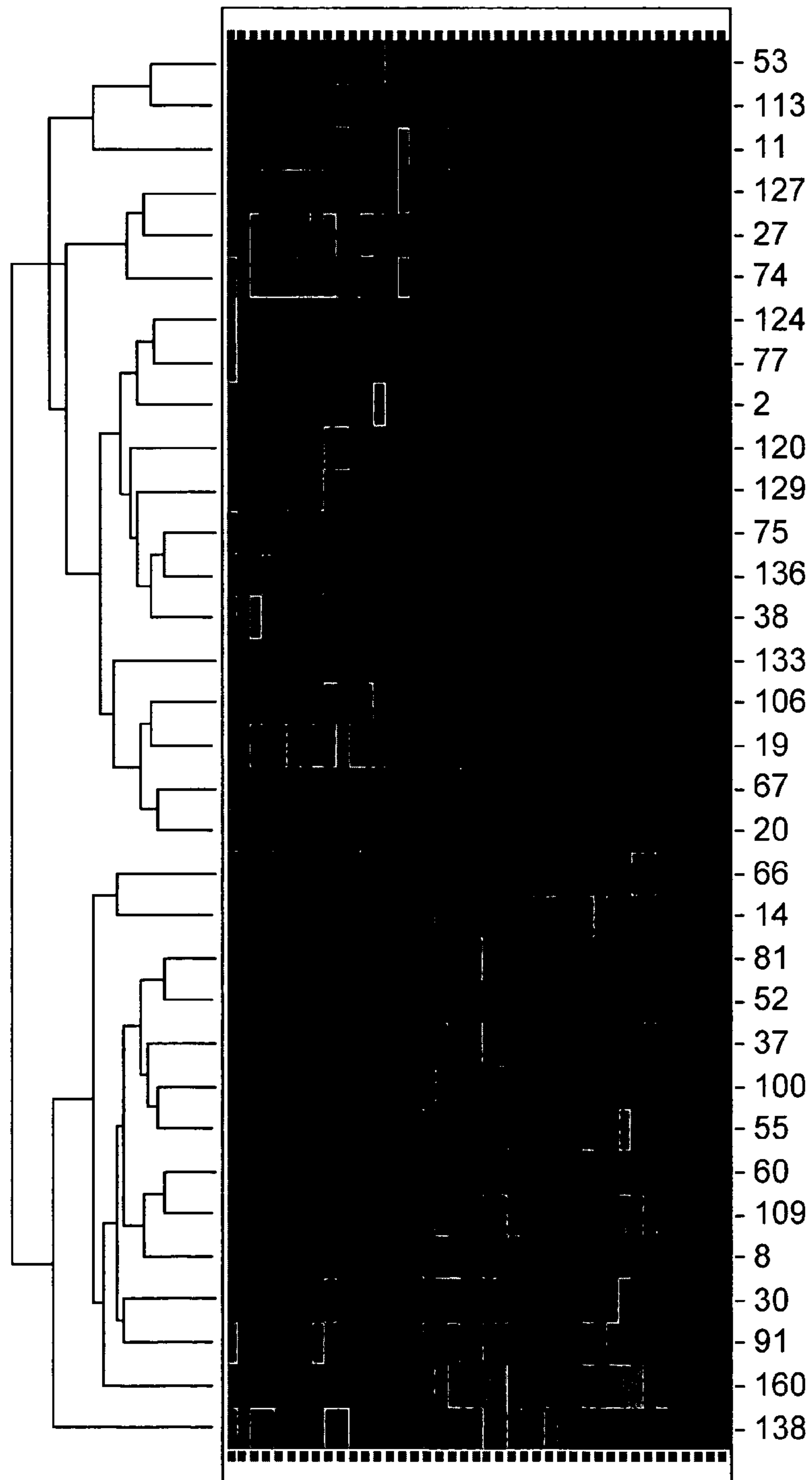
Principal Component Analysis using PRF1, GZMB, GNLY, CD8A, PRKCQ, FOXP3, IFNG, CCL5, GPR171 and TRBV19 genes



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FIG. 7

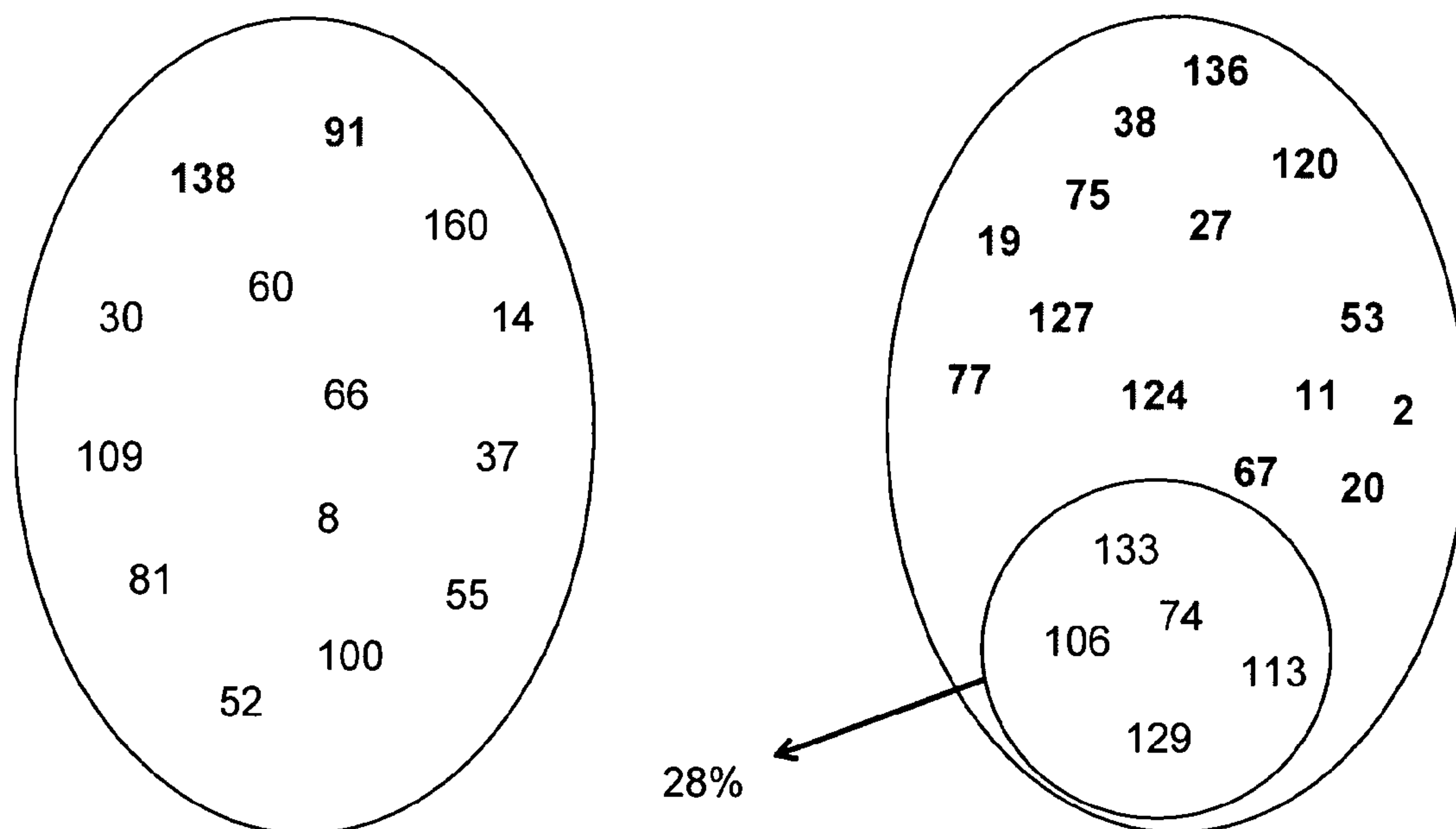
Hierarchical clustering of patients included into the AS15 arm.



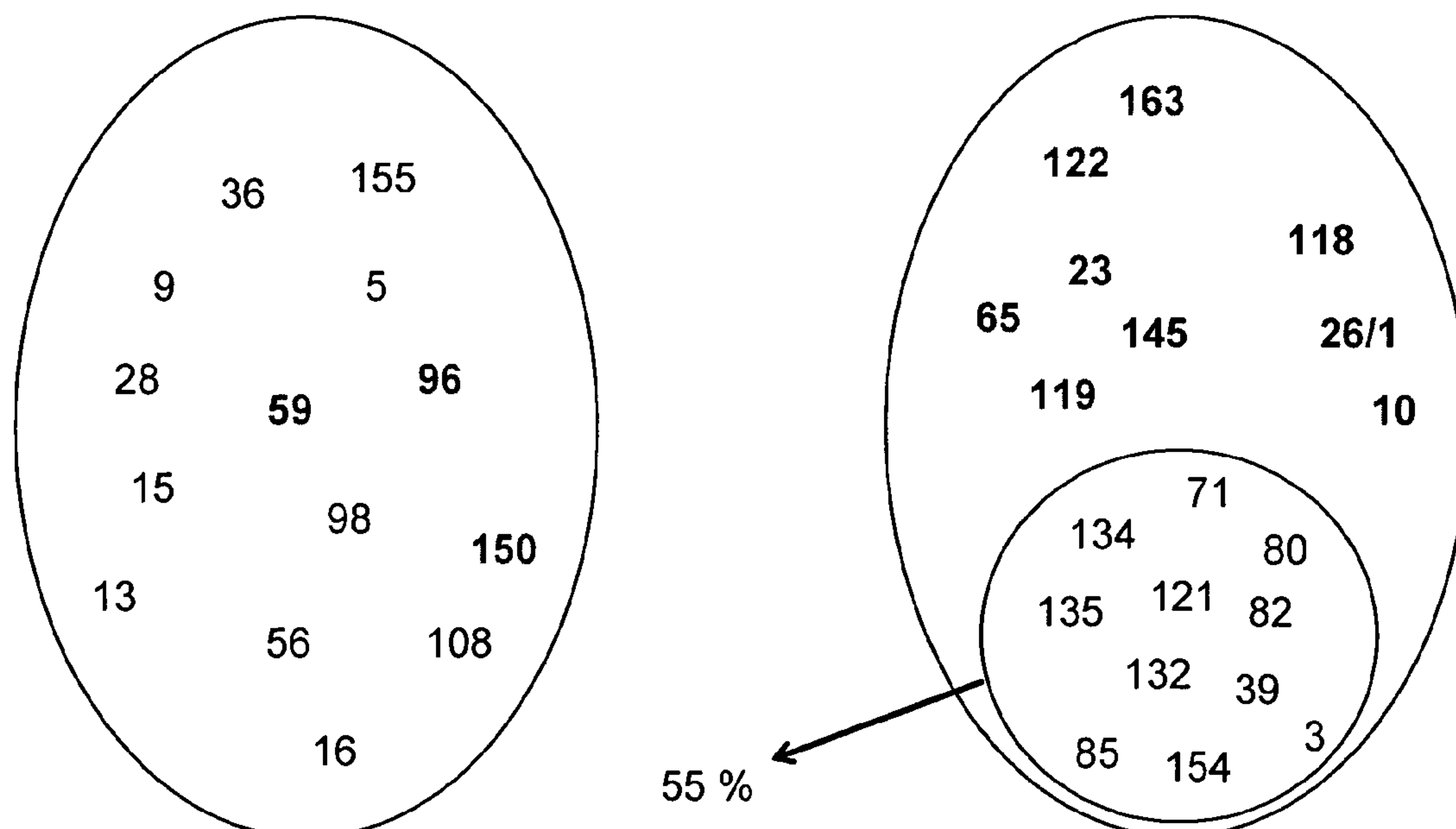
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FIG. 8

Hierarchical clustering of patients included into the AS15 arm.

**FIG. 10**

Hierarchical clustering of patients included into the AS02b arm.



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FIG. 9

Hierarchical clustering of patients included into the AS02b arm.

