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(54) **MHC GENES AND RISK OF GRAFT VERSUS HOST DISEASE**

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(57) **ABSTRACT**

The invention relates to the novel use of gene markers in a method of predicting the risk of or diagnosing a subject to develop graft versus host reaction (GvHR) or graft versus host disease (GvHD). In other aspects the invention also relates to methods of monitoring the efficacy of treatment of GvHR or GvHD, and methods of screening a candidate substance for the treatment of GvHR or GvHD.

Figure 1

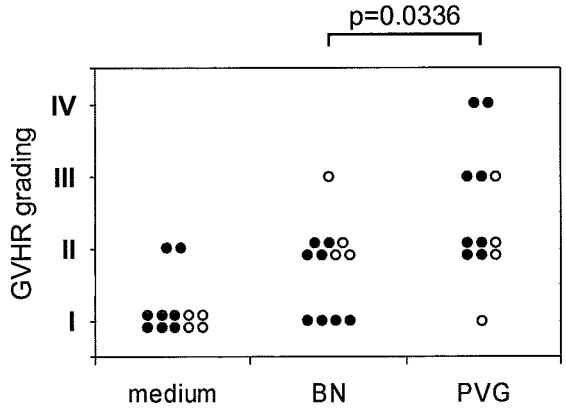


Figure 2

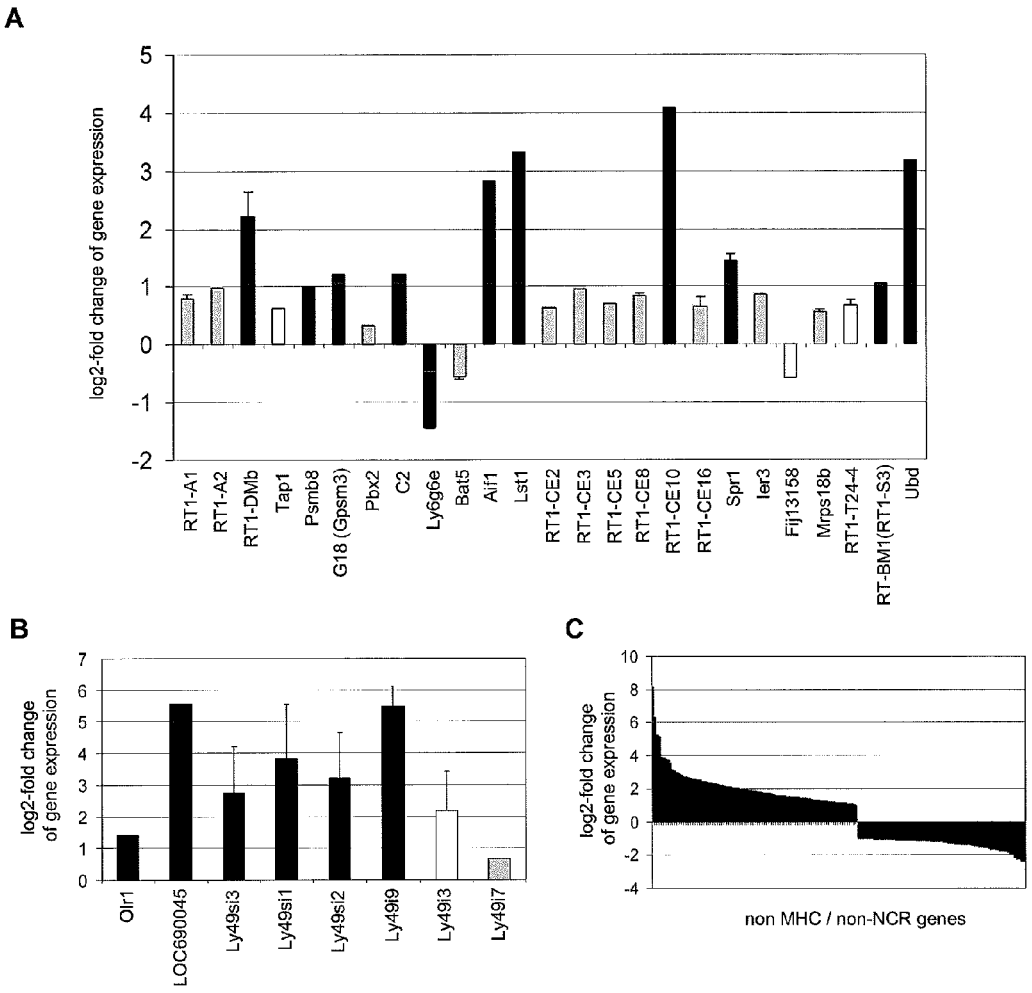

A
log2-fold change of gene expression
5
4
3
2
1
0
-1
-2
RT1-A1
RT1-A2
RT1-DMb
Tap1
Psmb8
G18 (Gpsm3)
Pbx2
C2
Ly6g6e
Bat5
Aif1
Lst1
RT1-CE2
RT1-CE3
RT1-CE5
RT1-CE8
RT1-CE10
RT1-CE16
Spr1
Ier3
Fij13158
Mrps18b
RT1-T24-4
RT-BM1(RT1-S3)
Ubd
B
log2-fold change of gene expression
7
6
5
4
3
2
1
0
Olr1
LOC690045
Ly49si3
Ly49si1
Ly49si2
Ly49i9
Ly49i3
Ly49i7
C
log2-fold change of gene expression
10
8
6
4
2
0
-2
-4
non MHC / non-NCR genes

Figure 3

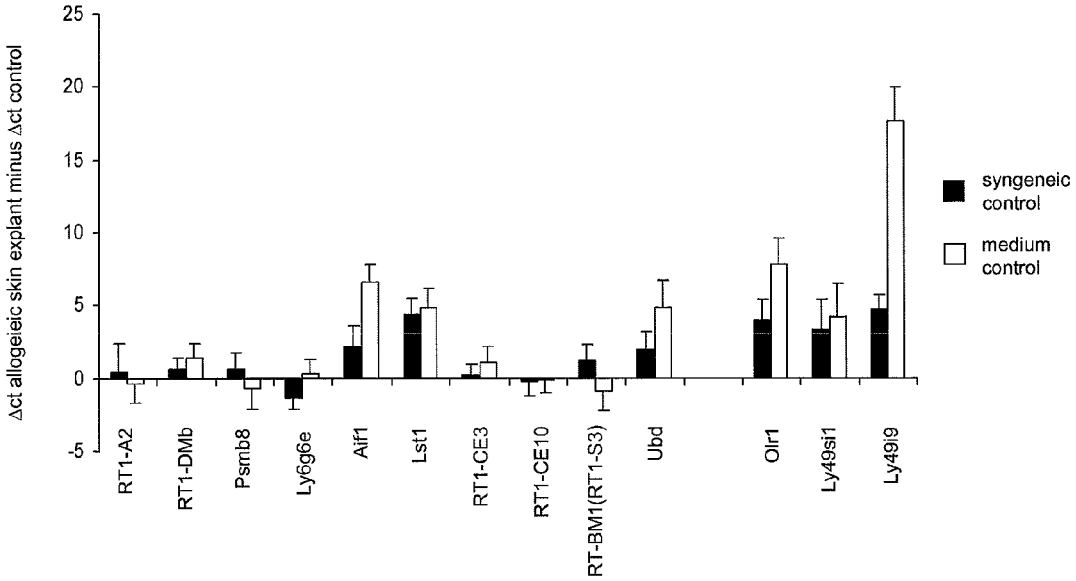

Δct allogeieic skin explant minus Δct control
25
20
15
10
5
0
-5
RT1-A2
RT1-DMb
Psmb8
Ly6g6e
Aif1
Lst1
RT1-CE3
RT1-CE10
RT-BM1(RT1-S3)
Ubd
Olr1
Ly49si1
Ly49i9
syngeneic control
medium control

Figure 4

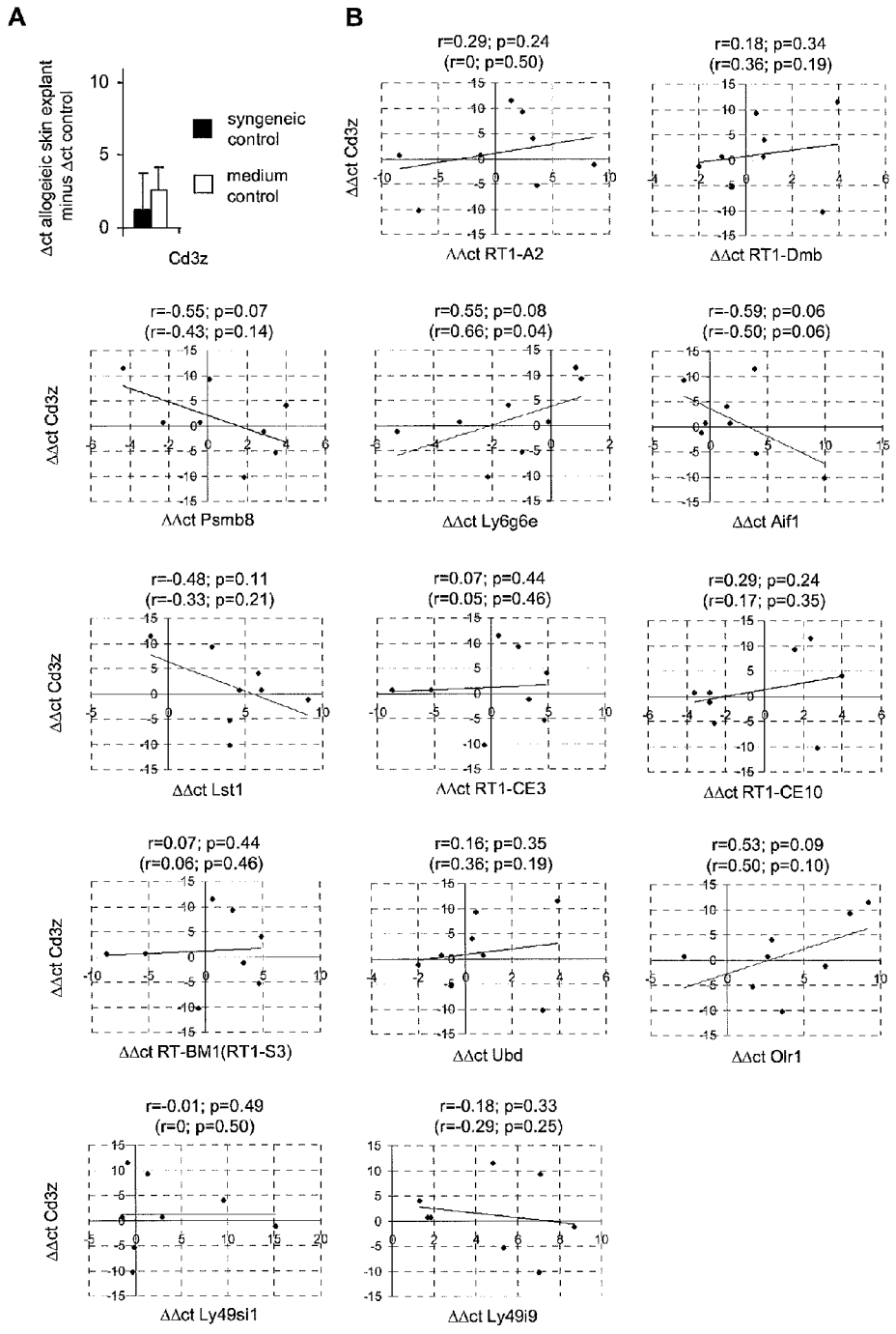

A
B
Δct allogeieic skin explant minus Δct control
syngeneic control
medium control
Cd3z
r=0.29; p=0.24
(r=0; p=0.50)
ΔΔct Cd3z
ΔΔct RT1-A2
r=0.18; p=0.34
(r=0.36; p=0.19)
ΔΔct RT1-Dmb
r=-0.55; p=0.07
(r=-0.43; p=0.14)
ΔΔct Psmb8
r=0.55; p=0.08
(r=0.66; p=0.04)
ΔΔct Ly6g6e
r=-0.59; p=0.06
(r=-0.50; p=0.06)
ΔΔct Aif1
r=-0.48; p=0.11
(r=-0.33; p=0.21)
ΔΔct Lst1
r=0.07; p=0.44
(r=0.05; p=0.46)
ΔΔct RT1-CE3
r=0.29; p=0.24
(r=0.17; p=0.35)
ΔΔct RT1-CE10
r=0.07; p=0.44
(r=0.06; p=0.46)
ΔΔct RT-BM1(RT1-S3)
r=0.16; p=0.35
(r=0.36; p=0.19)
ΔΔct Ubd
r=0.53; p=0.09
(r=0.50; p=0.10)
ΔΔct Olr1
r=-0.01; p=0.49
(r=0; p=0.50)
ΔΔct Ly49sl1
r=-0.18; p=0.33
(r=-0.29; p=0.25)
ΔΔct Ly49i9

Figure 5

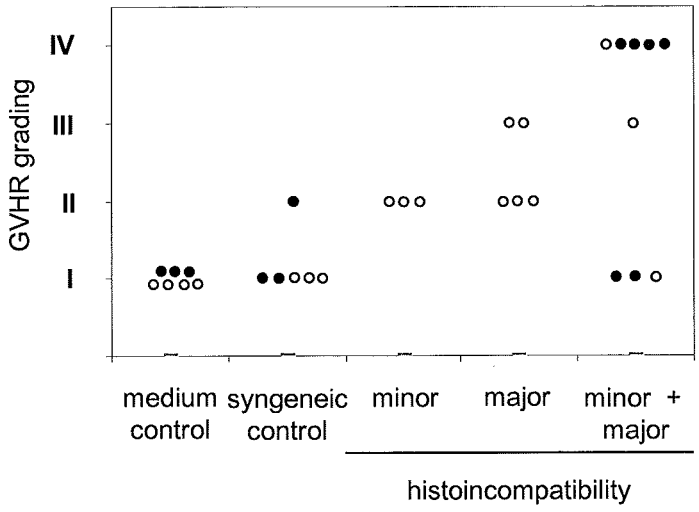

GVHR grading
IV
III
II
I
medium control
syngeneic control
minor
major
minor + major
histoincompatibility

Figure 6

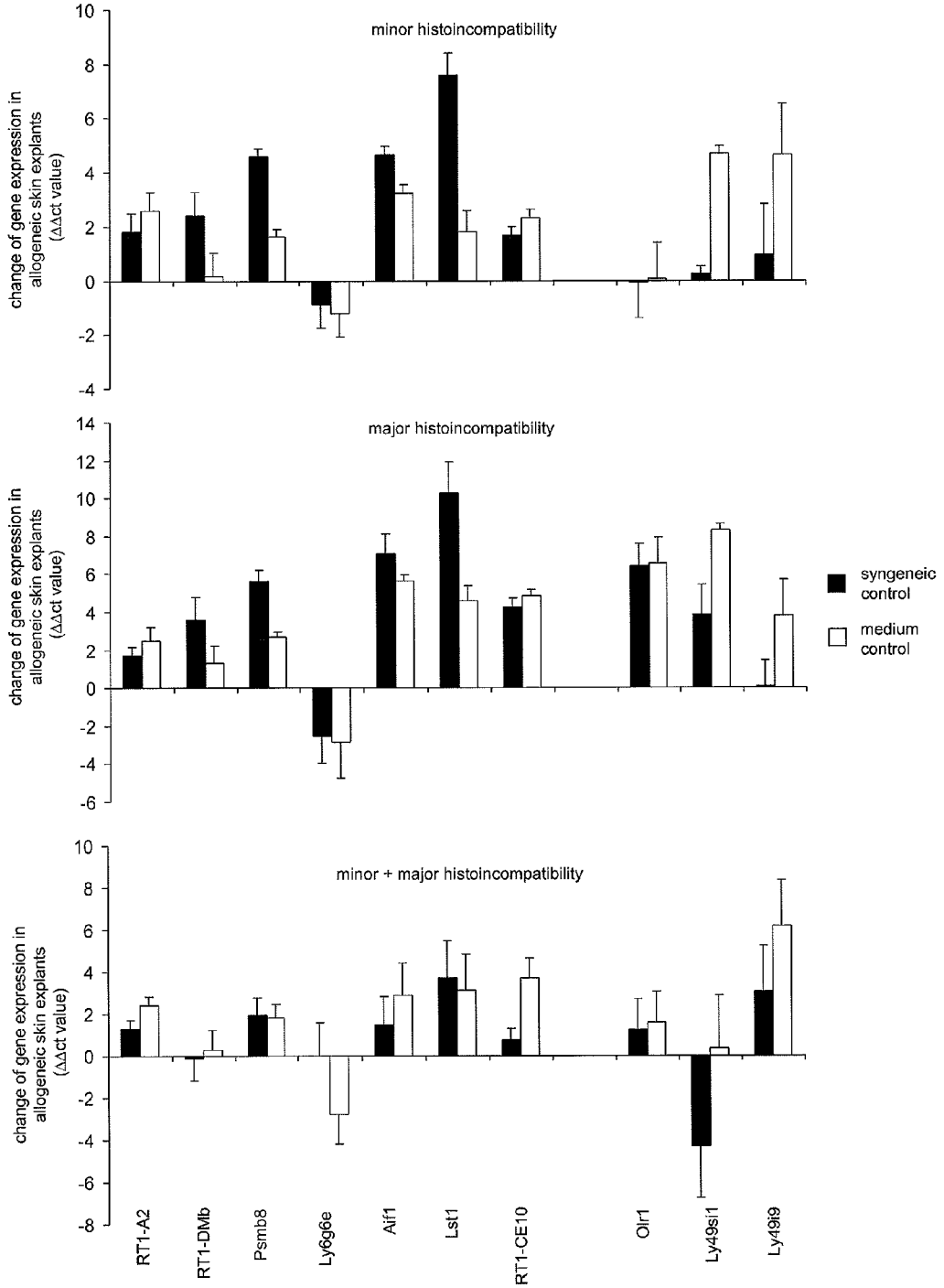

minor histoincompatibility
major histoincompatibility
minor + major histoincompatibility
change of gene expression in allogeneic skin explants (ΔΔct value)
syngeneic control
medium control
RT1-A2
RT1-DMb
Psmb8
Ly6g6e
Aif1
Lst1
RT1-CE10
Olr1
Ly49si1
Ly49i9

Figure 7

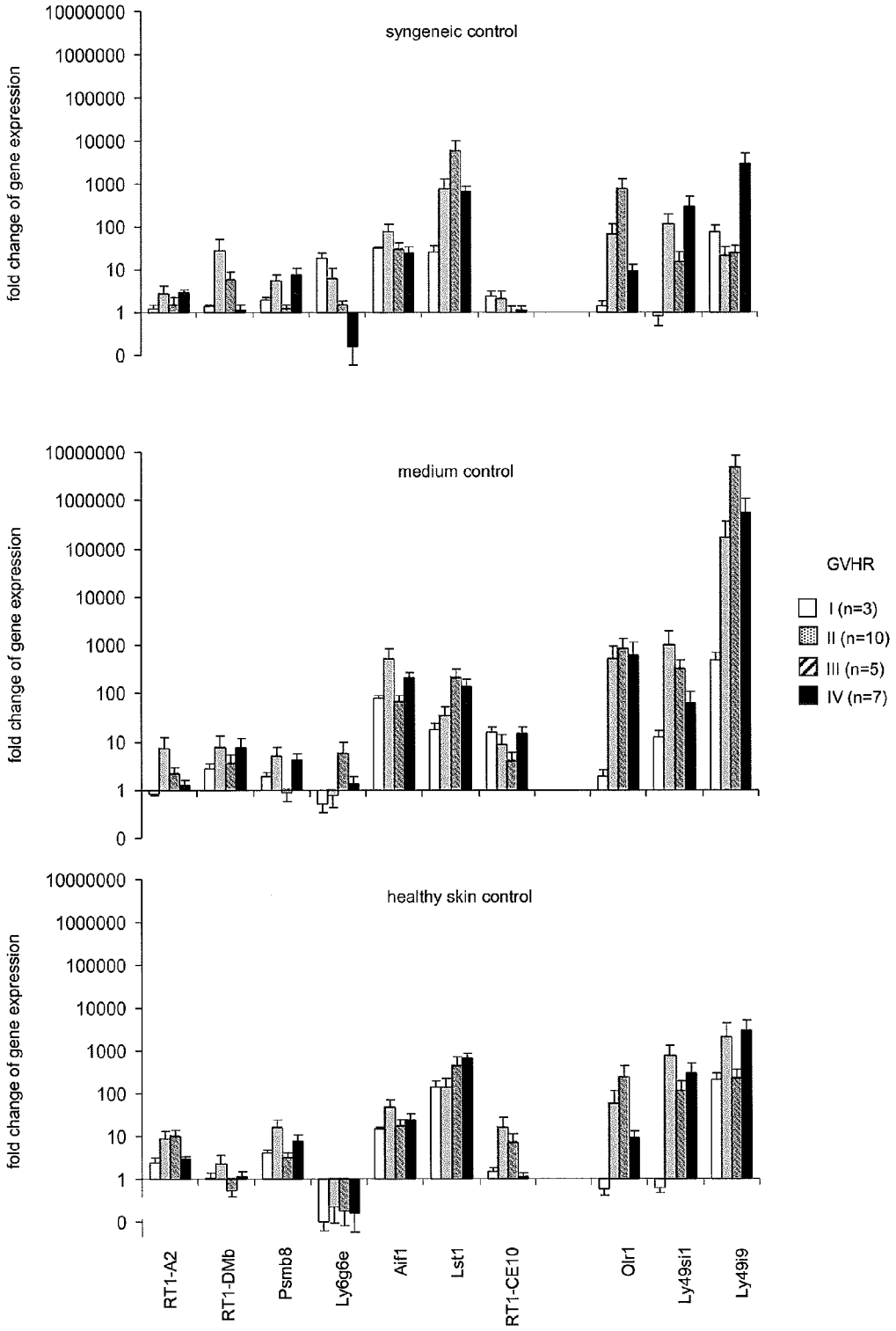
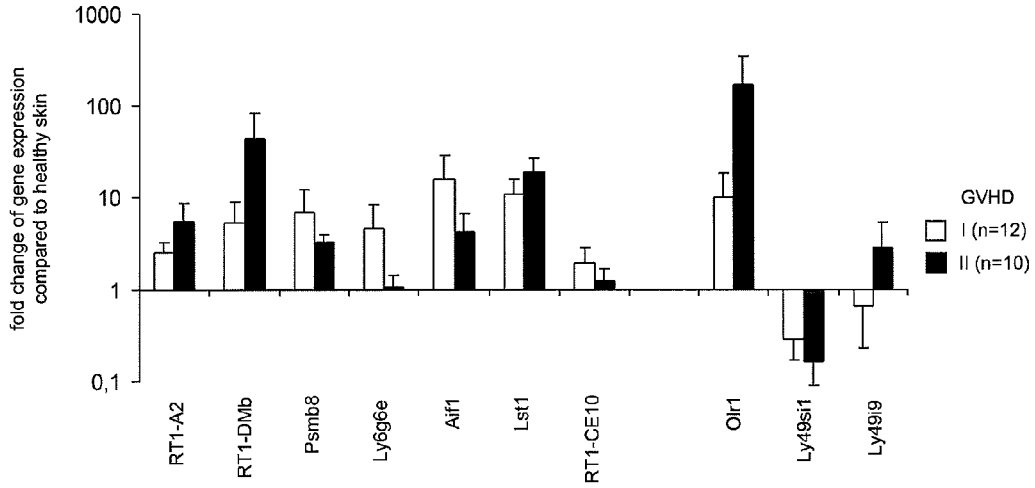

syngeneic control
medium control
healthy skin control
fold change of gene expression
10000000
1000000
100000
10000
1000
100
10
1
0
GVHR
I (n=3)
II (n=10)
III (n=5)
IV (n=7)
RT1-A2
RT1-DMb
Psmb8
Ly6g6e
Aif1
Lst1
RT1-CE10
Olr1
Ly49si1
Ly49i9

Figure 8


1000
100
10
1
0,1
fold change of gene expression compared to healthy skin
RT1-A2
RT1-DMb
Psmb8
Ly6g6e
Aif1
Lst1
RT1-CE10
Olr1
Ly49si1
Ly49i9
GVHD
I (n=12)
II (n=10)

MHC GENES AND RISK OF GRAFT VERSUS HOST DISEASE

FIELD OF THE INVENTION

[0001] The major histocompatibility complex (MHC) is the most important genomic region that contributes to the risk of graft versus host disease (GVHD) after haematopoietic stem cell transplantation. Matching of MHC class I and II genes is essential for the success of transplantation. However, the MHC contains additional genes that also contribute to the risk of developing acute GVHD. The inventors identified rat and human MHC and NKC genes but also non-MHC and non-NKC genes that are regulated during graft versus host reaction (GVHR) in skin explant assays and could therefore serve as biomarkers for GVHD. Several of the respective human genes, including HLA-DMB, C2, AIF1, SPR1, UBD, and OLR1, are polymorphic. These candidates may therefore contribute to the genetic risk of GVHD in patients.

BACKGROUND OF THE INVENTION

[0002] Haematopoietic stem cell transplantation (HSCT) is currently the only potentially curative treatment for many malignant and non-malignant haematological diseases. However, the overall survival rate after transplantation is still only 40% to 60% due to severe posttransplant complications, which include graft versus host disease (GVHD), relapse, and infection. Human leukocyte antigen (HLA) matching is essential to reduce the risk of graft rejection and GVHD. However, non-HLA genes also impact on transplant outcome and acute GVHD can be fatal even in patients receiving transplants from HLA-identical matched sibling donors (MSD). The cumulative incidence of grade 2 to 4 GVHD was 35% in a recent study evaluating 1960 MSD transplants. MSDs are currently available for about one third of the patients and, therefore, alternative donors are needed. HLA-matched unrelated donors (MUD) are more widely accepted than cord blood or mismatched related donors.

[0003] The level of HLA matching used for selection of MUDs has changed over time and usually includes now HLA-A, B, C, and DRB1 loci (8/8 match). In some studies matching has been extended to the HLA-DQB1 locus (10/10 match). A large recent study has compared MSD and 8/8 matched MUD transplants in a homogenous cohort of patients with chronic myeloid leukemia and found a 2.44 times higher risk of grade 2 to 4 acute GVHD in 8/8 matched MUD compared to MSD transplants (Arora M, et al. (2009) J Clin Oncol 27: 1644-1652). In another study, the incidence of grade 2 to 4 acute GVHD was still higher in 10/10 matched MUD compared to MSD transplants (Yakoub-Agha I, et al. (2006) J Clin Oncol 24: 5695-5702). The higher risk of GVHD after MUD compared to MSD transplants could be due to a higher degree of similarity in non-HLA genes for siblings, who share 50% of their genome with the respective recipient. However, also the HLA region itself could contribute to this difference since it harbors, in addition to the classical HLA class I and II genes, more than 200 other genes (Consortium T M S (1999) Nature 401: 921-923), many with immunological functions. In accordance with this hypothesis, mismatching of microsatellite markers in HLA class I, class II, and class III regions was associated with an increased risk of death in 10/10 matched MUD transplants. The HLA complex, as is the whole human genome, is organized into segments of closely linked genetic variants that are inherited as haplotypes on the same DNA strand. HLA haplotypes can be defined by HLA class I and II alleles and they are in strong linkage disequilibrium with defined genetic variants of non-class I/non-class II genes within the haplotype blocks within this region. Interestingly, HLA haplotype mismatching in 10/10 matched MUD transplants was associated with an increased risk of severe acute GVHD (Petersdorf E W, et al. (2007) PLoS Med 4: e8). This finding demonstrates that the HLA complex encodes in addition to HLA-A, B, C, DRB1, and DQB1 further unidentified genes that contribute significantly to the risk of developing acute GVHD. In case of disparity between donor and recipient alleles these genes may function as minor histocompatibility antigens. Alternatively, specific allelic variants may also increase the risk of GVHD, e.g., TNFA, a gene located within the class III region of the MHC encoding the pro-inflammatory cytokine tumor necrosis factor alpha (TNF-alpha). Several TNFA polymorphisms have been associated with an increased risk of GVHD and some of them are associated with increased TNF-alpha levels (Dickinson A M, et al. (2007) Expert Rev Mol Med 9: 1-19). The strong linkage disequilibrium within the HLA complex makes it very difficult to identify further non-class I/non-class II HLA genes involved in the pathophysiology of GVHD by genetic association studies alone.

[0004] HLA gene expression profiling may be an alternative strategy to identify HLA genes that are involved in the pathophysiology of GVHD. The inventors assumed that at least some non-class I/non-class II HLA genes that contribute to the risk of GVHD change their expression levels during disease progression. However, the genetic variation between clinical samples complicates the situation because allelic variation of gene expression could interfere with expression change in the pathophysiological process.

[0005] Accordingly, there is still a need for the identification of genes that contribute significantly to the risk of developing acute GVHD. These genes or gene markers may be used in the assessment of the risk to develop GVHD or GVHR, for the diagnosis of GVHD or GVHR, for monitoring treatment of GVHD or GVHR, and for screening for immunomodulating substances which may be useful in the treatment of GVHD or GVHR.

SUMMARY OF THE INVENTION

[0006] In a first aspect, the invention relates to a method of predicting the risk of a subject to develop graft versus host reaction (GvHR) or graft versus host disease (GvHD), comprising

[0007] (a) determining the expression level of one or more prognostic RNA transcripts, or their corresponding cDNAs, or their expression products, in a sample obtained from said subject, wherein said transcript(s) or expression products is/are the transcript or expression product of one or more genes selected from the group consisting of:

[0008] (i) Msr1, Pik3ap1, Pstpip1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Spic, Nfe2, Tnfaip8l2, and Ier3; or

[0009] (ii) Msr1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Spic, and Nfe2; or

[0010] (iii) Pik3ap1, Pstpip1, Tnfaip8l2, and Ier3;

[0011] (b) comparing the expression level of said one or more prognostic RNA transcript, or its corresponding

cDNA, or its expression product with a corresponding baseline value;

[0012] wherein

[0013] (i) for every unit of increased expression of Olr1, Msr1, Pik3ap1, and/or Pstpip1; or the corresponding cDNA or expression product, said subject is expected to develop GvHR or GvHD; and

[0014] (ii) for every unit of decreased expression of Ctss, Pbx2, Grem1, Ly6g6e, Spr1, Spic, Nfe2, Tnfaip8l2, and/or Ier3; or the corresponding cDNA or expression product, said subject is expected to develop GvHR or GvHD.

[0015] In a second aspect, the invention relates to a method of diagnosing graft versus host reaction (GvHR) or graft versus host disease (GvHD) in a subject following transplantation, comprising:

[0016] (a) determining the expression level of one or more prognostic RNA transcripts, or their corresponding cDNAs, or their expression products, in a sample obtained from said subject, wherein said transcript(s) or expression products is/are the transcript or expression product of one or more genes selected from the group consisting of:

[0017] (i) Msr1, Pik3ap1, Pstpip1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Spic, Nfe2 Tnfaip8l2, and Ier3; or

[0018] (ii) Msr1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Spic, and Nfe2; or

[0019] (iii) Pik3ap1, Pstpip1, Tnfaip8l2, and Ier3;

[0020] (b) comparing the expression level of said one or more prognostic RNA transcript, or its corresponding cDNA, or its expression product with a corresponding baseline value;

[0021] wherein

[0022] (i) every unit of increased expression of Olr1, Msr1, Pik3ap1, and/or Pstpip1, or the corresponding cDNA or expression product, is indicative of GvHR or GvHD; and

[0023] (ii) every unit of decreased expression of Ctss, Pbx2, Grem1, Ly6g6e, Spr1, Spic, Nfe2, Tnfaip8l2, and/or Ier3, or the corresponding cDNA or expression product, is indicative of GvHR or GvHD.

[0024] In a third aspect, the invention relates to a method of monitoring the efficacy of treatment of graft versus host reaction (GvHR) or graft versus host disease (GvHD) in a subject following transplantation, comprising:

[0025] (a) determining the expression level of one or more prognostic RNA transcripts, or their corresponding cDNAs, or their expression products, in a sample obtained from said subject at a first time point T1, and a later second time point T2, wherein said transcript(s) or expression products is/are the transcript or expression product of one or more genes selected from the group consisting of:

[0026] (i) Msr1, Pik3ap1, Pstpip1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Spic, Nfe2, Tnfaip8l2, and Ier3; or

[0027] (ii) Msr1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Spic, and Nfe2; or

[0028] (iii) Pik3ap1, Pstpip1, Tnfaip8l2, and Ier3;

[0029] (b) comparing the expression level of said one or more prognostic RNA transcript, or its corresponding cDNA, or its expression product at time point T1 ($\Delta 1$) and time point T2 ($\Delta 2$) with a corresponding baseline value;

[0030] wherein

[0031] (i) a decline in units of an increased expression of Olr1, Msr1, Pik3ap1, and/or Pstpip1; or the corresponding cDNA or expression product at time point T2 in comparison with the increased expression of said at least one gene at the time point T1 ($\Delta\Delta=\Delta 1-\Delta 2$), is indicative of effective treatment of GvHR or GvHD; and

[0032] (ii) a decline in units of a decreased expression of Ctss, Pbx2, Grem1, Ly6g6e, Spr1, Spic, Nfe2, Tnfaip8l2, and/or Ier3; or the corresponding cDNA or expression product at time point T2 in comparison with the decreased expression of said at least one gene at the time point T1($M=\Delta 1-\Delta 2$), is indicative of effective treatment of GvHR or GvHD.

[0033] In a fourth aspect, the invention relates to a method of screening for a candidate substance for treatment of graft versus host reaction (GvHR) or graft versus host disease (GvHD), comprising:

[0034] (a) monitoring the efficacy of treatment by said candidate substance by using the method according to the third aspect in

[0035] (i) a non-human animal model which suffers from GvHR or GvHD and to which the candidate substance has been administered, or

[0036] (ii) in an ex vivo model, including but not limited to cell-based and/or tissue-based GvHR or HvHD assay such as the Skin Explant Assay, wherein said cells and/or tissue have been contacted with said candidate substance; and

[0037] (b) selecting a candidate substance which shows effective treatment of GvHR or GvHD.

[0038] In a final aspect, the invention pertains to a use of a kit in a method of predicting the risk of developing graft versus host reaction (GvHR) or graft versus host disease (GvHD) according to the first aspect, or in a method of diagnosing GvHR or GvHD according to the second aspect, or in a method of monitoring the efficacy of treatment of GvHR or GvHD according to the third aspect, wherein the kit comprises at least one isolated polynucleotide, wherein each isolated polynucleotide independently comprises

[0039] (i) at least 20 contiguous nucleotides of the nucleotide sequence selected from SEQ ID NO: 1, 3, 5, 7, 8, 10, 12, 14, 16, 18, 20, 22, and/or 24; or SEQ ID NO: 26-47, or

[0040] (ii) a nucleotide sequence having at least 90% identity to (i), or

[0041] (iii) the coding region of a gene comprising a nucleotide sequence according to (i) or (ii), or

[0042] (iv) a nucleotide sequence that can specifically hybridize, under conditions of high stringency, to a polynucleotide having a nucleotide sequence according to (i), (ii) or (iii); and

wherein the kit comprises no more than 9000 isolated polynucleotides in total.

DETAILED DESCRIPTION OF THE INVENTION

[0043] In an exploratory experiment, the inventors analyzed the expression of 169 genes with human homologues, including the respective MHC and NKC region genes, identified in the rat in human skin explant samples (c.f. example 2, and Table 9). These human skin explants were cultured for 1, 2, or 3 days resulting in GVHR of grades I, II, and III, respectively. Notably, 69% of all tested human genes were found to be regulated in at least one of these human samples as predicted by the results of the rat expression profiling experiments. 21%, i.e. 36 of the tested genes, were regulated in all 3 human skin explant samples in accordance with the rat model, but this regulation varied depending on the GVHR grade and the time course of the skin explant assay. Although the inventors only validated these genes firstly on 3 samples,

the unexpectedly high concordance rate between the results of rat and human skin explant assays strongly suggests that the rat skin explant assay is an informative model for human GVHR and possibly GVHD.

[0044] Interestingly, for some of the genes that were found to be regulated in GVHR and GVHD in the rat, the human homologues are polymorphic and disease associations of gene polymorphisms have been described. These include HLA-DMB, C2, AIF1, SPR1, and possibly UBD. Therefore, these genes are especially interesting candidates of further non-class I/class II HLA genes that might confer an increased genetic risk of GVHD after HSCT depending on the genotype. In addition, the OLR1 gene in the NKC is polymorphic and polymorphisms of this gene have been associated with atherosclerosis, myocardial infarction, and Alzheimer's disease.

[0045] Several laboratory tests have been assessed for their ability to predict the risk of GVHD in patients. The skin explant assay has a predictive value of about 80% when cyclosporine alone is used for GVHD prophylaxis. A gene expression analysis of selected genes may help to further improve the predictive value of the assay. Pretransplant gene expression profiling of donor peripheral blood mononuclear cells (PBMC) has recently been shown to be a useful tool to predict the risk of GVHD. Post transplant differences in the gene expression profile of PBMC of patients with acute and chronic GVHD compared to non-GVHD samples have been described.

[0046] The inventors identified rat and human MHC and NKC genes but also non-MHC and non-NKC genes that are regulated during GVHR in skin explant assays and could therefore serve as biomarkers for GVHD. Several of the respective human genes, including HLA-DMB, C2, AIF1, SPR1, UBD, and OLR1, are polymorphic. These candidates may therefore contribute to the genetic risk of GVHD in patients.

[0047] The inventors observed a statistically significant and strong up or down regulation of 11 MHC, 6 NKC, and 168 genes encoded in other genomic regions, i.e. 4.9%, 14.0%, and 2.6% of the tested genes respectively. The regulation of 7 selected MHC and 3 NKC genes was confirmed by quantitative real-time PCR and in independent skin explant assays. In addition, similar regulations of most of the selected genes were observed in GVHD-affected skin lesions of transplanted rats and in human skin explant assays.

[0048] The inventors aimed to identify genes that are regulated during GVHR in the skin explant assay because these genes could be involved in the pathophysiology of GVHR and contribute to the genetic risk of GVHD. Special attention was given to genes encoded within the MHC region for the following reasons: Firstly, evidence has been presented that further risk genes for GVHD in addition to MHC class I and class II genes are present in this region. Secondly, those genes cannot easily be identified by genetic linkage analysis alone due to the strong linkage disequilibrium with MHC class I and class II genes so that expression profiling could be a worthwhile alternative approach. Thirdly, the inventors wanted to focus in this initial study on a fully characterized genomic region of special immunological importance rather than to follow a whole genome expression profiling approach. Importantly, 39% of the BN rat MHC genes (RT1″ haplotype) annotated by Hurt and colleagues (Hurt P, et al. (2004) Genome Res 14: 631-639) were at the time point of array construction not represented in the Agilent database and therefore not represented on the Agilent whole rat genome array. In addition to the MHC region, genes of the NKC region were included because this region encodes Ly49 genes and their products can function as receptors for the numerous MHC class Ia and Ib gene products encoded in the MHC. A higher percentage of MHC genes and NKC genes than genes in other regions of the genome were found to be regulated in the allogeneic skin explants compared to skin samples cocultured with syngeneic lymphocytes. Of the 25 MHC genes found to be significantly regulated ($p<0.05$), 5 are known to be involved in antigen processing and presentation. Besides two of three MHC class Ia genes in the BN strain (RT1-A1 and RT1-A2) that present peptides to cytotoxic T lymphocytes (CTL), the genes Tap1 and Psmb8, encoding a subunit of the antigen transporter and a subunit of the immunoproteasome (also known as LMP7), were found to be up-regulated. RT1-DMb encodes a homologue of HLA-DMB, a chaperone in the MHC class II presentation pathway. Furthermore, non-classical MHC class Ib genes (RT1-CE2, RT1-CE3, RT1-CE5, RT1-CE8, RT1-CE10, RT1-CE16, RT1-T24-4, RT-BM1) were up-regulated during GVHR in the skin explants. The function of the RT1-C/E/M class I genes is not well defined. It is known that they can become targets of CTL and function as ligands for activating or inhibitory NK receptors. RT1-C/E/M incompatibility has been shown to induce skin and pancreas graft rejection and to modulate the fate of MHC class IImismatched heart grafts. The RT1-T24-4 gene belongs to a family of genes that was originally identified as pseudogenes in the haplotype r21. In the RT1″ haplotype all four family members are presumably functional. However, their actual function has not been experimentally demonstrated so far. The RT-BM1 (RT1-S3) gene is assumed to be orthologous to the mouse H2-T23gene, which encodes the Qa-1 molecule. This is a functional homologue of HLA-E, which presents leader peptides of MHC class I molecules to the inhibitory NK receptor CD94/NKG2A. Interestingly, its expression can vary substantially depending on the RT1 haplotype. It has to be noticed that no human/rat orthology can be established for the class I genes in the various class I clusters. Therefore, with respect to class I genes, the rat cannot serve as a model for the HLA complex. However, the non-class I genes are clearly orthologous.

[0049] In addition to Tap1, Psmb8, and RT1-DMb, 12 further non-class I MHC genes were found to be regulated in the rat skin explant assays, some of them also involved in the immune response, such as the complement component C2, while such a role is strongly assumed for other genes. The allograft inflammatory factor 1 (Aif1), was cloned from chronically rejecting rat cardiac allografts and it was also found in transplanted human hearts. Persistent expression of AIF-1 is associated with the development of a cardiac allograft vasculopathy. The expression of AIF-1 is mostly limited to the monocyte/macrophage lineage, and can be augmented by interferon (IFN)-γ. The specific function of the leukocyte specific transcript 1 (Lst1) gene is not known, although its strong expression in dendritic cells and functional data suggest an immunomodulatory role. The expression of human LST1, specifically of splice variants encoding soluble isoforms, was increased in rheumatoid arthritis-affected blood and synovium and was up-regulated in response to IFN-γ. The immediate early response 3 (Ier3) gene is stress-inducible and is involved in the regulation of cell death and oncogenesis. The protein (also known as IEX-1 or IEX-1L) functions in the protection of cells from Fas or TNF-α-

induced apoptosis. However, it increases the rate of apoptosis in ultraviolet B irradiated keratinocytes. Distinct domains of the proteins were described to be responsible for pro and anti-apoptotic activities of the protein. The diubiquitin gene (UbM has been shown to be expressed in rat lymphoblasts, thymus, and testis. In the mouse it is expressed in dendritic cells and B cells, is inducible by IFN-γ, and can cause apoptosis. The protein (also known as FAT10) provides an ubiquitin-independent signal for proteasomal degradation. It has been suggested to participate in antigen processing, but its expression did not affect MHC class I expression or antigen presentation. In view of the reported roles of these genes in the immune response, a direct involvement in GVHD is conceivable.

[0050] For the other regulated MHC genes an involvement in immune functions has not been established so far. Spr1 (or Psors1c2) is the psoriasis susceptibility 1 candidate 2 gene and was found to be expressed in the thymus of rats. Its human homologue is expressed in normal and psoriasis skin and has been suggested to confer susceptibility to psoriasis. The function of the gene product is not known so far. G18 (Gpsm3) is an activator of G-protein signaling. Pbx2 encodes an ubiquitously expressed transcriptional activator. The Ly6g6e gene belongs to the lymphocyte antigen 6 (Ly-6) superfamily that encodes proteins attached to the cell surface by a glycosylphosphatidylinositol (GPI) anchor that is directly involved in signal transduction. Mouse Ly6g6e was found to be highly expressed at the leading edges of cells, on filopodia, which are normally involved in cell adhesion and migration. The mitochondrial ribosomal protein S18B (Mrsps18b) gene encodes a 28S subunit protein that belongs to the ribosomal protein S18P family. The functions of the HLA-B associated transcript 5 (Bat5) and Fij13158 (or RGD1303066) genes have not been characterized so far.

[0051] Many of the up-regulated MHC genes are inducible by IFN-γ, a type II cytokine that is primarily secreted by activated T and NK cells. Several studies have demonstrated an increased level of IFN-γ in the early phase of GVHD. Therefore, this cytokine might be highly important for the regulation of the expression of MHC genes during GVHR.

[0052] The inventors also included the NKC region in the expression profiling which harbors the Ly49 genes that encode NK receptors of the killer cell lectin-like receptor type and some of these have been shown to interact with both MHC class Ia and Ib molecules. In contrast to the MHC region, no reference sequence has been published for the NKC region of the rat. Therefore, 20 genes that were recently assigned to this region in the assembly RGSC v3.4 (Twigger et al. (2008) Nat. Genet. 40: 523-527) were not represented on the array. However, for most of them no function associated with the immune system has been reported. Interestingly, only Ly49 receptor genes which have an ITIM motif in their cytoplasmic region were up-regulated in the allogeneic skin explant assays. This includes also the LOC690045 gene which encodes an immunoreceptor similar to Ly49si1. It is not clear whether one of these gene products interacts with the MHC class Ib molecules that the inventors found to be up-regulated. Ly49 receptors are normally present mainly on NK cells and the skin explants harbored few leukocytes. However, skin resident lymphocytes can become activated in human skin explant assays. Although few NK cells infiltrating a tissue that normally does not contain these cells might cause a drastic relative change in the presence of Ly49 transcripts, the possibility should not be dismissed that other cells may express the receptors under pathological conditions. The role of NK cells for GVHR in skin explants needs to be further explored. In general NK cells are assumed to prevent GVHR, improve engraftment and to exert strong graft-versusleukemia effects without causing GVHD.

[0053] In the NKC region the inventors found one non-Ly49 gene to be regulated. The Olr1 gene encodes a receptor protein which belongs to the C-type lectin superfamily. The protein (also known as LOX-1) binds, internalizes and degrades oxidized low-density lipoprotein, which induces vascular endothelial cell activation and dysfunction, resulting in pro-inflammatory responses, pro-oxidative conditions and apoptosis. In addition, it acts as a receptor for extracellular heat shock protein 70 on dendritic cells. Binding and internalization of heat shock protein 70/peptide complexes channels peptides into the MHC class I presentation pathway. Thus, the protein is involved in antigen cross-presentation to naive T cells.

[0054] In addition to the MHC and NKC region genes, 168 further genes were significantly regulated in allogeneic skin explants. Many of them also have immunological functions and need to be analyzed in more detail in subsequent studies.

[0055] The results obtained in the MHC and NKC gene expression profiling experiment were confirmed in most tested cases by qRT-PCR on the skin explant samples. Some genes, e.g. Aif1 and Ly49i9, appeared to be up-regulated even in grade I GVHR. Olr1, in contrast, was up-regulated predominantly in grade II and III GVHR in all comparisons. Importantly, several of the MHC and NKC genes that were identified to be regulated in the skin explant assays, including Aif1, Lst1, and Olr1, were also regulated in the GVHD affected skin of transplanted animals. Thus, the skin explant assay can model GVHD not only histologically but also with respect to gene regulation. However, the up-regulation of the tested Ly49 genes (Ly49si1 and Ly49i9) that were observed in the skin explant was not clearly confirmed in the GVHD-affected skin of transplanted rats. Skin lesions from transplanted animals are likely to be more heterogeneous with respect to the dynamics of the pathophysiological process than skin explant samples, and this may contribute to the variation in results.

[0056] In conclusion, the MHC gene expression profiling approach in the rat skin explant assay identified a number of non-class I/class II genes that might contribute to the MHC-associated risk of GVHD following HSCT. These genes could be directly involved in the pathophysiology of GVHD or serve as molecular markers for GVHD and GVHR. The possibility should not be dismissed, however, that these marker genes could indicate that protective pathways are induced which modulate tissue damage during inflammation. Moreover, their human homologues may be useful for risk assessment, diagnosis, and as potential targets for therapy of GVHD in patients.

[0057] Accordingly, in a first aspect, the invention relates to a method of predicting the risk of a subject to develop graft versus host reaction (GvHR) or graft versus host disease (GvHD), comprising

[0058] (a) determining the expression level of one or more prognostic RNA transcripts, or their corresponding cDNAs, or their expression products, in a sample obtained from said subject, wherein said transcript(s) or expression products is/are the transcript or expression product of one or more genes selected from the group consisting of:

[0059] (i) Msr1, Pik3ap1, Pstpip1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Spic, Nfe2, Tnfaip8l2, and Ier3; or

[0060] (ii) Msr1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Spic, and Nfe2; or

[0061] (iii) Pik3ap1, Pstpip1, Tnfaip8l2, and Ier3;

[0062] (b) comparing the expression level of said one or more prognostic RNA transcript, or its corresponding cDNA, or its expression product with a corresponding baseline value;

[0063] wherein

[0064] (i) for every unit of increased expression of Olr1, Msr1, Pik3ap1, and/or is Pstpip1; or the corresponding cDNA or expression product, said subject is expected to develop GvHR or GvHD; and

[0065] (ii) for every unit of decreased expression of Ctss, Pbx2, Grem1, Ly6g6e, Spr1, Spic, Nfe2, Tnfaip8l2, and/or Ier3; or the corresponding cDNA or expression product, said subject is expected to develop GvHR or GvHD.

[0066] The term "predicting the risk of a subject" is used herein to refer to the prediction of the likelihood of a subject to develop graft versus host reaction (GvHR) or graft versus host disease (GvHD). The method of the invention may be used clinically in order to determine the best treatment modalities and regimen and/or to evaluate whether said patient is likely to respond favourably to a treatment, such as surgical intervention, as for example a transplantation, in particular with regard to dosage and/or drug combinations.

[0067] The terms "graft versus host reaction" and "graft versus host disease" may be used synonymously. Usually, 3 criteria must be met in order for GvHD to occur: (1) Administration of an immunocompetent graft, with viable and functional immune cells, (2) the recipient is immunologically disparate—histoincompatible, and (3) the recipient is immunocompromised and therefore cannot destroy or inactivate the transplanted cells. Following transplantation, T cells present in the graft, either as contaminants or intentionally introduced into the host, perceive host tissues as antigenically foreign and attack the tissues of the transplant recipient. GvHD occurs not only when there is a mismatch of a major MHC class I or II antigen but also in the context of disparities between minor histocompatibility antigens. GvHD is a common complication in recipients of bone marrow transplants from, e.g., HLA-identical siblings, who typically differ from each other in many polymorphic proteins encoded by genes unlinked to the MHC.

[0068] Clinically, GvHD is divided into acute and chronic forms. Acute and chronic GvHD appear to involve different immune cell subsets, different cytokine profiles, different host targets, and respond differently to treatment. For example, the acute form of GvHD is normally observed within the first 100 days post-transplant, and is a major challenge to transplants owing to associated morbidity and mortality. In contrast thereto, the chronic form of GvHD normally occurs after 100 days. The appearance of moderate to severe cases of chronic GvHD adversely influences long-term survival.

[0069] In order to determine the expression level of one or more prognostic RNA transcripts, or their corresponding cDNAs, or their expression products of one or more genes, a sample comprising cells from the subject and, thus, the prognostic RNA transcripts or their expression products is first derived from said subject.

[0070] The term "sample", as used herein, refers to a sample comprising cells of the subject to be tested, which may be the graft or the host in question, which cells may be homogenized and disrupted in order to release and optionally isolate the prognostic RNA transcripts. Preferably, the sample is a biopsy sample, preferably a biopsy sample of the tissue to be transplanted or of the tissue wherein the transplant is grafted, or a sample of Peripheral Blood Mononuclear Cells (PBMC). A peripheral blood mononuclear cell (PBMC) is a blood cell having a round nucleus. In general, these cells are immune cells, such as lymphocytes (e.g., T cells, B cells, and NK cells), monocytes or macrophages. These cells are often extracted from whole blood using ficoll, a hydrophilic polysaccharide that separates layers of blood, with monocytes and lymphocytes forming a buffy coat containing said PBMCs under a layer of plasma. Alternatively, PBMC can be extracted from whole blood using a hypotonic lysis which will preferentially lyse red blood cells. This method results in neutrophils and other polymorphonuclear (PMN) cells which are important in innate immune defence being obtained. However any other suitable method may be used in order to isolate PBMC from the subject.

[0071] Said RNA transcripts may subsequently be used directly or processed into another form, such as cRNA, cDNA or PCR amplification products, which still represent the expressed genes in said sample of cells, i.e. the transcripts of these genes. RNA can be isolated according to any of a number of methods well known to those of skill in the art. For example, mRNA is isolated using oligo d(T) column chromatography or glass beads. For example, RNA extraction may be performed by using TRIZOL reagent (Invitrogen, Carlsbad, Calif., USA), as described in more detail in the examples.

[0072] Alternatively, a cDNA may be reverse transcribed from said prognostic RNA transcript, RNA transcribed from that cDNA, a DNA amplified from that cDNA, RNA transcribed from the amplified DNA, or the like. Total mRNA can be converted to cDNA and amplified by conventional procedures, for example, by reverse transcription in a per se known manner. A cDNA may be amplified by any of a variety of conventional amplification procedures, including PCR. Suitable PCR primers can be selected using any well-known methods. Further examples of primers are given in the Examples section below.

[0073] For example, the level of expression of a prognostic RNA transcript or their corresponding cDNA in a sample is determined by hybridizing said RNA transcript or corresponding cDNA to a detectable probe, e.g. by performing a microarray, such as a DNA microarray. Alternatively, the expression level may be determined by using quantitative PCR. Then, the mRNA copy number may be calculated from the amount of hybridization, which generally reflects the level of expression of the polynucleotide in the cells of the sample, normalized to the amount of total RNA (or cDNA) or to the expression level of one or more housekeeping genes.

[0074] Methods for detecting hybridization are well known in the art. For example, the prognostic RNA transcript or corresponding cDNA may be labelled with a fluorescent label and levels and patterns of fluorescence indicative of hybridization are measured, e.g. by fluorescence microscopy, preferably confocal fluorescence microscopy. In this detection method, an argon ion laser excites the fluorescent label, emissions are directed to a photomultiplier and the amount of emitted light detected and quantitated. The detected signals are considered to be proportional to the amount of probe/target hybridization complex at each position of the microarray. Further, the fluorescence microscope may be associated

with a computer-driven scanner device to generate a quantitative two-dimensional image of hybridization intensity. The scanned image is examined to determine the abundance/expression level of each hybridized target transcript. Alternatively, a fluorescent imaging device, such as a microarray scanner, may be used.

[0075] Typically, array fluorescence intensities can be normalized to take into account variations in hybridization intensities when more than one array is used under similar test conditions. This may be achieved by using the intensities derived from internal normalization controls contained on each microarray, e.g. from housekeeping genes. Accordingly, "normalized" refers to the expression level of an RNA transcript relative to the expression level of the total RNA or relative to the expression level of a housekeeping gene. Housekeeping genes are genes that are constitutively transcribed at a relatively constant level across many or all known conditions, since the housekeeping gene's products are typically needed for maintenance of the cell. Examples of housekeeping genes include actin, GAPDH, and ubiquitin.

[0076] However, further methods for determining the amount of a polynucleotide are well known in the art and may include any suitable quantitative method. Examples for such further methods are, for example, quantitative PCR, such as real-time PCR, or reverse transcription PCR (RT-PCR), using primers specific for those polynucleotides. Methods for selecting suitable primers for detecting and quantitating the amplified product are known in the art and exemplified in the Examples section below.

[0077] Alternatively, the expression level may be determined by the expression product(s), i.e. by the polypeptides encoded by said genes. This may be accomplished using immunological methods involving the use of antibodies directed against said polypeptides, e.g. the expression level of the corresponding expression product(s) is determined by ELISA or immunohistochemistry.

[0078] In order to perform an ELISA the sample with an unknown amount of expression is product is immobilized on a solid support either non-specifically via adsorption to the surface of the solid support or specifically by a so called capture-antibody specific to the expression product. After the antigen is immobilized the detection antibody is added, forming a complex with the antigen. The detection antibody can itself be covalently linked to an enzyme, or can be detected by a secondary antibody linked to an enzyme. Between each step the plate is typically washed with a mild detergent solution to remove any proteins or antibodies that are not specifically bound. Detection occurs by adding an enzymatic substrate to produce a visible signal, which indicates the quantity of expression product in the sample. Immunohistochemistry refers to a method involving localizing the expression product in said cells of the sample using fluorescence labelled antibodies and determining the fluorescence intensity.

[0079] However, any suitable method may be used for determining the expression level of said expression product (s), such as by way of Western blotting, protein microarray, flow cytometry or surface plasmon resonance.

[0080] Thus, in a preferred embodiment, the expression level is determined by DNA microarray analysis or quantitative PCR and subsequent calculation of the mRNA copy number normalized to the amount of total RNA or to the expression level of one or more housekeeping genes. In another preferred embodiment the expression level of the corresponding expression product(s) is determined by ELISA, Western blotting, protein microarray or immunohistochemistry, flow cytometry or surface plasmon resonance.

[0081] The term "every unit of increased expression" and the term "every unit of decreased expression" as used herein refers to an expression level of one or more prognostic RNA transcripts, or their corresponding cDNAs, or their expression product(s) that has been found differentially expressed in subjects suffering or prone to suffer from GvHD or GvHR in comparison to healthy subjects. Thus, in case of "every unit of increased expression", the higher the expression level of a gene which is predominantly expressed in the cells of a subject who suffers or is prone to suffer from GvHD or GvHR, the higher is the risk that the subject to be tested is expected to develop GvHD or GvHR. Likewise, in case of "every unit of decreased expression", the lower the expression level of a gene which is predominantly expressed in healthy subjects but not in subjects suffering or prone to suffer from GvHD or GvHR, the higher is the risk that the subject to be tested develops GvHR or GvHD.

[0082] The determined expression level may be compared to a corresponding baseline value. As used herein, the term "corresponding baseline value" refers to the level of gene expression in normal cells or PBMCs, e.g. in a sample from a healthy subject or from a "pool" of samples derived from healthy subjects; or from a pool of one or more tissues from healthy subjects. Any of the above types of baseline values may be available in a database compiled from such values. Therefore, in a preferred embodiment, the baseline value may be the expression level of said at least one gene in at least one healthy subject.

[0083] An expression level of a gene may be considered as being increased if the log 2-fold change is at least 1, such as at least 1.1, or at least 1.2, preferably at least 1.25, such as at least 1.5 or at least 1.75, more preferably at least 2.0, such as at least 2.25 or at least 2.5, and most preferably at least 2.75 or even at least 3.0. Likewise, an expression level of a gene may be considered as being decreased if the log 2-fold change is at least −1, such as at least −1.1, or at least −1.2, preferably at least −1.25, such as at least −1.5 or at least −1.75, more preferably at least −2.0, such as at least −2.25 or at least −2.5, and most preferably at least −2.75 or even at least −3.0.

[0084] Alternatively, the term "increased" amount means herein an amount which is typically at least 120%, at least 130%, at least 140%, at least 150%, at least 175%, preferably at least 200%, at least 225%, at least 250%, at least 275%, more preferably at least 300%, at least 350%, or at least 400%, most preferably at least 500% of the baseline value.

[0085] Likewise, the term "decreased", as meant herein, refers to an amount which is typically less than 90%, less than 85%, less than 80%, less than 75%, more preferably less than 70%, less than 65%, less than 60%, even more preferably less than 50%, less than 40%, or less than 30%, most preferably less than 25%, less than 20%, or even less than 10% of the baseline value.

[0086] The term "one or more" as used herein means that either one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, or all thirteen expression level(s) of said genes is/are determined.

[0087] The term "corresponding", as used herein, refers to the baseline value of the same gene as determined in the sample. The genes and their respective reference sequence is given in Table 10 below as well as in SEQ ID NOs 1-25.

[0088] The following combinations of biomarkers are contemplated to be particularly useful:

Combination	Ctss	Pbx2	Grem1	Ly6g6e	Olr1	Spr1	Msr1	Spic	Nfe2	Tnfaip8l2	Ier3	Pik3ap1	Pstpip1
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		+		+									
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65					+	+							
66					+		+						
67					+			+					
68					+				+				
69					+					+			
70					+						+		
71					+							+	
72					+								+

-continued

Combination	Ctss	Pbx2	Grem1	Ly6g6e	Olr1	Spr1	Msr1	Spic	Nfe2	Tnfaip8l2	Ier3	Pik3ap1	Pstpip1
73						+							
74							+						
75								+					
76									+				
77										+			
78											+		
79												+	
80													+
81						+	+						
82						+		+					
83						+			+				
84						+				+			
85						+					+		
86						+						+	
87						+							+
88							+	+					
89							+		+				
90							+			+			
91							+				+		
92							+					+	
93							+						+
94								+	+				
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142			+	+								+	
143			+	+									+
144			+	+									
145				+	+	+							
146				+	+		+						
147				+	+			+					
148				+	+				+				
149				+	+					+			

-continued

Combination	Ctss	Pbx2	Grem1	Ly6g6e	Olr1	Spr1	Msr1	Spic	Nfe2	Tnfaip8l2	Ier3	Pik3ap1	Pstpip1
150				+	+						+		
151				+	+							+	
152				+	+								+
153					+	+							
154					+		+						
155					+			+					
156					+				+				
157					+					+			
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164						+				+			
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168						+	+	+					
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210			+	+	+								
211			+	+	+	+							
212			+	+	+		+						
213			+	+	+			+					
214			+	+	+				+				
215			+	+	+					+			
216			+	+	+						+		
217			+	+	+							+	
218			+	+	+								+
219				+	+	+							
220				+	+		+						
221				+	+			+					
222				+	+				+				
223				+	+					+			
224				+	+						+		

-continued

Combination	Ctss	Pbx2	Grem1	Ly6g6e	Olr1	Spr1	Msr1	Spic	Nfe2	Tnfaip8l2	Ier3	Pik3ap1	Pstpip1
225				+	+							+	
226				+	+								+
227					+	+	+						
228					+	+		+					
229					+	+			+				
230					+	+				+			
231					+	+					+		
232					+	+						+	
233					+	+							+
234						+	+	+					
235						+	+		+				
236						+	+			+			
237						+	+				+		
238						+	+					+	
239						+	+						+
240						+	+	+	+				
241						+	+	+		+			
242						+	+	+			+		
243						+	+	+				+	
244						+	+	+					+
245							+	+	+	+			
246							+	+	+		+		
247							+	+	+			+	
248							+	+	+				+
249								+	+	+	+		
250								+	+	+		+	
251								+	+	+			+
252									+	+	+	+	
253									+	+	+		+
254										+	+	+	+
255	+	+	+	+	+								
256	+	+	+	+									
257	+	+	+	+		+							
258	+	+	+	+			+						
259	+	+	+	+				+					
260	+	+	+	+					+				
261	+	+	+	+						+			
262	+	+	+	+							+		
263	+	+	+	+								+	
264	+	+	+	+									+
265		+	+	+	+								
266		+	+	+	+	+							
267		+	+	+	+		+						
268		+	+	+	+			+					
269		+	+	+	+				+				
270		+	+	+	+					+			
271		+	+	+	+						+		
272		+	+	+	+							+	
273		+	+	+	+								+
274			+	+	+	+							
275			+	+	+		+						
276			+	+	+			+					
277			+	+	+				+				
278			+	+	+					+			
279			+	+	+						+		
280			+	+	+							+	
281			+	+	+								+
282				+	+	+	+						
283				+	+	+		+					
284				+	+	+			+				
285				+	+	+				+			
286				+	+	+					+		
287				+	+	+						+	
288				+	+	+							+
289					+	+	+	+					
290					+	+	+		+				
291					+	+	+			+			
292					+	+	+				+		
293					+	+	+					+	
294					+	+	+						+
295						+	+	+	+				
296						+	+	+		+			
297						+	+	+			+		
298						+	+	+				+	
299						+	+	+					+

-continued

Combination	Ctss	Pbx2	Grem1	Ly6g6e	Olr1	Spr1	Msr1	Spic	Nfe2	Tnfaip8l2	Ier3	Pik3ap1	Pstpip1
300						+	+	+					
301						+	+	+					
302						+	+	+					
303						+	+	+	+	+			
304						+	+	+	+		+		
305						+	+	+	+			+	
306						+	+	+	+				+
307						+	+	+	+				
308						+	+	+	+				
309						+	+	+	+				
310							+	+	+	+	+		
311							+	+	+	+		+	
312							+	+	+	+			+
313								+	+	+	+	+	
314								+	+	+	+		+
315									+	+	+	+	+
316	+	+	+	+	+								
317	+	+	+	+	+	+							
318	+	+	+	+	+		+						
319	+	+	+	+	+			+					
320	+	+	+	+	+				+				
321	+	+	+	+	+					+			
322	+	+	+	+	+						+		
323	+	+	+	+	+							+	
324	+	+	+	+	+								+
325		+	+	+	+	+							
326		+	+	+	+		+						
327		+	+	+	+			+					
328		+	+	+	+				+				
329		+	+	+	+					+			
330		+	+	+	+						+		
331		+	+	+	+							+	
332		+	+	+	+								+
333			+	+	+	+	+						
334			+	+	+	+		+					
335			+	+	+	+			+				
336			+	+	+	+				+			
337			+	+	+	+					+		
338			+	+	+	+						+	
339			+	+	+	+							+
340				+	+	+	+	+					
341				+	+	+	+		+				
342				+	+	+	+			+			
343				+	+	+	+				+		
344				+	+	+	+					+	
345				+	+	+	+						+
346					+	+	+	+	+				
347					+	+	+	+		+			
348					+	+	+	+			+		
349					+	+	+	+				+	
350					+	+	+	+					+
351						+	+	+	+	+			
352						+	+	+	+		+		
353						+	+	+	+			+	
354						+	+	+	+				+
355						+	+	+	+	+	+		
356						+	+	+	+	+		+	
357						+	+	+	+	+			+
358							+	+	+	+	+	+	
359							+	+	+	+	+		+
360								+	+	+	+	+	+
361								+	+	+	+	+	
362	+	+	+	+	+	+							
363	+	+	+	+	+		+						
364	+	+	+	+	+			+					
365	+	+	+	+	+				+				
366	+	+	+	+	+					+			
367	+	+	+	+	+						+		
368	+	+	+	+	+							+	
369	+	+	+	+	+								+
370		+	+	+	+	+	+						
371		+	+	+	+	+		+					
372		+	+	+	+	+			+				
373		+	+	+	+	+				+			
374		+	+	+	+	+					+		

-continued

Combination	Ctss	Pbx2	Grem1	Ly6g6e	Olr1	Spr1	Msr1	Spic	Nfe2	Tnfaip8l2	Ier3	Pik3ap1	Pstpip1
375		+	+	+	+	+						+	
376		+	+	+	+	+							+
377			+	+	+	+	+	+					
378			+	+	+	+	+		+				
379			+	+	+	+	+			+			
380			+	+	+	+	+				+		
381			+	+	+	+	+					+	
382			+	+	+	+	+						+
383				+	+	+	+	+	+				
384				+	+	+	+	+		+			
385				+	+	+	+	+			+		
386				+	+	+	+	+				+	
387				+	+	+	+	+					+
388					+	+	+	+	+	+			
389					+	+	+	+	+		+		
390					+	+	+	+	+			+	
391					+	+	+	+	+				+
392						+	+	+	+	+	+		
393						+	+	+	+	+		+	
394						+	+	+	+	+			+
395						+	+	+	+	+	+	+	
396						+	+	+	+	+	+		+
397							+	+	+	+	+	+	+
398	+	+	+	+	+	+	+						
399	+	+	+	+	+	+		+					
400	+	+	+	+	+	+			+				
401	+	+	+	+	+	+				+			
402	+	+	+	+	+	+					+		
403	+	+	+	+	+	+						+	
404	+	+	+	+	+	+							+
405		+	+	+	+	+	+	+					
406		+	+	+	+	+	+		+				
407		+	+	+	+	+	+			+			
408		+	+	+	+	+	+				+		
409		+	+	+	+	+	+					+	
410		+	+	+	+	+	+						+
411			+	+	+	+	+	+	+				
412			+	+	+	+	+	+		+			
413			+	+	+	+	+	+			+		
414			+	+	+	+	+	+				+	
415			+	+	+	+	+	+					+
416				+	+	+	+	+	+	+			
417				+	+	+	+	+	+		+		
418				+	+	+	+	+	+			+	
419				+	+	+	+	+	+				+
420					+	+	+	+	+	+	+		
421					+	+	+	+	+	+		+	
422					+	+	+	+	+	+			+
423						+	+	+	+	+	+	+	
424						+	+	+	+	+	+		+
425						+	+	+	+	+	+	+	+
426	+	+	+	+	+	+	+	+					
427	+	+	+	+	+	+	+		+				
428	+	+	+	+	+	+	+			+			
429	+	+	+	+	+	+	+				+		
430	+	+	+	+	+	+	+					+	
431	+	+	+	+	+	+	+						+
432		+	+	+	+	+	+	+	+				
433		+	+	+	+	+	+	+		+			
434		+	+	+	+	+	+	+			+		
435		+	+	+	+	+	+	+				+	
436		+	+	+	+	+	+	+					+
437			+	+	+	+	+	+	+	+			
438			+	+	+	+	+	+	+		+		
439			+	+	+	+	+	+	+			+	
440			+	+	+	+	+	+	+				+
441				+	+	+	+	+	+	+	+		
442				+	+	+	+	+	+	+		+	
443				+	+	+	+	+	+	+			+
444					+	+	+	+	+	+	+	+	
445					+	+	+	+	+	+	+		+
446						+	+	+	+	+	+	+	+
447	+	+	+	+	+	+	+	+	+				
448	+	+	+	+	+	+	+	+		+			
449	+	+	+	+	+	+	+	+			+		

-continued

Combination	Ctss	Pbx2	Grem1	Ly6g6e	Olr1	Spr1	Msr1	Spic	Nfe2	Tnfaip8l2	Ier3	Pik3ap1	Pstpip1
450	+	+	+	+	+	+	+	+				+	
451	+	+	+	+	+	+	+	+					+
452		+	+	+	+	+	+	+	+	+			
453		+	+	+	+	+	+	+	+		+		
454		+	+	+	+	+	+	+	+			+	
455		+	+	+	+	+	+	+	+				+
456			+	+	+	+	+	+	+	+	+		
457			+	+	+	+	+	+	+	+		+	
458			+	+	+	+	+	+	+	+			+
459				+	+	+	+	+	+	+	+	+	
460				+	+	+	+	+	+	+	+		+
461					+	+	+	+	+	+	+	+	+
462	+	+	+	+	+	+	+	+	+	+			
463	+	+	+	+	+	+	+	+	+		+		
464	+	+	+	+	+	+	+	+	+			+	
465	+	+	+	+	+	+	+	+	+				+
466		+	+	+	+	+	+	+	+	+	+		
467		+	+	+	+	+	+	+	+	+		+	
468		+	+	+	+	+	+	+	+	+			+
469			+	+	+	+	+	+	+	+	+	+	
470			+	+	+	+	+	+	+	+	+		+
471				+	+	+	+	+	+	+	+	+	+
472	+	+	+	+	+	+	+	+	+	+	+		
473	+	+	+	+	+	+	+	+	+	+		+	
474	+	+	+	+	+	+	+	+	+	+			+
475		+	+	+	+	+	+	+	+	+	+	+	
476		+	+	+	+	+	+	+	+	+	+		+
477			+	+	+	+	+	+	+	+	+	+	+
478	+	+	+	+	+	+	+	+	+	+	+	+	
479	+	+	+	+	+	+	+	+	+	+	+		+
480	+	+	+	+	+	+	+	+	+	+	+	+	+
481							+					+	+

[0089] In a preferred embodiment, the subject is a mammal, preferably a mouse, rat, guinea pig, cat, dog, sheep, horse, cow, pig, more preferably the subject is a human.

[0090] In another preferred embodiment, the method further comprises determining the prognostic transcript of one or more genes selected from the group of genes consisting of Ubd, C2, Lst1, Aif1, C1QTNF7, CEACAM4, MME, IGFBP5, TAP1, CTGF, ANP32A, HCLS1, HTRA1, LGALS7, PTGER2, PTPN7, TGM2, TREM2 and CARD11; or their corresponding cDNAs, or their expression products, wherein

[0091] (i) for every unit of increased expression of one or more of Ubd, C2, Aif1, CEACAM4, TAP1, PTGER2, PTPN7, TGM2, TREM2, HCLS1 and/or CARD11; or the corresponding cDNA or expression product, said patient is expected to develop GvHR or GvHD; and

[0092] (ii) for every unit of decreased expression of one or more of Lst1, C1QTNF7, MME, CTGF, ANP32A, HTRA1, LGALS7 and/or IGFBP5; or the corresponding cDNAs or expression product(s), said patient is expected to develop GvHR or GvHD.

[0093] Accordingly, any combination of genes Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Msr1, Spic, Nfe2, Tnfaip8l2, Ier3, Pik3ap1, and Pstpip1 may be combined with any combination of genes Ubd, C2, Lst1, Aif1, C1QTNF7, CEACAM4, MME, IGFBP5, TAP1, CTGF, ANP32A, HCLS1, HTRA1, LGALS7, PTGER2, PTPN7, TGM2, TREM2 and CARD11.

[0094] In a second aspect, the invention relates to a method of diagnosing graft versus host reaction (GvHR) or graft versus host disease (GvHD) in a subject following transplantation, comprising:

[0095] (a) determining the expression level of one or more prognostic RNA transcripts, or their corresponding cDNAs, or their expression products, in a sample obtained from said subject, wherein said transcript(s) or expression products is/are the transcript or expression product of one or more genes selected from the group consisting of:

[0096] (i) Msr1, Pik3ap1, Pstpip1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Spic, Nfe2 Tnfaip8l2, and Ier3; or

[0097] (ii) Msr1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Spic, and Nfe2; or

[0098] (iii) Pik3ap1, Pstpip1, Tnfaip8l2, and Ier3;

[0099] (b) comparing the expression level of said one or more prognostic RNA transcript, or its corresponding cDNA, or its expression product with a corresponding baseline value;

[0100] wherein

[0101] (i) every unit of increased expression of Olr1, Msr1, Pik3ap1, and/or Pstpip1, or the corresponding cDNA or expression product, is indicative of GvHR or GvHD; and

[0102] (ii) every unit of decreased expression of Ctss, Pbx2, Grem1, Ly6g6e, Spr1, Spic, Nfe2, Tnfaip8l2, and/or Ier3, or the corresponding cDNA or expression product, is indicative of GvHR or GvHD.

[0103] The preferred embodiments of the first aspect are also preferred embodiments of the second aspect, and the same definitions apply.

[0104] However, in one particularly preferred embodiment, the baseline value is the expression level of said at least one gene in said subject prior to said transplantation and/or in at least one healthy subject.

[0105] In a preferred embodiment of the second aspect, said method further comprises determining the prognostic tran-

script of one or more genes selected from the group of genes consisting of Ubd, C2, Lst1, Aif1, C1QTNF7, CEACAM4, MME, IGFBP5, TAP1, CTGF, ANP32A, HCLS1, HTRA1, LGALS7, PTGER2, PTPN7, TGM2, TREM2 and CARD11; or their corresponding cDNAs, or their expression products, wherein

[0106] (i) every unit of increased expression of Ubd, C2, Aif1, CEACAM4, TAP1, PTGER2, PTPN7, TGM2, TREM2, HCLS1 and/or CARD11; or the corresponding cDNA or expression product, is indicative of GvHR or GvHD; and

[0107] (ii) every unit of decreased expression of Lst1, C1QTNF7, MME, CTGF, ANP32A, HTRA1, LGALS7 and/or IGFBP5; or the corresponding cDNA or expression product, is indicative of GvHR or GvHD.

[0108] In a third aspect, the invention relates to a method of monitoring the efficacy of treatment of graft versus host reaction (GvHR) or graft versus host disease (GvHD) in a subject following transplantation, comprising:

[0109] (a) determining the expression level of one or more prognostic RNA transcripts, or their corresponding cDNAs, or their expression products, in a sample obtained from said subject at a first time point T1, and a later second time point T2, wherein said transcript(s) or expression products is/are the transcript or expression product of one or more genes selected from the group consisting of:

[0110] (i) Msr1, Pik3ap1, Pstpip1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Spic, Nfe2, Tnfaip8l2, and Ier3; or

[0111] (ii) Msr1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Spic, and Nfe2; or

[0112] (iii) Pik3ap1, Pstpip1, Tnfaip8l2, and Ier3;

[0113] (b) comparing the expression level of said one or more prognostic RNA transcript, or its corresponding cDNA, or its expression product at time point T1 (Δ1) and time point T2 (Δ2) with a corresponding baseline value;

[0114] wherein

[0115] (i) a decline in units of an increased expression of Olr1, Msr1, Pik3ap1, and/or Pstpip1; or the corresponding cDNA or expression product at time point T2 in comparison with the increased expression of said at least one gene at the time point T1 (ΔΔ=Δ1−Δ2), is indicative of effective treatment of GvHR or GvHD; and

[0116] (ii) a decline in units of a decreased expression of Ctss, Pbx2, Grem1, Ly6g6e, Spr1, Spic, Nfe2, Tnfaip8l2, and/or Ier3; or the corresponding cDNA or expression product at time point T2 in comparison with the decreased expression of said at least one gene at the time point T1(ΔΔ=Δ1−Δ2), is indicative of effective treatment of GvHR or GvHD.

[0117] The preferred embodiments of the first and second aspect are also preferred embodiments of the third aspect, and the same definitions apply.

[0118] In another preferred embodiment, the method of the third aspect further comprises determining the prognostic transcript of one or more genes selected from the group of genes consisting of Ubd, C2, Lst1, Aif1, C1QTNF7, CEACAM4, MME, IGFBP5, Tap1, Ctgf, ANP32A, HCLS1, HTRA1, LGALS7, PTGER2, PTPN7, TGM2, TREM2 and CARD11; or their corresponding cDNAs, or their expression products, wherein

[0119] (i) a decline in units of an increased expression of Ubd, C2, Aif1, CEACAM4, Tap1, PTGER2, PTPN7, TGM2, TREM2, HCLS1 and/or CARD11; or the corresponding cDNA or expression product at time point T2 in comparison with the increased expression of said at least one gene at the time point T1 (M=Δ1−Δ2), is indicative of effective treatment of GvHR or GvHD; and

[0120] (ii) a decline in units of a decreased expression of Lst1, C1QTNF7, MME, Ctgf, ANP32A, HTRA1, LGALS7 and/or IGFBP5; or the corresponding cDNA or expression product at time point T2 in comparison with the decreased expression of said at least one gene at the time point T1(ΔΔ=Δ1−Δ2), is indicative of effective treatment of GvHR or GvHD.

[0121] In a very important fourth aspect, the invention further relates to a method of screening for a candidate substance for treatment of graft versus host reaction (GvHR) or graft versus host disease (GvHD), comprising:

[0122] (a) monitoring the efficacy of treatment by said candidate substance by using the method according to the third aspect in

[0123] (i) a non-human animal model which suffers from GvHR or GvHD and to which the candidate substance has been administered, or

[0124] (ii) in an ex vivo model, including but not limited to cell-based and/or tissue-based GvHR or HvHD assay such as the Skin Explant Assay, wherein said cells and/or tissue have been contacted with said candidate substance; and

[0125] (b) selecting a candidate substance which shows effective treatment of GvHR or GvHD.

[0126] Preferably, the screening method is carried out in vitro, i.e. in an ex vivo model, with cultured cells or with tissue, and by applying high throughput procedures. One example of such an ex vivo model is the Skin Explant Assay. This unique, non-artificial, (human) in vitro assay technology allows the study of primary and secondary immune responses in the presence of immunomodulatory drugs or allogeneic stem cells, reducing the need for extensive animal testing. Incubation with, for example, human skin, allows skin damage to be assessed by histopathology. The skin is graded for histological damage using criteria similar to that used and observed in the clinical setting. Results correlate with systemic disease and have been shown to predict outcome. The Skin Explant Assay is further exemplified in the Examples section and in the references cited therein.

[0127] Candidate substances selected by the screening method according to the invention may be subsequently also tested in vivo.

[0128] Alternatively, the screening assay may be directly performed in vivo by using a non-human animal model which suffers from GvHR or GvHD. Suitable non-human animal models include rats, mice, guinea pigs, pigs, dogs, and cats. However, it has to be made sure that the scientific gain outweighs any animal suffering, and that the testings are carried out in accordance with national restrictions for animal testings.

[0129] A variety of types of putative candidate substances may be tested and identified as suitable. For example, one can utilize known properties of a target protein to devise agents to stimulate or inhibit its production or activity, as desired. That is, one can devise a means to inhibit the action of, or bind, block, remove or otherwise diminish the presence, activity and/or availability of, a protein whose upregulation is associated with GvHD or GvHR; or one can devise a means to stimulate the action of, or to potentiate or enhance the activity of or availability of, a protein whose down-regulation is associated with GvHD or GvHR.

[0130] For example, in the case of a cellular receptor, one could expose the receptor to an antagonist, a soluble form of the receptor or a "decoy" ligand binding site of a receptor (to compete for ligand) to inhibit it. Antibodies may be administered to a cell to bind and inactivate (or compete with), or to enhance the activity of, secreted protein products or expressed cell-surface products of genes of interest.

[0131] Another approach is to employ antisense oligonucleotides or nucleic acid constructs that inhibit expression of a gene whose down-regulation is desired, in a highly specific manner. Methods to select, test and optimize putative antisense sequences are routine. Nucleic acid constructs may be used to express an antisense molecule of interest, or antisense oligonucleotides as such may be administered to a cell. The oligonucleotides can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotides can be modified at the base moiety, sugar moiety, or phosphate backbone. The oligonucleotide may include other appending groups such as peptides, or agents facilitating transport across the cell membrane, hybridization-triggered cleavage agents, or intercalating agents. Multiple antisense constructs or oligonucleotides specific for different genes can be employed together. The sequences of the down-regulated genes described herein can be used to design the antisense molecules. The antisense sequences may range from about 6 to about 50 nucleotides, and may be as large as 100 or 200 nucleotides, or larger. They may correspond to full-length coding sequences and/or may be genomic sequences that comprise non-coding sequences.

[0132] Another approach is to use ribozymes that can specifically cleave nucleic acids encoding the overexpressed genes disclosed herein. Such methods are routine in the art and methods of making and using any of a variety of appropriate ribozymes are well known to the skilled worker. A ribozyme having specificity for an mRNA of interest can be designed based upon the nucleotide sequence of, e.g., the corresponding cDNA. Alternatively, the sequence of an overexpressed gene disclosed herein can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules.

[0133] Another approach involves double stranded RNAs called small interfering RNAs. A siRNA is a double-stranded RNA molecule comprising self-complementary sense and antisense regions, wherein the antisense region comprises nucleotide sequence that is complementary to nucleotide sequence in a target nucleic acid molecule or a portion thereof, and the sense region has a nucleotide sequence corresponding to the target nucleic acid sequence or a portion thereof. The siRNA can be assembled from two separate oligonucleotides, where one strand is the sense strand and the other is the antisense strand, wherein the antisense and sense strands are self-complementary. The siRNA can be assembled from a single oligonucleotide, where the self-complementary sense and antisense regions of the siRNA are linked by means of a nucleic acid based or non-nucleic acid-based linker. The siRNA may be a polynucleotide having a hairpin secondary structure, i.e. having self-complementary sense and antisense regions. The siRNA may be a circular single-stranded polynucleotide having two or more loop structures and a stem comprising self-complementary sense and antisense regions, wherein the circular polynucleotide can be processed either in vivo or in vitro to generate an active siRNA molecule capable of mediating RNAi. In certain embodiments, the siRNA molecule comprises separate sense and antisense sequences or regions, wherein the sense and antisense regions are covalently linked by nucleotide or non-nucleotide linkers molecules as is known in the art, or are alternately non-covalently linked by ionic interactions, hydrogen bonding, van der Waals interactions, hydrophobic interactions, and/or stacking interactions. RNAi molecules may be used to inhibit gene expression, using conventional procedures.

[0134] Another approach is to use small molecules, or "compounds", isolated from natural sources or developed synthetically, e.g., by combinatorial chemistry. In general, such molecules are identified from large libraries of natural products or synthetic (or semisynthetic) extracts or chemical libraries according to methods known in the art. Those skilled in the field of drug discovery and development will understand that the precise source of test extracts or compounds is not critical to the methods of the invention. Accordingly, virtually any number of chemical extracts or compounds can be used in the methods described herein. Examples of such extracts or compounds include, but are not limited to, plant-, fungal-, prokaryotic- or animal-based extracts, fermentation broths, and synthetic compounds, as well as modification of existing compounds. Numerous methods are also available for generating random or directed synthesis (e.g., semi-synthesis or total synthesis) of any number of chemical compounds, including, but not limited to, saccharide-, lipid-, peptide-, polypeptide- and nucleic acid-based compounds. Synthetic compound libraries are commercially available, e.g., from Brandon Associates (Merrimack, N.H.) and Aldrich Chemical (Milwaukee, Wis.). Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant, and animal extracts are commercially available from a number of sources, e.g., Biotics (Sussex, UK), Xenova (Slough, UK), Harbor Branch Oceangraphics Institute (Ft. Pierce, Fla.), and PharmaMar, U.S.A. (Cambridge, Mass.). In addition, natural and synthetically produced libraries are generated, if desired, according to methods known in the art, e.g., by standard extraction and fractionation methods. Furthermore, if desired, any library or compound is readily modified using standard chemical, physical, or biochemical methods.

[0135] Methods for introducing candidate substances into cells are conventional. For example, methods of gene transfer may be used, wherein antisense molecules, ribozymes, or siRNAs are introduced into a rectal carcinoma cell of interest, or nucleic acids that encode proteins which modulate (up-regulate or down-regulate) the production or activity of one or more of the genes disclosed herein. Methods of gene transfer are conventional, and include virus-mediated gene transfer, for example, with retroviruses, lentiviruses, and recombinant adenovirus vectors. Adeno-associated virus (AAV) may also be used. Improved efficiency is attained by the use of promoter enhancer elements in the DNA constructs. In addition to virus-mediated gene transfer, physical means well-known in the art can be used for direct gene transfer, including administration of plasmid DNA and particle-bombardment mediated gene transfer. Furthermore, electroporation or calcium phosphate transfection, both well-known means to transfer genes into cell in vitro, may also be used. Gene transfer may also be achieved by using "carrier mediated gene transfer". Preferred carriers are targeted liposomes such as immunoliposomes, which can incorporate acylated monoclonal antibodies into the lipid bilayer, or polycations such as asialoglycoprotein/polylysine. Liposomes have been used to

encapsulate and deliver a variety of materials to cells, including nucleic acids and viral particles. Preformed liposomes that contain synthetic cationic lipids form stable complexes with polyanionic DNA. Cationic liposomes, liposomes comprising some cationic lipid, that contained a membrane fusion-promoting lipid dioctadecyldimethyl-ammonium-bromide (DDAB) have efficiently transferred heterologous genes into eukaryotic cells and can mediate high level cellular expression of transgenes, or mRNA, by delivering them into a variety of cultured cell lines.

[0136] In still a final aspect, the invention describes the use of a kit in a method of predicting the risk of developing graft versus host reaction (GvHR) or graft versus host disease (GvHD) according to the first aspect, or in a method of diagnosing GvHR or GvHD according to the second aspect, or in a method of monitoring the efficacy of treatment of GvHR or GvHD according to the third aspect, wherein the kit comprises at least one isolated polynucleotide, wherein each isolated polynucleotide independently comprises

[0137] (i) at least 20 contiguous nucleotides of the nucleotide sequence selected from SEQ ID NO: 1, 3, 5, 7, 8, 10, 12, 14, 16, 18, 20, 22, and/or 24; or SEQ ID NO: 26-47, or

[0138] (ii) a nucleotide sequence having at least 90% identity to (i), or

[0139] (iii) the coding region of a gene comprising a nucleotide sequence according to (i) or (ii), or

[0140] (iv) a nucleotide sequence that can specifically hybridize, under conditions of high stringency, to a polynucleotide having a nucleotide sequence according to (i), (ii) or (iii); and

wherein the kit comprises no more than 9000 isolated polynucleotides in total.

[0141] The isolated polynucleotide may have at least 90% identity to a polynucleotide cornprising a nucleotide sequence selected from the group of nucleotide sequences consisting of at least 20 contiguous nucleotides of the nucleotide sequence selected from SEQ ID NO: 1, 3, 5, 7, 8, 10, 12, 14, 16, 18, 20, 22, and/or 24; or SEQ ID NO: 26-47; more preferably to the CDS encoded therein. Preferably, said isolated polynucleotide, has a nucleotide sequence having at least 92%, at least 94%, at least 96%, at least 98%, or 99% nucleotide sequence identity to a polynucleotide comprising a nucleotide sequence selected from the group of nucleotide sequences consisting of at least 20 contiguous nucleotides of the nucleotide sequence selected from SEQ ID NO: 1, 3, 5, 7, 8, 10, 12, 14, 16, 18, 20, 22, and/or 24; or SEQ ID NO: 26-47; more preferably to the CDS encoded therein.

[0142] Generally, a nucleotide sequence has "at least x % identity" with another nucleotide sequence or any of the sequences given above if, when the sequence identity between those to aligned sequences is at least x %. Such an alignment can be performed using for example publicly available computer homology programs such as the "BLAST" program provided at the NCBI homepage at http://www.ncbi.nlm.nih.gov/blast/blast.cgi, using the default settings provided therein. Further methods of calculating sequence identity percentages of sets of nucleic acid sequences are known in the art.

[0143] Preferably, the isolated polynucleotides comprise at least 25, preferably at least 30, more preferably at least 35, even more preferably at least 40, most preferably 50, in particular 60 contiguous nucleotides.

[0144] In another preferred embodiment, the isolated polynucleotides are arranged in an array, in particular wherein the kit comprises no more than 8000, preferably no more than 7000, more preferably no more than 6000, even more preferably no more than 5000 or even no more than 4000, most preferably no more than 3000 or even no more than 2000, in particular no more than 1000 or even no more than 500 or no more than 100 isolated polynucleotides in total.

[0145] The isolated polynucleotides of the kit may be used as probes in a hybridization method, however, in a more preferred embodiment, the isolated polynucleotides are arranged in an array. The term "array", as used herein, means an ordered arrangement of addressable, accessible, spatially discrete or identifiable, molecules disposed on a surface. Moreover, the array may be a microarray (sometimes referred to as a DNA "chip"). Microarrays allow for massively parallel gene expression analysis. Furthermore, the hybridization signal from each of the array elements is individually distinguishable. Arrays can comprise any number of sites that comprise probes, from about 5 to, in the case of a microarray, tens to hundreds of thousands or more. Microfluidic devises are also contemplated.

[0146] Any suitable, compatible surfaces can be used in conjunction with this array. The surface (usually a solid, preferably a suitable rigid or semi-rigid support) may be any organic or inorganic material or a combination thereof, including, merely by way of example, plastics such as polypropylene or polystyrene; ceramic; silicon; (fused) silica, quartz or glass, which can have the thickness of, for example, a glass microscope slide or a glass cover slip; paper, such as filter paper; diazotized cellulose; nitrocellulose filters; nylon membrane; or polyacrylamide gel pad. Substrates that are trans-parent to light are useful when the method of performing an assay involves optical detection. Suitable surfaces include membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles, capillades, or the like. The surface can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which the isolated polynucleotides are bound. It can, for example, be a flat surface such as a square, rectangle, or circle; a curved surface; or a three dimensional surface such as a bead, particle, strand, precipitate, tube, sphere, etc.

[0147] Methods of making DNA arrays, including microarrays are conventional. For example, the probes may be synthesized directly on the surface; or preformed molecules, such as oligonucleotides or cDNAs, may be introduced onto (e.g., bound to, or otherwise immobilized on) the surface. Among suitable fabrication methods are photolithography, pipetting, drop-touch, piezoelectric printing (ink-jet), or the like.

[0148] Furthermore, the probes do not have to be directly bound to the substrate, but rather can be bound to the substrate through a linker group. The linker groups are typically about 6 to 50 atoms long to provide exposure to the attached nucleic acid probe. Preferred linker groups include ethylene glycol oligomers, diamines, diacids and the like. Reactive groups on the substrate surface react with one of the terminal portions of the linker to bind the linker to the substrate. The other terminal portion of the linker is then functionalized for binding the nucleic acid probe.

[0149] The kit may optionally further comprise, isolated polynucleotides that act as internal controls. The controls may be positive controls or negative controls, examples of which will be evident to the skilled worker. The determined

amounts obtained by use of the kit should reflect accurately the amounts of control target polynucleotide added to the sample.

[0150] The kit may further comprise means for carrying out a method of the invention, means for reading hybridization results and instructions for performing a method, such as a diagnostic method. Hybridization results may be units of fluorescence. Other optional elements of the kit may include suitable buffers, media components, or the like; a computer or computer-readable medium for storing and/or evaluating the assay results; containers; or packaging materials. Reagents for performing suitable controls may also be included. The reagents of the kit may be in containers in which the reagents are stable, e.g., in lyophilized form or stabilized liquids. The reagents may also be in single use form, e.g., in single reaction form for diagnostic use. The following examples are meant to further illustrate, but not limit, the invention. The examples comprise technical features, and it will be appreciated that the invention relates also to combinations of the technical features presented in this exemplifying section.

BRIEF DESCRIPTION OF THE FIGURES

[0151] FIG. **1**. Induction of a GVHR in BN rat skin explants exposed to PVG lymphocytes. A summary of the histological GVHR grading of BN skin samples cultured in medium alone, together with syngeneic BN lymphocytes, and together with pre-stimulated allogeneic PVG lymphocytes (n=12 in each group) is given. The samples represented by closed circles were used for both gene expression profiling and qRT-PCR experiments, whereas the other samples were only used for gene expression profiling. The pair-wise comparison (U test) indicated a significant difference between skin explant cultures with BN and PVG lymphocytes.

[0152] FIG. **2**. Expression profiling of BN skin explant samples exposed to allogeneic (PVG) lymphocytes in comparison to those exposed to syngeneic (BN) lymphocytes. (A) The log 2-fold changes in gene expression of significantly regulated MHC genes ($p<0.05$) are shown. (B) The log 2-fold changes in gene expression of significantly regulated NKC genes ($p<0.05$) are shown. (C) The log 2-fold changes in gene expression of 168 significantly ($p<0.05$) and strongly (log 2-fold change ≥ 1 or ≤ -1) regulated non-MHC and non-NKC genes indicate the range of observed alterations in gene expression levels among the 6342 tested genes. In panels A and B, black bars indicate a strong change (log 2-fold change or ≥ 1 or ≤ -1), dotted bars alterations below this amplitude, and white bars expression changes that were not detected at a significant level with all, but at least with 50% of the probes present on the array for that gene. When more than one probe indicated a significant change of gene expression the means and standard deviations of the log 2-fold changes are shown (see Tab. 5, 6, and 7 for further details).

[0153] FIG. **3**. Verification of the regulation in gene expression observed in the microarray experiment by qRT-PCR. A subgroup of 8 samples used for the microarray experiment (see FIG. **1**) was analyzed by qRT-PCR for the expression of 10 MHC and 3 NKC genes. The ΔΔct value was calculated, i.e. the Δct (Gapdh—gene of interest) of the allogeneic skin explant samples minus Δct (Gapdh—gene of interest) of the corresponding control sample. The control sample was either a parallel skin explant exposed to syngeneic lymphocytes as in the microarray experiment (syngeneic control, black bars) or a parallel skin explant sample cultured in medium only (medium control, white bars). The means of the ΔΔct values plus SEM are shown. A positive value indicates an up-regulation of gene expression in the allogeneic samples.

[0154] FIG. **4**. Analysis of T cell infiltration in skin explants. (A) Analysis of Cd3z gene expression in the same samples as shown in FIG. **3**. (B) Correlation of Cd3z and other gene expression levels (ΔΔct values for allogeneic skin explants minus syngeneic controls) in these samples. Pearson's correlation coefficients (r) and the p-values for the corresponding tests are given above the diagrams. In brackets Spearman's correlation coefficients (r) and the p-values for the corresponding tests are shown.

[0155] FIG. **5**. Induction of a GVHR in a second series of BN (filled circles) and LEW.1N (open circles) rat skin explants. Skin explants were co-cultured with pre-stimulated allogeneic lymphocytes from rats with a minor (BN lymphocytes and LEW.1N skin), major (LEW.1A ($RT1^a$) or LEW.1AV1 (Rn^{av1}) lymphocytes and LEW.1N skin), or a minor and major histoincompatibility (PVG lymphocytes ($RT1^c$) and BN skin or LOU/C ($RT1^U$) lymphocytes and LEW.1N skin). A summary of the histological GVHR grading of skin samples cultured in medium alone, together with syngeneic BN or LEW.1N lymphocytes, and together with allogeneic lymphocytes is given.

[0156] FIG. **6**. Verification of gene regulations observed in the microarray experiment by qRT-PCR in an independent set of 17 skin explant assays. Three samples were derived from skin explant assays with minor (upper panel), 5 with major (middle panel), and 9 with minor and major histoincompatibility (lower panel). The GVHR grading for these samples is shown in FIG. **5**. The expression of 7 MHC and 3 NKC was analyzed by qRT-PCR. The ΔΔct value, i.e. Δct (Gapdh—gene of interest) of the allogeneic skin explant samples minus mean of Δct (Gapdh—gene of interest) of the corresponding control samples (BN or LEW.1N, respectively), was calculated. The control samples were either skin explant samples exposed to syngeneic lymphocytes (syngeneic control) or skin explant samples cultured in medium only without added lymphocytes (medium control) and their GVHR grading is also shown in FIG. **5**. The means of the ΔΔct values plus SEM are shown. A positive value indicates an up-regulation of gene expression in the allogeneic samples.

[0157] FIG. **7**. Analysis of MHC and NKC gene regulation in skin explants exposed to pre-stimulated allogeneic lymphocytes depending on GVHR grading (from left to right: grade I (white), grade II (light grey/pointed), grade III (dark grey/striped), grade IV (black)). The expression of 7 MHC and 3 NKC was analyzed by qRT-PCR. The relative changes of gene expression levels were calculated using a mathematical model for relative quantification of real-time PCR data which also takes into account variations of the amplification efficiencies of different primer pairs (Pfaffl M W (2001) Nucleic Acids Res 29: e45). The means plus SEM are shown. A value >1 indicates an up-regulation of gene expression in the allogeneic samples. The control samples were either skin explant samples exposed to syngeneic lymphocytes (syngeneic control, upper panel), skin explant samples cultured in medium only (medium control, mean panel), or freshly frozen healthy skin samples (healthy skin control, lower panel).

[0158] FIG. **8**. Analysis of MHC and NKC gene regulation in GVHD skin lesions from transplanted animals. BN ($RT1^n$) rats were transplanted with bone marrow of PVG ($RT1^c$) rats. Rats that developed acute GVHD were scarified and skin lesions with signs of GVHD were obtained for RNA preparation and histology. The expression of 7 MHC and 3 NKC

was analyzed by qRT-PCR using the B2m gene as reference. The relative changes of gene expression levels were calculated (Pfaffl M W (2001) Nucleic Acids Res 29: e45). The means plus SEM are shown for skin lesion with grade I and grade II GVHD. A value >1 indicates an up-regulation of gene expression in the allogeneic samples. The control samples were freshly frozen skin samples from healthy BN rats (n=7).

EXAMPLES

Example 1

Expression Profiling of GVHR in Rat Skin Explants

[0159] The inventors decided to analyze a rat model of GVHD making use of genetically well-defined inbred stains. Importantly, the non-class I/non-class II genes of human (HLA) and rat (RT1) MHCs are highly conserved. However, the size and organization of MHC class I encoding regions are considerably variable and the rat possesses a significant number of MHC class Ib genes for which no human homologues exist. At least some of these genes have already been proven to encode ligands for inhibitory or activating natural killer (NK) receptors (Naper C, et al. (1999) Eur J Immunol 29: 2046-2053; Naper C, et al. (2005) J Immunol 174: 2702-2711). In the rat, in contrast to human, NK receptors of the Ly49 killer cell lectin-like receptor type predominate over killer cell Ig-like receptor genes. Therefore, the inventors also included the natural killer complex (NKC) in the expression profiling which harbors the Ly49 genes and additional natural cytotoxicity receptor genes.

[0160] To reduce the complexity of the experimental approach, the inventors used an invitro-model of the graft versus host reaction (GVHR)—the skin explant assay. This assay has been shown to be a sensitive predictor of GVHD in patients (Sviland L, et al. (2001) Hum Immunol 62: 1277-1281). It was also used to study the pathophysiology of GVHR (Dickinson A M, et al. (2002) Nat Med 8: 410-414). Recently, the inventors developed a rat skin explant assay (Novota P, et al. (2008) Transplantation 85: 1809-1816). This standardized in-vitro-model allows for studying gene expression during GVHR in a setting that is not influenced by undefined genetic differences between tissue samples which is unavoidable in human studies. Presently, the inventors used this model to analyze the MHC and NKC gene expression profiles of GVHR.

[0161] For the rat skin explant assays, rats of the inbred strains LEW.1N ($RT1^n$), LEW.1A ($RT1^a$), LEW.1AV1 ($RT1^{av1}$), LOU/C ($RT1^u$), and BUF ($RT1^b$) were bred in the central animal facility of the Medical Faculty of the University of Gottingen. Rats of the strains PVG/OlaHsd ($RT1^c$) and BN/RijHsd ($RT1^n$) were purchased from Harlan Winkelmann (Borchen, Germany). Animals between 10 and 20 weeks of age were used for the experiments. For transplantation experiments, PVG rats of the RT7.2 allotype (allelic variant $RT7^b$), originally obtained from Harlan OLAC, UK), were bred at the animal facility of the University of Oslo and BN rats were purchased from Harlan.

[0162] Rat skin explant assays were performed as previously described in detail (Novota P, Sviland L, Zinöcker S, Stocki P, Balavarca Y, et al. (2008) Correlation of Hsp70-1 and Hsp70-2 gene expression with the degree of graft-versus-host reaction in a rat skin explant model. Transplantation 85: 1809-1816). Briefly, mononuclear cells were obtained from rat spleens. Responder and irradiated (25 Gy) stimulator splenocytes were co-cultured in a MLR and the proliferation of responder lymphocytes was tested by [methyl-^{3}H]-thymidine (Amersham, Braunschweig, Germany) incorporation. The stimulation index was calculated as described (Novota P, et al. (2008), supra). After 7 days 10^6 responder lymphocytes were added to freshly obtained skin samples from the stimulator strain that were cultured in 200 μl $NaHCO_3$-buffered Dulbecco's modified Eagle's medium (DMEM; Biochrom) supplemented with 3% normal rat serum, 2 mM L-glutamine, 1 mM sodium pyruvate, and antibiotics in round-bottomed microtitre plates (Sarstedt, Nümbrecht, Germany). The skin samples were excised from the paws of rats after washing with 70% ethanol. The subcutaneous fat tissue was removed and the samples were trimmed to a size of approximately 1.5×1.5 mm. Skin samples cultured in medium only and samples co-cultured with lymphocytes from a "syngeneic MLR" were used as controls. After 3 days, the skin explants were washed with N-2-hydroxyethylpiperazine-N-2-ethanesulfonic acid (HEPES)-buffered DMEM and snap frozen in liquid nitrogen and stored at −80° C. for RNA preparation. Parallel samples were fixed in 10% neutral-buffered formalin, sectioned, and stained with hematoxylin and eosin (H&E). The histological evaluation of the skin explants was performed blind by an expert histopathologist (L.S.) based on the grading system described by Lerner (Lerner K G, et al. (1974) Transplant Proc 6: 367-371). To obtain skin explant samples for an expression profiling experiment, the inventors used BN rats ($RT1^n$) as recipients and PVG rats ($RT1^c$) as donors. This combination is mismatched for minor and major histocompatibility antigens, which gives rise to GVHR grades I to IV (Novota P, et al. (2008), supra). PVG splenocytes were stimulated for 7 days in a mixed lymphocyte reaction (MLR) with irradiated BN splenocytes. Syngeneic co-cultures (BN plus irradiated BN splenocytes) were performed as control experiments. The stimulation index indicated a specific proliferation of PVG lymphocytes in response to irradiated BN lymphocytes in contrast to syngeneic cultures of BN lymphocytes ($p<0.0001$, U test; n=12 responder animals per strain, data not shown). After 7 days the PVG and BN lymphocytes were harvested, added to fresh BN skin samples from 12 individual animals and cultured for 3 further days. For further controls, additional BN skin samples from the same animals were cultured in medium only. On day 3 the skin samples were harvested and snap frozen for RNA preparation. Parallel samples were fixed and assayed for histological evidence of GVHR (FIG. **1**). Co-culture of BN skin explants with pre-stimulated allogeneic PVG lymphocytes resulted in higher grade GVHR than co-culture with BN lymphocytes ($p=0.0336$; U test). As in a previous experimental series (Novota P, et al. (2008) Transplantation 85: 1809-1816), the syngeneic lymphocyte co-culture more frequently resulted in GVHR-like pathology of grade II or higher than culture of the skin explants in medium only.

[0163] RNA was prepared from the 24 BN skin explants exposed either to syngeneic (BN; n=12) or to allogeneic (PVG, n=12) lymphocytes and used for MHC gene expression profiling.

[0164] RNA extraction was carried out using TRIZOL reagent (Invitrogen, Carlsbad, Calif., USA) according to the manufacturer's recommendations. Afterwards, the RNA samples were treated with RQ1 RNase free DNase (Promega, Madison, Wis., USA) for 20 min at 37° C. in order to remove genomic DNA contaminations. The RNA was then purified as described previously (Novota P, et al. (2008) Transplantation

85: 1809-1816). Quantity and quality of extracted RNA were controlled by capillary electrophoresis

[0165] Microarray Experiment

[0166] For the expression profiling, a custom-designed oligo DNA microarray (Agilent) was designed. For this purpose the annotated sequence of the MHC of the BN strain was used (Hurt P, et al. (2004) Genome Res 14: 631-639). The 15K microarray covered 224 MHC genes by 649 oligonucleotide probes and 43 NKC genes by 101 probes. For 88 of these genes, i.e. 39.3%, the inventors had to design custom probes. A list of the MHC genes in the chromosomal order with all results obtained in the expression profiling experiment is given in the Table 5a.

[0167] These probes were spotted in triplicates. Further probes representing 6342 genes were added mainly to allow for data normalization. A two-color 12×2 paired swap design (Landgrebe J, et al. (2004) In Silico Biol 4: 461-470) using 24 arrays was applied, comparing RNA samples from 12 independent allogeneic and 12 independent syngeneic skin explant assays. Aliquots of total RNA (200 ng) were used as starting material. The "Low RNA Input linear Amplification Kit Plus, two color" (Agilent, 5188-5340) and the "RNA Spike-In Kit" (Agilent, 5188-5279) were used for cDNA synthesis and in-vitro transcription according to the manufacturer's recommendations. Quantity and dye incorporation rates of the amplified cRNAs were determined using the NanoDrop ND-1000 UV-VIS Spectrophotometer version 3.2.1 (NanoDrop Technologies, Wilmington, Del., USA). Afterwards, 300 ng aliquots of Cy3 and Cy5-labeled cRNAs from syngeneic and allogeneic skin explant assays, respectively, were mixed and hybridized to the microarrays. The hybridization was performed for 17 hours at 10 rpm and 65° C. After washing, Cy3 and Cy5 intensities were detected by two-color scanning using a DNA microarray scanner (Agilent, G2505B) at 5 micron resolution. Scanned image files were visually inspected for artifacts. The generated raw data were extracted using the Feature Extraction 9.1 software (Agilent).

[0168] The normalization of the raw microarray data was done with a non-linear loess regression (Yang Y H, et al. (2002) Nucleic Acids Res 30: e15). Differentially expressed genes were identified by an analysis of variance (ANOVA) mixed effects model (Landgrebe J, et al. (2004) In Silico Biol 4: 461-470) using SAS PROC MIXED. The resulting p-values were adjusted with the Benjamini-Hochberg method to control the false discovery rate (Benjamini Y, Hochberg Y (1995) J Roy Statist Soc Ser B 57: 289-300). The microarray data were generated conforming to the MIAME guidelines and have been deposited in NCBI's Gene Expression Omnibus (accessible through GEO series accession number GSE17928). For a general analysis of the gene expression data the PANTHER (Protein ANalysis THrough Evolutionary Relationships) system (Thomas P D, et al. (2003) Genome Res 13: 2129-2141) was used, which classifies genes by their functions (www.pantherdb.org/tools/genexAnalysis.jsp). The microarray data were mapped to PANTHER molecular function and biological process categories, as well as to biological pathways (Thomas P D, et al. (2006) Nucleic Acids Res 34: W645-650).

[0169] For 42 of the 224 MHC genes, a probe on the array indicated a significant regulation ($p<0.05$) in the allogeneic skin explant assays ($n=12$) compared to the syngeneic controls ($n=12$) (Tab. 5b). Eleven of these MHC genes showed on average at least a 2-fold up-regulation (log 2-fold change ≥ 1) or 50% reduction (log 2-fold change ≤ -1) of mRNA levels (FIG. **2**A, Tab. 5c). This amplitude of change is conventionally considered to be biologically relevant. Of these genes one was down-regulated (Ly6g6e) while 10 were up-regulated (FIG. **2**A). Fourteen further MHC genes were regulated significantly ($p<0.05$) but with smaller amplitude (Tab. 5c). The regulation of 17 MHC genes appeared to be more doubtful because less than 50% of the probes for that gene indicated a significant regulation. Thus, the inventors considered 25 MHC genes to be significantly regulated in the expression profiling experiment (FIG. **2**A). These included the classical class Ia genes RT1-A1 and RT1-A2, 8 non-classical class Ib genes (RT1-CE2, RT1-CE3, RT1-CE5, RT1-CE8, RT1-CE10, RT1-CE16, RT1-T24-4, RT-BM1) and 3 genes involved in antigen presentation (RT1-DMb, Tap1, Psmb8).

[0170] Furthermore, 43 genes of the NKC region, as a second important immune gene cluster, were represented on the array including all Ly49 genes in this region (Tab. 6a). For 8 of the 43 NKC genes represented on the array, a probe indicated a significant regulation ($p<0.05$) in the allogeneic skin explant assays compared to the syngeneic controls (Tab. 6b, 6c). In addition to the Olr1 gene, 6 Ly49 genes appeared to be up-regulated in the allogeneic skin explant assays (FIG. **2**B). Not all probes for the Ly49i3 gene indicated a significant up-regulation. However, all significant results for this gene indicated a strong regulation (log 2-fold change >2). A statistically significant ($p<0.05$) but only moderate up-regulation (log 2-fold change <1) was detected for the Ly49i7gene.

[0171] Probes for 6342 additional genes from all chromosomes were included mainly to allow for data normalization. For 168 of the non-MHC/non-NKC genes, a probe on the array indicated a significant ($p<0.05$) and strong (log 2-fold change ≥ 1 or ≤ -1) regulation in the allogeneic skin explant assays compared to the syngeneic controls (FIG. **3**C, Tab. 7). The 20 genes showing the strongest change in expression levels are shown in Table 1.

TABLE 1

The 20 most strongly regulated non-MHC/non-NKC genes in allogeneic skin explants compared to syngeneic controls as revealed by the microarray experiment

gene	log2-fold change	adjusted p-value	gene description
LOC685020	8.18	0.0100	paired immunoglobin-like type 2 receptor alpha
Ptpns1l3	6.36	0.0100	protein tyrosine phosphatase, non-receptor type substrate 1-like 3
Fcgr3a	5.24	0.0100	Fc fragment of IgG, low affinity IIIa, receptor
Nat8	5.14	0.0100	*Rattus norvegicus* endogenous retrovirus mRNA, partial sequence [AY212271]

TABLE 1-continued

The 20 most strongly regulated non-MHC/non-NKC genes in allogeneic skin explants compared to syngeneic controls as revealed by the microarray experiment

gene	log2-fold change	adjusted p-value	gene description
Ccl9	4.16	0.0100	chemokine (C-C motif) ligand 9
XM_226926	3.92	0.0149	*Rattus norvegicus* similar to protein tyrosine phosphatase, non-receptor type substrate; brain immunological-like with tyrosine-based motifs (LOC310212)
Hck	3.87	0.0100	hemopoietic cell kinase
Trem2	3.78	0.0100	triggering receptor expressed on myeloid cells 2
Ccl6	3.71	0.0100	*Rattus norvegicus* chemokine (C-C motif) ligand 6
Cd36	3.57	0.0100	CD36 antigen
Igf1	3.23	0.0100	insulin-like growth factor 1
Ctss	3.15	0.0100	cathepsin S
Gzmc	3.11	0.0373	granzyme C
LOC100048479	2.97	0.0373	one cut domain, family member 1
Plscr1	2.83	0.0100	phospholipid scramblase 1
Nfe2	2.74	0.0149	nuclear factor, erythroid derived 2
Prg4	2.74	0.0149	proteoglycan 4
Spic	2.68	0.0278	Spi-C transcription factor
Fcgr2b	2.62	0.0100	Fc receptor, IgG, low affinity IIb
LOC498277	2.61	0.0100	similar to Low affinity immunoglobulin gamma Fc region receptor III precursor

All 20 genes were up-regulated and they included several genes with functions clearly associated with the immune response such as genes encoding chemokines (Ccl9, Ccl6), Fc receptors (Fcgr3a, Fcgr2b), the proteases cathepsin S (Ctss) and granzyme C (Gzmc), and the inflammatory triggering receptor on myeloid cells 2 (Trem2).

[0172] The percentage of significantly ($p<0.05$) and strongly (log 2-fold change ≥ 1 or ≤ -1) up- or down-regulated genes was higher in the NKC region (14.0%) compared to MHC region (4.9%) and the genes encoded in other regions of the genome (2.6%). This difference was even more pronounced for up-regulated genes. 14.0% of the NKC, but only 4.5% of the MHC and 1.5% of the other genes were up-regulated (Tab. 2).

TABLE 2

Proportion of regulated genes as indicated by the gene expression profiling experiment

region	analyzed genes	regulated[1]	up-regulated	down-regulated
MHC	224	11 (4.9%)	10 (4.5%)	1 (0.4%)
NKC	43	6 (14.0%)	6 (14.0%)	0 (0%)
others	6342	168 (2.6%)	93 (1.5%)	75 (1.2%)

[1]Only those genes that were both significantly ($p < 0.05$) and strongly (log2-fold change ≥ 1 or ≤ -1) regulated were taken into account for this comparison.

[0173] For a general analysis of the gene expression data the PANTHER system (Thomas P D, et al. (2003) Genome Res 13: 2129-2141) was used. With this tool the inventors found a significant up-regulation of genes taking part in "immunity and defence" ($p<0.0001$, binominal test). More specifically, genes involved in "T cell-mediated immunity" ($p<0.0001$), "NK cell-mediated immunity" ($p<0.0001$), "cytokine and chemokine-mediated signaling" ($p=0.0032$), and "B cell and antibody-mediated immunity" ($p=0.0235$) were up-regulated. Genes involved in "complement-mediated immunity" ($p=0.0336$) and "cell adhesion" ($p=0.0003$) were down-regulated (data not shown).

[0174] Validation of Rat Candidate Genes by Quantitative Real-Time PCR

[0175] To determine the reliability of the microarray results, the inventors analyzed the expression of 13 selected genes from the MHC and NKC regions by qRT-PCR experiments in 8 of the sample pairs that had been used for the microarrays (see FIG. **1**). Specific primers for 10 MHC and 3 NKC genes were designed (Tab. 8). To generate external standard curves and to calculate the amplification efficiency of each primer pair, a pool of 20 random cDNAs was amplified in serial 10-fold dilutions (Pfaffl M W (2001) Nucleic Acids Res 29: e45). The amplification reactions were carried out as described previously (Novota P, et al. (2008) Transplantation 85: 1809-1816) using an ABI 7500 Real-Time PCR System. The data were analyzed with the ABI 7500 SDS software (Applied Biosystems). As internal control, mRNA expression of housekeeping genes Gapdh (Rn_Gapd_1_SG QuantiTect Primer Assay QT00199633, Qiagen, Hilden, Germany) or B2m were monitored. To normalize variations in the RNA concentration in different samples, the ct values obtained in real-time PCR for the genes were corrected by the ct-value obtained for the housekeeping gene in the same sample (Δct=ct housekeeping gene−ct gene of interest). For direct comparison with microarray data, the relative changes of mRNA expression were calculated using the $\Delta\Delta$ct method ($\Delta\Delta$ct=Δct sample of interest−Δct control sample) (Livak K J, Schmittgen T D (2001) Methods 25: 402-408). For additional analyses, the relative changes of gene expression levels were calculated using a mathematical model for relative quantification of real-time PCR data which takes into account variations of the amplification efficiencies of different primer pairs (Pfaffl M W (2001), supra).

[0176] For 12 genes the regulation that was observed in the microarray experiment was confirmed by qRT-PCR as indicated by a regulation into the same direction when the allogeneic and syngeneic skin explant assays were compared using the $\Delta\Delta$ cycle threshold (ct) method for relative quantification of gene expression (FIG. **3**). Only one gene, RT1-CE10, was found to be strongly up-regulated in allogeneic

skin explants in the microarray experiment but slightly down-regulated in qRT-PCR. In the qRT-PCR experiments, the inventors also included parallel skin explants that were cultured in medium only. Eight genes (RT1-DMb, Aif1, Lst1, RT1-CE3, Ubd, Olr1, Ly49si1, and Ly49i9) showed an up-regulation in the allogeneic skin explant assay also in this comparison (FIG. **3**). Six of these genes (Aif1, Lst1, Ubd, Olr1, Ly49si1, and Ly49i9) were clearly found to be up-regulated in both comparisons.

[0177] The up-regulation of genes in skin explants could be due to the change of gene expression in cells of the skin or due to infiltration of donor lymphocytes. Non-infiltrating or non-attaching donor lymphocytes were washed off before freezing of the skin explants and therefore would not contribute significantly to the results. Infiltrating lymphocytes were rarely seen in skin explants by histological analysis (data not shown). To further determine T cell infiltration at the RNA level, the inventors analyzed the expression of the CD3 zeta chain in qRT-PCR. Cd3z expression was found to be up-regulated in comparison to syngeneic controls and medium controls (FIG. **4**A). The expression of most tested genes showed no correlation with Cd3z mRNA levels (FIG. **40**). Only two of the genes analyzed in qRT-PCR (Ly6g6e and Olr1) showed a moderately positive correlation ($r>0.50$) with the Cd3z expression level (FIG. **4**B). Importantly, Ly6g6e was down- and not up-regulated in allogeneic skin explants. The expression levels of three up-regulated genes (Psmb8, Aif1, and Lst1) were even negatively associated with Cd3z expression (FIG. **4**B). Thus, of the tested genes only the increase of Olr1 expression may be formally explained by infiltrating T cells. However, Olr1 has not been described to be expressed in T cells. Therefore, infiltration of skin explants with T cells is unlikely to explain the observed gene expression changes.

[0178] Next the inventors determined the expression of 10 selected genes in an independent set of skin explant assays. Skin explants derived from BN ($RT1^n$) and LEW.1N ($RT1^n$) rats were co-cultured with pre-stimulated allogeneic lymphocytes from rats with minor (BN lymphocytes and LEW.1N skin), major (LEW.1A ($RT1^a$) or LEW.1AV1 ($RT1^{av1}$) lymphocytes and LEW.1N skin), or minor and major histoincompatibility (PVG lymphocytes ($RT1^c$) and BN skin or LOU/C ($RT1^u$) lymphocytes and LEW.1N skin). Skin samples cultured with syngeneic lymphocytes (BN or LEW.1N) or cultured in medium only served as controls. The GVHR grading obtained in these experiments is shown in FIG. **5**. The general regulation of the selected genes during GVHR was reproduced in this second experimental set when compared to skin explants exposed to syngeneic lymphocytes and also to samples cultured in medium only (FIG. **6**). Aif1 and Lst1 were the most consistently up-regulated genes in skin explants with minor, major, and minor plus major histoincompatibility. The samples with minor plus major histoincompatibility showed the highest variation in gene regulation (FIG. **6**). However, these samples were also most heterogeneous in the GVHR grading (FIG. **5**). Therefore, the inventors analyzed the gene regulation dependent from the GVHR grading in samples from both experimental sets.

[0179] Regulation of Selected MHC and NKC Genes During GVHR

[0180] The expression of 7 MHC and 3 NKC genes was evaluated in the skin explant samples showing grade I, II, III or IV GVHR (FIG. **7**). To provide an even more accurate comparison of the different genes in this evaluation of the data, the relative changes of gene expression levels were calculated using a mathematical model for relative quantification of real-time PCR data which takes into account variations in the amplification efficiencies of different primer pairs (Pfaffl M W (2001) Nucleic Acids Res 29: e45). When compared to skin explants exposed to syngeneic lymphocytes or to medium controls, the genes Aif1, Lst1, Olr1, and Ly49i9 were consistently up-regulated. Ly6g6e was down-regulated in some but not all comparisons. The expression of Aif1, Lst1 and Ly49i9 was found to be increased in all GVHR grades. The extremely high up-regulation of Ly49i9 encoding an NK receptor in comparison to medium controls might be explained by complete absence of NK cells in normal skin biopsies and infiltration of few NK cells during GVHR. When the gene expression was compared to freshly frozen healthy skin, the principal findings were confirmed. Interestingly, Olr1 was up-regulated mainly in grade II and III GVHR samples when compared to syngeneic control skin explants and healthy skin. Thus, this gene could be a marker of intermediate grade GVHR.

[0181] Regulation of Selected MHC and NKC Genes During GVHD

[0182] Next, the inventors wanted to know whether the genes found to be differentially expressed in GVHR in skin explant assays were also regulated in vivo in GVHD. For this purpose the inventors analyzed skin samples from BN rats that were transplanted with bone marrow from PVG rats and developed acute GVHD.

[0183] Transplantation experiments were approved by the Experimental Animal Board under the Ministry of Agriculture of Norway (ID 09.1514, 09.1515 and VIT 09.1512). Male PVG ($RT7^b$) rats served as bone marrow and lymph node donors. Mononuclear bone marrow cells were purified by density gradient centrifugation in Nycoprep 1.077A (Medinor ASA, Norway). The cells were depleted of T cells by magnetic separation using anti-CD5 (Ox19) and anti-αβ T cell receptor (R73) antibodies conjugated to pan-mouse IgG coated Dynabeads (Dynal Biotech ASA, Norway). This procedure reduced the $CD3^+$ T cell content in the bone marrow from 3% to less than 0.3%. Male BN rats were used as recipients. They were irradiated (9 Gy) and subsequently received an i.v. injection of 30×10^6 PVG.7b T cell-depleted bone marrow cells. 14 days post transplantation, 1.5×10^6 lymph node cells were injected i.v. to evoke GVHD. The rats were regularly monitored for GVHD symptoms. Rats suffering from irreversible GVHD were sacrificed and skin samples were processed for RNA preparation and histology in parallel.

[0184] The analyzed skin samples showed in histology a grade I or grade II GVHD. The results of qRT-PCR for 7 MHC genes and 3 NKC genes are shown in FIG. **8**. The strongest up-regulation in GVHD-affected skin was observed for RT1-DMb, Aif1, Lst1, and Olr1. Thus, most genes that were found to be regulated in GVHR in skin explants were also regulated in GVHD-affected skin. However, the Ly49si1 gene that was up-regulated consistently in allogeneic skin explants showing GVHR of grade II and above appeared to be down-regulated in GVHD. Compared to the skin explant samples, also the Ly49i9 gene was only moderately up-regulated in grade II GVHD samples from transplanted rats.

Example 2

Regulation of Selected MHC and NKC Genes During GVHR in Human Skin Explant Assays

[0185] Finally, the inventors explored the regulation of the identified genes during GVHR in human skin explant assays.

[0186] Validation of the rat candidate genes with human homologues was done by qRT-PCR on clinical samples of GvhD skin and normal skin samples. This was done by relative quantification using custom designed Taqman low density array (TLDA) cards (Applied Biosystems), each card contained 4 replicates of 95 unique genes and a control gene, 185. The qRT-PCR reactions were set up using Taqman x2 gene expression mastermix (Applied Biosystems), 50 ng RNA equivalent of cDNA and the total volume adjusted to 200 µl with nuclease free water (Quiagen). The TLDA cards were run on a 7900 qRT-PCR system (Applied Biosystems) using the TLDA block and analysed using the RQ manager 1.2 software (Applied Biosystems). To normalize variations in the RNA concentration and quality in different samples, the ct values obtained in real-time PCR for the genes were corrected by the ct-value obtained for the housekeeping gene in the same sample (Δct=ct housekeeping gene−ct gene of interest) then the relative changes in RNA expression were calculated using the ΔΔct method (ΔΔct=Δct sample of interest−Δct control sample) using the average Δct values of 5 normal skins as the control sample for each of the 9 GVHD skins.

[0187] At 1, 2 and 3 days of co-culture with alloreactive lymphocytes skin samples of one donor were taken and analyzed in comparison to parallel samples cultured in medium only. At day 1a GVHR of grade I was observed that increased to grade II at day 2 and grade III at day 3. The inventors determined the expression of 15 MHC and 1 NKC gene by qRT-PCR (Tab. 3).

TABLE 3

Regulation of MHC and NCR candidate genes in human skin explants

	regulation in rat	regulation in human skin explant assay			
	skin explant assays (expression profiling)	day 1 (GVHR I)	day 2 (GVHR II)	days (GVHR III)	concordance rate
MHC region					
HLA-DMB	↑[1]	—	↑	—	1/3
TAP1	(↑)	↑	↑	↑	3/3
PSMB8	↑	↑	↑	↑	3/3
G18 (GPSM3)	↑	n.d.	n.d.	n.d.	
PBX2	(↑)	↓	n.d.	↑	1/3
C2	↑	↑	↑	↓	2/3
LY6G6E	↓	n.d.	↑	n.d.	0/3
BAT5	↓	—	—	—	0/3
AIF1	↑	↓	↑	↓	1/3
LST1	↑	—	↑	n.d.	1/3
SPR1 (PSORS1C2)	↑	—	—	↑	1/3
IER3	↑	↓	↑	—	1/3
FLI13158	(↓)	↓	↓	—	2/3
MRPS18B	(↑)	↓	↓	↓	0/3
UBD	↑	↑	↑	↑	3/3
NCR region					
OLR1	↑	↑	↑	n.d.	2/3

[1]Explanation of symbols:

↑ up-regulated mRNA expression level (log2-fold change ≥1)

↓ down-regulated mRNA level (log2-fold change ≤−1)

— unchanged mRNA expression level (log2-fold change >−1 and <1)

(↑) significant ($p < 0.05$) but moderate up-regulation (log2-fold change <1) of mRNA expression level in the rat expression profiling experiment

(↓) significant ($p < 0.05$) but moderate down-regulation (log2-fold change >−1) of mRNA expression level

n.d. no mRNA detected

[0188] Of these 16 genes 12 (75%) were regulated at least in one skin explant sample in the way predicted by the results of the rat expression profiling experiments (Tab. 4). Three genes TAP1, PSMB8, and UBD were up-regulated in all 3 human skin explant samples. The genes C2, FLI13158, and OLR1 were regulated in 2 of the 3 samples as predicted by the rat experiments. In addition, the inventors determined the expression of 153 non-MHC/non-NCR genes that were identified to be regulated in rat skin explant assays. Also of these genes 105 (69%) were regulated in at least one of the human skin explant samples in accordance with the results obtained in the rat model (Tab. 4). These results suggest that the in vitro rat model of the skin explant assay gives evidences of gene expression changes that are very likely to occur also in human skin explant assays during GVHR.

TABLE 4

Proportion of concordantly regulated in MHC, NKC, and genes encoded in other regions in human skin explant assays in comparison to rat skin explant assays

	analyzed human	mRNA not	concordantly regulated in human skin explant assays in comparison to rat skin explant assays			not concordantly regulated
region	genes	detected	3/3	2/3	1/3	0/3
MHC	15	1 (7%)	3 (20%)	2 (13%)	6 (40%)	3 (20%)
NKC	1	0 (0%)	0 (0%)	1 (100%)	0 (0%)	0 (0%)
others	153	18 (12%)	33 (22%)	31 (20%)	41 (27%)	30 (20%)

[0189] In a follow-up study, 24 genes have been identified in additional validation tests. The results are shown in Table 9. The probes used and the reference sequences are shown in Table 10. The additional validation tests confirmed the significant regulation of gene expression, i.e. up-regulation or down-regulation, preferably down-regulation for Ctss, Pbx2, Spr1, Spic, Nfe2, Tnfaip8l2, Ier3, and Lst1.

[0190] Statistical Analyses not Related to Microarray Experiments

[0191] Paired comparisons between experimental groups were performed using the non-parametric Mann-Whitney U test. Pearson's and Spearman's correlation coefficients were calculated to determine the correlation between mRNA expression levels of two genes. The statistical analyses were performed using WinSTAT® software.

Example 3

mRNA Expression Profiling in Human Clinical GVHD Biopsies

[0192] Further studies were undertaken to evaluate the expression markers also under clinical conditions. Therefore, new tests were performed using skin explant assay as well as mRNA expression profiling studies directly on clinical GVHD biopsies to validate the results from the previous skin explant studies. The clinical GVHD biopsies were taken from hematopoietic stem cell transplantation (HSCT) patients. These data are summarized in Table 11.

[0193] Experimental Skin Explants Assays Using Autologous HSCT Patients and Normal Controls

[0194] Peripheral blood mononuclear cells (PBMC) and skin samples were obtained from autologous HSCT patients following informed consent and approval from the North Tyneside Research Ethics Committee. Buffy coat from HLA mismatched normal blood donations were obtained from Newcastle National Blood Service with consent. Skin explant assays were performed as previously described [5,6], 1×10^7 responder PBMC from healthy volunteers was cultured with an equal number of irradiated PBMC from autologous HSCT patients, in 10 ml complete medium (RPMI 1640 supplemented with antibiotics, 2 mM L-glutamine and 10% heat inactivated human AB serum) in a 25 cm^2 flask. Standard 4 mm punch skin biopsy specimens were obtained pretransplant from the auto HSCT patients and divided into 12 equal sized pieces. After 7 days of culture, the MLR primed lymphocytes were washed and resuspended in complete medium supplemented with 20% heat inactivated autologous (patient) serum and co-cultured in duplicate with patient skin at a cell concentration of 1×10^6 cells/well in a volume of 200 μl/well in 96-well round-bottomed microtitre plates. In addition each skin sample was also cultured in duplicate in culture medium alone as a negative or medium only control. A time course experiment was set up to enable RNA expression analysis to be assessed early, (day 1) and late, (days 2 and 3) to monitor the interaction of sensitised T cells with recipient skin. Parallel control skins were incubated in medium only on days 1, 2 and 3 and used as the comparators. The skin samples were removed from the time series, duplicate control and MLR skin explant on days one, two or three, one sample was fixed in 10% buffered formalin, sectioned and stained with H&E and duplicate sample placed in RNAlater (Ambion) and stored at −80° C. prior to RNA extraction.

[0195] The histopathological evaluation of the skin explants for graft versus host reaction (GVHR) was performed independently by at least two assessors. Grade I histopathological damage in skin biopsies was regarded as background and was normally observed in the medium control. All biopsies presenting histopathological damage of grade II or above were regarded as GVHR positive.

[0196] Clinical Biopsies

[0197] Standard 4 mm punch biopsies or scrape biopsies were obtained from 10 patients at various time points post transplant at onset of acute GvHD together with normal skin skin controls (n=10). RNA was extracted from these biopsies as described below.

[0198] RNA Extraction and cDNA Production

[0199] RNA was extracted from the skin samples stored in RNA later using the Ambion mirVana miRNA Isolation Kit according to the manufacturer's recommendations and quantified using the NanoDrop ND-1000 spectrophotometer (Thermo Scientific). cDNA was generated by random hexamer priming, briefly equal quantities of RNA and 2× strength cDNA mix containing random hexamer primers (Pharmacia), dNTPs (Roche), reverse transcriptase (MMLVRT—Invitrogen) and an RNase inhibitor (Rnasin—Promega) were incubated at 37° C. for 2 hours with a further incubation at 65° C. for 10 minutes to denature the reverse transcriptase.

[0200] Validation of Candidate Genes by Quantitative Real-Time PCR

[0201] Validation of the candidate genes in the human skin explant assay and clinical biopsies was done by qRT-PCR. For this relative quantification with three custom designed Taqman low density array (TLDA) cards (Applied Biosys-

tems) were used each card contained 4 replicates of 94 unique genes and two control genes, 18S and GAPDH, giving a total of 282 genes. The qRT-PCR reactions were set up using Taqman x2 gene expression mastermix (Applied Biosystems), 50 ng RNA equivalent of cDNA and the total volume adjusted to 200 μl with nuclease free water (Quiagen). The reaction mix was loaded onto the TLDA cards and the cards were run on a 7900 qRT-PCR system (Applied Biosystems) and analysed using the RQ manager 1.2 software (Applied Biosystems). The relative changes in RNA expression were calculated using the ΔΔct method, that is, ΔΔct=Δct sample of interest−Δct control sample, where the Δct is the ct of the control gene−the ct of the gene of interest.

[0202] Genes which showed a consistent change in expression between the medium only control skin and the MLR skin or in the clinical aGVHD skin compared to normal skin were investigated further using additional normal (n=10) and clinical aGVHD (n=10) skin samples. Real time PCR was carried out using individual TaqMan assays (Applied Biosystems) for the genes of interest and the control gene GAPDH (Applied Biosystems). The reactions were set up in triplicate using Taqman x2 gene expression mastermix, 10 to 20 ng RNA equivalent of cDNA and the manufacturer's recommended concentration of primer/probe mix. The reactions were run on a 7900 qRT-PCR system (Applied Biosystems) and analysed using the SDS 2.3 software, normalisation of expression was performed using GAPDH gene, expression results and ACT values were calculated as above.

[0203] Statistical Analysis

[0204] Comparisons between the experimental groups were carried out using the non-parametric Mann-Whitney U test using Graphpad prism 5 software (Graphpad Software inc.).

[0205] Table 5. Expression Profiling Results of MHC Genes

[0206] In Table 5a, results for all 224 MHC genes are shown in their chromosomal order (Hurt P, et al. (2004) Genome Res 14: 631-639). The expression profiling results of BN skin explant samples exposed to pre-stimulated allogeneic (PVG) lymphocytes in comparison to those exposed to syngeneic (BN) lymphocytes are given. The log 2-fold changes and the fold changes in gene expression are shown for every oligonucleotide probe used. The adjusted p-values are indicated. Significant change is defined by $p<0.05$ and strong change is defined by log 2-fold change ≥ 1 or ≤ -1; i.e. fold change ≥ 2 or ≤ 0.5. In addition, the identification numbers of the probes on the arrays are given (probe ID) together with the information whether these probes were taken from the Agilent database or custom designed. Table 5b contains the same information for all MHC genes for which at least one probe indicated a significant alteration of gene expression. In Table 5c, the data for those genes are summarized that are considered to be regulated significantly because either at least a single probe indicated a significant ($p<0.05$) and strong (log 2-fold change ≥ 1 or ≤ -1) regulation or at least 50% of the gene probes indicated a significant ($p<0.05$) regulation of gene expression.

TABLE 5a

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
1	3930402F13Rik (Zbtb9)	0.08	1.06	0.7687	zinc finger and BTB domain containing 9	A_43_P10072	Agilent
1	3930402F13Rik (Zbtb9)	0.04	1.03	0.8180	zinc finger and BTB domain containing 9	A_43_P20769	Agilent
2	Syngap1	−0.17	0.89	0.1557	synaptic Ras GTPase activating protein 1 homolog (rat)	A_44_P470444	Agilent
3	Cuta	0.21	1.16	0.4430	cutA divalent cation tolerance homolog (*E. coli*)	A_42_P765298	Agilent
4	Phf1	0.21	1.16	0.2688	PHD finger protein 1	A_44_P1057137	Agilent
5	Kifc1	−0.23	0.85	0.4351	kinesin family member C1	A_44_P1042372	Agilent
6	AA926063	−0.06	0.96	0.6022	gene corresponding to rat EST acc. no. AA926063	A_44_P128110	Agilent
7	Daxx	0.07	1.05	0.5495	Fas death domain-associated protein	A_42_P622574	Agilent
8	Znf297	−0.21	0.86	0.1375	zinc finger protein 297	A_43_P18449	Agilent
8	Znf297	−0.12	0.92	0.8050	zinc finger protein 297	A_42_P486012	Agilent
8	Znf297	−0.06	0.96	0.7324	zinc finger protein 297	A_43_P20215	Agilent
8	Znf297	0.12	1.09	0.4409	zinc finger protein 297	A_43_P20683	Agilent
9	Tapbp	0.31	1.24	0.3259	TAP binding protein	A_42_P698972	Agilent
10	Rab2l	−0.15	0.90	0.3580	RAB2, member RAS oncogene family-like	A_44_P465986	Agilent
11	Ke2	−0.07	0.95	0.8616	H2-K region expressed gene 2	A_44_P498712	Agilent
12	Bing4 (Wdr46)	−0.13	0.91	0.6702	WD repeat domain 46	A_44_P158675	Agilent
13	B3galt4	0.01	1.01	0.9910	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	A_42_P692926	Agilent
14	Rps18	−0.32	0.80	0.1017	ribosomal protein S18	A_42_P582859	Agilent
15	Sacm2l (Vps52)	0.00	1.00	0.9771	similar to vacuolar protein sorting 52	A_43_P12732	Agilent
16	RT1-A1	0.70	1.62	0.0149	RT1 class I	CUST_1_PI202535318	custom
16	RT1-A1	0.75	1.68	0.0100	RT1 class I	CUST_2_PI202535318	custom
16	RT1-A1	0.80	1.74	0.0149	RT1 class I	CUST_3_PI202535318	custom
16	RT1-A1	0.86	1.82	0.0100	RT1 class I	CUST_4_PI202535318	custom
16	RT1-A1	0.91	1.88	0.0100	RT1 class I	CUST_5_PI202535318	custom
17	RT1-A2	0.98	1.97	0.0100	RT1 class I	A_44_P296155	Agilent
18	RT1-A3	0.28	1.21	0.4444	RT1 class I	A_44_P501234	Agilent
19	Ring1	−0.14	0.91	0.5739	ring finger protein 1	A_44_P100117	Agilent
20	Hsd17b8	0.06	1.04	0.8435	hydroxysteroid (17-beta) dehydrogenase 8	A_43_P15081	Agilent
21	Ke4	−0.03	0.98	0.8962	RT1 class I, locus Ke4	CUST_1_PI195698117	custom
21	Ke4	−0.04	0.97	0.8617	RT1 class I, locus Ke4	CUST_2_PI195698117	custom
21	Ke4	−0.02	0.99	0.9361	RT1 class I, locus Ke4	CUST_3_PI195698117	custom
21	Ke4	0.01	1.01	0.9700	RT1 class I, locus Ke4	CUST_4_PI195698117	custom
21	Ke4	−0.05	0.97	0.7835	RT1 class I, locus Ke4	CUST_5_PI195698117	custom

TABLE 5a-continued

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
22	Rxrb	−0.14	0.91	0.5922	retinoid X receptor beta	A_52_P519689	Agilent
22	Rxrb	−0.06	0.96	0.8238	retinoid X receptor beta	CUST_11_PI207500742	custom
22	Rxrb	−0.03	0.98	0.8934	retinoid X receptor beta	CUST_12_PI207500742	custom
22	Rxrb	−0.08	0.95	0.6808	retinoid X receptor beta	CUST_13_PI207500742	custom
22	Rxrb	−0.03	0.98	0.9004	retinoid X receptor beta	CUST_14_PI207500742	custom
22	Rxrb	0.01	1.01	0.9575	retinoid X receptor beta	CUST_15_PI207500742	custom
23	Col11a2	−0.45	0.73	0.0533	procollagen, type XI, alpha 2	A_44_2527024	Agilent
24	RT1-Hb	0.04	1.03	0.7868	RT1 class II, H beta	A_44_P250763	Agilent
25	RT1-Ha	0.07	1.05	0.6681	RT1 class II, H alpha	CUST_1_PI195698201	custom
25	RT1-Ha	0.02	1.01	0.8589	RT1 class II, H alpha	CUST_2_PI195698201	custom
25	RT1-Ha	−0.11	0.93	0.5819	RT1 class II, H alpha	CUST_3_PI195698201	custom
25	RT1-Ha	0.00	1.00	0.9980	RT1 class II, H alpha	CUST_4_PI195698201	custom
25	RT1-Ha	−0.08	0.95	0.5019	RT1 class II, H alpha	CUST_5_PI195698201	custom
26	RT1-DOa	−0.06	0.96	0.7324	RT1 class II, locus DOa	A_44_P344228	Agilent
27	Brd2	0.46	1.38	0.0825	bromodomain containing 2	A_42_P558503	Agilent
28	RT1-DMa	0.87	1.83	0.0681	histocompatibility 2, class II, locus DMa	A_42_P473314	Agilent
29	RT1-DMb	2.59	6.02	0.0100	major histocompatibility complex, class II, DM beta	CUST_1_PI195698203	custom
29	RT1-DMb	2.77	6.82	0.0100	major histocompatibility complex, class II, DM beta	CUST_2_PI195698203	custom
29	RT1-DMb	1.93	3.81	0.0149	major histocompatibility complex, class II, DM beta	CUST_3_PI195698203	custom
29	RT1-DMb	1.87	3.66	0.0149	major histocompatibility complex, class II, DM beta	CUST_4_PI195698203	custom
29	RT1-DMb	1.94	3.84	0.0100	major histocompatibility complex, class II, DM beta	CUST_5_PI195698203	custom
30	Psmb9	0.50	1.41	0.1412	proteasome (prosome, macropain) subunit, beta type 9 (large multi-functional peptidase 2)	A_42_P759756	Agilent
31	Tap1	0.53	1.44	0.1159	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	A_43_P15763	Agilent
31	Tap1	0.63	1.55	0.0390	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	A_44_P451916	Agilent
32	Psmb8	1.00	2.00	0.0336	proteasome (prosome, macropain) subunit, beta type 8 (large multi-functional peptidase 7)	A_42_P761035	Agilent
33	Tap2	0.44	1.36	0.1639	transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)	A_42_P797381	Agilent
34	RT1-DOb	0.39	1.31	0.0573	RT1 class II, locus DOb	A_44_P294965	Agilent
35	RT1-Bb	−0.29	0.82	0.6142	RT1 class II, locus Bb	A_44_P552452	Agilent
36	RT1-Ba	−0.14	0.91	0.8110	RT1 class II, locus Ba	A_44_P128248	Agilent
36	RT1-Ba	0.18	1.13	0.2934	RT1 class II, locus Ba	A_44_P194167	Agilent
36	RT1-Ba	−0.09	0.94	0.8443	RT1 class II, locus Ba	A_43_P14429	Agilent
37	RT1-Db1	0.36	1.28	0.5390	RT1 class II, D beta 1	A_44_P130513	Agilent
38	RT1-Db2	0.62	1.54	0.2275	RT1 class II, D beta 2	CUST_1_PI201011278	custom
38	RT1-Db2	0.65	1.57	0.2267	RT1 class II, D beta 2	CUST_2_PI201011278	custom
38	RT1-Db2	0.67	1.59	0.1732	RT1 class II, D beta 2	CUST_3_PI201011278	custom
38	RT1-Db2	0.86	1.82	0.0856	RT1 class II, D beta 2	CUST_4_PI201011278	custom
38	RT1-Db2	1.00	2.00	0.0755	RT1 class II, D beta 2	CUST_5_PI201011278	custom
39	RT1-Da	0.22	1.16	0.6541	RT1 class II, D alpha	A_44_P991532	Agilent
40	Btnl2	−0.09	0.94	0.4427	butyrophilin-like 2 (MHC class II associated)	A_23_P376686	Agilent
41	Btnl3	−0.10	0.93	0.2949	butyrophilin-like 3	A_42_P788302	Agilent
42	Tesb	0.18	1.13	0.1346	testis specific basic protein	CUST_4_PI1956982050	custom
42	Tesb	0.14	1.10	0.5685	testis specific basic protein	CUST_5_PI1956982050	custom
43	Btnl4	0.75	1.68	0.1649	butyrophilin-like 4	CUST_44_PI2408728340	custom
43	Btnl4	0.71	1.64	0.1853	butyrophilin-like 4	CUST_45_PI2408728340	custom
44	Btnl5	0.20	1.15	0.4751	butyrophilin-like 5	CUST_7_PI207500742	custom
45	Btnl6	−0.08	0.95	0.3599	butyrophilin-like 6	CUST_1_PI201011255	custom
45	Btnl6	−0.29	0.82	0.0847	butyrophilin-like 6	CUST_2_PI201011255	custom
45	Btnl6	−0.01	0.99	0.9153	butyrophilin-like 6	CUST_3_PI201011255	custom
45	Btnl6	0.00	1.00	0.9864	butyrophilin-like 6	CUST_4_PI201011255	custom
45	Btnl6	0.06	1.04	0.5623	butyrophilin-like 6	CUST_5_PI201011255	custom
46	Btnl7	−0.12	0.92	0.2797	butyrophilin-like 7	A_44_P212575	Agilent
46	Btnl7	0.08	1.06	0.7469	butyrophilin-like 7	CUST_1_PI201011264	custom
46	Btnl7	−0.04	0.97	0.7249	butyrophilin-like 7	CUST_2_PI201011264	custom
46	Btnl7	−0.07	0.95	0.5583	butyrophilin-like 7	CUST_3_PI201011264	custom
46	Btnl7	−0.08	0.95	0.5922	butyrophilin-like 7	CUST_4_PI201011264	custom
46	Btnl7	−0.28	0.82	0.0879	butyrophilin-like 7	CUST_5_PI201011264	custom
47	Btnl8	0.09	1.06	0.4680	butyrophilin-like 8	A_44_P379412	Agilent
47	Btnl8	0.26	1.20	0.2238	butyrophilin-like 8	CUST_6_PI207500742	custom
47	Btnl8	−0.16	0.90	0.2688	butyrophilin-like 8	CUST_8_PI207500742	custom
47	Btnl8	−0.03	0.98	0.8236	butyrophilin-like 8	CUST_9_PI207500742	custom
47	Btnl8	0.12	1.09	0.3144	butyrophilin-like 8	CUST_10_PI207500742	custom
48	Btnl9	−0.03	0.98	0.8134	butyrophilin-like 9	A_32_P187951	Agilent
48	Btnl9	−0.11	0.93	0.3818	butyrophilin-like 9	A_23_P81280	Agilent
49	C4-2	−0.97	0.51	0.1521	complement component 4, gene 2	A_42_P494900	Agilent
50	Notch4	−0.90	0.54	0.1159	Notch homolog 4	A_42_P734094	Agilent
51	G18 (Gpsm3)	1.23	2.35	0.0315	G18 protein	A_42_P569708	Agilent
52	Pbx2	0.33	1.26	0.0466	pre-B-cell leukemia transcription factor 2	A_42_P592157	Agilent
53	Ager	0.10	1.07	0.4914	advanced glycosylation end product-specific receptor	A_43_P15393	Agilent

TABLE 5a-continued

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
54	Rnf5	0.57	1.48	0.0315	ring finger protein 5	A_51_P204582	Agilent
54	Rnf5	0.26	1.20	0.0674	ring finger protein 5	CUST_1_PI207500742	custom
54	Rnf5	0.21	1.16	0.1445	ring finger protein 5	CUST_2_PI207500742	custom
54	Rnf5	0.17	1.13	0.2905	ring finger protein 5	CUST_3_PI207500742	custom
54	Rnf5	0.22	1.16	0.1626	ring finger protein 5	CUST_4_PI207500742	custom
54	Rnf5	0.19	1.14	0.1707	ring finger protein 5	CUST_5_PI207500742	custom
55	Agpat1	0.14	1.10	0.6400	1-acylglycerol-3-phosphate O-acyltransferase 1	A_44_P419004	Agilent
56	Ng3	−0.18	0.88	0.3016	NG3 protein	CUST_51_PI209196805	custom
56	Ng3	0.07	1.05	0.6808	NG3 protein	CUST_52_PI209196805	custom
56	Ng3	−0.12	0.92	0.3181	NG3 protein	CUST_53_PI209196805	custom
56	Ng3	−0.29	0.82	0.2314	NG3 protein	CUST_54_PI209196805	custom
56	Ng3	−0.07	0.95	0.8401	NG3 protein	CUST_55_PI209196805	custom
57	Ppt2	−0.12	0.92	0.6876	palmitoyl-protein thioesterase 2	A_44_P343303	Agilent
58	Ng5	0.18	1.13	0.2523	NG5 protein	CUST_1_PI195698205	custom
58	Ng5	0.06	1.04	0.6520	NG5 protein	CUST_2_PI195698205	custom
58	Ng5	0.22	1.16	0.1750	NG5 protein	CUST_3_PI195698205	custom
58	Ng5	0.18	1.13	0.1494	NG5 protein	CUST_4_PI195698205	custom
58	Ng5	0.13	1.09	0.4775	NG5 protein	CUST_5_PI195698205	custom
59	Fkbpl	−0.05	0.97	0.8864	FK506 binding protein-like	A_44_P1048901	Agilent
60	Crebl1	0.36	1.28	0.5778	cAMP responsive element binding protein-like 1	A_44_P292503	Agilent
61	Tnx	0.04	1.03	0.6633	tenascin-X	CUST_2_PI2010111961	custom
61	Tnx	0.03	1.02	0.8015	tenascin-X	CUST_3_PI2010111961	custom
62	Cyp21a1	−0.09	0.94	0.3540	cytochrome P450, family 21, subfamily a, polypeptide 1	A_44_P381937	Agilent
63	C4-1	−0.76	0.59	0.1375	complement component 4, gene 1	A_43_P21634	Agilent
64	Stk19	0.28	1.21	0.2657	serine/threonine kinase 19	A_44_P491782	Agilent
65	Dom3z	0.27	1.21	0.3198	DOM-3 homolog Z	A_44_P158709	Agilent
66	Skiv2l	−0.24	0.85	0.3408	superkiller viralicidic activity 2-like	A_44_P292558	Agilent
67	Rdbp	−0.47	0.72	0.1367	RD RNA-binding protein	A_44_P266879	Agilent
68	Bf (CfB)	−0.71	0.61	0.3004	complement factor B	A_44_P419064	Agilent
69	C2	1.22	2.33	0.0325	complement component 2	A_44_P332606	Agilent
70	Ng35	−0.04	0.97	0.7095	Ng35 protein	A_43_P17778	Agilent
71	Bat8 (Ehmt2)	−0.23	0.85	0.5125	euchromatic histone lysine N-methyltransferase 2	A_44_P1057272	Agilent
72	Ng22 (Slc44a4)	−0.20	0.87	0.3134	solute carrier family 44, member 4	A_43_P18443	Agilent
72	Ng22 (Slc44a4)	−0.81	0.57	0.0598	solute carrier family 44, member 4	A_44_P1037285	Agilent
73	Neu1	0.22	1.16	0.3690	neuraminidase 1	A_43_P12574	Agilent
74	Hspa1b	0.06	1.04	0.5939	heat shock 70 kD protein 1B (mapped)	A_44_P532958	Agilent
75	Hspa1a	0.07	1.05	0.8419	heat shock 70 kD protein 1A	A_44_P1042876	Agilent
76	Hspa1l	−0.20	0.87	0.2682	heat shock 70 kD protein 1-like (mapped)	A_42_P541025	Agilent
77	Lsm2	0.08	1.06	0.8227	LSM2 homolog, U6 small nuclear RNA associated [*S. cerevisiae*]	A_51_P314931	Agilent
77	Lsm2	0.03	1.02	0.9332	LSM2 homolog, U6 small nuclear RNA associated [*S. cerevisiae*]	CUST_6_PI209196805	custom
77	Lsm2	0.12	1.09	0.7330	LSM2 homolog, U6 small nuclear RNA associated [*S. cerevisiae*]	CUST_7_PI209196805	custom
77	Lsm2	−0.04	0.97	0.8943	LSM2 homolog, U6 small nuclear RNA associated [*S. cerevisiae*]	CUST_8_PI209196805	custom
77	Lsm2	0.13	1.09	0.6868	LSM2 homolog, U6 small nuclear RNA associated [*S. cerevisiae*]	CUST_9_PI209196805	custom
77	Lsm2	0.06	1.04	0.8429	LSM2 homolog, U6 small nuclear RNA associated [*S. cerevisiae*]	CUST_10_PI209196805	custom
78	G7e	−0.35	0.78	0.8265	G7e pseudogen	CUST_1_PI2010111701	custom
78	G7e	−0.21	0.86	0.6235	G7e pseudogen	CUST_2_PI2010111701	custom
79	Vars2	0.08	1.06	0.7163	valyl-tRNA synthetase	A_42_P646976	Agilent
80	G7c	−0.14	0.91	0.2006	G7c protein	A_44_P325599	Agilent
80	G7c	−0.03	0.98	0.9121	G7c protein	CUST_26_PI209196805	custom
80	G7c	−0.10	0.93	0.6167	G7c protein	CUST_27_PI209196805	custom
80	G7c	−0.05	0.97	0.8127	G7c protein	CUST_28_PI209196805	custom
80	G7c	−0.10	0.93	0.3349	G7c protein	CUST_29_PI209196805	custom
80	G7c	−0.07	0.95	0.6486	G7c protein	CUST_30_PI209196805	custom
81	Ng23	0.00	1.00	0.9979	Ng23 protein	A_51_P233727	Agilent
82	Msh5	0.01	1.01	0.9515	mutS homolog 5 (*E. coli*)	A_43_P23342	Agilent
83	Clic1	0.05	1.04	0.7886	chloride intracellular channel 1	A_44_P1028007	Agilent
84	Ddah2	0.11	1.08	0.6564	dimethylarginine dimethylaminohydrolase 2	CUST_1_PI195698222	custom
84	Ddah2	0.17	1.13	0.3684	dimethylarginine dimethylaminohydrolase 2	CUST_2_PI195698222	custom
84	Ddah2	0.15	1.11	0.4977	dimethylarginine dimethylaminohydrolase 2	CUST_3_PI195698222	custom
84	Ddah2	0.13	1.09	0.5078	dimethylarginine dimethylaminohydrolase 2	CUST_4_PI195698222	custom
84	Ddah2	0.12	1.09	0.5019	dimethylarginine dimethylaminohydrolase 2	CUST_5_PI195698222	custom
85	G6b	−0.01	0.99	0.8795	G6b protein	A_44_P334847	Agilent
86	Ly6g6c	0.12	1.09	0.7567	lymphocyte antigen 6 complex, locus G6C	CUST_1_PI195698232	custom
86	Ly6g6c	0.11	1.08	0.7656	lymphocyte antigen 6 complex, locus G6C	CUST_2_PI195698232	custom
86	Ly6g6c	0.12	1.09	0.7537	lymphocyte antigen 6 complex, locus G6C	CUST_3_PI195698232	custom
86	Ly6g6c	0.37	1.29	0.2006	lymphocyte antigen 6 complex, locus G6C	CUST_4_PI195698232	custom
86	Ly6g6c	0.38	1.30	0.1845	lymphocyte antigen 6 complex, locus G6C	CUST_5_PI195698232	custom

TABLE 5a-continued

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
87	Ly6g6d	0.30	1.23	0.4948	lymphocyte antigen 6 complex, locus G6D	CUST_1_PI195698244	custom
87	Ly6g6d	0.28	1.21	0.4856	lymphocyte antigen 6 complex, locus G6D	CUST_2_PI195698244	custom
87	Ly6g6d	0.19	1.14	0.6310	lymphocyte antigen 6 complex, locus G6D	CUST_3_PI195698244	custom
87	Ly6g6d	0.47	1.39	0.3675	lymphocyte antigen 6 complex, locus G6D	CUST_4_PI195698244	custom
87	Ly6g6d	0.36	1.28	0.5300	lymphocyte antigen 6 complex, locus G6D	CUST_5_PI195698244	custom
88	Ly6g6e	−1.38	0.38	0.0416	lymphocyte antigen 6 complex, locus G6E	CUST_1_PI195698246	custom
88	Ly6g6e	−1.42	0.37	0.0523	lymphocyte antigen 6 complex, locus G6E	CUST_2_PI195698246	custom
88	Ly6g6e	−1.39	0.38	0.0623	lymphocyte antigen 6 complex, locus G6E	CUST_3_PI195698246	custom
88	Ly6g6e	−1.44	0.37	0.0416	lymphocyte antigen 6 complex, locus G6E	CUST_4_PI195698246	custom
88	Ly6g6e	−1.46	0.36	0.0433	lymphocyte antigen 6 complex, locus G6E	CUST_5_PI195698246	custom
89	G6f (Ly6g6f)	−0.15	0.90	0.2839	lymphocyte antigen 6 complex, locus G6F	CUST_1_PI195701417	custom
89	G6f (Ly6g6f)	0.22	1.16	0.0965	lymphocyte antigen 6 complex, locus G6F	CUST_2_PI195701417	custom
89	G6f (Ly6g6f)	−0.02	0.99	0.8965	lymphocyte antigen 6 complex, locus G6F	CUST_3_PI195701417	custom
89	G6f (Ly6g6f)	0.05	1.04	0.7887	lymphocyte antigen 6 complex, locus G6F	CUST_4_PI195701417	custom
89	G6f (Ly6g6f)	0.41	1.33	0.0716	lymphocyte antigen 6 complex, locus G6F	CUST_5_PI195701417	custom
90	Bat5	−0.60	0.66	0.0100	HLA-B associated transcript 5	CUST_1_PI195830595	custom
90	Bat5	−0.48	0.72	0.0100	HLA-B associated transcript 5	CUST_2_PI195830595	custom
90	Bat5	−0.54	0.69	0.0180	HLA-B associated transcript 5	CUST_3_PI195830595	custom
90	Bat5	−0.53	0.69	0.0229	HLA-B associated transcript 5	CUST_4_PI195830595	custom
90	Bat5	−0.58	0.67	0.0100	HLA-B associated transcript 5	CUST_5_PI195830595	custom
91	Ly6g5c	−0.18	0.88	0.4183	lymphocyte antigen 6 complex, locus G5C	A_44_P355842	Agilent
92	Ly6g5b	0.01	1.01	0.9526	lymphocyte antigen 6 complex, locus G5B	A_44_P111744	Agilent
93	Csnk2b	−0.40	0.76	0.4907	casein kinase 2, beta subunit	A_44_P453337	Agilent
94	Bat4	−0.06	0.96	0.7985	Bat4 gene	CUST_1_PI195941286	custom
94	Bat4	0.02	1.01	0.9500	Bat4 gene	CUST_2_PI195941286	custom
94	Bat4	0.00	1.00	0.9979	Bat4 gene	CUST_3_PI195941286	custom
94	Bat4	0.02	1.01	0.9284	Bat4 gene	CUST_4_PI195941286	custom
94	Bat4	0.04	1.03	0.8698	Bat4 gene	CUST_5_PI195941286	custom
95	G4	−0.12	0.92	0.6277	G4 protein	A_44_P327945	Agilent
96	Apom	−0.31	0.81	0.1188	apolipoprotein M	A_43_P15453	Agilent
97	Bat3	−0.04	0.97	0.8843	HLA-B-associated transcript 3	A_42_P506345	Agilent
98	Bat2	−0.08	0.95	0.6799	HLA-B associated transcript 2	CUST_1_PI195941289	custom
98	Bat2	−0.02	0.99	0.9413	HLA-B associated transcript 2	CUST_2_PI195941289	custom
98	Bat2	−0.07	0.95	0.7889	HLA-B associated transcript 2	CUST_3_PI195941289	custom
98	Bat2	−0.11	0.93	0.5007	HLA-B associated transcript 2	CUST_5_PI195941289	custom
98	Bat2	0.05	1.04	0.63	HLA-B associated transcript 2	CUST_4_PI195941289	custom
99	E230034O05Rik	−0.06	0.96	0.4994	E230034O05Rik gene	A_44_P255078	Agilent
100	Aif1	2.83	7.11	0.0100	allograft inflammatory factor 1	A_44_P421534	Agilent
101	Ncr3	−0.20	0.87	0.4300	natural cytotoxicity triggering receptor 3	A_43_P22986	Agilent
102	Lst1	3.32	9.99	0.0100	leucocyte specific transcript 1	A_43_P12274	Agilent
103	Ltb	1.15	2.22	0.0693	lymphotoxin B	A_42_P550914	Agilent
104	Tnf	0.32	1.25	0.0924	tumor necrosis factor	A_43_P11513	Agilent
105	Lta	1.10	2.14	0.0523	lymphotoxin A	A_43_P15592	Agilent
106	Nfkbil1	−0.01	0.99	0.9859	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1	CUST_1_PI195941300	custom
106	Nfkbil1	0.10	1.07	0.8117	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1	CUST_2_PI195941300	custom
106	Nfkbil1	0.10	1.07	0.8007	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1	CUST_3_PI195941300	custom
106	Nfkbil1	0.03	1.02	0.9472	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1	CUST_4_PI195941300	custom
106	Nfkbil1	0.17	1.13	0.6007	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1	CUST_5_PI195941300	custom
107	Atp6v1g2	−0.15	0.90	0.2622	ATPase, H+ transporting, V1 subunit G isoform 2	A_44_P484719	Agilent
108	Bat1a	−0.56	0.68	0.0769	HLA-B-associated transcript 1A	A_42_P784188	Agilent
109	RT1-CE1	0.45	1.37	0.0668	RT1 class I, CE1	A_44_P513029	Agilent
110	RT1-CE2	0.64	1.56	0.0278	RT1 class I, CE2	A_44_P107372	Agilent
111	RT1-CE3	0.96	1.95	0.0100	RT1 class I, CE3	A_44_P274061	Agilent
112	RT1-CE4	0.43	1.35	0.1222	RT1 class I, CE4	A_44_P440514	Agilent
113	RT1-CE5	0.70	1.62	0.0395	RT1 class I, CE5	A_44_P172850	Agilent
114	RT1-CE6	0.18	1.13	0.6413	RT1-CE6 gene	A_44_P547954	Agilent
115	RT1-CE7	0.45	1.37	0.1503	RT1 class I, CE7	A_42_P511265	Agilent
116	RT1-CE8	0.90	1.87	0.0278	RT1 class I, CE8	CUST_1_PI201011245	custom
116	RT1-CE8	0.91	1.88	0.0100	RT1 class I, CE8	CUST_2_PI201011245	custom
116	RT1-CE8	0.78	1.72	0.0229	RT1 class I, CE8	CUST_3_PI201011245	custom
116	RT1-CE8	0.84	1.79	0.0100	RT1 class I, CE8	CUST_4_PI201011245	custom
116	RT1-CE8	0.79	1.73	0.0149	RT1 class I, CE8	CUST_5_PI201011245	custom
117	RT1-CE9	0.80	1.74	0.0315	RT1 class I, CE9	CUST_1_PI201011241	custom
117	RT1-CE9	0.35	1.27	0.1745	RT1 class I, CE9	CUST_2_PI201011241	custom
117	RT1-CE9	0.74	1.67	0.0539	RT1 class I, CE9	CUST_3_PI201011241	custom
117	RT1-CE9	0.24	1.18	0.3698	RT1 class I, CE9	CUST_4_PI201011241	custom
117	RT1-CE9	0.81	1.75	0.0373	RT1 class I, CE9	CUST_5_PI201011241	custom
118	RT1-CE10	4.09	17.03	0.0100	RT1 class I, CE10	A_44_P389019	Agilent

TABLE 5a-continued

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
119	RT1-CE11	0.28	1.21	0.2867	RT1 class I, CE11	CUST_1_PI195941302	custom
119	RT1-CE11	0.65	1.57	0.0315	RT1 class I, CE11	CUST_2_PI195941302	custom
119	RT1-CE11	0.22	1.16	0.2638	RT1 class I, CE11	CUST_3_PI195941302	custom
119	RT1-CE11	0.16	1.12	0.3957	RT1 class I, CE11	CUST_4_PI195941302	custom
119	RT1-CE11	0.38	1.30	0.0980	RT1 class I, CE11	CUST_5_PI195941302	custom
120	RT1-CE12	0.43	1.35	0.1710	RT1 class I, CE12	CUST_1_PI195941305	custom
120	RT1-CE12	−0.10	0.93	0.4503	RT1 class I, CE12	CUST_2_PI195941305	custom
120	RT1-CE12	0.34	1.27	0.1043	RT1 class I, CE12	CUST_3_PI195941305	custom
120	RT1-CE12	0.04	1.03	0.8574	RT1 class I, CE12	CUST_4_PI195941305	custom
120	RT1-CE12	0.56	1.47	0.0310	RT1 class I, CE12	CUST_5_PI195941305	custom
121	RT1-CE13	−0.42	0.75	0.1923	RT1 class I, CE13	CUST_1_PI197795816	custom
121	RT1-CE13	−0.46	0.73	0.2116	RT1 class I, CE13	CUST_2_PI197795816	custom
121	RT1-CE13	0.37	1.29	0.1077	RT1 class I, CE13	CUST_3_PI197795816	custom
121	RT1-CE13	0.38	1.30	0.1263	RT1 class I, CE13	CUST_4_PI197795816	custom
121	RT1-CE13	0.40	1.32	0.0752	RT1 class I, CE13	CUST_5_PI197795816	custom
122	RT1-CE14	0.39	1.31	0.1076	RT1 class I, CE14	CUST_1_PI195941310	custom
122	RT1-CE14	0.35	1.27	0.1471	RT1 class I, CE14	CUST_2_PI195941310	custom
122	RT1-CE14	0.30	1.23	0.1626	RT1 class I, CE14	CUST_3_PI195941310	custom
122	RT1-CE14	0.25	1.19	0.2529	RT1 class I, CE14	CUST_4_PI195941310	custom
122	RT1-CE14	0.25	1.19	0.2735	RT1 class I, CE14	CUST_5_PI195941310	custom
123	RT1-CE15	0.28	1.21	0.2085	RT1 class I, CE15	CUST_1_PI195941312	custom
123	RT1-CE15	0.26	1.20	0.2210	RT1 class I, CE15	CUST_2_PI195941312	custom
123	RT1-CE15	0.30	1.23	0.1395	RT1 class I, CE15	CUST_3_PI195941312	custom
123	RT1-CE15	0.29	1.22	0.1795	RT1 class I, CE15	CUST_4_PI195941312	custom
123	RT1-CE15	0.35	1.27	0.1157	RT1 class I, CE15	CUST_5_PI195941312	custom
124	RT1-CE16	0.54	1.45	0.0325	RT1 class I, CE16 (RT1 class Ib, locus Cl)	A_44_P867246	Agilent
124	RT1-CE16	0.78	1.72	0.0206	RT1 class I, CE16 (RT1 class Ib. locus Cl)	A_44_P554925	Agilent
125	Pou5f1	0.02	1.01	0.8552	POU domain, class 5, transcription factor 1	CUST_1_PI195941317	custom
125	Pou5f1	−0.12	0.92	0.5977	POU domain, class 5, transcription factor 1	CUST_2_PI195941317	custom
125	Pou5f1	0.07	1.05	0.7099	POU domain, class 5, transcription factor 1	CUST_3_PI195941317	custom
125	Pou5f1	0.15	1.11	0.2432	POU domain, class 5, transcription factor 1	CUST_4_PI195941317	custom
125	Pou5f1	−0.07	0.95	0.5946	POU domain, class 5, transcription factor 1	CUST_5_PI195941317	custom
126	Tcf19	−0.19	0.88	0.5212	transcription factor 19	A_42_P591665	Agilent
127	Hcr	−0.19	0.88	0.1202	HCR (a-helix coiled-coil rod homolog)	A_52_P669964	Agilent
127	Hcr	−0.26	0.84	0.2118	HCR (a-helix coiled-coil rod homolog)	CUST_11_PI209196805	custom
127	Hcr	−0.26	0.84	0.2030	HCR (a-helix coiled-coil rod homolog)	CUST_12_PI209196805	custom
127	Hcr	−0.25	0.84	0.2461	HCR (a-helix coiled-coil rod homolog)	CUST_13_PI209196805	custom
127	Hcr	−0.16	0.90	0.3650	HCR (a-helix coiled-coil rod homolog)	CUST_14_PI209196805	custom
127	Hcr	−0.15	0.90	0.5193	HCR (a-helix coiled-coil rod homolog)	CUST_15_PI209196805	custom
128	Spr1	1.26	2.39	0.0206	psoriasis susceptibility 1 candidate 2 (human)	A_66_P100662	Agilent
128	Spr1	1.39	2.62	0.0180	psoriasis susceptibility 1 candidate 2 (human)	A_51_P212958	Agilent
128	Spr1	1.36	2.57	0.0206	psoriasis susceptibility 1 candidate 2 (human)	A_51_P212956	Agilent
128	Spr1	1.50	2.83	0.0100	psoriasis susceptibility 1 candidate 2 (human)	CUST_56_PI209196805	custom
128	Spr1	1.52	2.87	0.0100	psoriasis susceptibility 1 candidate 2 (human)	CUST_57_PI209196805	custom
128	Spr1	1.51	2.85	0.0100	psoriasis susceptibility 1 candidate 2 (human)	CUST_58_PI209196805	custom
128	Spr1	1.50	2.83	0.0100	psoriasis susceptibility 1 candidate 2 (human)	CUST_59_PI209196805	custom
128	Spr1	1.58	2.99	0.0100	psoriasis susceptibility 1 candidate 2 (human)	CUST_60_PI209196805	custom
129	Cdsn	0.37	1.29	0.2732	corneodesmosin	CUST_1_PI201011238	custom
129	Cdsn	0.84	1.79	0.0100	corneodesmosin	CUST_2_PI201011238	custom
129	Cdsn	0.38	1.30	0.2184	corneodesmosin	CUST_3_PI201011238	custom
129	Cdsn	0.32	1.25	0.3754	corneodesmosin	CUST_4_PI201011238	custom
129	Cdsn	0.40	1.32	0.1769	corneodesmosin	CUST_5_PI201011238	custom
130	Stg	0.13	1.09	0.4327	Stg protein	A_44_P161038	Agilent
130	Stg	0.06	1.04	0.8258	Stg protein	A_43_P12304	Agilent
131	CB741658	−0.09	0.94	0.3912	CB741658 gene	CUST_1_PI197795805	custom
131	CB741658	0.05	1.04	0.5990	CB741658 gene	CUST_2_PI197795805	custom
131	CB741658	−0.05	0.97	0.6299	CB741658 gene	CUST_3_PI197795805	custom
131	CB741658	−0.03	0.98	0.7498	CB741658 gene	CUST_4_PI197795805	custom
131	CB741658	−0.05	0.97	0.5704	CB741658 gene	CUST_5_PI197795805	custom
132	Dpcr1	−0.11	0.93	0.3540	diffuse panbronchiolitis critical region 1 (human)	A_66_P112041	Agilent
132	Dpcr1	−0.17	0.89	0.0877	diffuse panbronchiolitis critical region 1 (human)	CUST_36_PI209196805	custom
132	Dpcr1	−0.10	0.93	0.4426	diffuse panbronchiolitis critical region 1 (human)	CUST_37_PI209196805	custom
132	Dpcr1	−0.11	0.93	0.2585	diffuse panbronchiolitis critical region 1 (human)	CUST_38_PI209196805	custom
132	Dpcr1	−0.14	0.91	0.2435	diffuse panbronchiolitis critical region 1 (human)	CUST_39_PI209196805	custom
132	Dpcr1	−0.04	0.97	0.7474	diffuse panbronchiolitis critical region 1 (human)	CUST_40_PI209196805	custom
133	E030032D13Rik	−0.24	0.85	0.0701	E030032D13Rik gene	A_44_P341977	Agilent
134	Kiaa1885	−0.08	0.95	0.5867	KIAA1885 protein	A_44_P1007561	Agilent
135	Gtf2h4	−0.09	0.94	0.7537	general transcription factor II H, polypeptide 4	CUST_1_PI197795807	custom
135	Gtf2h4	−0.03	0.98	0.9410	general transcription factor II H, polypeptide 4	CUST_2_PI197795807	custom
135	Gtf2h4	−0.12	0.92	0.7090	general transcription factor II H, polypeptide 4	CUST_3_PI197795807	custom
135	Gtf2h4	−0.02	0.99	0.9552	general transcription factor II H, polypeptide 4	CUST_4_PI197795807	custom
135	Gtf2h4	−0.06	0.96	0.8501	general transcription factor II H, polypeptide 4	CUST_5_PI197795807	custom
136	Ddr1	−0.18	0.88	0.1499	discoidin domain receptor family, member 1	A_44_P515494	Agilent

TABLE 5a-continued

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
137	CB707485I	−0.01	0.99	0.9561	gene corresponding to rat EST CB707485	CUST_1_PI201011227	custom
137	CB707485I	0.08	1.06	0.5379	gene corresponding to rat EST CB707485	CUST_2_PI201011227	custom
137	CB707485I	0.04	1.03	0.7953	gene corresponding to rat EST CB707485	CUST_3_PI201011227	custom
137	CB707485I	0.07	1.05	0.5259	gene corresponding to rat EST CB707485	CUST_4_PI201011227	custom
137	CB707485I	−0.08	0.95	0.7190	gene corresponding to rat EST CB707485	CUST_5_PI201011227	custom
138	Ier3	0.87	1.83	0.0229	immediate early response 3	A_42_P515405	Agilent
139	Flot1	0.04	1.03	0.8901	flotillin 1	A_44_P1023498	Agilent
140	Tubb5	0.16	1.12	0.2875	tubulin, beta 5	A_44_P825566	Agilent
141	Kiaa0170 (Mdc1)	0.02	1.01	0.9108	mediator of DNA damage checkpoint 1	A_42_P627572	Agilent
142	Nrm	−0.06	0.96	0.8031	nurim (nuclear envelope membrane protein)	CUST_1_PI197795809	custom
142	Nrm	−0.11	0.93	0.6622	nurim (nuclear envelope membrane protein)	CUST_2_PI197795809	custom
142	Nrm	−0.20	0.87	0.3384	nurim (nuclear envelope membrane protein)	CUST_3_PI197795809	custom
142	Nrm	−0.05	0.97	0.8551	nurim (nuclear envelope membrane protein)	CUST_4_PI197795809	custom
142	Nrm	0.03	1.02	0.8504	nurim (nuclear envelope membrane protein)	CUST_5_PI197795809	custom
143	Kiaa1949	0.42	1.34	0.0481	KIAA1949 protein	CUST_1_PI201011218	custom
143	Kiaa1949	0.49	1.40	0.0457	KIAA1949 protein	CUST_2_PI201011218	custom
143	Kiaa1949	0.33	1.26	0.1378	KIAA1949 protein	CUST_3_PI201011218	custom
143	Kiaa1949	0.39	1.31	0.0993	KIAA1949 protein	CUST_4_PI201011218	custom
143	Kiaa1949	0.34	1.27	0.1184	KIAA1949 protein	CUST_5_PI201011218	custom
144	Ddx16	0.04	1.03	0.8954	DEAH (Asp-Glu-Ala-His) box polypeptide 16	A_44_P379461	Agilent
144	Ddx16	−0.27	0.83	0.0797	DEAH (Asp-Glu-Ala-His) box polypeptide 16	A_43_P20689	Agilent
145	Mgc15854 (RGD1302996)	0.12	1.09	0.5094	hypothetical protein MGC15854	A_42_P508754	Agilent
145	Mgc15854 (RGD1302996)	0.05	1.04	0.8290	hypothetical protein MGC15854	A_44_P1002280	Agilent
146	Flj13158 (RGD1303066)	−0.25	0.84	0.0832	hypothetical protein FLJ13158	A_44_P278509	Agilent
146	Flj13158 (RGD1303066)	−0.57	0.67	0.0378	hypothetical protein FLJ13158	A_44_P654250	Agilent
147	Mrps18b	0.52	1.43	0.0474	mitochondrial ribosomal protein S18B	CUST_1_PI197795811	custom
147	Mrps18b	0.49	1.40	0.0378	mitochondrial ribosomal protein S18B	CUST_2_PI197795811	custom
147	Mrps18b	0.57	1.48	0.0267	mitochondrial ribosomal protein S18B	CUST_3_PI197795811	custom
147	Mrps18b	0.59	1.51	0.0365	mitochondrial ribosomal protein S18B	CUST_4_PI197795811	custom
147	Mrps18b	0.62	1.54	0.0254	mitochondrial ribosomal protein S18B	CUST_5_PI197795811	custom
148	Ppp1r10	0.49	1.40	0.1582	protein phosphatase 1, regulatory subunit 10	A_42_P497323	Agilent
149	Abcf1	0.46	1.38	0.0832	ATP-binding cassette, sub-family F (GCN20), member 1	CUST_46_PI209196805	custom
149	Abcf1	0.44	1.36	0.1863	ATP-binding cassette, sub-family F (GCN20), member 1	CUST_47_PI209196805	custom
149	Abcf1	0.34	1.27	0.2797	ATP-binding cassette, sub-family F (GCN20), member 1	CUST_48_PI209196805	custom
149	Abcf1	0.30	1.23	0.3188	ATP-binding cassette, sub-family F (GCN20), member 1	CUST_49_PI209196805	custom
149	Abcf1	0.34	1.27	0.2180	ATP-binding cassette, sub-family F (GCN20), member 1	CUST_50_PI209196805	custom
150	Cat56 (Prr3)	−0.01	0.99	0.9791	proline-rich polypeptide 3	A_44_P299349	Agilent
151	Gnl1	0.05	1.04	0.8944	guanine nucleotide binding protein, related sequence 1	A_65_P05751	Agilent
151	Gnl1	−0.04	0.97	0.6698	guanine nucleotide binding protein, related sequence 1	A_66_P118660	Agilent
151	Gnl1	0.02	1.01	0.9496	guanine nucleotide binding protein, related sequence 1	A_51_P102809	Agilent
151	Gnl1	−0.15	0.90	0.5093	guanine nucleotide binding protein, related sequence 1	A_51_P102814	Agilent
151	Gnl1	0.07	1.05	0.8093	guanine nucleotide binding protein, related sequence 1	A_52_P491766	Agilent
151	Gnl1	−0.24	0.85	0.2708	guanine nucleotide binding protein, related sequence 1	CUST_41_PI209196805	custom
151	Gnl1	−0.17	0.89	0.4205	guanine nucleotide binding protein, related sequence 1	CUST_42_PI209196805	custom
151	Gnl1	0.03	1.02	0.9311	guanine nucleotide binding protein, related sequence 1	CUST_43_PI209196805	custom
151	Gnl1	0.02	1.01	0.9448	guanine nucleotide binding protein, related sequence 1	CUST_44_PI209196805	custom
151	Gnl1	0.03	1.02	0.8853	guanine nucleotide binding protein, related sequence 1	CUST_45_PI209196805	custom
152	RT1-T24-1	0.25	1.19	0.2040	RT1 class I, T24, gene 1	A_44_P187530	Agilent
153	RT1-T24-2	−0.01	0.99	0.9531	RT1 class I, T24, gene 2	A_44_P215023	Agilent
154	RT1-T24-3	0.31	1.24	0.1540	RT1 class I, T24, gene 3	CUST_1_PI201011214	custom
154	RT1-T24-3	0.42	1.34	0.0336	RT1 class I, T24, gene 3	CUST_2_PI201011214	custom
154	RT1-T24-3	0.27	1.21	0.1454	RT1 class I, T24, gene 3	CUST_3_PI201011214	custom
154	RT1-T24-3	0.31	1.24	0.0847	RT1 class I, T24, gene 3	CUST_4_PI201011214	custom
154	RT1-T24-3	0.08	1.06	0.6030	RT1 class I, T24, gene 3	CUST_5_PI201011214	custom
155	RT1-T24-4	0.57	1.48	0.0345	RT1 class I, T24, gene 4	CUST_1_PI197795813	custom
155	RT1-T24-4	0.76	1.69	0.0206	RT1 class I, T24, gene 4	CUST_2_PI197795813	custom
155	RT1-T24-4	0.72	1.65	0.0206	RT1 class I, T24, gene 4	CUST_3_PI197795813	custom
155	RT1-T24-4	0.39	1.31	0.0611	RT1 class I, T24, gene 4	CUST_4_PI197795813	custom
155	RT1-T24-4	0.51	1.42	0.0939	RT1 class I, T24, gene 4	CUST_5_PI197795813	custom
156	RT-BM1 (RT1-S3)	1.06	2.08	0.0416	RT1 class I, RT-BM1	A_44_P454420	Agilent
157	RT1-N3	0.20	1.15	0.3890	RT1 class I, N3	A_42_P521707	Agilent
158	RT1-O1	−0.03	0.98	0.8512	RT1 class I, O1	CUST_1_PI197795863	custom
158	RT1-O1	−0.05	0.97	0.6261	RT1 class I, O1	CUST_2_PI197795863	custom
158	RT1-O1	0.08	1.06	0.3128	RT1 class I, O1	CUST_3_PI197795863	custom
158	RT1-O1	0.01	1.01	0.8904	RT1 class I, O1	CUST_4_PI197795863	custom
158	RT1-O1	−0.15	0.90	0.3468	RT1 class I, O1	CUST_5_PI197795863	custom
159	RT1-S2	−0.31	0.81	0.2437	RT1 class I, S2	CUST_1_PI2010111700	custom
159	RT1-S2	−0.25	0.84	0.2765	RT1 class I, S2	CUST_5_PI2010111700	custom

TABLE 5a-continued

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
160	RT1-N2	0.06	1.04	0.7225	RT1 class I, N2	CUST_1_PI197795818	custom
160	RT1-N2	−0.02	0.99	0.9142	RT1 class I, N2	CUST_2_PI197795818	custom
160	RT1-N2	0.09	1.06	0.6061	RT1 class I, N2	CUST_3_PI197795818	custom
160	RT1-N2	0.01	1.01	0.9575	RT1 class I, N2	CUST_4_PI197795818	custom
160	RT1-N2	0.01	1.01	0.9481	RT1 class I, N2	CUST_5_PI197795818	custom
160	RT1-N2	0.02	1.01	0.9122	RT1 class I, N2	A_44_P379367	Agilent
161	RT1-O2	−0.38	0.77	0.2262	RT1 class I, O2	CUST_1_PI201011211	custom
161	RT1-O2	0.57	1.48	0.0345	RT1 class I, O2	CUST_2_PI201011211	custom
161	RT1-O2	−0.09	0.94	0.6330	RT1 class I, O2	CUST_3_PI201011211	custom
161	RT1-O2	0.55	1.46	0.0424	RT1 class I, O2	CUST_4_PI201011211	custom
161	RT1-O2	0.22	1.16	0.3389	RT1 class I, O2	CUST_5_PI201011211	custom
162	RT1-O3	−0.30	0.81	0.2438	RT1 class I, O3	CUST_1_PI201011202	custom
162	RT1-O3	−0.13	0.91	0.5468	RT1 class I, O3	CUST_2_PI201011202	custom
162	RT1-O3	0.50	1.41	0.0546	RT1 class I, O3	CUST_3_PI201011202	custom
162	RT1-O3	0.50	1.41	0.0457	RT1 class I, O3	CUST_4_PI201011202	custom
162	RT1-O3	0.23	1.17	0.2975	RT1 class I, O3	CUST_5_PI201011202	custom
163	RT1-V1	0.10	1.07	0.5153	RT1 class I, V1	CUST_1_PI201011196	custom
163	RT1-V1	0.05	1.04	0.6614	RT1 class I, V1	CUST_2_PI201011196	custom
163	RT1-V1	0.03	1.02	0.8018	RT1 class I, V1	CUST_3_PI201011196	custom
163	RT1-V1	0.03	1.02	0.7265	RT1 class I, V1	CUST_4_PI201011196	custom
163	RT1-V1	0.11	1.08	0.3219	RT1 class I, V1	CUST_5_PI201011196	custom
164	RT1-T18	0.12	1.09	0.5019	histocompatibility 2, T region locus 18	A_44_P358361	Agilent
164	RT1-T18	0.67	1.59	0.0828	histocompatibility 2, T region locus 18	A_44_P358358	Agilent
165	RT1-P1	0.42	1.34	0.1795	RT1 class I, P1	CUST_1_PI201011193	custom
165	RT1-P1	0.43	1.35	0.1897	RT1 class I, P1	CUST_2_PI201011193	custom
165	RT1-P1	0.33	1.26	0.3012	RT1 class I, P1	CUST_3_PI201011193	custom
165	RT1-P1	0.38	1.30	0.2049	RT1 class I, P1	CUST_4_PI201011193	custom
165	RT1-P1	0.31	1.24	0.2951	RT1 class I, P1	CUST_5_PI201011193	custom
166	RT1-V2	0.02	1.01	0.8517	RT1 class I, V2	CUST_1_PI201011189	custom
166	RT1-V2	0.07	1.05	0.3934	RT1 class I, V2	CUST_2_PI201011189	custom
166	RT1-V2	0.01	1.01	0.9606	RT1 class I, V2	CUST_3_PI201011189	custom
166	RT1-V2	−0.01	0.99	0.9455	RT1 class I, V2	CUST_4_PI201011189	custom
166	RT1-V2	0.06	1.04	0.6161	RT1 class I, V2	CUST_5_PI201011189	custom
167	RT1-P2	0.14	1.10	0.2561	RT1 class I, P2	CUST_1_PI201011184	custom
167	RT1-P2	−0.01	0.99	0.9599	RT1 class I, P2	CUST_2_PI201011184	custom
167	RT1-P2	−0.03	0.98	0.7705	RT1 class I, P2	CUST_3_PI201011184	custom
167	RT1-P2	0.01	1.01	0.9284	RT1 class I, P2	CUST_4_PI201011184	custom
167	RT1-P2	−0.03	0.98	0.8477	RT1 class I, P2	CUST_5_PI201011184	custom
168	Flj22638 (Rpp21)	0.10	1.07	0.6826	ribonuclease P 21 subunit	A_44_P1017763	Agilent
168	Flj22638 (Rpp21)	−0.02	0.99	0.8997	ribonuclease P 21 subunit	A_44_P1017757	Agilent
169	Trim39	−0.32	0.80	0.1210	tripartite motif-containing 39	A_44_P245427	Agilent
170	RT1-M10-1	0.02	1.01	0.8675	RT1 class I, M10, gene 1	CUST_1_PI201011161	custom
170	RT1-M10-1	−0.19	0.88	0.1707	RT1 class I, M10, gene 1	CUST_2_PI201011161	custom
170	RT1-M10-1	0.03	1.02	0.7954	RT1 class I, M10, gene 1	CUST_3_PI201011161	custom
170	RT1-M10-1	−0.01	0.99	0.9161	RT1 class I, M10, gene 1	CUST_4_PI201011161	custom
170	RT1-M10-1	−0.04	0.97	0.6779	RT1 class I, M10, gene 1	CUST_5_PI201011161	custom
171	RT1-M10-2	−0.09	0.94	0.2987	RT1 class I, M10, gene 2	CUST_1_PI201011180	custom
171	RT1-M10-2	−0.06	0.96	0.6569	RT1 class I, M10, gene 2	CUST_2_PI201011180	custom
171	RT1-M10-2	−0.01	0.99	0.9375	RT1 class I, M10, gene 2	CUST_3_PI201011180	custom
171	RT1-M10-2	0.03	1.02	0.7545	RT1 class I, M10, gene 2	CUST_4_PI201011180	custom
171	RT1-M10-2	−0.02	0.99	0.8053	RT1 class I, M10, gene 2	CUST_5_PI201011180	custom
172	RT1-M1-1	−0.01	0.99	0.9358	RT1 class I, M1, gene 1	CUST_1_PI201011178	custom
172	RT1-M1-1	−0.11	0.93	0.4445	RT1 class I, M1, gene 1	CUST_2_PI201011178	custom
172	RT1-M1-1	0.54	1.45	0.0278	RT1 class I, M1, gene 1	CUST_3_PI201011178	custom
172	RT1-M1-1	−0.17	0.89	0.1632	RT1 class I, M1, gene 1	CUST_4_PI201011178	custom
172	RT1-M1-1	−0.05	0.97	0.7839	RT1 class I, M1, gene 1	CUST_5_PI201011178	custom
173	RT1-M1-2	−0.11	0.93	0.3479	RT1 class I, M1, gene 2	CUST_1_PI197795822	custom
173	RT1-M1-2	−0.22	0.86	0.1078	RT1 class I, M1, gene 2	CUST_2_PI197795822	custom
173	RT1-M1-2	−0.03	0.98	0.7000	RT1 class I, M1, gene 2	CUST_3_PI197795822	custom
173	RT1-M1-2	−0.02	0.99	0.8325	RT1 class I, M1, gene 2	CUST_4_PI197795822	custom
173	RT1-M1-2	0.00	1.00	0.9910	RT1 class I, M1, gene 2	CUST_5_PI197795822	custom
174	RT1-M1-3	−0.10	0.93	0.2338	RT1 class I, M1, gene 3	CUST_1_PI201011175	custom
174	RT1-M1-3	−0.02	0.99	0.9164	RT1 class I, M1, gene 3	CUST_2_PI201011175	custom
174	RT1-M1-3	−0.01	0.99	0.9246	RT1 class I, M1, gene 3	CUST_3_PI201011175	custom
174	RT1-M1-3	0.03	1.02	0.7901	RT1 class I, M1, gene 3	CUST_4_PI201011175	custom
174	RT1-M1-3	−0.09	0.94	0.2805	RT1 class I, M1, gene 3	CUST_5_PI201011175	custom
175	RT1-M1-4	−0.23	0.85	0.1261	RT1 class I, M1, gene 4	A_44_P213221	Agilent
176	RT1-M1-5	0.04	1.03	0.7001	RT1 class I, M1, gene 5	A_44_P506413	Agilent
177	RT1-M7	−0.08	0.95	0.3109	RT1 class I, M7	CUST_1_PI201011173	custom
177	RT1-M7	−0.30	0.81	0.0433	RT1 class I, M7	CUST_2_PI201011173	custom
177	RT1-M7	0.04	1.03	0.5727	RT1 class I, M7	CUST_3_PI201011173	custom
177	RT1-M7	−0.05	0.97	0.7154	RT1 class I, M7	CUST_4_PI201011173	custom
177	RT1-M7	−0.32	0.80	0.1162	RT1 class I, M7	CUST_5_PI201011173	custom

TABLE 5a-continued

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
178	RT1-M8	−0.23	0.85	0.0654	RT1 class I, M8	CUST_1_PI201011170	custom
178	RT1-M8	−0.04	0.97	0.6168	RT1 class I, M8	CUST_2_PI201011170	custom
178	RT1-M8	−0.31	0.81	0.1655	RT1 class I, M8	CUST_3_PI201011170	custom
178	RT1-M8	−0.22	0.86	0.2766	RT1 class I, M8	CUST_5_PI201011170	custom
178	RT1-M8	0.01	1.01	0.9933	RT1 class I, M8	CUST_4_PI201011170	custom
179	RT1-M10-3	−0.02	0.99	0.9071	RT1 class I, M10, gene 3	CUST_1_PI201011167	custom
179	RT1-M10-3	−0.27	0.83	0.0424	RT1 class I, M10, gene 3	CUST_2_PI201011167	custom
179	RT1-M10-3	−0.06	0.96	0.6730	RT1 class I, M10, gene 3	CUST_3_PI201011167	custom
179	RT1-M10-3	−0.04	0.97	0.6161	RT1 class I, M10, gene 3	CUST_4_PI201011167	custom
179	RT1-M10-3	−0.06	0.96	0.5878	RT1 class I, M10, gene 3	CUST_5_PI201011167	custom
180	RT1-M10-4	0.08	1.06	0.4351	RT1 class I, M10, gene 4	CUST_1_PI197795820	custom
180	RT1-M10-4	0.09	1.06	0.4057	RT1 class I, M10, gene 4	CUST_2_PI197795820	custom
180	RT1-M10-4	0.26	1.20	0.3213	RT1 class I, M10, gene 4	CUST_3_PI197795820	custom
180	RT1-M10-4	−0.62	0.65	0.0539	RT1 class I, M10, gene 4	CUST_4_PI197795820	custom
180	RT1-M10-4	0.07	1.05	0.6195	RT1 class I, M10, gene 4	CUST_5_PI197795820	custom
181	Trim26	−0.04	0.97	0.8676	tripartite motif-containing 26	CUST_1_PI197795824	custom
181	Trim26	−0.04	0.97	0.8113	tripartite motif-containing 26	CUST_2_PI197795824	custom
181	Trim26	−0.20	0.87	0.1379	tripartite motif-containing 26	CUST_3_PI197795824	custom
181	Trim26	0.07	1.05	0.6779	tripartite motif-containing 26	CUST_4_PI197795824	custom
181	Trim26	−0.01	0.99	0.9756	tripartite motif-containing 26	CUST_5_PI197795824	custom
182	Trim15	−0.99	0.50	0.0539	tripartite motif-containing 15	CUST_1_PI201011159	custom
182	Trim15	−0.96	0.51	0.0722	tripartite motif-containing 15	CUST_2_PI201011159	custom
182	Trim15	−0.90	0.54	0.0858	tripartite motif-containing 15	CUST_3_PI201011159	custom
182	Trim15	−0.83	0.56	0.0654	tripartite motif-containing 15	CUST_4_PI201011159	custom
182	Trim15	−1.02	0.49	0.0603	tripartite motif-containing 15	CUST_5_PI201011159	custom
183	Trim10	−0.26	0.84	0.2418	tripartite motif protein 10	CUST_1_PI197795826	custom
183	Trim10	−0.18	0.88	0.5016	tripartite motif protein 10	CUST_2_PI197795826	custom
183	Trim10	−0.15	0.90	0.5471	tripartite motif protein 10	CUST_3_PI197795826	custom
183	Trim10	−0.26	0.84	0.2463	tripartite motif protein 10	CUST_4_PI197795826	custom
183	Trim10	−0.20	0.87	0.2290	tripartite motif protein 10	CUST_5_PI197795826	custom
184	Trim40	−0.22	0.86	0.0923	tripartite motif-containing 40	CUST_1_PI209196805	custom
184	Trim40	0.00	1.00	0.9664	tripartite motif-containing 40	CUST_2_PI209196805	custom
184	Trim40	0.08	1.06	0.5878	tripartite motif-containing 40	CUST_3_PI209196805	custom
184	Trim40	−0.06	0.96	0.6191	tripartite motif-containing 40	CUST_4_PI209196805	custom
184	Trim40	−0.08	0.95	0.4748	tripartite motif-containing 40	CUST_5_PI209196805	custom
185	Trim31	−0.04	0.97	0.8529	tripartite motif-containing 31	A_51_P490840	Agilent
185	Trim31	−0.04	0.97	0.7567	tripartite motif-containing 31	CUST_21_PI209196805	custom
185	Trim31	0.00	1.00	0.9980	tripartite motif-containing 31	CUST_22_PI209196805	custom
185	Trim31	−0.06	0.96	0.5133	tripartite motif-containing 31	CUST_23_PI209196805	custom
185	Trim31	−0.16	0.90	0.1958	tripartite motif-containing 31	CUST_24_PI209196805	custom
185	Trim31	−0.04	0.97	0.7351	tripartite motif-containing 31	CUST_25_PI209196805	custom
186	1700031A10Rik	−0.14	0.91	0.4950	gene corresponding to Riken clone 1700031A10	A_52_P515192	Agilent
186	1700031A10Rik	−0.10	0.93	0.2703	gene corresponding to Riken clone 1700031A10	CUST_31_PI209196805	custom
186	1700031A10Rik	−0.13	0.91	0.3373	gene corresponding to Riken clone 1700031A10	CUST_32_PI209196805	custom
186	1700031A10Rik	−0.08	0.95	0.5598	gene corresponding to Riken clone 1700031A10	CUST_33_PI209196805	custom
186	1700031A10Rik	−0.02	0.99	0.9034	gene corresponding to Riken clone 1700031A10	CUST_34_PI209196805	custom
186	1700031A10Rik	−0.05	0.97	0.7178	gene corresponding to Riken clone 1700031A10	CUST_35_PI209196805	custom
187	Rnf39	0.05	1.04	0.6605	Ring finger protein Lirf	CUST_1_PI195698208	custom
187	Rnf39	0.06	1.04	0.5793	Ring finger protein Lirf	CUST_2_PI195698208	custom
187	Rnf39	−0.02	0.99	0.8552	Ring finger protein Lirf	CUST_3_PI195698208	custom
187	Rnf39	−0.28	0.82	0.0579	Ring finger protein Lirf	CUST_4_PI195698208	custom
187	Rnf39	−0.06	0.96	0.6264	Ring finger protein Lirf	CUST_5_PI195698208	custom
188	Ppp1r11	0.14	1.10	0.5417	protein phosphatase 1, regulatory (inhibitor) subunit 11	CUST_1_PI197795829	custom
188	Ppp1r11	0.14	1.10	0.4917	protein phosphatase 1, regulatory (inhibitor) subunit 11	CUST_2_PI197795829	custom
188	Ppp1r11	0.10	1.07	0.6213	protein phosphatase 1, regulatory (inhibitor) subunit 11	CUST_3_PI197795829	custom
188	Ppp1r11	0.13	1.09	0.4615	protein phosphatase 1, regulatory (inhibitor) subunit 11	CUST_4_PI197795829	custom
188	Ppp1r11	0.09	1.06	0.6711	protein phosphatase 1, regulatory (inhibitor) subunit 11	CUST_5_PI197795829	custom
189	Znrd1	0.22	1.16	0.3879	zinc ribbon domain containing, 1	A_44_P404931	Agilent
190	Tctex4	−0.20	0.87	0.2497	t-complex testis-expressed 4, rat homologue	CUST_1_PI201011154	custom
190	Tctex4	−0.10	0.93	0.6520	t-complex testis-expressed 4, rat homologue	CUST_2_PI201011154	custom
190	Tctex4	−0.02	0.99	0.9728	t-complex testis-expressed 4, rat homologue	CUST_3_PI201011154	custom
190	Tctex4	−0.14	0.91	0.7705	t-complex testis-expressed 4, rat homologue	CUST_4_PI201011154	custom
190	Tctex4	−0.18	0.88	0.6959	t-complex testis-expressed 4, rat homologue	CUST_5_PI201011154	custom
191	RT1-M6-2	0.29	1.22	0.2232	RT1 class I, M6, gene 2	A_44_P309052	Agilent
192	RT1-M6-1	0.25	1.19	0.1939	RT1 class I, M6, gene 1	CUST_1_PI197795831	custom
192	RT1-M6-1	0.14	1.10	0.2419	RT1 class I, M6, gene 1	CUST_2_PI197795831	custom
192	RT1-M6-1	0.09	1.06	0.5742	RT1 class I, M6, gene 1	CUST_3_PI197795831	custom
192	RT1-M6-1	0.15	1.11	0.2707	RT1 class I, M6, gene 1	CUST_4_PI197795831	custom
192	RT1-M6-1	0.13	1.09	0.5124	RT1 class I, M6, gene 1	CUST_5_PI197795831	custom
193	RT1-M4	−0.05	0.97	0.6379	RT1 class I, M4	A_44_P260445	Agilent
193	RT1-M4	−0.03	0.98	0.8888	RT1 class I, M4	CUST_1_PI201011151	custom
193	RT1-M4	0.01	1.01	0.9694	RT1 class I, M4	CUST_2_PI201011151	custom
193	RT1-M4	0.25	1.19	0.2536	RT1 class I, M4	CUST_3_PI201011151	custom

TABLE 5a-continued

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
193	RT1-M4	−0.01	0.99	0.9413	RT1 class I, M4	CUST_4_PI201011151	custom
193	RT1-M4	−0.11	0.93	0.6425	RT1 class I, M4	CUST_5_PI201011151	custom
194	RT1-M5	−0.13	0.91	0.2545	RT1 class Ib, locus M5	CUST_1_PI197795834	custom
194	RT1-M5	−0.02	0.99	0.9122	RT1 class Ib, locus M5	CUST_2_PI197795834	custom
194	RT1-M5	−0.05	0.97	0.6483	RT1 class Ib, locus M5	CUST_3_PI197795834	custom
194	RT1-M5	0.03	1.02	0.8395	RT1 class Ib, locus M5	CUST_4_PI197795834	custom
194	RT1-M5	−0.05	0.97	0.6199	RT1 class Ib, locus M5	CUST_5_PI197795834	custom
195	Zfp57	0.13	1.09	0.6841	zinc finger protein 57	CUST_1_PI197795840	custom
195	Zfp57	−0.43	0.74	0.0681	zinc finger protein 57	CUST_2_PI197795840	custom
195	Zfp57	−0.40	0.76	0.0611	zinc finger protein 57	CUST_3_PI197795840	custom
195	Zfp57	−0.34	0.79	0.0401	zinc finger protein 57	CUST_4_PI197795840	custom
195	Zfp57	−0.29	0.82	0.0940	zinc finger protein 57	CUST_5_PI197795840	custom
196	Mog	−0.26	0.84	0.1591	myelin oligodendrocyte glycoprotein	A_43_P12283	Agilent
197	Gabbr1	−0.17	0.89	0.4183	gamma-aminobutyric acid (GABA) B receptor 1	A_43_P12481	Agilent
198	9430032L10Rik	0.05	1.04	0.5965	gene corresponding to Riken clone 9430032L10	CUST_1_PI201011147	custom
198	9430032L10Rik	0.02	1.01	0.8261	gene corresponding to Riken clone 9430032L10	CUST_2_PI201011147	custom
198	9430032L10Rik	0.02	1.01	0.8425	gene corresponding to Riken clone 9430032L10	CUST_3_PI201011147	custom
198	9430032L10Rik	0.04	1.03	0.8307	gene corresponding to Riken clone 9430032L10	CUST_4_PI201011147	custom
198	9430032L10Rik	−0.03	0.98	0.8685	gene corresponding to Riken clone 9430032L10	CUST_5_PI201011147	custom
199	Or1	−0.08	0.95	0.5471	olfactory receptor 1750 (predicted)	A_52_P410245	Agilent
199	Or1	−0.02	0.99	0.8675	olfactory receptor 1750 (predicted)	CUST_16_PI209196805	custom
199	Or1	−0.11	0.93	0.4597	olfactory receptor 1750 (predicted)	CUST_17_PI209196805	custom
199	Or1	−0.02	0.99	0.9034	olfactory receptor 1750 (predicted)	CUST_18_PI209196805	custom
199	Or1	−0.04	0.97	0.8090	olfactory receptor 1750 (predicted)	CUST_19_PI209196805	custom
199	Or1	−0.05	0.97	0.7090	olfactory receptor 1750 (predicted)	CUST_20_PI209196805	custom
200	Or2	−0.07	0.95	0.6299	olfactory receptor 1749 (predicted)	CUST_1_PI197795848	custom
200	Or2	−0.08	0.95	0.3091	olfactory receptor 1749 (predicted)	CUST_2_PI197795848	custom
200	Or2	0.07	1.05	0.5007	olfactory receptor 1749 (predicted)	CUST_3_PI197795848	custom
200	Or2	−0.05	0.97	0.6808	olfactory receptor 1749 (predicted)	CUST_4_PI197795848	custom
200	Or2	−0.03	0.98	0.8117	olfactory receptor 1749 (predicted)	CUST_5_PI197795848	custom
201	Or3	−0.11	0.93	0.4566	olfactory receptor 1748 (predicted)	CUST_1_PI197795850	custom
201	Or3	−0.13	0.91	0.2329	olfactory receptor 1748 (predicted)	CUST_2_PI197795850	custom
201	Or3	−0.17	0.89	0.1773	olfactory receptor 1748 (predicted)	CUST_3_PI197795850	custom
201	Or3	−0.06	0.96	0.6310	olfactory receptor 1748 (predicted)	CUST_4_PI197795850	custom
201	Or3	−0.27	0.83	0.1077	olfactory receptor 1748 (predicted)	CUST_5_PI197795850	custom
202	Or4	−0.20	0.87	0.2322	olfactory receptor 1747 (predicted)	CUST_1_PI201011143	custom
202	Or4	−0.01	0.99	0.9720	olfactory receptor 1747 (predicted)	CUST_2_PI201011143	custom
202	Or4	−0.21	0.86	0.1923	olfactory receptor 1747 (predicted)	CUST_3_PI201011143	custom
202	Or4	−0.18	0.88	0.2355	olfactory receptor 1747 (predicted)	CUST_4_PI201011143	custom
202	Or4	−0.10	0.93	0.5972	olfactory receptor 1747 (predicted)	CUST_5_PI201011143	custom
203	Or5	0.10	1.07	0.4571	olfactory receptor 1746 (predicted)	CUST_1_PI197795852	custom
203	Or5	0.04	1.03	0.7809	olfactory receptor 1746 (predicted)	CUST_2_PI197795852	custom
203	Or5	−0.03	0.98	0.8583	olfactory receptor 1746 (predicted)	CUST_3_PI197795852	custom
203	Or5	0.13	1.09	0.3836	olfactory receptor 1746 (predicted)	CUST_4_PI197795852	custom
203	Or5	−0.02	0.99	0.9090	olfactory receptor 1746 (predicted)	CUST_5_PI197795852	custom
204	Ubd	3.19	9.13	0.0345	ubiquitin D	A_42_P602724	Agilent
205	Or6	0.03	1.02	0.8855	olfactory receptor 1745 (predicted)	CUST_1_PI201011139	custom
205	Or6	0.14	1.10	0.2994	olfactory receptor 1745 (predicted)	CUST_2_PI201011139	custom
205	Or6	−0.06	0.96	0.6676	olfactory receptor 1745 (predicted)	CUST_3_PI201011139	custom
205	Or6	−0.09	0.94	0.8444	olfactory receptor 1745 (predicted)	CUST_4_PI201011139	custom
205	Or6	−0.09	0.94	0.7413	olfactory receptor 1745 (predicted)	CUST_5_PI201011139	custom
206	Or7	0.14	1.10	0.2389	olfactory receptor 1744 (predicted)	CUST_1_PI197795854	custom
206	Or7	0.00	1.00	0.9829	olfactory receptor 1744 (predicted)	CUST_2_PI197795854	custom
206	Or7	−0.09	0.94	0.6165	olfactory receptor 1744 (predicted)	CUST_3_PI197795854	custom
206	Or7	0.12	1.09	0.5423	olfactory receptor 1744 (predicted)	CUST_4_PI197795854	custom
206	Or7	−0.07	0.95	0.4992	olfactory receptor 1744 (predicted)	CUST_5_PI197795854	custom
207	Or8	0.01	1.01	0.9701	olfactory receptor 1743 (predicted)	CUST_1_PI197795856	custom
207	Or8	−0.10	0.93	0.5207	olfactory receptor 1743 (predicted)	CUST_2_PI197795856	custom
207	Or8	−0.14	0.91	0.2325	olfactory receptor 1743 (predicted)	CUST_3_PI197795856	custom
207	Or8	−0.10	0.93	0.4321	olfactory receptor 1743 (predicted)	CUST_4_PI197795856	custom
207	Or8	−0.31	0.81	0.0310	olfactory receptor 1743 (predicted)	CUST_5_PI197795856	custom
208	Or9	−0.02	0.99	0.8743	olfactory receptor 1742 (predicted)	A_44_P365332	Agilent
208	Or9	0.03	1.02	0.8131	olfactory receptor 1742 (predicted)	CUST_1_PI197795876	custom
208	Or9	−0.19	0.88	0.1014	olfactory receptor 1742 (predicted)	CUST_2_PI197795876	custom
208	Or9	−0.26	0.84	0.0623	olfactory receptor 1742 (predicted)	CUST_3_PI197795876	custom
208	Or9	−0.04	0.97	0.6038	olfactory receptor 1742 (predicted)	CUST_4_PI197795876	custom
208	Or9	−0.02	0.99	0.9014	olfactory receptor 1742 (predicted)	CUST_5_PI197795876	custom
209	RT1-M3-2	−0.07	0.95	0.8384	RT1 class Ib, locus M3	CUST_1_PI201011135	custom
209	RT1-M3-2	−0.03	0.98	0.9327	RT1 class Ib, locus M3	CUST_2_PI201011135	custom
209	RT1-M3-2	−0.08	0.95	0.8425	RT1 class Ib, locus M3	CUST_3_PI201011135	custom
209	RT1-M3-2	−0.13	0.91	0.6541	RT1 class Ib, locus M3	CUST_4_PI201011135	custom
209	RT1-M3-2	−0.10	0.93	0.7667	RT1 class Ib, locus M3	CUST_5_PI201011135	custom
210	Or10	0.07	1.05	0.6326	olfactory receptor 1740 (predicted)	CUST_1_PI201011133	custom

TABLE 5a-continued

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
210	Or10	−0.10	0.93	0.2049	olfactory receptor 1740 (predicted)	CUST_2_PI201011133	custom
210	Or10	−0.09	0.94	0.5788	olfactory receptor 1740 (predicted)	CUST_3_PI201011133	custom
210	Or10	−0.08	0.95	0.5345	olfactory receptor 1740 (predicted)	CUST_4_PI201011133	custom
210	Or10	−0.10	0.93	0.2687	olfactory receptor 1740 (predicted)	CUST_5_PI201011133	custom
211	RT1-M3-1	0.24	1.18	0.4938	RT1 class Ib, locus M3	CUST_1_PI197795861	custom
211	RT1-M3-1	0.27	1.21	0.5424	RT1 class Ib, locus M3	CUST_2_PI197795861	custom
211	RT1-M3-1	0.25	1.19	0.5596	RT1 class Ib, locus M3	CUST_3_PI197795861	custom
211	RT1-M3-1	0.03	1.02	0.9375	RT1 class Ib, locus M3	CUST_4_PI197795861	custom
211	RT1-M3-1	0.14	1.10	0.7567	RT1 class Ib, locus M3	CUST_5_PI197795861	custom
212	Or11	0.03	1.02	0.7761	olfactory receptor 1739 (predicted)	A_44_P433163	Agilent
213	Or12	−0.07	0.95	0.6171	olfactory receptor 1738 (predicted)	CUST_1_PI197795865	custom
213	Or12	−0.21	0.86	0.1188	olfactory receptor 1738 (predicted)	CUST_2_PI197795865	custom
213	Or12	−0.19	0.88	0.1498	olfactory receptor 1738 (predicted)	CUST_3_PI197795865	custom
213	Or12	0.02	1.01	0.9088	olfactory receptor 1738 (predicted)	CUST_4_PI197795865	custom
213	Or12	0.06	1.04	0.6232	olfactory receptor 1738 (predicted)	CUST_5_PI197795865	custom
214	Or13	−0.01	0.99	0.9278	olfactory receptor 1737 (predicted)	CUST_1_PI197795867	custom
214	Or13	−0.38	0.77	0.0345	olfactory receptor 1737 (predicted)	CUST_2_PI197795867	custom
214	Or13	−0.07	0.95	0.6831	olfactory receptor 1737 (predicted)	CUST_3_PI197795867	custom
214	Or13	0.06	1.04	0.6537	olfactory receptor 1737 (predicted)	CUST_4_PI197795867	custom
214	Or13	0.02	1.01	0.8695	olfactory receptor 1737 (predicted)	CUST_5_PI197795867	custom
215	Or14	0.04	1.03	0.6686	olfactory receptor 1736 (predicted)	CUST_1_PI197795870	custom
215	Or14	0.00	1.00	0.9849	olfactory receptor 1736 (predicted)	CUST_2_PI197795870	custom
215	Or14	0.01	1.01	0.9194	olfactory receptor 1736 (predicted)	CUST_3_PI197795870	custom
215	Or14	−0.26	0.84	0.2740	olfactory receptor 1736 (predicted)	CUST_4_PI197795870	custom
215	Or14	−0.14	0.91	0.1027	olfactory receptor 1736 (predicted)	CUST_5_PI197795870	custom
216	Or15	−0.07	0.95	0.3931	olfactory receptor 1735 (predicted)	CUST_1_PI197795872	custom
216	Or15	−0.14	0.91	0.2867	olfactory receptor 1735 (predicted)	CUST_2_PI197795872	custom
216	Or15	0.00	1.00	0.9952	olfactory receptor 1735 (predicted)	CUST_3_PI197795872	custom
216	Or15	−0.08	0.95	0.6808	olfactory receptor 1735 (predicted)	CUST_4_PI197795872	custom
216	Or15	−0.07	0.95	0.5993	olfactory receptor 1735 (predicted)	CUST_5_PI197795872	custom
217	Or27	−0.04	0.97	0.8286	olfactory receptor 1716 (predicted)	CUST_1_PI201011130	custom
217	Or27	−0.09	0.94	0.4929	olfactory receptor 1716 (predicted)	CUST_2_PI201011130	custom
217	Or27	−0.01	0.99	0.9401	olfactory receptor 1716 (predicted)	CUST_3_PI201011130	custom
217	Or27	−0.04	0.97	0.6989	olfactory receptor 1716 (predicted)	CUST_4_PI201011130	custom
217	Or27	−0.07	0.95	0.6330	olfactory receptor 1716 (predicted)	CUST_5_PI201011130	custom
218	Or26	−0.07	0.95	0.4471	olfactory receptor 1718 (predicted)	A_44_P505752	Agilent
219	Or28	−0.05	0.97	0.5892	olfactory receptor 1714 (predicted)	CUST_1_PI197795859	custom
219	Or28	−0.24	0.85	0.0490	olfactory receptor 1714 (predicted)	CUST_2_PI197795859	custom
219	Or28	−0.01	0.99	0.9454	olfactory receptor 1714 (predicted)	CUST_3_PI197795859	custom
219	Or28	−0.02	0.99	0.8444	olfactory receptor 1714 (predicted)	CUST_4_PI197795859	custom
219	Or28	−0.03	0.98	0.8464	olfactory receptor 1714 (predicted)	CUST_5_PI197795859	custom
220	RT1-M3-3	−0.12	0.92	0.3297	RT1 class Ib, locus M3	CUST_1_PI201011128	custom
220	RT1-M3-3	−0.06	0.96	0.6580	RT1 class Ib, locus M3	CUST_2_PI201011128	custom
220	RT1-M3-3	−0.08	0.95	0.3186	RT1 class Ib, locus M3	CUST_3_PI201011128	custom
220	RT1-M3-3	−0.12	0.92	0.3465	RT1 class Ib, locus M3	CUST_4_PI201011128	custom
220	RT1-M3-3	−0.18	0.88	0.3305	RT1 class Ib, locus M3	CUST_5_PI201011128	custom
222	Or29	−0.02	0.99	0.8250	olfactory receptor 29	A_44_P411999	Agilent
223	RT1-M2	0.04	1.03	0.6219	RT1 class Ib, locus M2	A_44_P154023	Agilent
224	Or30	0.03	1.02	0.7708	olfactory receptor 1730 (predicted)	CUST_1_PI197795878	custom
224	Or30	−0.06	0.96	0.5708	olfactory receptor 1730 (predicted)	CUST_2_PI197795878	custom
224	Or30	0.00	1.00	0.9771	olfactory receptor 1730 (predicted)	CUST_3_PI197795878	custom
224	Or30	−0.36	0.78	0.0940	olfactory receptor 1730 (predicted)	CUST_4_PI197795878	custom
224	Or30	0.05	1.04	0.7708	olfactory receptor 1730 (predicted)	CUST_5_PI197795878	custom

TABLE 5b

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
16	RT1-A1	0.70	1.62	0.0149	RT1 class I	CUST_1_PI202535318	custom
16	RT1-A1	0.75	1.68	0.0100	RT1 class I	CUST_2_PI202535318	custom
16	RT1-A1	0.80	1.74	0.0149	RT1 class I	CUST_3_PI202535318	custom
16	RT1-A1	0.86	1.82	0.0100	RT1 class I	CUST_4_PI202535318	custom
16	RT1-A1	0.91	1.88	0.0100	RT1 class I	CUST_5_PI202535318	custom
17	RT1-A2	0.98	1.97	0.0100	RT1 class I	A_44_P296155	Agilent
29	RT1-DMb	2.59	6.02	0.0100	major histocompatibility complex, class II, DM beta	CUST_1_PI195698203	custom
29	RT1-DMb	2.77	6.82	0.0100	major histocompatibility complex, class II, DM beta	CUST_2_PI195698203	custom
29	RT1-DMb	1.93	3.81	0.0149	major histocompatibility complex, class II, DM beta	CUST_3_PI195698203	custom
29	RT1-DMb	1.87	3.66	0.0149	major histocompatibility complex, class II, DM beta	CUST_4_PH95698203	custom
29	RT1-DMb	1.94	3.84	0.0100	major histocompatibility complex, class II, DM beta	CUST_5_PI195698203	custom

TABLE 5b-continued

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
31	Tap1	0.53	1.44	0.1159	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	A_43_P15763	Agilent
31	Tap1	0.63	1.55	0.0390	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	A_44_P451916	Agilent
32	Psmb8	1.00	2.00	0.0336	proteasome (prosome, macropain) subunit, beta type 8 (large multi-functional peptidase 7)	A_42_P761035	Agilent
51	G18 (Gpsm3)	1.23	2.35	0.0315	G18 protein	A_42_P569708	Agilent
52	Pbx2	0.33	1.26	0.0466	pre-B-cell leukemia transcription factor 2	A_42_P592157	Agilent
54	Rnf5	0.57	1.48	0.0315	ring finger protein 5	A_51_P204582	Agilent
54	Rnf5	0.26	1.20	0.0674	ring finger protein 5	CUST_1_PI207500742	custom
54	Rnf5	0.21	1.16	0.1445	ring finger protein 5	CUST_2_PI207500742	custom
54	Rnf5	0.17	1.13	0.2905	ring finger protein 5	CUST_3_PI207500742	custom
54	Rnf5	0.22	1.16	0.1626	ring finger protein 5	CUST_4_PI207500742	custom
54	Rnf5	0.19	1.14	0.1707	ring finger protein 5	CUST_5_PI207500742	custom
69	C2	1.22	2.33	0.0325	complement component 2	A_44_P332606	Agilent
88	Ly6g6e	−1.38	0.38	0.0416	lymphocyte antigen 6 complex, locus G6E	CUST_1_PI195698246	custom
88	Ly6g6e	−1.42	0.37	0.0523	lymphocyte antigen 6 complex, locus G6E	CUST_2_PI195698246	custom
88	Ly6g6e	−1.39	0.38	0.0623	lymphocyte antigen 6 complex, locus G6E	CUST_3_PI195698246	custom
88	Ly6g6e	−1.44	0.37	0.0416	lymphocyte antigen 6 complex, locus G6E	CUST_4_PI195698246	custom
88	Ly6g6e	−1.46	0.36	0.0433	lymphocyte antigen 6 complex, locus G6E	CUST_5_PI195698246	custom
90	Bat5	−0.60	0.66	0.0100	HLA-B associated transcript 5	CUST_1_PI195830595	custom
90	Bat5	−0.48	0.72	0.0100	HLA-B associated transcript 5	CUST_2_PI195830595	custom
90	Bat5	−0.54	0.69	0.0180	HLA-B associated transcript 5	CUST_3_PI195830595	custom
90	Bat5	−0.53	0.69	0.0229	HLA-B associated transcript 5	CUST_4_PI195830595	custom
90	Bat5	−0.58	0.67	0.0100	HLA-B associated transcript 5	CUST_5_PI195830595	custom
100	Aif1	2.83	7.11	0.0100	allograft inflammatory factor 1	A_44_P421534	Agilent
102	Lst1	3.32	9.99	0.0100	leucocyte specific transcript 1	A_43_P12274	Agilent
110	RT1-CE2	0.64	1.56	0.0278	RT1 class I, CE2	A_44_P107372	Agilent
111	RT1-CE3	0.96	1.95	0.0100	RT1 class I, CE3	A_44_P274061	Agilent
113	RT1-CE5	0.70	1.62	0.0395	RT1 class I, CE5	A_44_P172850	Agilent
116	RT1-CE8	0.90	1.87	0.0278	RT1 class I, CE8	CUST_1_PI201011245	custom
116	RT1-CE8	0.91	1.88	0.0100	RT1 class I, CE8	CUST_2_PI201011245	custom
116	RT1-CE8	0.78	1.72	0.0229	RT1 class I, CE8	CUST_3_PI201011245	custom
116	RT1-CE8	0.84	1.79	0.0100	RT1 class I, CE8	CUST_4_PI201011245	custom
116	RT1-CE8	0.79	1.73	0.0149	RT1 class I, CE8	CUST_5_PI201011245	custom
117	RT1-CE9	0.80	1.74	0.0315	RT1 class I, CE9	CUST_1_PI201011241	custom
117	RT1-CE9	0.35	1.27	0.1745	RT1 class I, CE9	CUST_2_PI201011241	custom
117	RT1-CE9	0.74	1.67	0.0539	RT1 class I, CE9	CUST_3_PI201011241	custom
117	RT1-CE9	0.24	1.18	0.3698	RT1 class I, CE9	CUST_4_PI201011241	custom
117	RT1-CE9	0.81	1.75	0.0373	RT1 class I, CE9	CUST_5_PI201011241	custom
118	RT1-CE10	4.09	17.03	0.0100	RT1 class I, CE10	A_44_P389019	Agilent
119	RT1-CE11	0.28	1.21	0.2867	RT1 class I, CE11	CUST_1_PI195941302	custom
119	RT1-CE11	0.65	1.57	0.0315	RT1 class I, CE11	CUST_2_PI195941302	custom
119	RT1-CE11	0.22	1.16	0.2638	RT1 class I, CE11	CUST_3_PI195941302	custom
119	RT1-CE11	0.16	1.12	0.3957	RT1 class I, CE11	CUST_4_PI195941302	custom
119	RT1-CE11	0.38	1.30	0.0980	RT1 class I, CE11	CUST_5_PI195941302	custom
120	RT1-CE12	0.43	1.35	0.1710	RT1 class I, CE12	CUST_1_PI195941305	custom
120	RT1-CE12	−0.10	0.93	0.4503	RT1 class I, CE12	CUST_2_PI195941305	custom
120	RT1-CE12	0.34	1.27	0.1043	RT1 class I, CE12	CUST_3_PI195941305	custom
120	RT1-CE12	0.04	1.03	0.8574	RT1 class I, CE12	CUST_4_PH95941305	custom
120	RT1-CE12	0.56	1.47	0.0310	RT1 class I, CE12	CUST_5_PI195941305	custom
124	RT1-CE16	0.54	1.45	0.0325	RT1 class I, CE16 (RT1 class Ib, locus Cl)	A_44_P867246	Agilent
124	RT1-CE16	0.78	1.72	0.0206	RT1 class I, CE16 (RT1 class Ib, locus Cl)	A_44_P554925	Agilent
128	Spr1	1.26	2.39	0.0206	psoriasis susceptibility 1 candidate 2 (human)	A_66_P100662	Agilent
128	Spr1	1.39	2.62	0.0180	psoriasis susceptibility 1 candidate 2 (human)	A_51_P212958	Agilent
128	Spr1	1.36	2.57	0.0206	psoriasis susceptibility 1 candidate 2 (human)	A_51_P212956	Agilent
128	Spr1	1.50	2.83	0.0100	psoriasis susceptibility 1 candidate 2 (human)	CUST_56_PI209196805	custom
128	Spr1	1.52	2.87	0.0100	psoriasis susceptibility 1 candidate 2 (human)	CUST_57_PI209196805	custom
128	Spr1	1.51	2.85	0.0100	psoriasis susceptibility 1 candidate 2 (human)	CUST_58_PI209196805	custom
128	Spr1	1.50	2.83	0.0100	psoriasis susceptibility 1 candidate 2 (human)	CUST_59_PI209196805	custom
128	Spr1	1.58	2.99	0.0100	psoriasis susceptibility 1 candidate 2 (human)	CUST_60_PI209196805	custom
129	Cdsn	0.37	1.29	0.2732	corneodesmosin	CUST_1_PI201011238	custom
129	Cdsn	0.84	1.79	0.0100	corneodesmosin	CUST_2_PI201011238	custom
129	Cdsn	0.38	1.30	0.2184	corneodesmosin	CUST_3_PI201011238	custom
129	Cdsn	0.32	1.25	0.3754	corneodesmosin	CUST_4_PI201011238	custom
129	Cdsn	0.40	1.32	0.1769	corneodesmosin	CUST_5_PI201011238	custom
138	Ier3	0.87	1.83	0.0229	immediate early response 3	A_42_P515405	Agilent
143	Kiaa1949	0.42	1.34	0.0481	KIAA1949 protein	CUST_1_PI201011218	custom
143	Kiaa1949	0.49	1.40	0.0457	KIAA1949 protein	CUST_2_PI201011218	custom
143	Kiaa1949	0.33	1.26	0.1378	KIAA1949 protein	CUST_3_PI201011218	custom
143	Kiaa1949	0.39	1.31	0.0993	KIAA1949 protein	CUST_4_PI201011218	custom
143	Kiaa1949	0.34	1.27	0.1184	KIAA1949 protein	CUST_5_PI201011218	custom
146	Flj13158 (RGD1303066)	−0.25	0.84	0.0832	hypothetical protein FLJ13158	A_44_P278509	Agilent

TABLE 5b-continued

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
146	Flj13158 (RGD1303066)	−0.57	0.67	0.0378	hypothetical protein FLJ13158	A_44_P654250	Agilent
147	Mrps18b	0.52	1.43	0.0474	mitochondrial ribosomal protein S18B	CUST_1_PI197795811	custom
147	Mrps18b	0.49	1.40	0.0378	mitochondrial ribosomal protein S18B	CUST_2_PI197795811	custom
147	Mrps18b	0.57	1.48	0.0267	mitochondrial ribosomal protein S18B	CUST_3_PI197795811	custom
147	Mrps18b	0.59	1.51	0.0365	mitochondrial ribosomal protein S18B	CUST_4_PI197795811	custom
147	Mrps18b	0.62	1.54	0.0254	mitochondrial ribosomal protein S18B	CUST_5_PI197795811	custom
154	RT1-T24-3	0.31	1.24	0.1540	RT1 class I, T24, gene 3	CUST_1_PI201011214	custom
154	RT1-T24-3	0.42	1.34	0.0336	RT1 class I, T24, gene 3	CUST_2_PI201011214	custom
154	RT1-T24-3	0.27	1.21	0.1454	RT1 class I, T24, gene 3	CUST_3_PI201011214	custom
154	RT1-T24-3	0.31	1.24	0.0847	RT1 class I, T24, gene 3	CUST_4_PI201011214	custom
154	RT1-T24-3	0.08	1.06	0.6030	RT1 class I, T24, gene 3	CUST_5_PI201011214	custom
155	RT1-T24-4	0.57	1.48	0.0345	RT1 class I, T24, gene 4	CUST_1_PI197795813	custom
155	RT1-T24-4	0.76	1.69	0.0206	RT1 class I, T24, gene 4	CUST_2_PI197795813	custom
155	RT1-T24-4	0.72	1.65	0.0206	RT1 class I, T24, gene 4	CUST_3_PI197795813	custom
155	RT1-T24-4	0.39	1.31	0.0611	RT1 class I, T24, gene 4	CUST_4_PI197795813	custom
155	RT1-T24-4	0.51	1.42	0.0939	RT1 class I, T24, gene 4	CUST_5_PI197795813	custom
156	RT-BM1 (RT1-S3)	1.06	2.08	0.0416	RT1 class I, RT-BM1	A_44_P454420	Agilent
161	RT1-O2	−0.38	0.77	0.2262	RT1 class I, O2	CUST_1_PI201011211	custom
161	RT1-O2	0.57	1.48	0.0345	RT1 class I, O2	CUST_2_PI201011211	custom
161	RT1-O2	−0.09	0.94	0.6330	RT1 class I, O2	CUST_3_PI201011211	custom
161	RT1-O2	0.55	1.46	0.0424	RT1 class I, O2	CUST_4_PI201011211	custom
161	RT1-O2	0.22	1.16	0.3389	RT1 class I, O2	CUST_5_PI201011211	custom
162	RT1-O3	−0.30	0.81	0.2438	RT1 class I, O3	CUST_1_PI201011202	custom
162	RT1-O3	−0.13	0.91	0.5468	RT1 class I, O3	CUST_2_PI201011202	custom
162	RT1-O3	0.50	1.41	0.0546	RT1 class I, O3	CUST_3_PI201011202	custom
162	RT1-O3	0.50	1.41	0.0457	RT1 class I, O3	CUST_4_PI201011202	custom
162	RT1-O3	0.23	1.17	0.2975	RT1 class I, O3	CUST_5_PI201011202	custom
172	RT1-M1-1	−0.01	0.99	0.9358	RT1 class I, M1, gene 1	CUST_1_PI201011178	custom
172	RT1-M1-1	−0.11	0.93	0.4445	RT1 class I, M1, gene 1	CUST_2_PI201011178	custom
172	RT1-M1-1	0.54	1.45	0.0278	RT1 class I, M1, gene 1	CUST_3_PI201011178	custom
172	RT1-M1-1	−0.17	0.89	0.1632	RT1 class I, M1, gene 1	CUST_4_PI201011178	custom
172	RT1-M1-1	−0.05	0.97	0.7839	RT1 class I, M1, gene 1	CUST_5_PI201011178	custom
177	RT1-M7	−0.08	0.95	0.3109	RT1 class I, M7	CUST_1_PI201011173	custom
177	RT1-M7	−0.30	0.81	0.0433	RT1 class I, M7	CUST_2_PI201011173	custom
177	RT1-M7	0.04	1.03	0.5727	RT1 class I, M7	CUST_3_PI201011173	custom
177	RT1-M7	−0.05	0.97	0.7154	RT1 class I, M7	CUST_4_PI201011173	custom
177	RT1-M7	−0.32	0.80	0.1162	RT1 class I, M7	CUST_5_PI201011173	custom
179	RT1-M10-3	−0.02	0.99	0.9071	RT1 class I, M10, gene 3	CUST_1_PI201011167	custom
179	RT1-M10-3	−0.27	0.83	0.0424	RT1 class I, M10, gene 3	CUST_2_PI201011167	custom
179	RT1-M10-3	−0.06	0.96	0.6730	RT1 class I, M10, gene 3	CUST_3_PI201011167	custom
179	RT1-M10-3	−0.04	0.97	0.6161	RT1 class I, M10, gene 3	CUST_4_PI201011167	custom
179	RT1-M10-3	−0.06	0.96	0.5878	RT1 class I, M10, gene 3	CUST_5_PI201011167	custom
195	Zfp57	0.13	1.09	0.6841	zinc finger protein 57	CUST_1_PI197795840	custom
195	Zfp57	−0.43	0.74	0.0681	zinc finger protein 57	CUST_2_PI197795840	custom
195	Zfp57	−0.40	0.76	0.0611	zinc finger protein 57	CUST_3_PI197795840	custom
195	Zfp57	−0.34	0.79	0.0401	zinc finger protein 57	CUST_4_PI197795840	custom
195	Zfp57	−0.29	0.82	0.0940	zinc finger protein 57	CUST_5_PI197795840	custom
204	Ubd	3.19	9.13	0.0345	ubiquitin D	A_42_P602724	Agilent
207	Or8	0.01	1.01	0.9701	olfactory receptor 1743 (predicted)	CUST_1_PI197795856	custom
207	Or8	−0.10	0.93	0.5207	olfactory receptor 1743 (predicted)	CUST_2_PI197795856	custom
207	Or8	−0.14	0.91	0.2325	olfactory receptor 1743 (predicted)	CUST_3_PI197795856	custom
207	Or8	−0.10	0.93	0.4321	olfactory receptor 1743 (predicted)	CUST_4_PI197795856	custom
207	Or8	−0.31	0.81	0.0310	olfactory receptor 1743 (predicted)	CUST_5_PI197795856	custom
214	Or13	−0.01	0.99	0.9278	olfactory receptor 1737 (predicted)	CUST_1_PI197795867	custom
214	Or13	−0.38	0.77	0.0345	olfactory receptor 1737 (predicted)	CUST_2_PI197795867	custom
214	Or13	−0.07	0.95	0.6831	olfactory receptor 1737 (predicted)	CUST_3_PI197795867	custom
214	Or13	0.06	1.04	0.6537	olfactory receptor 1737 (predicted)	CUST_4_PI197795867	custom
214	Or13	0.02	1.01	0.8695	olfactory receptor 1737 (predicted)	CUST_5_PI197795867	custom
219	Or28	−0.05	0.97	0.5892	olfactory receptor 1714 (predicted)	CUST_1_PI197795859	custom
219	Or28	−0.24	0.85	0.0490	olfactory receptor 1714 (predicted)	CUST_2_PI197795859	custom
219	Or28	−0.01	0.99	0.9454	olfactory receptor 1714 (predicted)	CUST_3_PI197795859	custom
219	Or28	−0.02	0.99	0.8444	olfactory receptor 1714 (predicted)	CUST_4_PI197795859	custom
219	Or28	−0.03	0.98	0.8464	olfactory receptor 1714 (predicted)	CUST_5_PI197795859	custom

TABLE 5c

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
16	RT1-A1	0.70	1.62	0.0149	RT1 class I	CUST_1_PI202535318	custom
16	RT1-A1	0.75	1.68	0.0100	RT1 class I	CUST_2_PI202535318	custom
16	RT1-A1	0.80	1.74	0.0149	RT1 class I	CUST_3_PI202535318	custom
16	RT1-A1	0.86	1.82	0.0100	RT1 class I	CUST_4_PI202535318	custom
16	RT1-A1	0.91	1.88	0.0100	RT1 class I	CUST_5_PI202535318	custom
17	RT1-A2	0.98	1.97	0.0100	RT1 class I	A_44_P296155	Agilent
29	RT1-DMb	2.59	6.02	0.0100	major histocompatibility complex, class II, DM beta	CUST_1_PI195698203	custom
29	RT1-DMb	2.77	6.82	0.0100	major histocompatibility complex, class II, DM beta	CUST_2_PI195698203	custom
29	RT1-DMb	1.93	3.81	0.0149	major histocompatibility complex, class II, DM beta	CUST_3_PI195698203	custom
29	RT1-DMb	1.87	3.66	0.0149	major histocompatibility complex, class II, DM beta	CUST_4_PI195698203	custom
29	RT1-DMb	1.94	3.84	0.0100	major histocompatibility complex, class II, DM beta	CUST_5_PI195698203	custom
31	Tap1	0.63	1.55	0.0390	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	A_44_P451916	Agilent
32	Psmb8	1.00	2.00	0.0336	proteasome (prosome, macropain) subunit, beta type 8 (large multi-functional peptidase 7)	A_42_P761035	Agilent
51	G18 (Gpsm3)	1.23	2.35	0.0315	G18 protein	A_42_P569708	Agilent
52	Pbx2	0.33	1.26	0.0466	pre-B-cell leukemia transcription factor 2	A_42_P592157	Agilent
69	C2	1.22	2.33	0.0325	complement component 2	A_44_P332606	Agilent
88	Ly6g6e	−1.38	0.38	0.0416	lymphocyte antigen 6 complex, locus G6E	CUST_1_PI195698246	custom
88	Ly6g6e	−1.44	0.37	0.0416	lymphocyte antigen 6 complex, locus G6E	CUST_4_PI195698246	custom
88	Ly6g6e	−1.46	0.36	0.0433	lymphocyte antigen 6 complex, locus G6E	CUST_5_PI195698246	custom
90	Bat5	−0.60	0.66	0.0100	HLA-B associated transcript 5	CUST_1_PI195830595	custom
90	Bat5	−0.48	0.72	0.0100	HLA-B associated transcript 5	CUST_2_PI195830595	custom
90	Bat5	−0.54	0.69	0.0180	HLA-B associated transcript 5	CUST_3_PI195830595	custom
90	Bat5	−0.53	0.69	0.0229	HLA-B associated transcript 5	CUST_4_PI195830595	custom
90	Bat5	−0.58	0.67	0.0100	HLA-B associated transcript 5	CUST_5_PI195830595	custom
100	Aif1	2.83	7.11	0.0100	allograft inflammatory factor 1	A_44_P421534	Agilent
102	Lst1	3.32	9.99	0.0100	leucocyte specific transcript 1	A_43_P12274	Agilent
110	RT1-CE2	0.64	1.56	0.0278	RT1 class I, CE2	A_44_P107372	Agilent
111	RT1-CE3	0.96	1.95	0.0100	RT1 class I, CE3	A_44_P274061	Agilent
113	RT1-CE5	0.70	1.62	0.0395	RT1 class I, CE5	A_44_P172850	Agilent
116	RT1-CE8	0.90	1.87	0.0278	RT1 class I, CE8	CUST_1_PI201011245	custom
116	RT1-CE8	0.91	1.88	0.0100	RT1 class I, CE8	CUST_2_PI201011245	custom
116	RT1-CE8	0.78	1.72	0.0229	RT1 class I, CE8	CUST_3_PI201011245	custom
116	RT1-CE8	0.84	1.79	0.0100	RT1 class I, CE8	CUST_4_PI201011245	custom
116	RT1-CE8	0.79	1.73	0.0149	RT1 class I, CE8	CUST_5_PI201011245	custom
118	RT1-CE10	4.09	17.03	0.0100	RT1 class I, CE10	A_44_P389019	Agilent
124	RT1-CE16	0.54	1.45	0.0325	RT1 class I, CE16 (RT1 class Ib, locus Cl)	A_44_P867246	Agilent
124	RT1-CE16	0.78	1.72	0.0206	RT1 class I, CE16 (RT1 class Ib, locus Cl)	A_44_P554925	Agilent
128	Spr1	1.26	2.39	0.0206	psoriasis susceptibility 1 candidate 2 (human)	A_66_P100662	Agilent
128	Spr1	1.39	2.62	0.0180	psoriasis susceptibility 1 candidate 2 (human)	A_51_P212958	Agilent
128	Spr1	1.36	2.57	0.0206	psoriasis susceptibility 1 candidate 2 (human)	A_51_P212956	Agilent
128	Spr1	1.50	2.83	0.0100	psoriasis susceptibility 1 candidate 2 (human)	CUST_56_PI209196805	custom
128	Spr1	1.52	2.87	0.0100	psoriasis susceptibility 1 candidate 2 (human)	CUST_57_PI209196805	custom
128	Spr1	1.51	2.85	0.0100	psoriasis susceptibility 1 candidate 2 (human)	CUST_58_PI209196805	custom
128	Spr1	1.50	2.83	0.0100	psoriasis susceptibility 1 candidate 2 (human)	CUST_59_PI209196805	custom
128	Spr1	1.58	2.99	0.0100	psoriasis susceptibility 1 candidate 2 (human)	CUST_60_PI209196805	custom
138	Ier3	0.87	1.83	0.0229	immediate early response 3	A_42_P515405	Agilent
146	Flj13158 (RGD1303066)	−0.57	0.67	0.0378	hypothetical protein FLJ13158	A_44_P654250	Agilent
147	Mrps18b	0.52	1.43	0.0474	mitochondrial ribosomal protein S18B	CUST_1_PI197795811	custom
147	Mrps18b	0.49	1.40	0.0378	mitochondrial ribosomal protein S18B	CUST_2_PI197795811	custom
147	Mrps18b	0.57	1.48	0.0267	mitochondrial ribosomal protein S18B	CUST_3_PI197795811	custom
147	Mrps18b	0.59	1.51	0.0365	mitochondrial ribosomal protein S18B	CUST_4_PI197795811	custom
147	Mrps18b	0.62	1.54	0.0254	mitochondrial ribosomal protein S18B	CUST_5_PI197795811	custom
155	RT1-T24-4	0.57	1.48	0.0345	RT1 class I, T24, gene 4	CUST_1_PI197795813	custom
155	RT1-T24-4	0.76	1.69	0.0206	RT1 class I, T24, gene 4	CUST_2_PI197795813	custom
155	RT1-T24-4	0.72	1.65	0.0206	RT1 class I, T24, gene 4	CUST_3_PI197795813	custom
156	RT-BM1 (RT1-S3)	1.06	2.08	0.0416	RT1 class I, RT-BM1	A_44_P454420	Agilent
204	Ubd	3.19	9.13	0.0345	ubiquitin D	A_42_P602724	Agilent

[0207] Table 6. Expression Profiling Results of NKC Genes

[0208] In Table 6a, results for all 43 NKC genes investigated are indicated in their chromosomal order (Klrg; Pzp to Csda). The expression profiling results of BN skin explant samples exposed to pre-stimulated allogeneic (PVG) lymphocytes in comparison to those exposed to syngeneic (BN) lymphocytes are given. The log 2-fold changes and the fold changes in gene expression are shown for every oligonucleotide probe used. The adjusted p-values are indicated. Significant change is defined by $p<0.05$ and strong change is defined by log 2-fold change ≥ 1 or ≤ -1; i.e. fold change ≥ 2 or ≤ 0.5. In addition, the identification numbers of the probes on the arrays are given (probe ID) together with the information whether these probes were taken from the Agilent database or custom designed. Table 6b contains the information for all NKC genes for which at least one probe indicted a significant alteration of gene expression. In Table 6c, the data for those genes are summarized that are considered to be regulated significantly because either at least a single probe indicated a significant ($p<0.05$) and strong (log 2-fold change ≥ 1 or ≤ -1) regulation or at least 50% of the probes indicated a significant ($p<0.05$) regulation of gene expression.

TABLE 6a

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
1	Klrg1	−0.05	0.97	0.7388	*Rattus norvegicus* killer cell lectin-like receptor subfamily G, member 1 (Klrg1)	A_43_P15509	Agilent
2	Pzp	0.20	1.15	0.1307	pregnancy zone protein	A_44_P214900	Agilent
3	RGD1565709	nt			similar to ovostatin-2		
4	Klrb1a	0.27	1.21	0.1808	killer cell lectin-like receptor subfamily B member 1a	A_42_P598304	Agilent
5	Klrb1b	−0.08	0.95	0.7253	killer cell lectin-like receptor subfamily B member 1B	A_44_P210547	Agilent
6	LOC500331	−0.10	0.93	0.5986	*Rattus norvegicus* similar to osteoclast inhibitory lectin (LOC500331)	A_44_P311870	Agilent
7	RGD1562831	−0.10	0.93	0.5986	similar to osteoclast inhibitory lectin	A_44_P311870	Agilent
8	LOC689757 (Clec2d3)	nt			similar to osteoclast inhibitory lectin		
9	LOC689770 (Clr4, Clec2d4)	nt			similar to osteoclast inhibitory lectin		
10	Clec2d (Ocil)	−0.33	0.80	0.3029	C-type lectin domain family 2, member D (osteoclast inhibitory lectin)	A_44_P137003	Agilent
11	Cle2dl1	nt			C-type lectin domain family 2 member d-like 1		
12	LOC689800	−0.02	0.99	0.9178	similar to osteoclast inhibitory lectin	A_44_P391750	Agilent
13	Klrb1f	nt			killer cell lectin-like receptor subfamily B member 1F		
14	Clec2h	nt			C-type lectin domain family 2, member h		
15	Clec2e	nt			C-type lectin domain family 2, member E		
16	RGD1563148 (Clrb, Clec2d11)	−0.02	0.99	0.9178	similar to osteoclast inhibitory lectin	A_44_P391750	Agilent
17	Cd69	0.69	1.61	0.1845	CD69 antigen	A_43_P16166	Agilent
18	RGD1564770	nt			similar to CD69 antigen (p60, early T-cell activation antigen)		
19	Clec12b	nt			C-type lectin domain family 12, member B		
20	Clec1b	0.93	1.91	0.0500	C-type lectin domain family 1, member b	A_44_P869774	Agilent
21	Clec9a	nt			C-type lectin domain family 9, member a		
22	Clec1a	nt			C-type lectin domain family 1, member a		
23	Clec7a	nt			C-type lectin domain family 7, member a		
24	Olr1	1.41	2.66	0.0390	oxidized low density lipoprotein (lectin-like) receptor 1	A_44_P377266	Agilent
25	LOC689963	nt			hypothetical protein LOC689963		
26	Gabarapl1	0.26	1.20	0.2049	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	CUST_6_PI209816013	custom
26	Gabarapl1	0.21	1.16	0.3468	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	CUST_7_PI209816013	custom
26	Gabarapl1	0.18	1.13	0.4143	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	CUST_8_PI209816013	custom
26	Gabarapl1	0.12	1.09	0.5487	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	CUST_9_PI209816013	custom
26	Gabarapl1	0.19	1.14	0.2042	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	CUST_10_PI209816013	custom
27	Klre1	−0.17	0.89	0.2053	killer cell lectin-like receptor family E member 1	A_44_P536089	Agilent
27	Klre1	−0.12	0.92	0.6467	killer cell lectin-like receptor family E member 1	A_43_P16744	Agilent
28	Klrd1	0.21	1.16	0.3290	killer cell lectin-like receptor, subfamily D, member 1, CD94	A_43_P11543	Agilent
29	Klrk1	−0.02	0.99	0.9332	killer cell lectin-like receptor subfamily K, member 1, NKG2D	A_43_P13194	Agilent
30	Klrc3	−0.13	0.91	0.6020	killer cell lectin-like receptor subfamily C member 3	A_44_P255149	Agilent
31	Klrc2	0.00	1.00	0.9796	killer cell lectin-like receptor subfamily C, member 2	A_43_P11997	Agilent
32	Klrc1	−0.13	0.91	0.6020	killer cell lectin-like receptor subfamily C member 1, NKG2A	A_44_P2551491	Agilent
33	Klri1	−0.18	0.88	0.3321	killer cell lectin-like receptor family I member 1	CUST_46_PI209816013	custom
33	Klri1	−0.14	0.91	0.4180	killer cell lectin-like receptor family I member 1	CUST_47_PI209816013	custom

TABLE 6a-continued

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
33	Klri1	0.16	1.12	0.5780	killer cell lectin-like receptor family I member 1	CUST_48_PI209816013	custom
33	Klri1	−0.11	0.93	0.5043	killer cell lectin-like receptor family I member 1	CUST_49_PI209816013	custom
33	Klri1	−0.16	0.90	0.3331	killer cell lectin-like receptor family I member 1	CUST_50_PI209816013	custom
34	Klri2	−0.12	0.92	0.2434	killer cell lectin-like receptor family I member 2	A_44_P590906	Agilent
35	Klrh1	−0.08	0.95	0.6380	killer cell lectin-like receptor subfamily H, member 1	A_43_P13373	Agilent
36	LOC690020	nt			similar to killer cell lectin-like receptor, subfamily A, member 17		
37	LOC690045	5.56	47.18	0.0100	similar to immunoreceptor Ly49si1	A_43_P10690	Agilent
38	Ly49si3	3.67	12.73	0.0180	immunoreceptor Ly49si3	CUST_21_PI209816013	custom
38	Ly49si3	4.82	28.25	0.0100	immunoreceptor Ly49si3	CUST_22_PI209816013	custom
38	Ly49si3	2.23	4.69	0.0310	immunoreceptor Ly49si3	CUST_23_PI209816013	custom
38	Ly49si3	1.22	2.33	0.0411	immunoreceptor Ly49si3	CUST_24_PI209816013	custom
38	Ly49si3	1.79	3.46	0.0365	immunoreceptor Ly49si3	CUST_25_PI209816013	custom
39	RGD1561306	nt			similar to immunoreceptor Ly49si3		
40	Ly49si1	1.82	3.53	0.0517	immunoreceptor Ly49si1	CUST_56_PI209816013	custom
40	Ly49si1	2.71	6.54	0.0325	immunoreceptor Ly49si1	CUST_57_PI209816013	custom
40	Ly49si1	2.18	4.53	0.0362	immunoreceptor Ly49si1	CUST_58_PI209816013	custom
40	Ly49si1	5.79	55.33	0.0100	immunoreceptor Ly49si1	CUST_59_PI209816013	custom
40	Ly49si1	4.67	25.46	0.0100	immunoreceptor Ly49si1	CUST_60_PI209816013	custom
41	RGD1563110	nt			similar to immunoreceptor Ly49si3		
42	Ly49si2	3.64	12.47	0.0180	immunoreceptor Ly49si2	CUST_36_PI209816013	custom
42	Ly49si2	4.60	24.25	0.0100	immunoreceptor Ly49si2	CUST_37_PI209816013	custom
42	Ly49si2	4.44	21.71	0.0100	immunoreceptor Ly49si2	CUST_38_PI209816013	custom
42	Ly49si2	1.76	3.39	0.0310	immunoreceptor Ly49si2	CUST_39_PI209816013	custom
42	Ly49si2	1.67	3.18	0.0373	immunoreceptor Ly49si2	CUST_40_PI209816013	custom
43	LOC690097	nt			similar to immunoreceptor Ly49si3		
44	LOC502907	nt			similar to immunoreceptor Ly49si1		
45	Ly49i9	5.27	38.59	0.0100	Ly49 inhibitory receptor 9	CUST_66_PI209816013	custom
45	Ly49i9	5.13	35.02	0.0100	Ly49 inhibitory receptor 9	CUST_67_PI209816013	custom
45	Ly49i9	5.15	35.51	0.0100	Ly49 inhibitory receptor 9	CUST_68_PI209816013	custom
45	Ly49i9	5.29	39.12	0.0100	Ly49 inhibitory receptor 9	CUST_69_PI209816013	custom
45	Ly49i9	6.60	97.01	0.0100	Ly49 inhibitory receptor 9	CUST_70_PI209816013	custom
46	Ly49s5	0.01	1.01	0.9723	Ly49 stimulatory receptor 5	CUST_41_PI209816013	custom
46	Ly49s5	−0.07	0.95	0.5774	Ly49 stimulatory receptor 5	CUST_42_PI209816013	custom
46	Ly49s5	−0.11	0.93	0.3468	Ly49 stimulatory receptor 5	CUST_43_PI209816013	custom
46	Ly49s5	−0.03	0.98	0.8268	Ly49 stimulatory receptor 5	CUST_44_PI209816013	custom
46	Ly49s5	−0.08	0.95	0.5682	Ly49 stimulatory receptor 5	CUST_45_PI209816013	custom
47	Ly49i5	−0.06	0.96	0.8065	Ly49 inhibitory receptor 5	CUST_76_PI209816013	custom
47	Ly49i5	0.07	1.05	0.5957	Ly49 inhibitory receptor 5	CUST_77_PI209816013	custom
47	Ly49i5	−0.01	0.99	0.9703	Ly49 inhibitory receptor 5	CUST_78_PI209816013	custom
47	Ly49i5	0.00	1.00	0.9905	Ly49 inhibitory receptor 5	CUST_79_PI209816013	custom
47	Ly49i5	0.05	1.04	0.6808	Ly49 inhibitory receptor 5	CUST_80_PI209816013	custom
48	Klra22	−0.04	0.97	0.7497	killer cell lectin-like receptor subfamily A, member 22	A_44_P266817	Agilent
49	Ly49s6	0.19	1.14	0.1938	Ly49 stimulatory receptor 6	CUST_26_PI209816013	custom
49	Ly49s6	−0.01	0.99	0.9561	Ly49 stimulatory receptor 6	CUST_27_PI209816013	custom
49	Ly49s6	0.02	1.01	0.9047	Ly49 stimulatory receptor 6	CUST_28_PI209816013	custom
49	Ly49s6	−0.18	0.88	0.2611	Ly49 stimulatory receptor 6	CUST_29_PI209816013	custom
49	Ly49s6	−0.14	0.91	0.3529	Ly49 stimulatory receptor 6	CUST_30_PI209816013	custom
50	Ly49s4	0.15	1.11	0.2267	Ly49 stimulatory receptor 4	CUST_61_PI209816013	custom
50	Ly49s4	0.09	1.06	0.2799	Ly49 stimulatory receptor 4	CUST_62_PI209816013	custom
50	Ly49s4	0.06	1.04	0.3468	Ly49 stimulatory receptor 4	CUST_63_PI209816013	custom
50	Ly49s4	−0.03	0.98	0.7923	Ly49 stimulatory receptor 4	CUST_64_PI209816013	custom
50	Ly49s4	−0.07	0.95	0.5814	Ly49 stimulatory receptor 4	CUST_65_PI209816013	custom
51	Ly49s3	0.09	1.06	0.4744	Ly-49 stimulatory receptor 3	A_44_P111662	Agilent
52	Ly49i4	−0.01	0.99	0.9090	Ly49 inhibitory receptor 4	A_44_P250375	Agilent
53	Ly49i3	−0.14	0.91	0.3217	Ly49 inhibitory receptor 3	CUST_81_PI209816013	custom
53	Ly49i3	0.14	1.10	0.1803	Ly49 inhibitory receptor 3	CUST_82_PI209816013	custom
53	Ly49i3	1.30	2.46	0.0325	Ly49 inhibitory receptor 3	CUST_84_PI209816013	custom
53	Ly49i3	3.06	8.34	0.0180	Ly49 inhibitory receptor 3	CUST_85_PI209816013	custom
53	Ly49i3	0.01	1.01	0.9333	Ly49 inhibitory receptor 3	CUST_83_PI209816013	custom
54	Ly49i2	0.03	1.02	0.8446	Ly49 inhibitory receptor 2	A_44_P360539	Agilent
55	Ly49i6	0.05	1.04	0.7829	Ly49 inhibitory receptor 6	CUST_71_PI209816013	custom
55	Ly49i6	0.18	1.13	0.1258	Ly49 inhibitory receptor 6	CUST_72_PI209816013	custom
55	Ly49i6	0.14	1.10	0.4065	Ly49 inhibitory receptor 6	CUST_73_PI209816013	custom
55	Ly49i6	−0.07	0.95	0.6385	Ly49 inhibitory receptor 6	CUST_74_PI209816013	custom
55	Ly49i6	0.05	1.04	0.7708	Ly49 inhibitory receptor 6	CUST_75_PI209816013	custom
56	Ly49s8	0.01	1.01	0.9448	Ly49 stimulatory receptor 8	CUST_11_PI209816013	custom
56	Ly49s8	0.69	1.61	0.0755	Ly49 stimulatory receptor 8	CUST_12_PI209816013	custom
56	Ly49s8	1.12	2.17	0.1471	Ly49 stimulatory receptor 8	CUST_13_PI209816013	custom
56	Ly49s8	0.55	1.46	0.0733	Ly49 stimulatory receptor 8	CUST_14_PI209816013	custom

TABLE 6a-continued

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
56	Ly49s8	0.66	1.58	0.1253	Ly49 stimulatory receptor 8	CUST_15_PI209816013	custom
57	Ly49s7	0.12	1.09	0.3177	Ly49 stimulatory receptor 7	A_44_P118897	Agilent
58	Klra5	1.27	2.41	0.0984	killer cell lectin-like receptor, subfamily A, member 5	CUST_1_PI209816013	custom
58	Klra5	0.46	1.38	0.2146	killer cell lectin-like receptor, subfamily A, member 5	CUST_2_PI209816013	custom
58	Klra5	1.00	2.00	0.0940	killer cell lectin-like receptor, subfamily A, member 5	CUST_3_PI209816013	custom
58	Klra5	0.99	1.99	0.0844	killer cell lectin-like receptor, subfamily A, member 5	CUST_4_PI209816013	custom
58	Klra5	0.90	1.87	0.0845	killer cell lectin-like receptor, subfamily A, member 5	CUST_5_PI209816013	custom
59	Ly49i7	0.67	1.59	0.0395	immunoreceptor Ly49i7	A_44_P821875	Agilent
60	Ly49i8	0.07	1.05	0.5972	immunoreceptor Ly49i8	A_44_P652293	Agilent
61	LOC690303	nt			similar to mago-nashi homolog		
62	Styk1	nt			serine/threonine/tyrosine kinase 1		
63	Csda	−0.50	0.71	0.09	cold shock domain protein A	A_42_P631493	Agilent

TABLE 6b

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
24	Olr1	1.41	2.66	0.0390	oxidized low density lipoprotein (lectin-like) receptor 1	A_44_P377266	Agilent
37	LOC690045	5.56	47.18	0.0100	similar to immunoreceptor Ly49si1	A_43_P10690	Agilent
38	Ly49si3	3.67	12.73	0.0180	immunoreceptor Ly49si3	CUST_21_PI209816013	custom
38	Ly49si3	4.82	28.25	0.0100	immunoreceptor Ly49si3	CUST_22_PI209816013	custom
38	Ly49si3	2.23	4.69	0.0310	immunoreceptor Ly49si3	CUST_23_PI209816013	custom
38	Ly49si3	1.22	2.33	0.0411	immunoreceptor Ly49si3	CUST_24_PI209816013	custom
38	Ly49si3	1.79	3.46	0.0365	immunoreceptor Ly49si3	CUST_25_PI209816013	custom
40	Ly49si1	1.82	3.53	0.0517	immunoreceptor Ly49si1	CUST_56_PI209816013	custom
40	Ly49si1	2.71	6.54	0.0325	immunoreceptor Ly49si1	CUST_57_PI209816013	custom
40	Ly49si1	2.18	4.53	0.0362	immunoreceptor Ly49si1	CUST_58_PI209816013	custom
40	Ly49si1	5.79	55.33	0.0100	immunoreceptor Ly49si1	CUST_59_PI209816013	custom
40	Ly49si1	4.67	25.46	0.0100	immunoreceptor Ly49si1	CUST_60_PI209816013	custom
42	Ly49si2	3.64	12.47	0.0180	immunoreceptor Ly49si2	CUST_36_PI209816013	custom
42	Ly49si2	4.60	24.25	0.0100	immunoreceptor Ly49si2	CUST_37_PI209816013	custom
42	Ly49si2	4.44	21.71	0.0100	immunoreceptor Ly49si2	CUST_38_PI209816013	custom
42	Ly49si2	1.76	3.39	0.0310	immunoreceptor Ly49si2	CUST_39_PI209816013	custom
42	Ly49si2	1.67	3.18	0.0373	immunoreceptor Ly49si2	CUST_40_PI209816013	custom
45	Ly49i9	5.27	38.59	0.0100	Ly49 inhibitory receptor 9	CUST_66_PI209816013	custom
45	Ly49i9	5.13	35.02	0.0100	Ly49 inhibitory receptor 9	CUST_67_PI209816013	custom
45	Ly49i9	5.15	35.51	0.0100	Ly49 inhibitory receptor 9	CUST_68_PI209816013	custom
45	Ly49i9	5.29	39.12	0.0100	Ly49 inhibitory receptor 9	CUST_69_PI209816013	custom
45	Ly49i9	6.60	97.01	0.0100	Ly49 inhibitory receptor 9	CUST_70_PI209816013	custom
53	Ly49i3	−0.14	0.91	0.3217	Ly49 inhibitory receptor 3	CUST_81_PI209816013	custom
53	Ly49i3	0.14	1.10	0.1803	Ly49 inhibitory receptor 3	CUST_82_PI209816013	custom
53	Ly49i3	1.30	2.46	0.0325	Ly49 inhibitory receptor 3	CUST_84_PI209816013	custom
53	Ly49i3	3.06	8.34	0.0180	Ly49 inhibitory receptor 3	CUST_85_PI209816013	custom
53	Ly49i3	0.01	1.01	0.9333	Ly49 inhibitory receptor 3	CUST_83_PI209816013	custom
59	Ly49i7	0.67	1.59	0.0395	immunoreceptor Ly49i7	A_44_P821875	Agilent

TABLE 6c

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
24	Olr1	1.41	2.66	0.0390	oxidized low density lipoprotein (lectin-like) receptor 1	A_44_P377266	Agilent
37	LOC690045	5.56	47.18	0.0100	similar to immunoreceptor Ly49si1	A_43_P10690	Agilent
38	Ly49si3	3.67	12.73	0.0180	immunoreceptor Ly49si3	CUST_21_PI209816013	custom
38	Ly49si3	4.82	28.25	0.0100	immunoreceptor Ly49si3	CUST_22_PI209816013	custom
38	Ly49si3	2.23	4.69	0.0310	immunoreceptor Ly49si3	CUST_23_PI209816013	custom
38	Ly49si3	1.22	2.33	0.0411	immunoreceptor Ly49si3	CUST_24_PI209816013	custom
38	Ly49si3	1.79	3.46	0.0365	immunoreceptor Ly49si3	CUST_25_PI209816013	custom
40	Ly49si1	2.71	6.54	0.0325	immunoreceptor Ly49si1	CUST_57_PI209816013	custom
40	Ly49si1	2.18	4.53	0.0362	immunoreceptor Ly49si1	CUST_58_PI209816013	custom
40	Ly49si1	5.79	55.33	0.0100	immunoreceptor Ly49si1	CUST_59_PI209816013	custom
40	Ly49si1	4.67	25.46	0.0100	immunoreceptor Ly49si1	CUST_60_PI209816013	custom
42	Ly49si2	3.64	12.47	0.0180	immunoreceptor Ly49si2	CUST_36_PI209816013	custom

TABLE 6c-continued

Gene order	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID	Probe Design
42	Ly49si2	4.60	24.25	0.0100	immunoreceptor Ly49si2	CUST_37_PI209816013	custom
42	Ly49si2	4.44	21.71	0.0100	immunoreceptor Ly49si2	CUST_38_PI209816013	custom
42	Ly49si2	1.76	3.39	0.0310	immunoreceptor Ly49si2	CUST_39_PI209816013	custom
42	Ly49si2	1.67	3.18	0.0373	immunoreceptor Ly49si2	CUST_40_PI209816013	custom
45	Ly49i9	5.27	38.59	0.0100	Ly49 inhibitory receptor 9	CUST_66_PI209816013	custom
45	Ly49i9	5.13	35.02	0.0100	Ly49 inhibitory receptor 9	CUST_67_PI209816013	custom
45	Ly49i9	5.15	35.51	0.0100	Ly49 inhibitory receptor 9	CUST_68_PI209816013	custom
45	Ly49i9	5.29	39.12	0.0100	Ly49 inhibitory receptor 9	CUST_69_PI209816013	custom
45	Ly49i9	6.60	97.01	0.0100	Ly49 inhibitory receptor 9	CUST_70_PI209816013	custom
53	Ly49i3	1.30	2.46	0.0325	Ly49 inhibitory receptor 3	CUST_84_PI209816013	custom
53	Ly49i3	3.06	8.34	0.0180	Ly49 inhibitory receptor 3	CUST_85_PI209816013	custom
59	Ly49i7	0.67	1.59	0.0395	immunoreceptor Ly49i7	A_44_P821875	Agilent

TABLE 7

Regulated non-MHC non-NKC genes

The expression profiling results of non-MHC non-NKC genes are given for those genes that were both significantly ($p < 0.05$) and strongly (log2-fold change ≥1 or ≤−1; i.e. fold change ≥2 or ≤0.5) regulated. The log2-fold changes and the fold changes in gene expression are shown. The adjusted p-values are indicated. For 20 of these genes at least two different probes were present on the array. In 8 cases (indicated by gene symbols in bold) the second probe indicated the same strong and significant regulation and in 7 further cases (indicated by gene symbols in italics) the second probe indicated a regulation with borderline amplitude or significance. In 5 cases (indicated by gene symbols in blue font) the results of the two probes for a gene did not confirm each other. Furthermore, the identification numbers of the probes on the arrays are given (probe ID) together with the information whether these probes were taken from the Agilent database or custom designed.

Genes	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID
106	NCAM1	−2.42	0.19	0.0180	neural cell adhesion molecule 1	A_43_P12573
118	Pdzrn3	−2.41	0.19	0.0100	PDZ domain containing RING finger 3	A_42_P481087
142	Serpine1	−2.26	0.21	0.0149	serine (or cysteine) peptidase inhibitor, clade E, member 1	A_42_P758220
110	Nfe2l3	−2.24	0.21	0.0254	nuclear factor, erythroid derived 2, like 3	A_44_P393978
46	Drd5	−2.19	0.22	0.0336	dopamine receptor 5	A_43_P15525
86	Lmcd1	−1.96	0.26	0.0206	LIM and cysteine-rich domains 1	A_42_P749591
146	SNAP25	−1.92	0.26	0.0416	synaptosomal-associated protein 25	A_43_P12469
85	Lgals7	−1.87	0.27	0.0149	lectin, galactose binding, soluble 7	A_43_P12249
98	Lox	−1.80	0.29	0.0229	*Rattus norvegicus* lysyl oxidase (Lox), mRNA [NM_017061]	A_42_P585695
59	Grem1	−1.78	0.29	0.0315	gremlin 1	A_42_P495820
29	Cfi	−1.77	0.29	0.0362	complement factor I	A_42_P693316
30	Chl1	−1.77	0.29	0.0100	cell adhesion molecule with homology to L1CAM	A_44_P1029697
124	Postn	−1.73	0.30	0.0310	periostin, osteoblast specific factor	A_44_P525235
132	Ptprd	−1.68	0.31	0.0416	protein tyrosine phosphatase, receptor type, D	A_43_P10925
115	Pcdh21	−1.65	0.32	0.0325	protocadherin 21	A_42_P596050
137	Rarres2	−1.65	0.32	0.0100	*Rattus norvegicus* retinoic acid receptor responder (tazarotene induced) 2 (Rarres2), mRNA [NM_001013427]	A_42_P628853
19	Ccl27	−1.61	0.33	0.0373	chemokine (C-C motif) ligand 27	A_42_P683840
33	COL12A1	−1.57	0.34	0.0149	collagen, type XII, alpha 1	A_43_P15760
102	Mme	−1.57	0.34	0.0278	membrane metallo endopeptidase	A_43_P11484
42	Cxcl12	−1.56	0.34	0.0365	chemokine (C—X—C motif) ligand 12	A_43_P12144
152	Tgfbi	−1.54	0.34	0.0100	transforming growth factor, beta induced	A_44_P620106
9	Apoe	−1.52	0.35	0.0206	apolipoprotein E	A_44_P171440
15	C1s	−1.47	0.36	0.0149	complement component 1, s sub-component	A_43_P15364
34	Col1a2	−1.47	0.36	0.0149	collagen, type I, alpha 2	A_43_P12783
7	Anp32a	−1.45	0.37	0.0278	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	A_43_P11613
36	Col8a1	−1.40	0.38	0.0229	collagen, type VIII, alpha 1	A_44_P140684
40	Cthrc1	−1.40	0.38	0.0490	collagen triple helix repeat containing 1	A_44_P144591
60	Grin2c	−1.39	0.38	0.0373	*Rattus norvegicus* glutamate receptor, ionotropic, NMDA2C (Grin2c), mRNA [NM_012575]	A_42_P738337

TABLE 7-continued

Regulated non-MHC non-NKC genes

The expression profiling results of non-MHC non-NKC genes are given for those genes that were both significantly ($p < 0.05$) and strongly (log2-fold change ≥1 or ≤−1; i.e. fold change ≥2 or ≤0.5) regulated. The log2-fold changes and the fold changes in gene expression are shown. The adjusted p-values are indicated. For 20 of these genes at least two different probes were present on the array. In 8 cases (indicated by gene symbols in bold) the second probe indicated the same strong and significant regulation and in 7 further cases (indicated by gene symbols in italics) the second probe indicated a regulation with borderline amplitude or significance. In 5 cases (indicated by gene symbols in blue font) the results of the two probes for a gene did not confirm each other. Furthermore, the identification numbers of the probes on the arrays are given (probe ID) together with the information whether these probes were taken from the Agilent database or custom designed.

Genes	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID
94	*LOC684607*	−1.39	0.38	0.0345	similar to nuclear receptor binding protein	A_44_P191287
73	Igfbp5	−1.36	0.39	0.0433	*Rattus norvegicus* cDNA clone IMAGE: 7110383 [BC087030]	A_44_P264240
119	Perp	−1.36	0.39	0.0267	PERP, TP53 apoptosis effector	A_42_P768883
127	Prom2	−1.35	0.39	0.0416	prominin 2	A_42_P530761
31	Chn1	−1.32	0.40	0.0100	chimerin (chimaerin) 1	A_43_P15576
87	LOC100044927	−1.30	0.41	0.0449	similar to TNF-stimulated gene 6 protein	A_43_P16110
35	Col5a3	−1.28	0.41	0.0395	collagen, type V, alpha 3	A_44_P197290
165	Wisp1	−1.27	0.41	0.0100	WNT1 inducible signaling pathway protein 1	A_42_P816427
37	Cpe	−1.25	0.42	0.0100	carboxypeptidase E	A_42_P708169
42	Cxcl12	−1.24	0.42	0.0365	chemokine (C—X—C motif) ligand 12	A_44_P337351
108	Nell2	−1.23	0.43	0.0365	*Rattus norvegicus* nel-like 2 homolog (chicken) (Nell2), mRNA [NM_031070]	A_43_P12500
151	*Tcfap2b*	−1.21	0.43	0.0100	transcription factor AP-2 beta	A_42_P463781
3	Adcy2	−1.20	0.44	0.0449	adenylate cyclase 2	A_43_P15311
32	Clu	−1.20	0.44	0.0310	clusterin	A_44_P311126
55	Fst	−1.20	0.44	0.0298	follistatin	A_44_P108588
56	Fzd1	−1.20	0.44	0.0149	frizzled homolog 1 (*Drosophila*)	A_44_P170527
1	Abcc1	−1.18	0.44	0.0310	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	A_44_P252417
81	Itpr3	−1.18	0.44	0.0100	inositol 1,4,5-triphosphate receptor 3	A_42_P572461
126	Prkcdbp	−1.18	0.44	0.0180	protein kinase C, delta binding protein	A_42_P736812
150	Tacstd2	−1.18	0.44	0.0206	tumor-associated calcium signal transducer 2	A_42_P468712
10	Asam	−1.15	0.45	0.0298	adipocyte-specific adhesion molecule	A_44_P292495
44	Dclk1	−1.15	0.45	0.0267	doublecortin-like kinase 1	A_42_P787216
135	Ptprz1	−1.15	0.45	0.0100	protein tyrosine phosphatase, receptor type Z, polypeptide 1	A_42_P475885
47	EGR1	−1.14	0.45	0.0149	early growth response 1	A_42_P623792
58	Gpr98	−1.14	0.45	0.0206	G protein-coupled receptor 98	A_42_P478080
84	Lgals1	−1.13	0.46	0.0229	lectin, galactose binding, soluble 1	A_42_P759159
111	*Nfib*	−1.13	0.46	0.0533	nuclear factor I/B	A_42_P752916
4	Adcy8	−1.12	0.46	0.0149	adenylate cyclase 8	A_42_P466362
27	Cdh5_predicted	−1.12	0.46	0.0254	PREDICTED: *Rattus norvegicus* cadherin 5 (predicted) (Cdh5_predicted), mRNA [XM_226213]	A_44_P121658
44	Dclk1	−1.12	0.46	0.0278	doublecortin-like kinase 1	A_44_P172645
154	*Thbs4*	−1.12	0.46	0.0466	thrombospondin 4	A_44_P337311
69	Htra1	−1.11	0.46	0.0100	HtrA serine peptidase 1	A_43_P12648
133	Ptprf	−1.10	0.47	0.0345	protein tyrosine phosphatase, receptor type, F	A_43_P11993
104	Mtss1_predicted	−1.09	0.47	0.0325	PREDICTED: *Rattus norvegicus* metastasis suppressor 1 (predicted) (Mtss1_predicted), mRNA [XM_001064860]	A_44_P554679
144	Serpinf1	−1.09	0.47	0.0206	serine (or cysteine) peptidase inhibitor, clade F, member 1	A_42_P709525
14	C1qtnf7	−1.08	0.47	0.0310	C1q and tumor necrosis factor related protein 7	A_44_P248172
51	Fam89a	−1.08	0.47	0.0481	family with sequence similarity 89, member A	A_42_P619403
143	Serpine2	−1.08	0.47	0.0481	serine (or cysteine) peptidase inhibitor, clade E, member 2	A_43_P15697
61	Gsn	−1.06	0.48	0.0267	gelsolin	A_44_P1014163
101	Med13l	−1.06	0.48	0.0229	mediator complex subunit 13-like	A_44_P169863
113	Ntrk2	−1.06	0.48	0.0100	neurotrophic tyrosine kinase, receptor, type 2	A_42_P538400

TABLE 7-continued

Regulated non-MHC non-NKC genes

The expression profiling results of non-MHC non-NKC genes are given for those genes that were both significantly ($p < 0.05$) and strongly (log2-fold change ≥1 or ≤−1; i.e. fold change ≥2 or ≤0.5) regulated. The log2-fold changes and the fold changes in gene expression are shown. The adjusted p-values are indicated. For 20 of these genes at least two different probes were present on the array. In 8 cases (indicated by gene symbols in bold) the second probe indicated the same strong and significant regulation and in 7 further cases (indicated by gene symbols in italics) the second probe indicated a regulation with borderline amplitude or significance. In 5 cases (indicated by gene symbols in blue font) the results of the two probes for a gene did not confirm each other. Furthermore, the identification numbers of the probes on the arrays are given (probe ID) together with the information whether these probes were taken from the Agilent database or custom designed.

Genes	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID
117	Pdgfrb	−1.05	0.48	0.0206	platelet derived growth factor receptor, beta polypeptide	A_43_P15740
149	Sulf1	−1.05	0.48	0.0325	sulfatase 1	A_43_P13252
39	Ctgf	−1.04	0.49	0.0466	connective tissue growth factor	A_42_P484738
50	Ercc5	−1.04	0.49	0.0315	excision repair cross-complementing rodent repair deficiency, complementation group 5	A_44_P1019654
100	Ltbp1	−1.04	0.49	0.0180	latent transforming growth factor beta binding protein 1	A_43_P14871
114	Papss2	−1.04	0.49	0.0395	3'-phosphoadenosine 5'-phosphosulfate synthase 2	A_42_P513050
111	*Nfib*	−1.03	0.49	0.0457	nuclear factor I/B	A_43_P15686
68	Hrh3	−1.02	0.49	0.0395	histamine receptor H3	A_43_P15338
23	Ccnd1	−1.01	0.50	0.0100	cyclin D1	A_44_P189299
94	*LOC684607*	−0.88	0.54	0.0634	similar to nuclear receptor binding protein	A_44_P250983
154	*Thbs4*	−0.87	0.55	0.0648	thrombospondin 4	A_43_P15768
151	*Tcfap2b*	−0.85	0.55	0.0345	transcription factor AP-2 beta	A_43_P18397
113	Ntrk2	−0.37	0.77	0.2827	neurotrophic tyrosine kinase, receptor, type 2	A_42_P631184
101	Med13l	−0.32	0.80	0.1024	mediator complex subunit 13-like	A_44_P473186
166	Wnt7a	−0.21	0.86	0.2198	wingless-related MMTV integration site 7A	A_44_P623953
114	Papss2	0.02	1.01	0.9620	3'-phosphoadenosine 5'-phosphosulfate synthase 2	A_44_P119160
66	Hmha1	0.22	1.16	0.1958	histocompatibility (minor) HA-1	A_43_P20339
168	Zfp36	0.54	1.45	0.2006	zinc finger protein 36	A_44_P435596
18	Ccl1	0.60	1.52	0.0791	chemokine (C-C motif) ligand 1	CUST_51_PI240872834
76	*Il1rn*	0.73	1.66	0.0100	interleukin 1 receptor antagonist	A_43_P15503
163	Tyrobp	0.91	1.88	0.0229	Tyro protein tyrosine kinase binding protein	A_44_P526676
22	Ccl9	1.00	2.00	0.0254	chemokine (C-C motif) ligand 9	A_43_P22206
153	Tgm2	1.00	2.00	0.0254	transglutaminase 2, C polypeptide	A_44_P1007347
121	Plaur	1.02	2.03	0.0229	plasminogen activator, urokinase receptor	A_44_P468141
128	Pstpip1	1.07	2.10	0.0325	proline-serine-threonine phosphatase-interacting protein 1	A_44_P180717
64	Hcls1	1.09	2.13	0.0325	hematopoietic cell specific Lyn substrate 1	A_43_P21322
160	Treml1	1.10	2.14	0.0373	triggering receptor expressed on myeloid cells-like 1	A_44_P798023
18	Ccl1	1.12	2.17	0.0298	chemokine (C-C motif) ligand 1	CUST_52_PI240872834
77	*Il2rb*	1.13	2.19	0.0815	interleukin 2 receptor, beta chain	A_44_P265709
26	Cd8b1	1.16	2.23	0.0229	CD8b molecule	A_42_P480723
79	Itgax	1.16	2.23	0.0457	*Rattus norvegicus* integrin alpha X (Itgax), mRNA [NM_031691]	A_42_P700646
20	*Ccl3*	1.17	2.25	0.0762	chemokine (C-C motif) ligand 3	A_42_P714311
112	Nfkbia	1.18	2.27	0.0180	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	A_42_P544487
122	Plk3	1.18	2.27	0.0315	polo-like kinase 3 (*Drosophila*)	A_44_P135224
147	Snx10	1.18	2.27	0.0345	sorting nexin 10	A_43_P16967
49	Epha2	1.20	2.30	0.0278	Eph receptor A2	A_42_P569711
145	Slfn2	1.20	2.30	0.0206	schlafen 2	A_44_P469113
120	Pik3ap1	1.21	2.31	0.0278	phosphoinositide-3-kinase adaptor protein 1	A_43_P21121
18	Ccl1	1.23	2.35	0.0378	chemokine (C-C motif) ligand 1	CUST_53_PI240872834
166	Wnt7a	1.24	2.36	0.0336	wingless-related MMTV integration site 7A	A_44_P135238

TABLE 7-continued

Regulated non-MHC non-NKC genes

The expression profiling results of non-MHC non-NKC genes are given for those genes that were both significantly ($p < 0.05$) and strongly (log2-fold change ≥1 or ≤−1; i.e. fold change ≥2 or ≤0.5) regulated. The log2-fold changes and the fold changes in gene expression are shown. The adjusted p-values are indicated. For 20 of these genes at least two different probes were present on the array. In 8 cases (indicated by gene symbols in bold) the second probe indicated the same strong and significant regulation and in 7 further cases (indicated by gene symbols in italics) the second probe indicated a regulation with borderline amplitude or significance. In 5 cases (indicated by gene symbols in blue font) the results of the two probes for a gene did not confirm each other. Furthermore, the identification numbers of the probes on the arrays are given (probe ID) together with the information whether these probes were taken from the Agilent database or custom designed.

Genes	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID
78	Itgam	1.25	2.38	0.0424	integrin alpha M	A_43_P15993
11	AW141130	1.27	2.41	0.0254	EST291162 Normalized rat brain, Bento Soares *Rattus* sp. cDNA clone RGIBD16 5' end similar to interleukin-3 receptor B subunit, mRNA sequence [AW141130]	A_44_P635423
161	Trib3	1.27	2.41	0.0278	tribbles homolog 3 (*Drosophila*)	A_42_P543774
5	Adipor2	1.31	2.48	0.0254	adiponectin receptor 2	A_44_P1013376
5	Adipor2	1.31	2.48	0.0100	adiponectin receptor 2	A_42_P523357
82	L37967	1.32	2.50	0.0345	RATTCRAL *Rattus norvegicus* T-cell receptor alpha-chain mRNA [L37967]	A_43_P16248
134	Ptprj	1.37	2.58	0.0378	protein tyrosine phosphatase, receptor type, J	A_43_P15275
18	Ccl1	1.38	2.60	0.0325	chemokine (C-C motif) ligand 1	CUST_54_PI240872834
2	Adcy10	1.40	2.64	0.0325	adenylate cyclase 10	A_42_P460021
38	Csf2	1.40	2.64	0.0401	colony stimulating factor 2 (granulocyte-macrophage)	A_43_P16294
71	Ifitm1	1.43	2.69	0.0180	interferon induced transmembrane protein 1	A_42_P676304
138	RGD1561143	1.45	2.73	0.0310	similar to cell surface receptor FDFACT	A_44_P182601
92	LOC681069	1.46	2.75	0.0401	similar to paired immunoglobin-like type 2 receptor beta	A_44_P330565
168	Zfp36	1.47	2.77	0.0378	zinc finger protein 36	A_42_P648055
48	Emb	1.49	2.81	0.0315	embigin	A_44_P304220
99	Lpxn	1.49	2.81	0.0278	leupaxin	A_43_P23014
66	Hmha1	1.51	2.85	0.0365	histocompatibility (minor) HA-1	A_44_P992516
141	Rhoh	1.52	2.87	0.0378	ras homolog gene family, member H	A_43_P23152
18	Ccl1	1.53	2.89	0.0390	chemokine (C-C motif) ligand 1	CUST_55_PI240872834
76	*Il1rn*	1.56	2.95	0.0100	interleukin 1 receptor antagonist	A_44_P462661
6	AF216218	1.57	2.97	0.0254	AF216218 *Rattus norvegicus* orphanin FQ receptor gene (OFQR), complete cds, alternatively spliced [AF216218]	A_44_P442838
67	Hmox1	1.57	2.97	0.0100	heme oxygenase (decycling) 1	A_42_P652275
157	Tnfsf13	1.57	2.97	0.0278	tumor necrosis factor (ligand) superfamily, member 13	A_42_P773636
93	LOC683463	1.58	2.99	0.0325	similar to paired-Ig-like receptor B	A_42_P841620
70	Ifi47	1.65	3.14	0.0310	interferon gamma inducible protein 47	A_44_P174992
25	Cd83	1.68	3.20	0.0481	CD83 antigen	A_42_P767128
65	Hk3	1.70	3.25	0.0206	hexokinase 3	A_44_P114207
45	Dok3	1.72	3.29	0.0325	docking protein 3	A_42_P468452
28	Ceacam10	1.74	3.34	0.0254	CEA-related cell adhesion molecule 10	A_43_P13426
83	Lcp2	1.78	3.43	0.0310	lymphocyte cytosolic protein 2	A_42_P671389
116	Pcsk1	1.80	3.48	0.0395	proprotein convertase subtilisin/kexin type 1	A_42_P570848
16	C5ar1	1.83	3.56	0.0298	complement component 5a receptor 1	A_42_P572521
129	Ptger2	1.85	3.61	0.0278	prostaglandin E receptor 2, sub-type EP2	A_43_P12508
77	*Il2rb*	1.86	3.63	0.0365	interleukin 2 receptor, beta chain	A_42_P555801
53	Fcgr3	1.89	3.71	0.0100	Fc receptor, IgG, low affinity III	A_44_P168405
164	Vav1	1.89	3.71	0.0229	vav 1 oncogene	A_42_P572413
17	Card11	1.93	3.81	0.0206	caspase recruitment domain family, member 11	A_44_P421727
158	Trem1	1.94	3.84	0.0206	triggering receptor expressed on myeloid cells 1	A_44_P354415
155	Tlr2	1.95	3.86	0.0315	toll-like receptor 2	A_43_P19763
136	Rarres1	2.00	4.00	0.0345	retinoic acid receptor responder (tazarotene induced) 1	A_42_P528691

TABLE 7-continued

Regulated non-MHC non-NKC genes

The expression profiling results of non-MHC non-NKC genes are given for those genes that were both significantly ($p < 0.05$) and strongly (log2-fold change ≥1 or ≤−1; i.e. fold change ≥2 or ≤0.5) regulated. The log2-fold changes and the fold changes in gene expression are shown. The adjusted p-values are indicated. For 20 of these genes at least two different probes were present on the array. In 8 cases (indicated by gene symbols in bold) the second probe indicated the same strong and significant regulation and in 7 further cases (indicated by gene symbols in italics) the second probe indicated a regulation with borderline amplitude or significance. In 5 cases (indicated by gene symbols in blue font) the results of the two probes for a gene did not confirm each other. Furthermore, the identification numbers of the probes on the arrays are given (probe ID) together with the information whether these probes were taken from the Agilent database or custom designed.

Genes	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID
89	LOC498277	2.05	4.14	0.0100	similar to Low affinity immunoglobulin gamma Fc region receptor III precursor (IgG Fc receptor III) (Fc-gamma RIII) (FcRIII)	A_44_P482476
96	LOC685157	2.05	4.14	0.0180	similar to paired immunoglobin-like type 2 receptor beta	A_44_P745407
12	Batf	2.06	4.17	0.0310	basic leucine zipper transcription factor, ATF-like	A_42_P624111
13	Bcl2a1d	2.08	4.23	0.0254	B-cell leukemia/lymphoma 2 related protein A1d	A_43_P13182
20	*Ccl3*	2.11	4.32	0.0278	chemokine (C-C motif) ligand 3	A_43_P11666
163	Tyrobp	2.14	4.41	0.0100	Tyro protein tyrosine kinase binding protein	A_42_P807697
8	Apob48r	2.15	4.44	0.0373	apolipoprotein B48 receptor	A_44_P194387
57	Gpnmb	2.19	4.56	0.0149	glycoprotein (transmembrane) nmb	A_42_P517381
43	Cxcl2	2.21	4.63	0.0206	chemokine (C—X—C motif) ligand 2	A_43_P12885
103	Msr1	2.22	4.66	0.0373	macrophage scavenger receptor 1	A_44_P928825
130	Ptpn7	2.26	4.79	0.0206	protein tyrosine phosphatase, non-receptor type 7	A_42_P653257
91	LOC680910	2.31	4.96	0.0180	similar to paired imnnunoglobin-like type 2 receptor beta	A_44_P187246
162	Trpv2	2.32	4.99	0.0100	transient receptor potential cation channel, subfamily V, member 2	A_42_P816020
156	Tnfaip8l2	2.33	5.03	0.0100	tumor necrosis factor, alpha-induced protein 8-like 2	A_43_P20022
74	Igsf6	2.34	5.06	0.0395	immunoglobulin superfamily, member 6	A_42_P588738
140	Rgs1	2.36	5.13	0.0373	regulator of G-protein signaling 1	A_43_P16318
107	Ncf1	2.40	5.28	0.0100	neutrophil cytosolic factor 1	A_44_P298049
75	Il1b	2.43	5.39	0.0395	interleukin 1 beta	A_43_P14911
139	RGD1561778	2.55	5.86	0.0206	similar to dendritic cell-derived immunoglobulin(Ig)-like receptor 1, DIgR1 - mouse	A_44_P176053
80	Itgb2	2.56	5.90	0.0100	integrin beta 2	A_42_P591344
91	LOC680910	2.59	6.02	0.0229	similar to paired immunoglobin-like type 2 receptor beta	A_44_P463899
72	Igf1	2.61	6.11	0.0100	insulin-like growth factor 1	A_44_P126021
90	LOC498277	2.61	6.11	0.0100	similar to Low affinity immunoglobulin gamma Fc region receptor III precursor (IgG Fc receptor III) (Fc-gamma RIII) (FcRIII)	A_43_P12955
52	Fcgr2b	2.62	6.15	0.0100	Fc receptor, IgG, low affinity IIb	A_42_P735417
148	Spic	2.68	6.41	0.0278	Spi-C transcription factor (Spi-1/PU.1 related)	A_42_P526140
109	Nfe2	2.74	6.68	0.0149	nuclear factor, erythroid derived 2	A_42_P464736
125	Prg4	2.74	6.68	0.0149	proteoglycan 4 (megakaryocyte stimulating factor, articular superficial zone protein)	A_43_P14460
123	Plscr1	2.83	7.11	0.0100	phospholipid scramblase 1	A_44_P1025102
88	LOC100048479	2.97	7.84	0.0373	one cut domain, family member 1	A_42_P701060
62	Gzmc	3.11	8.63	0.0373	granzyme C	A_42_P774527
41	Ctss	3.15	8.88	0.0100	cathepsin S	A_44_P1004731
72	Igf1	3.23	9.38	0.0100	insulin-like growth factor 1	A_44_P366723
24	Cd36	3.57	11.88	0.0100	CD36 antigen	A_43_P12588
21	Ccl6	3.71	13.09	0.0100	*Rattus norvegicus* chemokine (C-C motif) ligand 6 (Ccl6), mRNA [NM_001004202]	A_43_P16707
159	Trem2	3.78	13.74	0.0100	triggering receptor expressed on myeloid cells 2	A_42_P512838
63	Hck	3.87	14.62	0.0100	hemopoietic cell kinase	A_43_P11749
167	XM_226926	3.92	15.14	0.0149	*Rattus norvegicus* similar to protein tyrosine phosphatase, non-	A_44_P375194

TABLE 7-continued

Regulated non-MHC non-NKC genes

The expression profiling results of non-MHC non-NKC genes are given for those genes that were both significantly ($p < 0.05$) and strongly (log2-fold change ≥1 or ≤−1; i.e. fold change ≥2 or ≤0.5) regulated. The log2-fold changes and the fold changes in gene expression are shown. The adjusted p-values are indicated. For 20 of these genes at least two different probes were present on the array. In 8 cases (indicated by gene symbols in bold) the second probe indicated the same strong and significant regulation and in 7 further cases (indicated by gene symbols in italics) the second probe indicated a regulation with borderline amplitude or significance. In 5 cases (indicated by gene symbols in blue font) the results of the two probes for a gene did not confirm each other. Furthermore, the identification numbers of the probes on the arrays are given (probe ID) together with the information whether these probes were taken from the Agilent database or custom designed.

Genes	Gene Symbol	log2-Fold Change	Fold Change	adj. P-value	Gene Description	Probe ID
					receptor type substrate; brain immunological-like with tyrosine-based motifs (LOC310212), mRNA [XM_226926]	
22	Ccl9	4.16	17.88	0.0100	chemokine (C-C motif) ligand 9	A_42_P560084
105	Nat8	5.14	35.26	0.0100	*Rattus norvegicus* endogenous retrovirus mRNA, partial sequence [AY212271]	A_44_P594411
54	Fcgr3a	5.24	37.79	0.0100	Fc fragment of IgG, low affinity IIIa, receptor	A_42_P798429
131	Ptpns1l3	6.36	82.14	0.0100	protein tyrosine phosphatase, non-receptor type substrate 1-like 3	A_44_P248248
95	LOC685020	8.18	290.02	0.0100	paired immunoglobin-like type 2 receptor alpha	A_44_P715240

TABLE 8

Primer sequences used for mRNA expression analysis

	Primer sequence 5'-3'[1]	Amplicon (bp)	Proximity to poly-A (bp)	Efficiency coefficient (E)[2]
RT1-A2	F: TCCCTCCCTGCTACCCTGAG (SEQ ID NO: 48) R: GCCATCCACACTTGGGTCAA (SEQ ID NO: 49)	103	105	1.93
RT1-DMb	F: TCAAATCTGCCTCGGGTGTTT (SEQ ID NO: 50) R: GACAAGGTGGGGCTTTCAGG (SEQ ID NO: 51)	80	53	1.87
Psmb8	F: CACTGCTGGGCAGACATCCT (SEQ ID NO: 52) R: GCTTTGTCTCCAGCCCAGGT (SEQ ID NO: 53)	109	91	1.92
Ly6g6e	F: CCCAGGCAAAGGGACAGAAG (SEQ ID NO: 54) R: TGAGACCCTCAGGCACCAAG (SEQ ID NO: 55)	87	151	1.97
Aif1	F: TCCCCCAGCCAAGAAAGCTA (SEQ ID NO: 56) R: TCTTTTCCCATGCTGCTGTCA (SEQ ID NO: 57)	99	51	1.86
Lst1	F: GGGCAGGAGCTCCACTACG (SEQ ID NO: 58) R: CGATGCAGGCATAGTCAGTGC (SEQ ID NO: 59)	118	20	1.89
RT1-CE3	F: TGTCGTCCTTGGAGCCATCT (SEQ ID NO: 60) R: TCCTCACAACAGGCACCAGA (SEQ ID NO: 61)	62	106	1.91

TABLE 8-continued

Primer sequences used for mRNA expression analysis

	Primer sequence 5'-3'[1]	Amplicon (bp)	Proximity to poly-A (bp)	Efficiency coefficient (E)[2]
RT1-CE10	F: ACACAGGTGGGGAAGGAGGA (SEQ ID NO: 62) R: CAATCTGGGAGGGACACATCAG (SEQ ID NO: 63)	82	10	1.94
RT-BM1 (RT1-S3)	F: GCAGCTATGCTCATGTTCTAGGC (SEQ ID NO: 64) R: TGCCTTCTGAGGCCAGTCAG (SEQ ID NO: 65)	62	7	1.89
Ubd	F: TGGGGTGATGAGAAGCTCAAAA (SEQ ID NO: 66) R: CCCCACCTCAAATCTTTATTTC ATTC (SEQ ID NO: 67)	105	7	1.92
Olr1	F: GGAAGTCAGAAGAGGGCATGG (SEQ ID NO: 68) R: TCCTGGGTTCAATTTCCAGAGT (SEQ ID NO: 69)	89	271	1.90
Ly49si1	F: TGGCCAATCTGAATTTTCCTTG (SEQ ID NO: 70) R: ACATGGGAAGGGGTTCATGC (SEQ ID NO: 71)	115	36	1.84
Ly49i9	F: GGGACTTGGCAACCTCAGGA (SEQ ID NO: 72) R: TTGGAACATCTGCACAATGGAA (SEQ ID NO: 73)	110	179	1.88
Cd3z	F: AGTGCCTGCTGGGATTTAGC (SEQ ID NO: 74) R: CATCCATGGTCACAGGCACTT (SEQ ID NO: 75)	118	50	1.93
B2m	F: GAGCAGGTTGCTCCACAGGT (SEQ ID NO: 76) R: CAAGCTTTGAGTGCAAGAGATTGA (SEQ ID NO: 77)	128	246	1.94

[1]F: forward primer, R: reverse primer

[2]The real-time PCR efficiency coefficient (E) of one cycle in the exponential phase was calculated according to the equation: $E = 10^{[-1/slope\ of\ standard\ curve]}$

TABLE 9

Gene	Gene description	Tested organism	Log2-fold change (rat microarray)	Tested organism	Concordance rate first 3 human skin explants	Concordance rate in further human skin explants	Log2-fold change (human data)
Ctss	cathepsin S	*Rattus novegicus*	3.15	*Homo sapiens*	3/3	7/9	−1.25
Pbx2	Pre-B-cell leukemia homeobox 2	*Rattus novegicus*	0.33	*Homo sapiens*	1/3	7/9	−1.5
Grem1	Gremlin-1 inhibitor in the TGF beta signaling pathway	*Rattus novegicus*	−1.78	*Homo sapiens*	2/3	6/9	−3
Ly6g6e	lymphocyte antigen 6 complex, locus G6E	*Rattus novegicus*	−1.43	*Homo sapiens*	0/3	6/9	−2.25
Spr1	psoriasis susceptibility 1 candidate 2 (human)	*Rattus novegicus*	1.45	*Homo sapiens*	1/3	5/5	−1.25
Msr1	macrophage scavenger protein	*Rattus novegicus*	2.22	*Homo sapiens*	1/3	4/9	1.5
Spic	Spi-C transcription factor	*Rattus novegicus*	2.68	*Homo sapiens*	0/3	4/9	−2
Nfe2	nuclear factor, erythroid derived 2	*Rattus novegicus*	2.74	*Homo sapiens*	0/3	3/9	−1.5
Tnfaip8l2	tumor necrosis factor, alpha-induced protein 8-like 2	*Rattus novegicus*	2.33	*Homo sapiens*	3/3	3/9	−1.5
Ier3	Immediate early response 3	*Rattus novegicus*	0.87	*Homo sapiens*	1/3	2/9	−1.5
Pik3ap1	phosphoinositide-3-kinase adaptor protein 1	*Rattus novegicus*	1.21	*Homo sapiens*	3/3	1/9	1

TABLE 9-continued

Gene	Gene description	Tested organism	Log2-fold change (rat microarray)	Tested organism	Concordance rate first 3 human skin explants	Concordance rate in further human skin explants	Log2-fold change (human data)
Pstpip1	proline-serine-threonine phosphatase-interacting protein 1	*Rattus novegicus*	1.07	*Homo sapiens*	3/3	1/9	2
Ubd	ubiquitin D	*Rattus novegicus*	3.19	*Homo sapiens*	3/3	4/9	1.25
C2	complement component 2	*Rattus novegicus*	1.22	*Homo sapiens*	2/3	1/9	1
Lst1	leukocyte specific transcript 1	*Rattus novegicus*	3.32	*Homo sapiens*	1/3	5/9	−1.25
Aif1	allograft inflammatory factor 1	*Rattus novegicus*	2.83	*Homo sapiens*	1/3	3/9	1.25
C1QTNF7	C1q and TNF related protein 7	*Rattus novegicus*	−1.08	*Homo sapiens*	0/3	8/9	−2
MME	Membrane metallo-endopeptidase expressed by B and T cells upon induction of apotosis	*Rattus novegicus*	−1.75	*Homo sapiens*	3/3	6/9	−2
IGFBP5	Insulin-like growth factor-binding protein 5	*Rattus novegicus*	−1.36	*Homo sapiens*	1/3	6/9	−2
CARD11	apoptosis and scaffolding	*Rattus novegicus*	1.93	*Homo sapiens*	3/3	6/9	−2

TABLE 10

Gene	RefSeq (human)	Probe ID Applied Biosys-tems TLDA card (human)	Probe ID Agilent microarray chip (rat)	RefSeq (rat)	Entrez GeneID (rat)	Sequence (Agilent microarray chip, rat)
Ctss	NM_004079.3	CTSS-Hs00175403_m1	A_44_P1004731	NM_017320	ID: 50654	CTGGCTTACAGCTTGTTTGTTTTATAACTT-TACCTCTCTCTGAAAAGTCTGTAAGCAAGG (SEQ ID NO: 26)
Pbx2	NM_002586.4	PBX2-Hs00855025_s1	A_42_P592157	NM_001002828	ID: 406164	AAAGCTTTCGGTTTTGTTTTTTAAACTGTT-TGCAGAGTGGAGAAGATCGATCAGGAAGGG (SEQ ID NO: 27)
Grem1	NM_013372.5	GREM1-Hs00171951_m1	A_42_P495820	NM_019282	ID: 50566	ATTATGCAGGCTATGACGGAACTACTACCT-TGCTATGGATGAGGGTTGGGCAGGATTTAA (SEQ ID NO: 28)
Ly6g6e	NR_003673	LY6G6E-Hs00225567_m1	CUST_1_PI195698246	NM_027366	ID: 406866	GTCTCAAGAACAGAGGGCTACCTTGGGGAG-CCATAAAGAGTGTATTTAATAAAACGGGCT (SEQ ID NO: 29)
Spr1	NM_014069.2	PSORS1C2-Hs00204152_m1	A_66_P100662	NM_020576	ID: 57390	TTTGTGGTCCCTGTTCAGTCATTATGTTGT-CCCTTCGCTTCTCTTGATCAGCAGAAAGCA (SEQ ID NO: 31)
Msr1	NM_138715.2	MSR1-Hs00234007_m1	A_44_P928825	XM_573919	ID: 498638	GAACGTGTGCACAAAGTATCAGCAGAAATC-CAGTCTGTGAAAGAAGAACAAGAGCATGTG (SEQ ID NO: 32)
Spic	NM_152323.1	SPIC-Hs00951473_g1	A_42_P526140	NM_011461	ID: 20728	CTCAGTGTCCGTGAATTGGGTATCCAAGAA-CATCCTGAAGCCAGAATGTCTTCTCAGAAA (SEQ ID NO: 33)
Nfe2	NM_001136023	NFE2-Hs00232351_m1	A_42_P464736	NM_001012224	ID: 366998	AGGCTGAGTTCTCCAGACCAAAAGACCATT-TGGAAGTTCAAAGATGTATTTGAGGTTTGC (SEQ ID NO: 34)
Tnfaip8l2	NM_024575.3	TNFAIP8L2-Hs00226190_m1	A_43_P20022	NM_027206	ID: 310663	AGCTCTGAGGCTCCTGAGCTCAGCACACTG-GACTTTGGCAAAATGACTGACCGGGAAACG (SEQ ID NO: 35)
Ier3	NM_003897.3	IER3-Hs00174674_m1	A_42_P515405	NM_212505	ID: 15937	ATTTATTCTAACTTATGCAGGGGTGCGAGA-TATGCCCCCTTGCTGTGACACAGATATTTA (SEQ ID NO: 36)
Pik3ap1	NM_152309.2	PIK3AP1-Hs00381030_m1	A_43_P21121	NM_001106368	ID: 294048	ACCTGGAGACCCACTGTCACTGGTGATGGT-GTAGCCCTGCTGGTTTGGGTGATCCTTGAA (SEQ ID NO: 37)

TABLE 10-continued

Gene	RefSeq (human)	Probe ID Applied Biosys-tems TLDA card (human)	Probe ID Agilent microarray chip (rat)	RefSeq (rat)	Entrez GeneID (rat)	Sequence (Agilent microarray chip, rat)
Pstpip1	NM_003978.3	PSTPIP1-Hs00182777_m1	A_44_P180717	NM_011193	ID: 19200	TGGTGTGATAAAGAGGTTCTCTGGGCTGCT-ACATGGAAGTCCCAAGACCACACCTTCTCA (SEQ ID NO: 38)
Ubd	NM_006398.3	UBD-Hs00197374_m1	A_42_P602724	NM_053299	ID: 29168	GTGACTACGGGAGTGGGGTGATGAGAAGCT-CAAAACCGACTTCCTTTAATCAATTAACCA (SEQ ID NO: 39)
C2	NM_006987.2	C2-Hs00163794_m1	A_44_P332606	NM_172222	ID: 12263	CCTGGTGAGTTGGGGTCTTTTTGACCCTTG-TCACGGTTCCTCCAACAAAAACTTGCGCAG (SEQ ID NO: 40)
Lst1	NM_001166538	LST1-Hs00394683_m1	A_43_P12274	NM_022634	ID: 64569	AGGCAGAGGAGAAGGTGAAGGCGTAAAAGA-AGACGCCAGCACTGACTATGCCTGCATCGT (SEQ ID NO: 41)
Aif1	NM_001623.3	AIF1-Hs00610419_g1	A_44_P421534	NM_019467	ID: 11629	TTTCTCAGAATGATGCTGGGCAAGAGATCT-GCCATCTTGAGAATGATTCTGATGTATGAG (SEQ ID NO: 42)
C1QTNF7	NM_001135170.1	C1QTNF7-Hs00230467_m1	A_44_P248172	NM_175425	ID: 109323	GGTTTCTCCTCTATGTTGATACAGATTACC-TGGATTCTATATCAGAAGACGATGAGTTGT (SEQ ID NO: 43)
MME	NM_002426.4	MME-Hs00153519_m1	A_43_P11484	NM_012608	ID: 24590	ATCATATTGCTGAAAATCTTCAAACACAAA-CTCTGGGGTGAGCATTACCATTGAACAGTT (SEQ ID NO: 45)
IGFBP5	NM_000599.3	IGFBP5-Hs01052296_m1	A_44_P285534	NM_012817	ID: 16011	ACCCCGGAAACGTATTCCTATTTGAAGCAA-GTTGAACGGACAGAGAAGGGAAGAAGAGAA (SEQ ID NO: 46)
CARD11	NM_032415.3	CARD11-Hs01060620_m1	A_44_P421727	XM_001073551	ID: 108723	GAGATGAGTACCTCCGGAAACAGAAGACGG-AGACCATCATCTACTCCCGAGAAAAGAACC (SEQ ID NO: 47)

TABLE 11

gene	p value	log2-fold changes	regulation in human clinical GVHD biopsies	Gene Seq. Ref. (human)
ANP32A	0.022	−2.03	Down	NM_012903
CARD11	0.0015	2.68	Up	NM_032415.3
C1QTNF7	0.0002	−3.26	Down	NM_001135170.1
CEACAM4	0.003	4.86	Up	NM_001817.2
HCLS1	0.0006	2.53	Up	NM_008225
HTRA1	0.02	−1.01	Down	NM_031721
LGALS7	0.0172	−0.82	Down	NM_022582
LST1	0.0138	−0.75	Down	NM_001166538
MSR1	0.0133	3.94	Up	NM_138715.2
PIK3AP1	0.0279	3.39	Up	NM_152309.2
PSTPIP1	0.0057	2.40	Up	NM_003978.3
PTGER2	0.0435	1.99	Up	NM_031088
PTPN7	0.0003	4.14	Up	NM_177081
TAP1	0.0174	3.83	Up	NM_032055
TGM2	0.003	5.12	Up	NM_019386
TREM2	0.001	4.23	Up	NM_031254
UBD	0.0441	2.38	Up	NM_006398.3
CTGF	0.036	−1.90	Down	NM_001901.2

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SEQUENCE LISTING

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Gln Ala Lys Lys His Ala Leu Asn Cys His Arg Met Lys Pro Ala Leu
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Gly Leu Gly Leu Val Ser Gly Glu Pro Gly Gly Pro Gly Glu Pro Pro
            20                  25                  30

Gly Gly Gly Asp Pro Gly Gly Gly Ser Gly Gly Val Pro Gly Gly Arg
        35                  40                  45

Gly Lys Gln Asp Ile Gly Asp Ile Leu Gln Gln Ile Met Thr Ile Thr
    50                  55                  60

Asp Gln Ser Leu Asp Glu Ala Gln Ala Lys Lys His Ala Leu Asn Cys
65                  70                  75                  80

His Arg Met Lys Pro Ala Leu Phe Ser Val Leu Cys Glu Ile Lys Glu
                85                  90                  95

Lys Thr Gly Leu Ser Ile Arg Ser Ser Gln Glu Glu Glu Pro Val Asp
            100                 105                 110

Pro Gln Leu Met Arg Leu Asp Asn Met Leu Leu Ala Glu Gly Val Ala
        115                 120                 125

Gly Pro Glu Lys Gly Gly Gly Ser Ala Ala Ala Ala Ala Ala Ala Ala
    130                 135                 140

Ala Ser Gly Gly Gly Val Ser Pro Asp Asn Ser Ile Glu His Ser Asp
145                 150                 155                 160

Tyr Arg Ser Lys Leu Ala Gln Ile Arg His Ile Tyr His Ser Glu Leu
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                165                 170                 175

Glu Lys Tyr Glu Gln Ala Cys Asn Glu Phe Thr Thr His Val Met Asn
            180                 185                 190

Leu Leu Arg Glu Gln Ser Arg Thr Arg Pro Val Ala Pro Lys Glu Met
        195                 200                 205

Glu Arg Met Val Ser Ile Ile His Arg Lys Phe Ser Ala Ile Gln Met
    210                 215                 220

Gln Leu Lys Gln Ser Thr Cys Glu Ala Val Met Ile Leu Arg Ser Arg
225                 230                 235                 240

Phe Leu Asp Ala Arg Arg Lys Arg Arg Asn Phe Ser Lys Gln Ala Thr
                245                 250                 255

Glu Val Leu Asn Glu Tyr Phe Tyr Ser His Leu Ser Asn Pro Tyr Pro
            260                 265                 270

Ser Glu Glu Ala Lys Glu Glu Leu Ala Lys Lys Cys Gly Ile Thr Val
        275                 280                 285

Ser Gln Val Ser Asn Trp Phe Gly Asn Lys Arg Ile Arg Tyr Lys Lys
    290                 295                 300

Asn Ile Gly Lys Phe Gln Glu Glu Ala Asn Ile Tyr Ala Val Lys Thr
305                 310                 315                 320

Ala Val Ser Val Thr Gln Gly Gly His Ser Arg Thr Ser Ser Pro Thr
                325                 330                 335

Pro Pro Ser Ser Ala Gly Ser Gly Gly Ser Phe Asn Leu Ser Gly Ser
            340                 345                 350

Gly Asp Met Phe Leu Gly Met Pro Gly Leu Asn Gly Asp Ser Tyr Ser
        355                 360                 365

Ala Ser Gln Val Glu Ser Leu Arg His Ser Met Gly Pro Gly Gly Tyr
    370                 375                 380

Gly Asp Asn Leu Gly Gly Gly Gln Met Tyr Ser Pro Arg Glu Met Arg
385                 390                 395                 400

Ala Asn Gly Ser Trp Gln Glu Ala Val Thr Pro Ser Ser Val Thr Ser
                405                 410                 415

Pro Thr Glu Gly Pro Gly Ser Val His Ser Asp Thr Ser Asn
            420                 425                 430


<210> SEQ ID NO 5
<211> LENGTH: 4150
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (160)..(714)
<223> OTHER INFORMATION: Grem1

<400> SEQUENCE: 5

actcggtgcg ccttccgcgg accgggcgac ccagtgcacg gccgccgcgt cactctcggt     60

cccgctgacc ccgcgccgag ccccggcggc tctggccgcg gccgcactca gcgccacgcg    120

tcgaaagcgc aggccccgag gacccgccgc actgacagt atg agc cgc aca gcc       174
                                              Met Ser Arg Thr Ala
                                              1               5

tac acg gtg gga gcc ctg ctt ctc ctc ttg ggg acc ctg ctg ccg gct      222
Tyr Thr Val Gly Ala Leu Leu Leu Leu Leu Gly Thr Leu Leu Pro Ala
                10                  15                  20

gct gaa ggg aaa aag aaa ggg tcc caa ggt gcc atc ccc ccg cca gac      270
Ala Glu Gly Lys Lys Lys Gly Ser Gln Gly Ala Ile Pro Pro Pro Asp
            25                  30                  35
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aag gcc cag cac aat gac tca gag cag act cag tcg ccc cag cag cct      318
Lys Ala Gln His Asn Asp Ser Glu Gln Thr Gln Ser Pro Gln Gln Pro
        40                  45                  50

ggc tcc agg aac cgg ggg cgg ggc caa ggg cgg ggc act gcc atg ccc      366
Gly Ser Arg Asn Arg Gly Arg Gly Gln Gly Arg Gly Thr Ala Met Pro
    55                  60                  65

ggg gag gag gtg ctg gag tcc agc caa gag gcc ctg cat gtg acg gag      414
Gly Glu Glu Val Leu Glu Ser Ser Gln Glu Ala Leu His Val Thr Glu
70                  75                  80                  85

cgc aaa tac ctg aag cga gac tgg tgc aaa acc cag ccg ctt aag cag      462
Arg Lys Tyr Leu Lys Arg Asp Trp Cys Lys Thr Gln Pro Leu Lys Gln
                90                  95                  100

acc atc cac gag gaa ggc tgc aac agt cgc acc atc atc aac cgc ttc      510
Thr Ile His Glu Glu Gly Cys Asn Ser Arg Thr Ile Ile Asn Arg Phe
            105                 110                 115

tgt tac ggc cag tgc aac tct ttc tac atc ccc agg cac atc cgg aag      558
Cys Tyr Gly Gln Cys Asn Ser Phe Tyr Ile Pro Arg His Ile Arg Lys
        120                 125                 130

gag gaa ggt tcc ttt cag tcc tgc tcc ttc tgc aag ccc aag aaa ttc      606
Glu Glu Gly Ser Phe Gln Ser Cys Ser Phe Cys Lys Pro Lys Lys Phe
    135                 140                 145

act acc atg atg gtc aca ctc aac tgc cct gaa cta cag cca cct acc      654
Thr Thr Met Met Val Thr Leu Asn Cys Pro Glu Leu Gln Pro Pro Thr
150                 155                 160                 165

aag aag aag aga gtc aca cgt gtg aag cag tgt cgt tgc ata tcc atc      702
Lys Lys Lys Arg Val Thr Arg Val Lys Gln Cys Arg Cys Ile Ser Ile
                170                 175                 180

gat ttg gat taa gccaaatcca ggtgcaccca gcatgtccta ggaatgcagc          754
Asp Leu Asp

cccaggaagt cccagaccta aaacaaccag attcttactt ggcttaaacc tagaggccag    814

aagaaccccc agctgcctcc tggcaggagc ctgcttgtgc gtagttcgtg tgcatgagtg    874

tggatgggtg cctgtgggtg tttttagaca ccagagaaaa cacagtctct gctagagagc    934

actccctatt ttgtaaacat atctgcttta atggggatgt accagaaacc cacctcaccc    994

cggctcacat ctaaaggggc ggggccgtgg tctggttctg actttgtgtt tttgtgccct   1054

cctggggacc agaatctcct ttcggaatga atgttcatgg aagaggctcc tctgagggca   1114

agagacctgt tttagtgctg cattcgacat ggaaaagtcc ttttaacctg tgcttgcatc   1174

ctcctttcct cctcctcctc acaatccatc tcttcttaag ttgatagtga ctatgtcagt   1234

ctaatctctt gtttgccaag gttcctaaat taattcactt aaccatgatg caaatgtttt   1294

tcattttgtg aagaccctcc agactctggg agaggctggt gtgggcaagg acaagcagga   1354

tagtggagtg agaaagggag ggtggagggt gaggccaaat caggtccagc aaaagtcagt   1414

agggacattg cagaagcttg aaaggccaat accagaacac aggctgatgc ttctgagaaa   1474

gtcttttcct agtatttaac agaacccaag tgaacagagg agaaatgaga ttgccagaaa   1534

gtgattaact ttggccgttg caatctgctc aaacctaaca ccaaactgaa aacataaata   1594

ctgaccactc ctatgttcgg acccaagcaa gttagctaaa ccaaaccaac tcctctgctt   1654

tgtccctcag gtggaaaaga gaggtagttt agaactctct gcataggggt gggaattaat   1714

caaaaacctc agaggctgaa attcctaata cctttccttt atcgtggtta tagtcagctc   1774

atttccattc cactatttcc cataatgctt ctgagagcca ctaacttgat tgataaagat   1834

cctgcctctg ctgagtgtac ctgacagtag tctaagatga gagagtttag ggactactct   1894
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gttttagcaa gagatatttt gggggtcttt ttgttttaac tattgtcagg agattgggct 1954

aaagagaaga cgacgagagt aaggaaataa agggaattgc ctctggctag agagtagtta 2014

ggtgttaata cctggtagag atgtaaggga tatgacctcc ctttctttat gtgctcactg 2074

aggatctgag gggaccctgt taggagagca tagcatcatg atgtattagc tgttcatctg 2134

ctactggttg gatggacata actattgtaa ctattcagta tttactggta ggcactgtcc 2194

tctgattaaa cttggcctac tggcaatggc tacttaggat tgatctaagg gccaaagtgc 2254

agggtgggtg aactttattg tactttggat ttggttaacc tgttttcttc aagcctgagg 2314

ttttatatac aaactccctg aatactcttt ttgccttgta tcttctcagc ctcctagcca 2374

agtcctatgt aatatggaaa acaaacactg cagacttgag attcagttgc cgatcaaggc 2434

tctggcattc agagaaccct tgcaactcga gaagctgttt ttatttcgtt tttgttttga 2494

tccagtgctc tcccatctaa caactaaaca ggagccattt caaggcggga gatattttaa 2554

acacccaaaa tgttgggtct gattttcaaa cttttaaact cactactgat gattctcacg 2614

ctaggcgaat ttgtccaaac acatagtgtg tgtgttttgt atacactgta tgaccccacc 2674

ccaaatcttt gtattgtcca cattctccaa caataaagca cagagtggat ttaattaagc 2734

acacaaatgc taaggcagaa ttttgagggt gggagagaag aaaagggaaa gaagctgaaa 2794

atgtaaaacc acaccaggga ggaaaaatga cattcagaac cagcaaacac tgaatttctc 2854

ttgttgtttt aactctgcca caagaatgca atttcgttaa cggagatgac ttaagttggc 2914

agcagtaatc ttcttttagg agcttgtacc acagtcttgc acataagtgc agatttggct 2974

caagtaaaga gaatttcctc aacactaact tcactgggat aatcagcagc gtaactaccc 3034

taaaagcata tcactagcca aagagggaaa tatctgttct tcttactgtg cctatattaa 3094

gactagtaca aatgtggtgt gtcttccaac tttcattgaa aatgccatat ctataccata 3154

ttttattcga gtcactgatg atgtaatgat atatttttc attattatag tagaatattt 3214

ttatggcaag atatttgtgg tcttgatcat acctattaaa ataatgccaa acaccaaata 3274

tgaattttat gatgtacact ttgtgcttgg cattaaaaga aaaaaacaca catcctggaa 3334

gtctgtaagt tgtttttgt tactgtaggt cttcaaagtt aagagtgtaa gtgaaaaatc 3394

tggaggagag gataatttcc actgtgtgga atgtgaatag ttaaatgaaa agttatggtt 3454

atttaatgta attattactt caaatccttt ggtcactgtg atttcaagca tgttttcttt 3514

ttctccttta tatgactttc tctgagttgg gcaaagaaga agctgacaca ccgtatgttg 3574

ttagagtctt ttatctggtc aggggaaaca aaatcttgac ccagctgaac atgtcttcct 3634

gagtcagtgc ctgaatcttt attttttaaa ttgaatgttc cttaaaggtt aacatttcta 3694

aagcaatatt aagaaagact ttaaatgtta ttttggaaga cttacgatgc atgtatacaa 3754

acgaatagca gataatgatg actagttcac acataaagtc cttttaagga gaaaatctaa 3814

aatgaaaagt ggataaacag aacatttata agtgatcagt taatgcctaa gagtgaaagt 3874

agttctattg acattcctca agatatttaa tatcaactgc attatgtatt atgtctgctt 3934

aaatcattta aaaacggcaa agaattatat agactatgag gtaccttgct gtgtaggagg 3994

atgaaagggg agttgatagt ctcataaaac taatttggct tcaagtttca tgaatctgta 4054

actagaattt aattttcacc ccaataatgt tctatatagc ctttgctaaa gagcaactaa 4114

taaattaaac ctattctttc tgtgaaaaaa aaaaaa 4150

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<210> SEQ ID NO 6
<211> LENGTH: 184
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 6

Met Ser Arg Thr Ala Tyr Thr Val Gly Ala Leu Leu Leu Leu Leu Gly
1 5 10 15

Thr Leu Leu Pro Ala Ala Glu Gly Lys Lys Lys Gly Ser Gln Gly Ala
20 25 30

Ile Pro Pro Pro Asp Lys Ala Gln His Asn Asp Ser Glu Gln Thr Gln
35 40 45

Ser Pro Gln Gln Pro Gly Ser Arg Asn Arg Gly Arg Gly Gln Gly Arg
50 55 60

Gly Thr Ala Met Pro Gly Glu Glu Val Leu Glu Ser Ser Gln Glu Ala
65 70 75 80

Leu His Val Thr Glu Arg Lys Tyr Leu Lys Arg Asp Trp Cys Lys Thr
85 90 95

Gln Pro Leu Lys Gln Thr Ile His Glu Glu Gly Cys Asn Ser Arg Thr
100 105 110

Ile Ile Asn Arg Phe Cys Tyr Gly Gln Cys Asn Ser Phe Tyr Ile Pro
115 120 125

Arg His Ile Arg Lys Glu Glu Gly Ser Phe Gln Ser Cys Ser Phe Cys
130 135 140

Lys Pro Lys Lys Phe Thr Thr Met Met Val Thr Leu Asn Cys Pro Glu
145 150 155 160

Leu Gln Pro Pro Thr Lys Lys Lys Arg Val Thr Arg Val Lys Gln Cys
165 170 175

Arg Cys Ile Ser Ile Asp Leu Asp
180

<210> SEQ ID NO 7
<211> LENGTH: 652
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: misc_feature
<223> OTHER INFORMATION: Ly6g6e

<400> SEQUENCE: 7

agagacaaca tgctgagaga gcagaggaga ccctccaggc aagggcagac tccttgcagg 60

ggcaggctgg gggcccccgc tgcctgctgg gtcaggctgg tgaatctggt catggttccg 120

ccccccagat tcactcccta ggtgtgtttg tttactggtt cctcactgtc ttgctcaaat 180

gctccaactc tacaaatccc gggatctcgg ggtgcagatc acctctccca gattcctgag 240

cctgtgtctg gccatgggca cctccagcat cttcctctgc gtgctgttcc tctgtggggc 300

actgggtctc accatgtccc ctgcccgggg aaggctccgc tgctacatct gtggcttcac 360

caaaccctgc caccctgttc ccaccgagtg tcgggacgat gaagcttgtg gcatcagtat 420

tggcacttca gaccagagtg agatcactga gtgaaaaagc tgcctctcaa gggcccagtg 480

ccctctgcca ggctatgcca cctactggct gcactcctac actctgtggc accactgctg 540

cgagcaggac ctgtgcaaca tagccgcttc cccacagcag ctcaccagcc tcctcgcctc 600

cctgcccctc tttgtggcca gcttcgctgg gagaggacac ctcctccact ag 652

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<210> SEQ ID NO 8
<211> LENGTH: 2533
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (115)..(936)
<223> OTHER INFORMATION: Olr1

<400> SEQUENCE: 8

attcttctat tagataacag tagctattta aatacttctg cagaagctca catattttta 60

gtttgttgaa gttcgtgact gcttcactct ctcattctta gcttgaattt ggaa atg 117
Met
1

act ttt gat gac cta aag atc cag act gtg aag gac cag cct gat gag 165
Thr Phe Asp Asp Leu Lys Ile Gln Thr Val Lys Asp Gln Pro Asp Glu
5 10 15

aag tca aat gga aaa aaa gct aaa ggt ctt cag ttt ctt tac tct cca 213
Lys Ser Asn Gly Lys Lys Ala Lys Gly Leu Gln Phe Leu Tyr Ser Pro
20 25 30

tgg tgg tgc ctg gct gct gcg act cta ggg gtc ctt tgc ctg gga tta 261
Trp Trp Cys Leu Ala Ala Ala Thr Leu Gly Val Leu Cys Leu Gly Leu
35 40 45

gta gtg acc att atg gtg ctg ggc atg caa tta tcc cag gtg tct gac 309
Val Val Thr Ile Met Val Leu Gly Met Gln Leu Ser Gln Val Ser Asp
50 55 60 65

ctc cta aca caa gag caa gca aac cta act cac cag aaa aag aaa ctg 357
Leu Leu Thr Gln Glu Gln Ala Asn Leu Thr His Gln Lys Lys Lys Leu
70 75 80

gag gga cag atc tca gcc cgg caa caa gca gaa gaa gct tca cag gag 405
Glu Gly Gln Ile Ser Ala Arg Gln Gln Ala Glu Glu Ala Ser Gln Glu
85 90 95

tca gaa aac gaa ctc aag gaa atg ata gaa acc ctt gct cgg aag ctg 453
Ser Glu Asn Glu Leu Lys Glu Met Ile Glu Thr Leu Ala Arg Lys Leu
100 105 110

aat gag aaa tcc aaa gag caa atg gaa ctt cac cac cag aat ctg aat 501
Asn Glu Lys Ser Lys Glu Gln Met Glu Leu His His Gln Asn Leu Asn
115 120 125

ctc caa gaa aca ctg aag aga gta gca aat tgt tca gct cct tgt ccg 549
Leu Gln Glu Thr Leu Lys Arg Val Ala Asn Cys Ser Ala Pro Cys Pro
130 135 140 145

caa gac tgg atc tgg cat gga gaa aac tgt tac cta ttt tcc tcg ggc 597
Gln Asp Trp Ile Trp His Gly Glu Asn Cys Tyr Leu Phe Ser Ser Gly
150 155 160

tca ttt aac tgg gaa aag agc caa gag aag tgc ttg tct ttg gat gcc 645
Ser Phe Asn Trp Glu Lys Ser Gln Glu Lys Cys Leu Ser Leu Asp Ala
165 170 175

aag ttg ctg aaa att aat agc aca gct gat ctg gac ttc atc cag caa 693
Lys Leu Leu Lys Ile Asn Ser Thr Ala Asp Leu Asp Phe Ile Gln Gln
180 185 190

gca att tcc tat tcc agt ttt cca ttc tgg atg ggg ctg tct cgg agg 741
Ala Ile Ser Tyr Ser Ser Phe Pro Phe Trp Met Gly Leu Ser Arg Arg
195 200 205

aac ccc agc tac cca tgg ctc tgg gag gac ggt tct cct ttg atg ccc 789
Asn Pro Ser Tyr Pro Trp Leu Trp Glu Asp Gly Ser Pro Leu Met Pro
210 215 220 225

cac tta ttt aga gtc cga ggc gct gtc tcc cag aca tac cct tca ggt 837
His Leu Phe Arg Val Arg Gly Ala Val Ser Gln Thr Tyr Pro Ser Gly
230 235 240

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acc tgt gca tat ata caa cga gga gct gtt tat gcg gaa aac tgc att      885
Thr Cys Ala Tyr Ile Gln Arg Gly Ala Val Tyr Ala Glu Asn Cys Ile
            245                 250                 255

tta gct gcc ttc agt ata tgt cag aag aag gca aac cta aga gca cag      933
Leu Ala Ala Phe Ser Ile Cys Gln Lys Lys Ala Asn Leu Arg Ala Gln
        260                 265                 270

tga atttgaaggc tctggaagaa aagaaaaaag tctttgagtt ttattctgga           986

atttaagcta ttctttgtca cttgggtgcc aaacatgaga gcccagaaaa ctgtcattta   1046

gctggctgca gaactccttt gcagaaactg gggttccagg tgcctggcac ctttatgtca   1106

acatttttga ttctagctac ctgtattatt tcacctagct tgtcccaagc ttccctgcca   1166

gcctgaagtc cattttcccc tttttatttt aaaatttgac tcctcttcaa gcttgaaaac   1226

cctctgaact cagtcttctt tacctcatta tcaccttccc ctcacactcc taaaattgca   1286

tgaaagacag aacatggaga acttgctcaa gtgcaggcag agagcaaaaa ggggaaatat   1346

gtctgggaaa aagtgcacgt gaagaaacaa agaaggacag aggccattcc gaaatcaaga   1406

aactcatgtt cttaacttta aaaaaggtat caatccttgg tttttaaact gtggtccatc   1466

tccagactct accacttacg gacagacaga cagacagaca cacacacaca cacacacaca   1526

cattttggga caagtgggga gcccaagaaa gtaattagta agtgagtggt cttttctgta   1586

agctaatcca caacctgtta ccacttcctg aatcagttat tatttcttca ttttttttc    1646

taccagagga cagattaata gatttaaccc ttcacaacag ttcttgttag aatcatggga   1706

tgtgtggccc agaggtaaga atagaatttc tttccctaaa gaacatacct tttgtagatg   1766

aactcttctc aactctgttt tgctatgcta taattccgaa acatacaaga caaaaaaaat   1826

gaagacactc aatctagaac aaactaagcc aggtatgcaa atatcgctga atagaaacag   1886

atggaattag aaatatatct tctattttta ggcttctatt tcctttccac ccactcttca   1946

caggctattc tactttaaag gaagcctttt tattttgctg cacacaatct agcaggaatc   2006

ttttttttt tttaagagct gtgtcatcct tatgtaggca agagatgttt gcttttgtta   2066

aaagctttat tgagatataa ttaacataaa ataaactgaa catatttaaa gtgtactatt   2126

tgataagttt tcacaccttg tggagaacat gcatactaca attaagagag tgaacatatc   2186

catcatccct caaagtgtca caatgctcct cctgatgact cctccccaga aaaccaccaa   2246

tcggctttca ttttgcattt tgtagtttta tgtgaatgga atcatatagt atgtcttttt   2306

tttttgtctg gcttctttca ctttgcataa ttattttgag attcatatgt ctccatcttg   2366

atgctcgtat gaattcattc ttttaaatgt tgaatattcc cttgtatgga tataccacaa   2426

ttcatttacc catttacttg ttgatgacat ttgggttgtt ttagttttgg gatattacaa   2486

ataaagctgc tgtgaacatt tgtgtacaag aaaaaaaaaa aaaaaaa                 2533


<210> SEQ ID NO 9
<211> LENGTH: 273
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

Met Thr Phe Asp Asp Leu Lys Ile Gln Thr Val Lys Asp Gln Pro Asp
1               5                   10                  15

Glu Lys Ser Asn Gly Lys Lys Ala Lys Gly Leu Gln Phe Leu Tyr Ser
            20                  25                  30
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Pro Trp Trp Cys Leu Ala Ala Ala Thr Leu Gly Val Leu Cys Leu Gly
        35                  40                  45

Leu Val Val Thr Ile Met Val Leu Gly Met Gln Leu Ser Gln Val Ser
    50                  55                  60

Asp Leu Leu Thr Gln Glu Gln Ala Asn Leu Thr His Gln Lys Lys Lys
65                  70                  75                  80

Leu Glu Gly Gln Ile Ser Ala Arg Gln Gln Ala Glu Glu Ala Ser Gln
                85                  90                  95

Glu Ser Glu Asn Glu Leu Lys Glu Met Ile Glu Thr Leu Ala Arg Lys
            100                 105                 110

Leu Asn Glu Lys Ser Lys Glu Gln Met Glu Leu His His Gln Asn Leu
        115                 120                 125

Asn Leu Gln Glu Thr Leu Lys Arg Val Ala Asn Cys Ser Ala Pro Cys
    130                 135                 140

Pro Gln Asp Trp Ile Trp His Gly Glu Asn Cys Tyr Leu Phe Ser Ser
145                 150                 155                 160

Gly Ser Phe Asn Trp Glu Lys Ser Gln Glu Lys Cys Leu Ser Leu Asp
                165                 170                 175

Ala Lys Leu Leu Lys Ile Asn Ser Thr Ala Asp Leu Asp Phe Ile Gln
            180                 185                 190

Gln Ala Ile Ser Tyr Ser Ser Phe Pro Phe Trp Met Gly Leu Ser Arg
        195                 200                 205

Arg Asn Pro Ser Tyr Pro Trp Leu Trp Glu Asp Gly Ser Pro Leu Met
    210                 215                 220

Pro His Leu Phe Arg Val Arg Gly Ala Val Ser Gln Thr Tyr Pro Ser
225                 230                 235                 240

Gly Thr Cys Ala Tyr Ile Gln Arg Gly Ala Val Tyr Ala Glu Asn Cys
                245                 250                 255

Ile Leu Ala Ala Phe Ser Ile Cys Gln Lys Lys Ala Asn Leu Arg Ala
            260                 265                 270

Gln
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<210> SEQ ID NO 10
<211> LENGTH: 1185
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (325)..(735)
<223> OTHER INFORMATION: Spr1

<400> SEQUENCE: 10

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gtgattacgg agatgccaag tgggtattga ctgctccagg atgtggatgg agggtgtgaa     60

aaccagggtg gggtgacgca ggctctgggt catgataggg agagcaggca gctgggtcct    120

gggctggagg actaaaataa gggacgccac cttcaggggt gacacatcag cccaggcctt    180

cccaacgggt ttgaccagtt ctgttctgat ggtattcctg tgccactggg ctggtccctc    240

ctccactcct cccctataaa gcctcttggg gttcccaggc acccagactc agcccacccc    300

agctttgggg gccagtacat agcc atg atc ctc aac tgg aag ctc ctg ggg       351
                           Met Ile Leu Asn Trp Lys Leu Leu Gly
                           1               5

atc ctg gtc ctt tgc ctg cac acc aga ggc atc tca ggc agc gag ggc      399
Ile Leu Val Leu Cys Leu His Thr Arg Gly Ile Ser Gly Ser Glu Gly
10                  15                  20                  25
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cac ccc tct cac cca ccc gca gag gac cga gag gag gca ggc tcc cca      447
His Pro Ser His Pro Pro Ala Glu Asp Arg Glu Glu Ala Gly Ser Pro
                30                  35                  40

aca ttg cct cag ggc ccc cca gtc ccc ggt gac cct tgg cca ggg gca      495
Thr Leu Pro Gln Gly Pro Pro Val Pro Gly Asp Pro Trp Pro Gly Ala
            45                  50                  55

ccc cct ctc ttt gaa gat cct ccg cct acc cgc ccc agt cgt ccc tgg      543
Pro Pro Leu Phe Glu Asp Pro Pro Pro Thr Arg Pro Ser Arg Pro Trp
        60                  65                  70

aga gac ctg cct gaa act gga gtc tgg ctc cct gaa ccg cct aga acg      591
Arg Asp Leu Pro Glu Thr Gly Val Trp Leu Pro Glu Pro Pro Arg Thr
    75                  80                  85

gat cct cct caa cct ccc cgg cct gac gac cct tgg ccg gca gga ccc      639
Asp Pro Pro Gln Pro Pro Arg Pro Asp Asp Pro Trp Pro Ala Gly Pro
90                  95                  100                 105

cag ccc cca gaa aac ccc tgg cct cct gcc cct gag gtg gac aac cga      687
Gln Pro Pro Glu Asn Pro Trp Pro Pro Ala Pro Glu Val Asp Asn Arg
                110                 115                 120

cct cag gag gag cca gac cta gac cca ccc cgg gaa gag tac aga taa      735
Pro Gln Glu Glu Pro Asp Leu Asp Pro Pro Arg Glu Glu Tyr Arg
            125                 130                 135

tggagtcccc tcagccgttc tgttcccagg catctccagg cacccacgcc ctctccaccc    795

tctgattccc cgtgaattct tcccaattta gcctgtctcc ttaaacctct tcctcattcc    855

ctcggtttta ttctgaaccc gtaaggtggt gttctcaata tttcctgtcc cctcctgaga    915

tccatactta gtcctcacat cgcccgtttt ttcctctgac agcctaagcc tactctccta    975

cctcgcctcc aggcctcggc cgcacctacc tcccacccgg tcttcctgcc cgcgcgatcg   1035

ctggggcagg gctatggtac tgtgttccct tctgccacct ggtggccggc ggcaggaact   1095

atcagtagac agctgctgct tccatgaaac ggaaaaataa aaatcatgtt ttcttaaaaa   1155

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa                                    1185


<210> SEQ ID NO 11
<211> LENGTH: 136
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

Met Ile Leu Asn Trp Lys Leu Leu Gly Ile Leu Val Leu Cys Leu His
1               5                   10                  15

Thr Arg Gly Ile Ser Gly Ser Glu Gly His Pro Ser His Pro Pro Ala
            20                  25                  30

Glu Asp Arg Glu Glu Ala Gly Ser Pro Thr Leu Pro Gln Gly Pro Pro
        35                  40                  45

Val Pro Gly Asp Pro Trp Pro Gly Ala Pro Pro Leu Phe Glu Asp Pro
    50                  55                  60

Pro Pro Thr Arg Pro Ser Arg Pro Trp Arg Asp Leu Pro Glu Thr Gly
65                  70                  75                  80

Val Trp Leu Pro Glu Pro Pro Arg Thr Asp Pro Pro Gln Pro Pro Arg
                85                  90                  95

Pro Asp Asp Pro Trp Pro Ala Gly Pro Gln Pro Pro Glu Asn Pro Trp
            100                 105                 110

Pro Pro Ala Pro Glu Val Asp Asn Arg Pro Gln Glu Glu Pro Asp Leu
        115                 120                 125

Asp Pro Pro Arg Glu Glu Tyr Arg
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    130                 135


<210> SEQ ID NO 12
<211> LENGTH: 3761
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (199)..(1554)
<223> OTHER INFORMATION: Msr1

<400> SEQUENCE: 12

aaatttagat tttgcaaacc tgtgcattga tgagagtgct attgaaacac attaagaaag     60

attttcaacg caggaatgtg tcatttcctt tcttcatgta ccagatgctg aaatactatg    120

agataaagat tttaggtttc aattgtaaag agagagaagt ggataaatca gtgctgcttt    180

ctttaggacg aaagaagt atg gag cag tgg gat cac ttt cac aat caa cag      231
                  Met Glu Gln Trp Asp His Phe His Asn Gln Gln
                  1               5                   10

gag gac act gat agc tgc tcc gaa tct gtg aaa ttt gat gct cgc tca      279
Glu Asp Thr Asp Ser Cys Ser Glu Ser Val Lys Phe Asp Ala Arg Ser
            15                  20                  25

atg aca gct ttg ctt cct ccg aat cct aaa aac agc cct tcc ctt caa      327
Met Thr Ala Leu Leu Pro Pro Asn Pro Lys Asn Ser Pro Ser Leu Gln
        30                  35                  40

gag aaa ctg aag tcc ttc aaa gct gca ctg att gcc ctt tac ctc ctc      375
Glu Lys Leu Lys Ser Phe Lys Ala Ala Leu Ile Ala Leu Tyr Leu Leu
    45                  50                  55

gtg ttt gca gtt ctc atc cct ctc att gga ata gtg gca gct caa ctc      423
Val Phe Ala Val Leu Ile Pro Leu Ile Gly Ile Val Ala Ala Gln Leu
60                  65                  70                  75

ctg aag tgg gaa acg aag aat tgc tca gtt agt tca act aat gca aat      471
Leu Lys Trp Glu Thr Lys Asn Cys Ser Val Ser Ser Thr Asn Ala Asn
                80                  85                  90

gat ata act caa agt ctc acg gga aaa gga aat gac agc gaa gag gaa      519
Asp Ile Thr Gln Ser Leu Thr Gly Lys Gly Asn Asp Ser Glu Glu Glu
            95                  100                 105

atg aga ttt caa gaa gtc ttt atg gaa cac atg agc aac atg gag aag      567
Met Arg Phe Gln Glu Val Phe Met Glu His Met Ser Asn Met Glu Lys
        110                 115                 120

aga atc cag cat att tta gac atg gaa gcc aac ctc atg gac aca gag      615
Arg Ile Gln His Ile Leu Asp Met Glu Ala Asn Leu Met Asp Thr Glu
    125                 130                 135

cat ttc caa aat ttc agc atg aca act gat caa aga ttt aat gac att      663
His Phe Gln Asn Phe Ser Met Thr Thr Asp Gln Arg Phe Asn Asp Ile
140                 145                 150                 155

ctt ctg cag cta agt acc ttg ttt tcc tca gtc cag gga cat ggg aat      711
Leu Leu Gln Leu Ser Thr Leu Phe Ser Ser Val Gln Gly His Gly Asn
                160                 165                 170

gca ata gat gaa atc tcc aag tcc tta ata agt ttg aat acc aca ttg      759
Ala Ile Asp Glu Ile Ser Lys Ser Leu Ile Ser Leu Asn Thr Thr Leu
            175                 180                 185

ctt gat ttg cag ctc aac ata gaa aat ctg aat ggc aaa atc caa gag      807
Leu Asp Leu Gln Leu Asn Ile Glu Asn Leu Asn Gly Lys Ile Gln Glu
        190                 195                 200

aat acc ttc aaa caa caa gag gaa atc agt aaa tta gag gag cgt gtt      855
Asn Thr Phe Lys Gln Gln Glu Glu Ile Ser Lys Leu Glu Glu Arg Val
    205                 210                 215

tac aat gta tca gca gaa att atg gct atg aaa gaa gaa caa gtg cat      903
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Tyr Asn Val Ser Ala Glu Ile Met Ala Met Lys Glu Glu Gln Val His
220                 225                 230                 235

ttg gaa cag gaa ata aaa gga gaa gtg aaa gta ctg aat aac atc act      951
Leu Glu Gln Glu Ile Lys Gly Glu Val Lys Val Leu Asn Asn Ile Thr
                240                 245                 250

aat gat ctc aga ctg aaa gat tgg gaa cat tct cag acc ttg aga aat      999
Asn Asp Leu Arg Leu Lys Asp Trp Glu His Ser Gln Thr Leu Arg Asn
            255                 260                 265

atc act tta att caa ggt cct cct gga ccc ccg ggt gaa aaa gga gat     1047
Ile Thr Leu Ile Gln Gly Pro Pro Gly Pro Pro Gly Glu Lys Gly Asp
        270                 275                 280

cga ggt ccc act gga gaa agt ggt cca cga gga ttt cca ggt cca ata     1095
Arg Gly Pro Thr Gly Glu Ser Gly Pro Arg Gly Phe Pro Gly Pro Ile
    285                 290                 295

ggt cct ccg ggt ctt aaa ggt gat cgg gga gca att ggc ttt cct gga     1143
Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Ala Ile Gly Phe Pro Gly
300                 305                 310                 315

agt cga gga ctc cca gga tat gcc gga agg cca gga aat tct gga cca     1191
Ser Arg Gly Leu Pro Gly Tyr Ala Gly Arg Pro Gly Asn Ser Gly Pro
                320                 325                 330

aaa ggc cag aaa ggg gaa aag ggg agt gga aac aca tta act cca ttt     1239
Lys Gly Gln Lys Gly Glu Lys Gly Ser Gly Asn Thr Leu Thr Pro Phe
            335                 340                 345

acg aaa gtt cga ctg gtc ggt ggg agc ggc cct cac gag ggg agg gtg     1287
Thr Lys Val Arg Leu Val Gly Gly Ser Gly Pro His Glu Gly Arg Val
        350                 355                 360

gag ata ctc cac agc ggc cag tgg ggt aca att tgt gac gat cgc tgg     1335
Glu Ile Leu His Ser Gly Gln Trp Gly Thr Ile Cys Asp Asp Arg Trp
    365                 370                 375

gaa gtg cgc gtt gga cag gtc gtc tgt agg agc ttg gga tac cca ggt     1383
Glu Val Arg Val Gly Gln Val Val Cys Arg Ser Leu Gly Tyr Pro Gly
380                 385                 390                 395

gtt caa gcc gtg cac aag gca gct cac ttt gga caa ggt act ggt cca     1431
Val Gln Ala Val His Lys Ala Ala His Phe Gly Gln Gly Thr Gly Pro
                400                 405                 410

ata tgg ctg aat gaa gtg ttt tgt ttt ggg aga gaa tca tct att gaa     1479
Ile Trp Leu Asn Glu Val Phe Cys Phe Gly Arg Glu Ser Ser Ile Glu
            415                 420                 425

gaa tgt aaa att cgg caa tgg ggg aca aga gcc tgt tca cat tct gaa     1527
Glu Cys Lys Ile Arg Gln Trp Gly Thr Arg Ala Cys Ser His Ser Glu
        430                 435                 440

gat gct gga gtc act tgc act tta taa tgcatcatat tttcattcac           1574
Asp Ala Gly Val Thr Cys Thr Leu
    445                 450

aactatgaaa tcgctgctca aaaatgattt tattaccttg ttcctgtaaa atccatttaa   1634

tcaatattta agagattaag aatattgccc aaataatatt ttagattaca ggattaatat   1694

attgaacacc ttcatgctta ctattttatg tctatattta aatcatttta acttctatag   1754

gtttttaaat ggaattttct aatataatga cttatatgct gaattgaaca ttttgaagtt   1814

tatagcttcc agattacaaa ggccaagggt aatagaaatg cataccagta attggctcca   1874

attcataata tgttcaccag gagattacaa ttttttgctc ttcttgtctt tgtaatctat   1934

ttagttgatt ttaattactt tctgaataac ggaagggatc agaagatatc ttttgtgcct   1994

agattgcaaa atctccaatc cacacatatt gttttaaaat aagaatgtta tccaactatt   2054

aagatatctc aatgtgcaat aacttgtgta ttagatatca atgttaatga tatgtcttgg   2114
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ccactatgga ccagggagct tatttttctt gtcatgtact gacaactgtt taattgaatc   2174

atgaagtaaa ttgaaagcag gacatatgag aaaactgacc atcagtatat ttgtccagat   2234

aattggtgga tcaaaaatgc cacttaacag gaagtttagt ttgttatgca ctttaaatgg   2294

aataattagc ttgttacaat tctaggacat ggtgtttaaa atttaaatct gattaatcca   2354

ttttaacaaa caatgcaaac atcttcagtg cagaaggaag agtggtttca actgtttgga   2414

gtcttttatg aagtcagtca acatttacaa ccaaagggcg gggggggggg tgggggtgc    2474

gtctttagtc ctaaagggac aataactctg agcatgcccc aaaaaagtag tttagcaacc   2534

ttttgttggt agtcaaccca tccccagggc catagtgtag agtgtgaaaa gctaccctga   2594

aacccagtaa ttctaccctg aaagtgactg cctgcagaaa gaccagcagt tgatattaaa   2654

gcgcaaatga attcaacctc agccctgaaa ataacagaat tctgaagttt cctatgacta   2714

attcacaaaa aaagtaattg taaactagta ctattatgga attactctac tgttctttct   2774

ttaatagtgg caaatgaaag cataagctta agcatttttt catattctga agtctcacca   2834

cacataataa ccaagtggta gactcacagc cgtccaactt aaaaaggcaa aaccttacct   2894

tggaattgga attactgtaa acagcctact gaaaatgcat ttttatcatg taacattctt   2954

ctacttgttt aacattgctg attttctctg gcagcataat tttgtggtta agagaatgaa   3014

ttctgaatgt acactttctg tctcaaaccc tggctgtaat ttcagctagt taataattct   3074

ttgtgttcag ttccactatc taggtatttt cttcaaaagg taaatacaat ggtttctgaa   3134

agaatcattt gcattatcag cctgtttggg atgtctgaga tcagtgcctc tgggttgtta   3194

atactgtatt gctgtatggt atatgtatgc tgatttacta cttatgcgta agtggtatgc   3254

atgggatgtc tgaaatcagt gcctatgggt tgtcaatagt attaactatt agtgttaact   3314

gttagtatta actattagta ttattaacac taataatagt actattacta ttactatttt   3374

tattttaaaa taaaatttac ctttaaaata ataatagtac tattgctagt actagtacta   3434

ttgctattac tagtactatt actagtacta gtactatgac actgttaata gtactattaa   3494

caacccatag gcacttggga tgtctgagat cagtgcctat gggttgttaa tactatattg   3554

ctgtatggta tatgcatgct gatttaccac ttatgcatag atatatcttt aataagtaat   3614

ctaaaaatcc tttttgtatt tgagagaatc tactaagttc agtccagtca agaaaagaac   3674

ctaatagcac caatacaaat tgaggactta atttactttg gaatgttgaa ttgcatttgt   3734

tccattaaaa aaaacagaaa tttgcga                                      3761
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<210> SEQ ID NO 13
<211> LENGTH: 451
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 13

```
Met Glu Gln Trp Asp His Phe His Asn Gln Gln Glu Asp Thr Asp Ser
1               5                   10                  15

Cys Ser Glu Ser Val Lys Phe Asp Ala Arg Ser Met Thr Ala Leu Leu
            20                  25                  30

Pro Pro Asn Pro Lys Asn Ser Pro Ser Leu Gln Glu Lys Leu Lys Ser
        35                  40                  45

Phe Lys Ala Ala Leu Ile Ala Leu Tyr Leu Leu Val Phe Ala Val Leu
    50                  55                  60

Ile Pro Leu Ile Gly Ile Val Ala Ala Gln Leu Leu Lys Trp Glu Thr
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65                  70                  75                  80

Lys Asn Cys Ser Val Ser Ser Thr Asn Ala Asn Asp Ile Thr Gln Ser
                85                  90                  95

Leu Thr Gly Lys Gly Asn Asp Ser Glu Glu Glu Met Arg Phe Gln Glu
            100                 105                 110

Val Phe Met Glu His Met Ser Asn Met Glu Lys Arg Ile Gln His Ile
        115                 120                 125

Leu Asp Met Glu Ala Asn Leu Met Asp Thr Glu His Phe Gln Asn Phe
    130                 135                 140

Ser Met Thr Thr Asp Gln Arg Phe Asn Asp Ile Leu Leu Gln Leu Ser
145                 150                 155                 160

Thr Leu Phe Ser Ser Val Gln Gly His Gly Asn Ala Ile Asp Glu Ile
                165                 170                 175

Ser Lys Ser Leu Ile Ser Leu Asn Thr Thr Leu Leu Asp Leu Gln Leu
            180                 185                 190

Asn Ile Glu Asn Leu Asn Gly Lys Ile Gln Glu Asn Thr Phe Lys Gln
        195                 200                 205

Gln Glu Glu Ile Ser Lys Leu Glu Glu Arg Val Tyr Asn Val Ser Ala
    210                 215                 220

Glu Ile Met Ala Met Lys Glu Glu Gln Val His Leu Glu Gln Glu Ile
225                 230                 235                 240

Lys Gly Glu Val Lys Val Leu Asn Asn Ile Thr Asn Asp Leu Arg Leu
                245                 250                 255

Lys Asp Trp Glu His Ser Gln Thr Leu Arg Asn Ile Thr Leu Ile Gln
            260                 265                 270

Gly Pro Pro Gly Pro Pro Gly Glu Lys Gly Asp Arg Gly Pro Thr Gly
        275                 280                 285

Glu Ser Gly Pro Arg Gly Phe Pro Gly Pro Ile Gly Pro Pro Gly Leu
    290                 295                 300

Lys Gly Asp Arg Gly Ala Ile Gly Phe Pro Gly Ser Arg Gly Leu Pro
305                 310                 315                 320

Gly Tyr Ala Gly Arg Pro Gly Asn Ser Gly Pro Lys Gly Gln Lys Gly
                325                 330                 335

Glu Lys Gly Ser Gly Asn Thr Leu Thr Pro Phe Thr Lys Val Arg Leu
            340                 345                 350

Val Gly Gly Ser Gly Pro His Glu Gly Arg Val Glu Ile Leu His Ser
        355                 360                 365

Gly Gln Trp Gly Thr Ile Cys Asp Asp Arg Trp Glu Val Arg Val Gly
    370                 375                 380

Gln Val Val Cys Arg Ser Leu Gly Tyr Pro Gly Val Gln Ala Val His
385                 390                 395                 400

Lys Ala Ala His Phe Gly Gln Gly Thr Gly Pro Ile Trp Leu Asn Glu
                405                 410                 415

Val Phe Cys Phe Gly Arg Glu Ser Ser Ile Glu Glu Cys Lys Ile Arg
            420                 425                 430

Gln Trp Gly Thr Arg Ala Cys Ser His Ser Glu Asp Ala Gly Val Thr
        435                 440                 445

Cys Thr Leu
    450


<210> SEQ ID NO 14
<211> LENGTH: 1116
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (27)..(773)
<223> OTHER INFORMATION: Spic

<400> SEQUENCE: 14

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cagaattgtc aatttattaa tgaaat atg acg tgt gtt gaa caa gac aag ctg      53
                            Met Thr Cys Val Glu Gln Asp Lys Leu
                            1               5

ggt caa gca ttt gaa gat gct ttt gag gtt ctg agg caa cat tca act      101
Gly Gln Ala Phe Glu Asp Ala Phe Glu Val Leu Arg Gln His Ser Thr
10                  15                  20                  25

gga gat ctt cag tac tcg cca gat tac aga aat tac ctg gct tta atc      149
Gly Asp Leu Gln Tyr Ser Pro Asp Tyr Arg Asn Tyr Leu Ala Leu Ile
                30                  35                  40

aac cat cgt cct cat gtc aaa gga aat tcc agc tgc tat gga gtg ttg      197
Asn His Arg Pro His Val Lys Gly Asn Ser Ser Cys Tyr Gly Val Leu
            45                  50                  55

cct aca gag gag cct gtc tat aat tgg aga acg gta att aac agt gct      245
Pro Thr Glu Glu Pro Val Tyr Asn Trp Arg Thr Val Ile Asn Ser Ala
        60                  65                  70

gcg gac ttc tat ttt gaa gga aat att cat caa tct ctg cag aac ata      293
Ala Asp Phe Tyr Phe Glu Gly Asn Ile His Gln Ser Leu Gln Asn Ile
    75                  80                  85

act gaa aac cag ctg gta caa ccc act ctt ctc cag caa aag ggg gga      341
Thr Glu Asn Gln Leu Val Gln Pro Thr Leu Leu Gln Gln Lys Gly Gly
90                  95                  100                 105

aaa ggc agg aag aag ctc cga ctg ttt gaa tac ctt cac gaa tcc ctg      389
Lys Gly Arg Lys Lys Leu Arg Leu Phe Glu Tyr Leu His Glu Ser Leu
                110                 115                 120

tat aat ccg gag atg gca tct tgt att cag tgg gta gat aaa acc aaa      437
Tyr Asn Pro Glu Met Ala Ser Cys Ile Gln Trp Val Asp Lys Thr Lys
            125                 130                 135

ggc atc ttt cag ttt gta tca aaa aac aaa gaa aaa ctt gcc gag ctt      485
Gly Ile Phe Gln Phe Val Ser Lys Asn Lys Glu Lys Leu Ala Glu Leu
        140                 145                 150

tgg ggg aaa aga aaa ggc aac agg aag acc atg act tac cag aaa atg      533
Trp Gly Lys Arg Lys Gly Asn Arg Lys Thr Met Thr Tyr Gln Lys Met
    155                 160                 165

gcc agg gca ctc aga aat tac gga aga agt ggg gaa att acc aaa atc      581
Ala Arg Ala Leu Arg Asn Tyr Gly Arg Ser Gly Glu Ile Thr Lys Ile
170                 175                 180                 185

cgg agg aag ctg act tac cag ttc agt gag gcc att ctc caa aga ctc      629
Arg Arg Lys Leu Thr Tyr Gln Phe Ser Glu Ala Ile Leu Gln Arg Leu
                190                 195                 200

tct cca tcc tat ttc ctg ggg aaa gag atc ttc tat tca cag tgt gtt      677
Ser Pro Ser Tyr Phe Leu Gly Lys Glu Ile Phe Tyr Ser Gln Cys Val
            205                 210                 215

caa cct gat caa gaa tat ctc agt tta aat aac tgg aat gca aat tat      725
Gln Pro Asp Gln Glu Tyr Leu Ser Leu Asn Asn Trp Asn Ala Asn Tyr
        220                 225                 230

aat tat aca tat gcc aat tac cat gag cta aat cac cat gat tgc taa      773
Asn Tyr Thr Tyr Ala Asn Tyr His Glu Leu Asn His His Asp Cys
    235                 240                 245

atatactttc atatttcatg gtttactggc atcggaaatc tctacaagtt ttaatgattt    833

ctccctccct ctctttttt cctcctctga agaaatttag gatttttctc ttaaagcaaa    893
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tactaaagag gaaaaaaaat taactttatt gttgctttta tcaaagagta tgtaatctat 953

actaacttgt tgggaaattc tgccaatgaa caacttttt ataataaaaa aaaaaaaaaa 1013

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1073

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1116

<210> SEQ ID NO 15
<211> LENGTH: 248
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 15

Met Thr Cys Val Glu Gln Asp Lys Leu Gly Gln Ala Phe Glu Asp Ala
1 5 10 15

Phe Glu Val Leu Arg Gln His Ser Thr Gly Asp Leu Gln Tyr Ser Pro
20 25 30

Asp Tyr Arg Asn Tyr Leu Ala Leu Ile Asn His Arg Pro His Val Lys
35 40 45

Gly Asn Ser Ser Cys Tyr Gly Val Leu Pro Thr Glu Glu Pro Val Tyr
50 55 60

Asn Trp Arg Thr Val Ile Asn Ser Ala Ala Asp Phe Tyr Phe Glu Gly
65 70 75 80

Asn Ile His Gln Ser Leu Gln Asn Ile Thr Glu Asn Gln Leu Val Gln
85 90 95

Pro Thr Leu Leu Gln Gln Lys Gly Gly Lys Gly Arg Lys Lys Leu Arg
100 105 110

Leu Phe Glu Tyr Leu His Glu Ser Leu Tyr Asn Pro Glu Met Ala Ser
115 120 125

Cys Ile Gln Trp Val Asp Lys Thr Lys Gly Ile Phe Gln Phe Val Ser
130 135 140

Lys Asn Lys Glu Lys Leu Ala Glu Leu Trp Gly Lys Arg Lys Gly Asn
145 150 155 160

Arg Lys Thr Met Thr Tyr Gln Lys Met Ala Arg Ala Leu Arg Asn Tyr
165 170 175

Gly Arg Ser Gly Glu Ile Thr Lys Ile Arg Arg Lys Leu Thr Tyr Gln
180 185 190

Phe Ser Glu Ala Ile Leu Gln Arg Leu Ser Pro Ser Tyr Phe Leu Gly
195 200 205

Lys Glu Ile Phe Tyr Ser Gln Cys Val Gln Pro Asp Gln Glu Tyr Leu
210 215 220

Ser Leu Asn Asn Trp Asn Ala Asn Tyr Asn Tyr Thr Tyr Ala Asn Tyr
225 230 235 240

His Glu Leu Asn His His Asp Cys
245

<210> SEQ ID NO 16
<211> LENGTH: 1663
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (264)..(1385)
<223> OTHER INFORMATION: Nfe2

<400> SEQUENCE: 16

gtgcgcctgc ttggggctcc tgtgctcagc tcagcctgag cttccacact cagcgctcag 60

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caatggcccg ggggcggggc gcggtcctcg cagattctca aaggtagccg ggatcctcgt    120

ccagcagtgt cagctcaggc tcagcctccc cagagacaac accgggagcc tcatctctct    180

cctcaccctg ctgtgactcc accacaggtt tctagagcca tctgggcttt ccgggaacct    240

ggaccagact ctggcccagt agg atg tcc ccg tgt cct ccc cag cag agc agg    293
                        Met Ser Pro Cys Pro Pro Gln Gln Ser Arg
                        1               5                  10

aac agg gtg ata cag ctg tcc act tca gag cta gga gag atg gaa ctg      341
Asn Arg Val Ile Gln Leu Ser Thr Ser Glu Leu Gly Glu Met Glu Leu
                15                  20                  25

act tgg cag gag atc atg tcc atc acc gag ctg cag ggt ctg aat gct      389
Thr Trp Gln Glu Ile Met Ser Ile Thr Glu Leu Gln Gly Leu Asn Ala
            30                  35                  40

cca agt gag cca tca ttt gag ccc caa gcc cca gct cca tac ctt gga      437
Pro Ser Glu Pro Ser Phe Glu Pro Gln Ala Pro Ala Pro Tyr Leu Gly
        45                  50                  55

cct cca cca ccc aca act tac tgc ccc tgc tca atc cac cca gat tct      485
Pro Pro Pro Pro Thr Thr Tyr Cys Pro Cys Ser Ile His Pro Asp Ser
    60                  65                  70

ggc ttc cca ctt cct cca cca cct tat gag ctc cca gca tcc aca tcc      533
Gly Phe Pro Leu Pro Pro Pro Pro Tyr Glu Leu Pro Ala Ser Thr Ser
75                  80                  85                  90

cat gtc cca gat ccc cca tac tcc tat ggc aac atg gcc ata cca gtc      581
His Val Pro Asp Pro Pro Tyr Ser Tyr Gly Asn Met Ala Ile Pro Val
                95                  100                 105

tcc aag cca ctg agc ctc tca ggc ctg ctc agt gag ccg ctc caa gac      629
Ser Lys Pro Leu Ser Leu Ser Gly Leu Leu Ser Glu Pro Leu Gln Asp
            110                 115                 120

ccc tta gcc ctc ctg gac att ggg ctg cca gca ggg cca cct aag ccc      677
Pro Leu Ala Leu Leu Asp Ile Gly Leu Pro Ala Gly Pro Pro Lys Pro
        125                 130                 135

caa gaa gac cca gaa tcc gac tca gga tta tcc ctc aac tat agc gat      725
Gln Glu Asp Pro Glu Ser Asp Ser Gly Leu Ser Leu Asn Tyr Ser Asp
    140                 145                 150

gct gaa tct ctt gag ctg gag ggg aca gag gct ggt cgg cgg cgc agc      773
Ala Glu Ser Leu Glu Leu Glu Gly Thr Glu Ala Gly Arg Arg Arg Ser
155                 160                 165                 170

gaa tat gta gag atg tac cca gtg gag tac ccc tac tca ctc atg ccc      821
Glu Tyr Val Glu Met Tyr Pro Val Glu Tyr Pro Tyr Ser Leu Met Pro
                175                 180                 185

aac tcc ttg gcc cac tcc aac tat acc ttg cca gct gct gag acc ccc      869
Asn Ser Leu Ala His Ser Asn Tyr Thr Leu Pro Ala Ala Glu Thr Pro
            190                 195                 200

ttg gcc tta gag ccc tcc tca ggc cct gtg cgg gct aag ccc act gca      917
Leu Ala Leu Glu Pro Ser Ser Gly Pro Val Arg Ala Lys Pro Thr Ala
        205                 210                 215

cgg ggg gag gca ggg agt cgg gat gaa cgt cgg gcc ttg gcc atg aag      965
Arg Gly Glu Ala Gly Ser Arg Asp Glu Arg Arg Ala Leu Ala Met Lys
    220                 225                 230

att cct ttt cct acg gac aag att gtc aac ttg ccg gta gat gac ttt     1013
Ile Pro Phe Pro Thr Asp Lys Ile Val Asn Leu Pro Val Asp Asp Phe
235                 240                 245                 250

aat gag cta ttg gca agg tac ccg ctg aca gag agc cag cta gcg cta     1061
Asn Glu Leu Leu Ala Arg Tyr Pro Leu Thr Glu Ser Gln Leu Ala Leu
                255                 260                 265

gtc cgg gac atc cga cga cgg ggc aaa aac aag gtg gca gcc cag aac     1109
Val Arg Asp Ile Arg Arg Arg Gly Lys Asn Lys Val Ala Ala Gln Asn
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            270                 275                 280

tgc cgc aag agg aag ctg gaa acc att gtg cag ctg gag cgg gag ctg     1157
Cys Arg Lys Arg Lys Leu Glu Thr Ile Val Gln Leu Glu Arg Glu Leu
        285                 290                 295

gag cgg ctg acc aat gaa cgg gag cgg ctt ctc agg gcc cgc ggg gag     1205
Glu Arg Leu Thr Asn Glu Arg Glu Arg Leu Leu Arg Ala Arg Gly Glu
    300                 305                 310

gca gac cgg acc ctg gag gtc atg cgc caa cag ctg aca gag ctg tac     1253
Ala Asp Arg Thr Leu Glu Val Met Arg Gln Gln Leu Thr Glu Leu Tyr
315                 320                 325                 330

cgt gac att ttc cag cac ctt cgg gat gaa tca ggc aac agc tac tct     1301
Arg Asp Ile Phe Gln His Leu Arg Asp Glu Ser Gly Asn Ser Tyr Ser
                335                 340                 345

cct gaa gag tac gcg ctg caa cag gct gcc gat ggg acc atc ttc ctt     1349
Pro Glu Glu Tyr Ala Leu Gln Gln Ala Ala Asp Gly Thr Ile Phe Leu
            350                 355                 360

gtg ccc cgg ggg acc aag atg gag gcc aca gac tga gctggcccag          1395
Val Pro Arg Gly Thr Lys Met Glu Ala Thr Asp
        365                 370

aggggtggaa ctgctgatgg gatttccttc attcccttct gataaaggta ctccccaacc   1455

ctgagtccca gaaggagctg agttctctag accagaagag gatgacaatg gcaacaagtg   1515

tttggaagtt ccaaggtgtg ttcaaagagg cttgccttga gggagggctg gaatctgtct   1575

tccctgactc ggctcctcag gtctttagcc tccaccttgt ctaagctttg gtctataaag   1635

tgcgctacag aaaaaaaaaa aaaaaaaa                                      1663


<210> SEQ ID NO 17
<211> LENGTH: 373
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 17

Met Ser Pro Cys Pro Pro Gln Gln Ser Arg Asn Arg Val Ile Gln Leu
1               5                   10                  15

Ser Thr Ser Glu Leu Gly Glu Met Glu Leu Thr Trp Gln Glu Ile Met
            20                  25                  30

Ser Ile Thr Glu Leu Gln Gly Leu Asn Ala Pro Ser Glu Pro Ser Phe
        35                  40                  45

Glu Pro Gln Ala Pro Ala Pro Tyr Leu Gly Pro Pro Pro Pro Thr Thr
    50                  55                  60

Tyr Cys Pro Cys Ser Ile His Pro Asp Ser Gly Phe Pro Leu Pro Pro
65                  70                  75                  80

Pro Pro Tyr Glu Leu Pro Ala Ser Thr Ser His Val Pro Asp Pro Pro
                85                  90                  95

Tyr Ser Tyr Gly Asn Met Ala Ile Pro Val Ser Lys Pro Leu Ser Leu
            100                 105                 110

Ser Gly Leu Leu Ser Glu Pro Leu Gln Asp Pro Leu Ala Leu Leu Asp
        115                 120                 125

Ile Gly Leu Pro Ala Gly Pro Pro Lys Pro Gln Glu Asp Pro Glu Ser
    130                 135                 140

Asp Ser Gly Leu Ser Leu Asn Tyr Ser Asp Ala Glu Ser Leu Glu Leu
145                 150                 155                 160

Glu Gly Thr Glu Ala Gly Arg Arg Arg Ser Glu Tyr Val Glu Met Tyr
                165                 170                 175
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Pro Val Glu Tyr Pro Tyr Ser Leu Met Pro Asn Ser Leu Ala His Ser
            180                 185                 190

Asn Tyr Thr Leu Pro Ala Ala Glu Thr Pro Leu Ala Leu Glu Pro Ser
        195                 200                 205

Ser Gly Pro Val Arg Ala Lys Pro Thr Ala Arg Gly Glu Ala Gly Ser
    210                 215                 220

Arg Asp Glu Arg Arg Ala Leu Ala Met Lys Ile Pro Phe Pro Thr Asp
225                 230                 235                 240

Lys Ile Val Asn Leu Pro Val Asp Asp Phe Asn Glu Leu Leu Ala Arg
                245                 250                 255

Tyr Pro Leu Thr Glu Ser Gln Leu Ala Leu Val Arg Asp Ile Arg Arg
            260                 265                 270

Arg Gly Lys Asn Lys Val Ala Ala Gln Asn Cys Arg Lys Arg Lys Leu
        275                 280                 285

Glu Thr Ile Val Gln Leu Glu Arg Glu Leu Glu Arg Leu Thr Asn Glu
    290                 295                 300

Arg Glu Arg Leu Leu Arg Ala Arg Gly Glu Ala Asp Arg Thr Leu Glu
305                 310                 315                 320

Val Met Arg Gln Gln Leu Thr Glu Leu Tyr Arg Asp Ile Phe Gln His
                325                 330                 335

Leu Arg Asp Glu Ser Gly Asn Ser Tyr Ser Pro Glu Glu Tyr Ala Leu
            340                 345                 350

Gln Gln Ala Ala Asp Gly Thr Ile Phe Leu Val Pro Arg Gly Thr Lys
        355                 360                 365

Met Glu Ala Thr Asp
    370


<210> SEQ ID NO 18
<211> LENGTH: 1248
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (127)..(681)
<223> OTHER INFORMATION: Tnfaip8l2

<400> SEQUENCE: 18

ggccaagcca aagggctctc acactaagtg aagcttctcc attctgtaag ctttccggga     60

acatccaagg caagactggc acccagcaca gcagtgactg accacatacc ccactctcca    120

ggaccc atg gag tcc ttc agc tca aag agc ctg gca ctg caa gca gag       168
       Met Glu Ser Phe Ser Ser Lys Ser Leu Ala Leu Gln Ala Glu
       1               5                   10

aag aag cta ctg agt aag atg gcg ggt cgc tct gtg gct cat ctc ttc      216
Lys Lys Leu Leu Ser Lys Met Ala Gly Arg Ser Val Ala His Leu Phe
15                  20                  25                  30

ata gat gag aca agc agt gag gtg cta gat gag ctc tac cgt gtg tcc      264
Ile Asp Glu Thr Ser Ser Glu Val Leu Asp Glu Leu Tyr Arg Val Ser
                35                  40                  45

aag gag tac acg cac agc cgg ccc cag gcc cag cgc gtg atc aag gac      312
Lys Glu Tyr Thr His Ser Arg Pro Gln Ala Gln Arg Val Ile Lys Asp
            50                  55                  60

ctg atc aaa gtg gcc atc aag gtg gct gtg ctg cac cgc aat ggc tcc      360
Leu Ile Lys Val Ala Ile Lys Val Ala Val Leu His Arg Asn Gly Ser
        65                  70                  75

ttt ggc ccc agt gag ctg gcc ctg gct acc cgc ttt cgc cag aag ctg      408
Phe Gly Pro Ser Glu Leu Ala Leu Ala Thr Arg Phe Arg Gln Lys Leu
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    80                  85                  90

cgg cag ggt gcc atg acg gca ctt agc ttt ggt gag gta gac ttc acc      456
Arg Gln Gly Ala Met Thr Ala Leu Ser Phe Gly Glu Val Asp Phe Thr
95                  100                 105                 110

ttc gag gct gct gtt ctg gct ggc ctg ctg acc gag tgc cgg gat gtg      504
Phe Glu Ala Ala Val Leu Ala Gly Leu Leu Thr Glu Cys Arg Asp Val
                115                 120                 125

ctg cta gag ttg gtg gaa cac cac ctc acg ccc aag tca cat ggc cgc      552
Leu Leu Glu Leu Val Glu His His Leu Thr Pro Lys Ser His Gly Arg
            130                 135                 140

atc cgc cac gtg ttt gat cac ttc tct gac cca ggt ctg ctc acg gcc      600
Ile Arg His Val Phe Asp His Phe Ser Asp Pro Gly Leu Leu Thr Ala
        145                 150                 155

ctc tat ggg cct gac ttc act cag cac ctt ggc aag atc tgt gac gga      648
Leu Tyr Gly Pro Asp Phe Thr Gln His Leu Gly Lys Ile Cys Asp Gly
    160                 165                 170

ctc agg aag ctg cta gac gaa ggg aag ctc tga gagccctgag cctagcacat    701
Leu Arg Lys Leu Leu Asp Glu Gly Lys Leu
175                 180

tccaccttga caaaatggtt gactgagaaa acacagataa tgggcttcct aaccctgctc    761

acctggcact aacacttttc aatcttcagg cttcattcct tcccaagagt gcttttgact    821

ctgagaccag cccaccccca aacagctagt ggagaaggag caatgctgag gggtgaggcc    881

tctctcccac tccagcccca ggacaggaaa cagaactgcc tgaaaaaggt gaagtgaaac    941

ttggatctct atttctccca taagggactt ctgaaacagg gaagcccccc cccatgtgaa   1001

ccaaggaaag gaggcacagc ccagagaacc cctttgggga tactaaagac agaagagggg   1061

aaggtggccc ttagagacag agcttggaca gatgccagag gctctgttcc agagtgcagg   1121

aagaaggggc tagggcaggg gagattctca taggggaaat aaaactacta aaatatgaaa   1181

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa   1241

aaaaaaa                                                            1248


<210> SEQ ID NO 19
<211> LENGTH: 184
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 19

Met Glu Ser Phe Ser Ser Lys Ser Leu Ala Leu Gln Ala Glu Lys Lys
1               5                   10                  15

Leu Leu Ser Lys Met Ala Gly Arg Ser Val Ala His Leu Phe Ile Asp
            20                  25                  30

Glu Thr Ser Ser Glu Val Leu Asp Glu Leu Tyr Arg Val Ser Lys Glu
        35                  40                  45

Tyr Thr His Ser Arg Pro Gln Ala Gln Arg Val Ile Lys Asp Leu Ile
    50                  55                  60

Lys Val Ala Ile Lys Val Ala Val Leu His Arg Asn Gly Ser Phe Gly
65                  70                  75                  80

Pro Ser Glu Leu Ala Leu Ala Thr Arg Phe Arg Gln Lys Leu Arg Gln
                85                  90                  95

Gly Ala Met Thr Ala Leu Ser Phe Gly Glu Val Asp Phe Thr Phe Glu
            100                 105                 110

Ala Ala Val Leu Ala Gly Leu Leu Thr Glu Cys Arg Asp Val Leu Leu
        115                 120                 125
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Glu Leu Val Glu His His Leu Thr Pro Lys Ser His Gly Arg Ile Arg
    130                 135                 140

His Val Phe Asp His Phe Ser Asp Pro Gly Leu Leu Thr Ala Leu Tyr
145                 150                 155                 160

Gly Pro Asp Phe Thr Gln His Leu Gly Lys Ile Cys Asp Gly Leu Arg
                165                 170                 175

Lys Leu Leu Asp Glu Gly Lys Leu
            180


<210> SEQ ID NO 20
<211> LENGTH: 1254
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (33)..(503)
<223> OTHER INFORMATION: Ier3

<400> SEQUENCE: 20

ctcacttggc cttacactcc gctcggctca cc atg tgt cac tct cgc agc tgc       53
                                  Met Cys His Ser Arg Ser Cys
                                  1               5

cac ccg acc atg acc atc ctg cag gcc ccg acc ccg gcc ccc tcc acc      101
His Pro Thr Met Thr Ile Leu Gln Ala Pro Thr Pro Ala Pro Ser Thr
        10                  15                  20

atc ccg gga ccc cgg cgg ggc tcc ggt cct gag atc ttc acc ttc gac      149
Ile Pro Gly Pro Arg Arg Gly Ser Gly Pro Glu Ile Phe Thr Phe Asp
    25                  30                  35

cct ctc ccg gag ccc gca gcg gcc cct gcc ggg cgc ccc agc gcc tct      197
Pro Leu Pro Glu Pro Ala Ala Ala Pro Ala Gly Arg Pro Ser Ala Ser
40                  45                  50                  55

cgc ggg cac cga aag cgc agc cgc agg gtt ctc tac cct cga gtg gtc      245
Arg Gly His Arg Lys Arg Ser Arg Arg Val Leu Tyr Pro Arg Val Val
                60                  65                  70

cgg cgc cag ctg cca gtc gag gaa ccg aac cca gcc aaa agg ctt ctc      293
Arg Arg Gln Leu Pro Val Glu Glu Pro Asn Pro Ala Lys Arg Leu Leu
            75                  80                  85

ttt ctg ctg ctc acc atc gtc ttc tgc cag atc ctg atg gct gaa gag      341
Phe Leu Leu Leu Thr Ile Val Phe Cys Gln Ile Leu Met Ala Glu Glu
        90                  95                  100

ggt gtg ccg gcg ccc ctg cct cca gag gac gcc cct aac gcc gca tcc      389
Gly Val Pro Ala Pro Leu Pro Pro Glu Asp Ala Pro Asn Ala Ala Ser
    105                 110                 115

ctg gcg ccc acc cct gtg tcc gcc gtc ctc gag ccc ttt aat ctg act      437
Leu Ala Pro Thr Pro Val Ser Ala Val Leu Glu Pro Phe Asn Leu Thr
120                 125                 130                 135

tcg gag ccc tcg gac tac gct ctg gac ctc agc act ttc ctc cag caa      485
Ser Glu Pro Ser Asp Tyr Ala Leu Asp Leu Ser Thr Phe Leu Gln Gln
                140                 145                 150

cac ccg gcc gcc ttc taa ctgtgactcc ccgcactccc caaaaagaat             533
His Pro Ala Ala Phe
            155

ccgaaaaacc acaaagaaac accaggcgta cctggtgcgc gagagcgtat ccccaactgg    593

gacttccgag gcaacttgaa ctcagaacac tacagcggag acgccacccg gtgcttgagg    653

cgggaccgag gcgcacagag accgaggcgc atagagaccg aggcacagcc cagctggggc    713

taggcccggt gggaaggaga gcgtcgttaa tttatttctt attgctccta attaatattt    773
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atatgtattt atgtacgtcc tcctaggtga tggagatgtg tacgtaatat ttattttaac    833

ttatgcaagg gtgtgagatg ttccccctgc tgtaaatgca ggtctcttgg tatttattga    893

gctttgtggg actggtggaa gcaggacacc tggaactgcg gcaaagtagg agaagaaatg    953

gggaggactc gggtgggga ggacgtcccg gctgggatga agtctggtgg tgggtcgtaa   1013

gtttaggagg tgactgcatc ctccagcatc tcaactccgt ctgtctactg tgtgagactt   1073

cggcggacca ttaggaatga gatccgtgag atccttccat cttcttgaag tcgcctttag   1133

ggtggctgcg aggtagaggg ttgggggttg gtgggctgtc acggagcgac tgtcgagatc   1193

gcctagtatg ttctgtgaac acaaataaaa ttgatttact gtctgcaaaa aaaaaaaaaa   1253

a                                                                   1254
```

<210> SEQ ID NO 21
<211> LENGTH: 156
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 21

```
Met Cys His Ser Arg Ser Cys His Pro Thr Met Thr Ile Leu Gln Ala
1               5                   10                  15

Pro Thr Pro Ala Pro Ser Thr Ile Pro Gly Pro Arg Arg Gly Ser Gly
            20                  25                  30

Pro Glu Ile Phe Thr Phe Asp Pro Leu Pro Glu Pro Ala Ala Ala Pro
        35                  40                  45

Ala Gly Arg Pro Ser Ala Ser Arg Gly His Arg Lys Arg Ser Arg Arg
    50                  55                  60

Val Leu Tyr Pro Arg Val Val Arg Arg Gln Leu Pro Val Glu Glu Pro
65                  70                  75                  80

Asn Pro Ala Lys Arg Leu Leu Phe Leu Leu Leu Thr Ile Val Phe Cys
                85                  90                  95

Gln Ile Leu Met Ala Glu Glu Gly Val Pro Ala Pro Leu Pro Pro Glu
            100                 105                 110

Asp Ala Pro Asn Ala Ala Ser Leu Ala Pro Thr Pro Val Ser Ala Val
        115                 120                 125

Leu Glu Pro Phe Asn Leu Thr Ser Glu Pro Ser Asp Tyr Ala Leu Asp
    130                 135                 140

Leu Ser Thr Phe Leu Gln Gln His Pro Ala Ala Phe
145                 150                 155
```

<210> SEQ ID NO 22
<211> LENGTH: 4817
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (129)..(2546)
<223> OTHER INFORMATION: Pik3ap1

<400> SEQUENCE: 22

```
gaagcgccag agcggcggcc ggtcccgcgc ggagcccggc gcccctccag cccgagccag     60

gacgccgccg gccccggtcc cggccccggg cacgcagcga gccagggatg tgagcggcgc    120

cccgcggc atg gca gcc tca ggg gtg ccc aga gga tgc gac atc ctc atc     170
       Met Ala Ala Ser Gly Val Pro Arg Gly Cys Asp Ile Leu Ile
       1               5                   10

gtc tac agc ccg gat gcc gag gaa tgg tgc cag tac ctg cag acc ctg      218
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Val Tyr Ser Pro Asp Ala Glu Glu Trp Cys Gln Tyr Leu Gln Thr Leu
15                  20                  25                  30

ttc ctg tcc agt cgg cag gtc cgc agc cag aag ata ctg act cac agg      266
Phe Leu Ser Ser Arg Gln Val Arg Ser Gln Lys Ile Leu Thr His Arg
                35                  40                  45

ctg ggc ccc gag gcc tcc ttc tcg gca gag gac cta agc ctt ttc ctc      314
Leu Gly Pro Glu Ala Ser Phe Ser Ala Glu Asp Leu Ser Leu Phe Leu
            50                  55                  60

agc acc cgc tgt gtc gtg gtg ctg ctg tcc gcg gag ctg gtg cag cac      362
Ser Thr Arg Cys Val Val Val Leu Leu Ser Ala Glu Leu Val Gln His
        65                  70                  75

ttc cac aag ccc gcc ttg ctg ccc ctg ctg cag aga gct ttc cat cct      410
Phe His Lys Pro Ala Leu Leu Pro Leu Leu Gln Arg Ala Phe His Pro
    80                  85                  90

ccg cac cgc gtg gtc agg ctg ctc tgc ggc gtg cgg gac agc gag gag      458
Pro His Arg Val Val Arg Leu Leu Cys Gly Val Arg Asp Ser Glu Glu
95                  100                 105                 110

ttc cta gac ttc ttt cca gat tgg gcc cat tgg cag gag ctc acc tgt      506
Phe Leu Asp Phe Phe Pro Asp Trp Ala His Trp Gln Glu Leu Thr Cys
                115                 120                 125

gac gat gag cca gag acc tac gtg gca gct gtg aaa aaa gcc att tcc      554
Asp Asp Glu Pro Glu Thr Tyr Val Ala Ala Val Lys Lys Ala Ile Ser
            130                 135                 140

gaa gat tct ggc tgt gac tca gtc act gac act gag cct gag gac gag      602
Glu Asp Ser Gly Cys Asp Ser Val Thr Asp Thr Glu Pro Glu Asp Glu
        145                 150                 155

aag gtt gtt tcc tac tcg aag cag cag aac ctg ccg acg gtg act tca      650
Lys Val Val Ser Tyr Ser Lys Gln Gln Asn Leu Pro Thr Val Thr Ser
    160                 165                 170

cct ggg aac ctg atg gtg gtg cag ccg gac cgc att cgc tgt ggg gca      698
Pro Gly Asn Leu Met Val Val Gln Pro Asp Arg Ile Arg Cys Gly Ala
175                 180                 185                 190

gaa acc act gtc tat gtt att gtg aga tgt aag ctg gat gac agg gtg      746
Glu Thr Thr Val Tyr Val Ile Val Arg Cys Lys Leu Asp Asp Arg Val
                195                 200                 205

gcg aca gaa gca gag ttt tct cct gag gat tct ccc tct gta agg atg      794
Ala Thr Glu Ala Glu Phe Ser Pro Glu Asp Ser Pro Ser Val Arg Met
            210                 215                 220

gaa gcc aag gtg gag aat gag tac acc att tca gtg aag gct ccc aac      842
Glu Ala Lys Val Glu Asn Glu Tyr Thr Ile Ser Val Lys Ala Pro Asn
        225                 230                 235

ctt tca tct ggg aac gtt tct ctg aag ata tat tct gga gac tta gtg      890
Leu Ser Ser Gly Asn Val Ser Leu Lys Ile Tyr Ser Gly Asp Leu Val
    240                 245                 250

gtg tgt gaa acc gtt atc agc tat tat act gac atg gaa gaa att ggg      938
Val Cys Glu Thr Val Ile Ser Tyr Tyr Thr Asp Met Glu Glu Ile Gly
255                 260                 265                 270

aat tta ttg tcc aat gcc gcg aat cct gtg gaa ttc atg tgt cag gcc      986
Asn Leu Leu Ser Asn Ala Ala Asn Pro Val Glu Phe Met Cys Gln Ala
                275                 280                 285

ttt aaa att gtg ccc tac aac aca gag acc ctt gat aaa ctg cta acc     1034
Phe Lys Ile Val Pro Tyr Asn Thr Glu Thr Leu Asp Lys Leu Leu Thr
            290                 295                 300

gaa tcc ctg aag aac aat atc cct gca agc gga ctg cac ctc ttt gga     1082
Glu Ser Leu Lys Asn Asn Ile Pro Ala Ser Gly Leu His Leu Phe Gly
        305                 310                 315

atc aac cag ctg gaa gaa gaa gat atg atg aca aat cag agg gat gaa     1130
Ile Asn Gln Leu Glu Glu Glu Asp Met Met Thr Asn Gln Arg Asp Glu
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    320                 325                 330

gag ctg ccc acc ctg ttg cat ttt gct gcg aag tat gga ctg aag aac     1178
Glu Leu Pro Thr Leu Leu His Phe Ala Ala Lys Tyr Gly Leu Lys Asn
335                 340                 345                 350

ctc act gcc ttg ttg ctc acc tgc cca gga gcc ctg cag gcg tac agc     1226
Leu Thr Ala Leu Leu Leu Thr Cys Pro Gly Ala Leu Gln Ala Tyr Ser
                355                 360                 365

gtg gcc aac aag cat ggc cac tac ccc aac acc atc gct gag aaa cac     1274
Val Ala Asn Lys His Gly His Tyr Pro Asn Thr Ile Ala Glu Lys His
            370                 375                 380

ggc ttc agg gac ctg cgg cag ttc atc gac gag tat gtg gaa acg gtg     1322
Gly Phe Arg Asp Leu Arg Gln Phe Ile Asp Glu Tyr Val Glu Thr Val
        385                 390                 395

gac atg ctc aag agt cac att aaa gag gaa ctg atg cac ggg gag gag     1370
Asp Met Leu Lys Ser His Ile Lys Glu Glu Leu Met His Gly Glu Glu
    400                 405                 410

gct gat gct gtg tac gag tcc atg gcc cac ctt tcc aca gac ctg ctt     1418
Ala Asp Ala Val Tyr Glu Ser Met Ala His Leu Ser Thr Asp Leu Leu
415                 420                 425                 430

atg aaa tgc tcg ctc aac ccc ggc tgt gac gag gat ctc tat gag tcc     1466
Met Lys Cys Ser Leu Asn Pro Gly Cys Asp Glu Asp Leu Tyr Glu Ser
                435                 440                 445

atg gct gcc ttt gtc cca gct gcc act gaa gac ctc tat gtt gaa atg     1514
Met Ala Ala Phe Val Pro Ala Ala Thr Glu Asp Leu Tyr Val Glu Met
            450                 455                 460

ctt cag gcc agt aca tct aac cca atc cct gga gat ggt ttc tct cgg     1562
Leu Gln Ala Ser Thr Ser Asn Pro Ile Pro Gly Asp Gly Phe Ser Arg
        465                 470                 475

gcc act aag gac tct atg atc cgc aag ttt tta gaa ggc aac agc atg     1610
Ala Thr Lys Asp Ser Met Ile Arg Lys Phe Leu Glu Gly Asn Ser Met
    480                 485                 490

gga atg acc aat ctg gag aga gat cag tgc cat ctt ggt cag gaa gaa     1658
Gly Met Thr Asn Leu Glu Arg Asp Gln Cys His Leu Gly Gln Glu Glu
495                 500                 505                 510

gat gtt tat cac acg gtg gat gac gat gag gcc ttt tct gtg gac ctg     1706
Asp Val Tyr His Thr Val Asp Asp Asp Glu Ala Phe Ser Val Asp Leu
                515                 520                 525

gcc agc agg ccc cct gtc cca gtg ccc aga cca gag acc act gct cct     1754
Ala Ser Arg Pro Pro Val Pro Val Pro Arg Pro Glu Thr Thr Ala Pro
            530                 535                 540

ggt gct cac cag ctg cct gac aac gaa cca tac att ttt aaa gtt ttt     1802
Gly Ala His Gln Leu Pro Asp Asn Glu Pro Tyr Ile Phe Lys Val Phe
        545                 550                 555

gca gaa aaa agt caa gag cgg cct ggg aat ttc tac gtt tcc tca gag     1850
Ala Glu Lys Ser Gln Glu Arg Pro Gly Asn Phe Tyr Val Ser Ser Glu
    560                 565                 570

agc atc agg aaa ggg ccg ccc gtc aga cca tgg agg gac agg ccc cag     1898
Ser Ile Arg Lys Gly Pro Pro Val Arg Pro Trp Arg Asp Arg Pro Gln
575                 580                 585                 590

tcg agt ata tat gac cct ttt gcg gga atg aaa acg cca ggc cag cgg     1946
Ser Ser Ile Tyr Asp Pro Phe Ala Gly Met Lys Thr Pro Gly Gln Arg
                595                 600                 605

cag ctt atc acc ctc cag gag cag gtg aag ctg ggc att gtc aac gtg     1994
Gln Leu Ile Thr Leu Gln Glu Gln Val Lys Leu Gly Ile Val Asn Val
            610                 615                 620

gat gag gct gtg ctc cac ttc aaa gag tgg cag ctc aac cag aag aaa     2042
Asp Glu Ala Val Leu His Phe Lys Glu Trp Gln Leu Asn Gln Lys Lys
        625                 630                 635
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cga tcg gag tcc ttt cgt ttc cag cag gaa aat ctt aaa cgg cta aga     2090
Arg Ser Glu Ser Phe Arg Phe Gln Gln Glu Asn Leu Lys Arg Leu Arg
    640                 645                 650

gac agc atc acc cga aga cag aga gag aag caa aaa tca gga aag cag     2138
Asp Ser Ile Thr Arg Arg Gln Arg Glu Lys Gln Lys Ser Gly Lys Gln
655                 660                 665                 670

aca gac ttg gag atc acg gtc cca att cgg cac tca cag cac ctg cct     2186
Thr Asp Leu Glu Ile Thr Val Pro Ile Arg His Ser Gln His Leu Pro
                675                 680                 685

gca aaa gtg gag ttt gga gtc tat gag agt ggc ccc agg aaa agt gtc     2234
Ala Lys Val Glu Phe Gly Val Tyr Glu Ser Gly Pro Arg Lys Ser Val
            690                 695                 700

att ccc cct agg acg gag ctg aga cga gga gac tgg aaa aca gac agc     2282
Ile Pro Pro Arg Thr Glu Leu Arg Arg Gly Asp Trp Lys Thr Asp Ser
        705                 710                 715

acc tcc agc aca gca agt agc aca agt aac cgc tcc agc acc cgg agc     2330
Thr Ser Ser Thr Ala Ser Ser Thr Ser Asn Arg Ser Ser Thr Arg Ser
    720                 725                 730

ctc ctc agt gtg agc agc ggg atg gaa ggg gac aac gag gat aat gaa     2378
Leu Leu Ser Val Ser Ser Gly Met Glu Gly Asp Asn Glu Asp Asn Glu
735                 740                 745                 750

gtc cct gag gtt acc aga agt cgc agt cca ggc ccc cca caa gtg gat     2426
Val Pro Glu Val Thr Arg Ser Arg Ser Pro Gly Pro Pro Gln Val Asp
                755                 760                 765

ggg aca ccc acc atg tcc ctc gag aga ccc ccc agg gtg cct ccg aga     2474
Gly Thr Pro Thr Met Ser Leu Glu Arg Pro Pro Arg Val Pro Pro Arg
            770                 775                 780

gct gcc tca cag agg cct ccg acc agg gag acc ttc cat cct cct cca     2522
Ala Ala Ser Gln Arg Pro Pro Thr Arg Glu Thr Phe His Pro Pro Pro
        785                 790                 795

cct gtt cca ccc aga gga cgc tga ttccacctcc taaaacctgc ctacttcagg    2576
Pro Val Pro Pro Arg Gly Arg
    800                 805

actttaagac tcacagtctt cagcctgtta atgatgtctt catgttgagt tttatagcat   2636

gactgttgac cttaagatcc attctcattg ctgataatgc tgcagccctg ctggtttggg   2696

cttgcctcga agattttatt aaggcacgaa gaagtgaaaa actaagggct tcattcacca   2756

tcaccaagta tatcgaacca tatacttgtt tgccaaaagg atgaagactt aatcgaaata   2816

cttacctcta atttgccata tcagaagcct aaaaagaatg atcataaatg tacttcacca   2876

gtgattttac tgaaatgcac ttatattagt ctttatgtat ttgctagttc agcctgattt   2936

ctagaagagg ttatagtgtg agacttgtag tattcaagta agataagtga cctaatttta   2996

aaataattct tctacttttc tgtatattca gcagggtatt taagtgctag ggctggtcac   3056

acacaaccaa ctgaaaaaga ctagagggat tagtacaaac tcctcttata cagaaggcaa   3116

atctgaggtt ccacagaagt ctggaaccaa gactattcag ttggttaaat aaagaggtta   3176

gtctagactg ggcctgctca ttctaggtca ccacattttc catctccaaa tagccaggcc   3236

ctctctccct caagaaatgc ccagatgtag aaattcatca gtgcctattg gtcttccaga   3296

attttccatc ttccgtatct cccaggcatg agactaccaa gtttgtttgt tttctttcca   3356

atttgggaat ttatacttca gtatggtttc aacgcagtta tgtttccaga gaacatctag   3416

aagtggctgg aaaccagaag ctggggattc cagggacccc acttagtgct ctatttcctt   3476

tataggtttt atttctggtc atagagagag aaggaccttt gacttttttct tcgttgaggc   3536
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ttctgaggag gaaaaacaaa cctaaaatag aaatacagtc agcctttcaa atccatgggt   3596

tctgtgtccg tggattcaac caaccttgga tcaaaaatat ttgaaaaaaa atctacaaag   3656

tttcaaaaag caaaacttga atttgctgca tgccaagaag tatgttgaat tcatgtaaat   3716

gaagtgatgt gtaggcattg tattagatat tataagaaat ctagaaatga tttaaagcat   3776

acaggaggat gtgcataggt tatatgcaaa tactatgcta ttttatatat gggacttgag   3836

catttgtgga ttttgatact gggggatcct ggaaccaatc ccccatggat accaaagtac   3896

gactgtagtt atctattttt tacatactta ttattaccac catgctcagt aagtccattt   3956

ttgcatggaa tatggagcct taaaacatgt catgaatttg gagtccctgg cacataaatc   4016

taccttcaaa tcagaggtcc ttaatgatgc ctaaacatac agtaaaatta gaatcagaaa   4076

tacttcttta aaaaatattc aaaatgtgtt tgtttcccat gggattattc tctatcccac   4136

acgaatgtaa aaaaatccac attaatgatc catttaagta tagttttatt gggtcctttt   4196

ctaatgatta aaggttcttt ctcaatttca ttcctcagtc ctgcaagtaa ggactcatac   4256

tgaagagtac tgaaacaagg acttcttgtc agaaacagct tctggaatct tgggttttgt   4316

ttttgttttt tgacaaaata cactattggc catgtccatc acgagagtgt ttgtagtaat   4376

taattacctt gtacaggacc tggcacttag tagcattctt caaatgttcc ctcagtgatc   4436

cttttactct ccttgtcact tatttgggag aaataggggc acgtgagata agaagaagaa   4496

taattttgat gttggtatgc ttgccctgtt acttatagac agtctttgtc ataggcaaac   4556

ttgaatttga tttaaaatag ggctgggaaa aatattcaat aactgtaagc ccccttttgg   4616

atgccaaact tagaattttg tacattctct gatgaacaag catttagatc gtaacatggt   4676

aaagcctatt accagccaat gttgttagca tctttgtatg cacatcactg tttgtgcaat   4736

atatgaatat tttgttgcat tgtattctta tataaaaata agtagaaaac ataaaattga   4796

aattgctgat gagaaaaaaa a                                             4817
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<210> SEQ ID NO 23
<211> LENGTH: 805
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 23

Met Ala Ala Ser Gly Val Pro Arg Gly Cys Asp Ile Leu Ile Val Tyr
1               5                   10                  15

Ser Pro Asp Ala Glu Glu Trp Cys Gln Tyr Leu Gln Thr Leu Phe Leu
            20                  25                  30

Ser Ser Arg Gln Val Arg Ser Gln Lys Ile Leu Thr His Arg Leu Gly
        35                  40                  45

Pro Glu Ala Ser Phe Ser Ala Glu Asp Leu Ser Leu Phe Leu Ser Thr
    50                  55                  60

Arg Cys Val Val Val Leu Leu Ser Ala Glu Leu Val Gln His Phe His
65                  70                  75                  80

Lys Pro Ala Leu Leu Pro Leu Leu Gln Arg Ala Phe His Pro Pro His
                85                  90                  95

Arg Val Val Arg Leu Leu Cys Gly Val Arg Asp Ser Glu Glu Phe Leu
            100                 105                 110

Asp Phe Phe Pro Asp Trp Ala His Trp Gln Glu Leu Thr Cys Asp Asp
        115                 120                 125

Glu Pro Glu Thr Tyr Val Ala Ala Val Lys Lys Ala Ile Ser Glu Asp
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    130                 135                 140

Ser Gly Cys Asp Ser Val Thr Asp Thr Glu Pro Glu Asp Glu Lys Val
145                 150                 155                 160

Val Ser Tyr Ser Lys Gln Gln Asn Leu Pro Thr Val Thr Ser Pro Gly
                165                 170                 175

Asn Leu Met Val Val Gln Pro Asp Arg Ile Arg Cys Gly Ala Glu Thr
            180                 185                 190

Thr Val Tyr Val Ile Val Arg Cys Lys Leu Asp Asp Arg Val Ala Thr
        195                 200                 205

Glu Ala Glu Phe Ser Pro Glu Asp Ser Pro Ser Val Arg Met Glu Ala
    210                 215                 220

Lys Val Glu Asn Glu Tyr Thr Ile Ser Val Lys Ala Pro Asn Leu Ser
225                 230                 235                 240

Ser Gly Asn Val Ser Leu Lys Ile Tyr Ser Gly Asp Leu Val Val Cys
                245                 250                 255

Glu Thr Val Ile Ser Tyr Tyr Thr Asp Met Glu Glu Ile Gly Asn Leu
            260                 265                 270

Leu Ser Asn Ala Ala Asn Pro Val Glu Phe Met Cys Gln Ala Phe Lys
        275                 280                 285

Ile Val Pro Tyr Asn Thr Glu Thr Leu Asp Lys Leu Leu Thr Glu Ser
    290                 295                 300

Leu Lys Asn Asn Ile Pro Ala Ser Gly Leu His Leu Phe Gly Ile Asn
305                 310                 315                 320

Gln Leu Glu Glu Glu Asp Met Met Thr Asn Gln Arg Asp Glu Glu Leu
                325                 330                 335

Pro Thr Leu Leu His Phe Ala Ala Lys Tyr Gly Leu Lys Asn Leu Thr
            340                 345                 350

Ala Leu Leu Leu Thr Cys Pro Gly Ala Leu Gln Ala Tyr Ser Val Ala
        355                 360                 365

Asn Lys His Gly His Tyr Pro Asn Thr Ile Ala Glu Lys His Gly Phe
    370                 375                 380

Arg Asp Leu Arg Gln Phe Ile Asp Glu Tyr Val Glu Thr Val Asp Met
385                 390                 395                 400

Leu Lys Ser His Ile Lys Glu Glu Leu Met His Gly Glu Glu Ala Asp
                405                 410                 415

Ala Val Tyr Glu Ser Met Ala His Leu Ser Thr Asp Leu Leu Met Lys
            420                 425                 430

Cys Ser Leu Asn Pro Gly Cys Asp Glu Asp Leu Tyr Glu Ser Met Ala
        435                 440                 445

Ala Phe Val Pro Ala Ala Thr Glu Asp Leu Tyr Val Glu Met Leu Gln
    450                 455                 460

Ala Ser Thr Ser Asn Pro Ile Pro Gly Asp Gly Phe Ser Arg Ala Thr
465                 470                 475                 480

Lys Asp Ser Met Ile Arg Lys Phe Leu Glu Gly Asn Ser Met Gly Met
                485                 490                 495

Thr Asn Leu Glu Arg Asp Gln Cys His Leu Gly Gln Glu Glu Asp Val
            500                 505                 510

Tyr His Thr Val Asp Asp Asp Glu Ala Phe Ser Val Asp Leu Ala Ser
        515                 520                 525

Arg Pro Pro Val Pro Val Pro Arg Pro Glu Thr Thr Ala Pro Gly Ala
    530                 535                 540
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His Gln Leu Pro Asp Asn Glu Pro Tyr Ile Phe Lys Val Phe Ala Glu
545                 550                 555                 560

Lys Ser Gln Glu Arg Pro Gly Asn Phe Tyr Val Ser Ser Glu Ser Ile
                565                 570                 575

Arg Lys Gly Pro Pro Val Arg Pro Trp Arg Asp Arg Pro Gln Ser Ser
            580                 585                 590

Ile Tyr Asp Pro Phe Ala Gly Met Lys Thr Pro Gly Gln Arg Gln Leu
        595                 600                 605

Ile Thr Leu Gln Glu Gln Val Lys Leu Gly Ile Val Asn Val Asp Glu
    610                 615                 620

Ala Val Leu His Phe Lys Glu Trp Gln Leu Asn Gln Lys Lys Arg Ser
625                 630                 635                 640

Glu Ser Phe Arg Phe Gln Gln Glu Asn Leu Lys Arg Leu Arg Asp Ser
                645                 650                 655

Ile Thr Arg Arg Gln Arg Glu Lys Gln Lys Ser Gly Lys Gln Thr Asp
            660                 665                 670

Leu Glu Ile Thr Val Pro Ile Arg His Ser Gln His Leu Pro Ala Lys
        675                 680                 685

Val Glu Phe Gly Val Tyr Glu Ser Gly Pro Arg Lys Ser Val Ile Pro
    690                 695                 700

Pro Arg Thr Glu Leu Arg Arg Gly Asp Trp Lys Thr Asp Ser Thr Ser
705                 710                 715                 720

Ser Thr Ala Ser Ser Thr Ser Asn Arg Ser Ser Thr Arg Ser Leu Leu
                725                 730                 735

Ser Val Ser Ser Gly Met Glu Gly Asp Asn Glu Asp Asn Glu Val Pro
            740                 745                 750

Glu Val Thr Arg Ser Arg Ser Pro Gly Pro Pro Gln Val Asp Gly Thr
        755                 760                 765

Pro Thr Met Ser Leu Glu Arg Pro Pro Arg Val Pro Pro Arg Ala Ala
    770                 775                 780

Ser Gln Arg Pro Pro Thr Arg Glu Thr Phe His Pro Pro Pro Pro Val
785                 790                 795                 800

Pro Pro Arg Gly Arg
                805


<210> SEQ ID NO 24
<211> LENGTH: 1870
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (451)..(1701)
<223> OTHER INFORMATION: Pstpip1

<400> SEQUENCE: 24

acaaaccttc ctgcgcaggc ctcgggctgc ctgcctgcct gcctgcctgg cccggcccga     60

gctccagcct gcctcttcca ctggccactg cctcccaccc agggctggca tccctgctcc    120

ctgccctggg tcccagactg tgtcctccat caccgcaggg tcggtgaggg gctgggctgg    180

acaccagggc ccgccctccc atcactgagc tccactcctt cctcattttg ctgctgattc    240

tagccccaaa caaaacaggt tgagcttttt cctcccctca gaagctcctc tctggctcgt    300

ggctgccttc tgagtgttgc agacggcgcc ggccgggaag gggggcctgg gccagccctg    360

ccaggactgg gacgctgctg ctggcgcctg gccctccatc aggccagcct gtggcaggag    420
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agtgagcttt gccgcggcag acgcctgagg atg atg ccc cag ctg cag ttc aaa     474
                                Met Met Pro Gln Leu Gln Phe Lys
                                1               5

gat gcc ttt tgg tgc agg gac ttc aca gcc cac acg ggc tac gag gtg      522
Asp Ala Phe Trp Cys Arg Asp Phe Thr Ala His Thr Gly Tyr Glu Val
    10                  15                  20

ctg ctg cag cgg ctt ctg gat ggc agg aag atg tgc aaa gac atg gag      570
Leu Leu Gln Arg Leu Leu Asp Gly Arg Lys Met Cys Lys Asp Met Glu
25                  30                  35                  40

gag cta ctg agg cag agg gcc cag gcg gag gag cgg tac ggg aag gag      618
Glu Leu Leu Arg Gln Arg Ala Gln Ala Glu Glu Arg Tyr Gly Lys Glu
                45                  50                  55

ctg gtg cag atc gca cgg aag gca ggt ggc cag acg gag atc aac tcc      666
Leu Val Gln Ile Ala Arg Lys Ala Gly Gly Gln Thr Glu Ile Asn Ser
            60                  65                  70

ctg agg gcc tcc ttt gac tcc ttg aag cag caa atg gag aat gtg ggc      714
Leu Arg Ala Ser Phe Asp Ser Leu Lys Gln Gln Met Glu Asn Val Gly
        75                  80                  85

agc tca cac atc cag ctg gcc ctg acc ctg cgt gag gag ctg cgg agt      762
Ser Ser His Ile Gln Leu Ala Leu Thr Leu Arg Glu Glu Leu Arg Ser
    90                  95                  100

ctc gag gag ttt cgt gag agg cag aag gag cag agg aag aag tat gag      810
Leu Glu Glu Phe Arg Glu Arg Gln Lys Glu Gln Arg Lys Lys Tyr Glu
105                 110                 115                 120

gcc gtc atg gac cgg gtc cag aag agc aag ctg tcg ctc tac aag aag      858
Ala Val Met Asp Arg Val Gln Lys Ser Lys Leu Ser Leu Tyr Lys Lys
                125                 130                 135

gcc atg gag tcc aag aag aca tac gag cag aag tgc cgg gac gcg gac      906
Ala Met Glu Ser Lys Lys Thr Tyr Glu Gln Lys Cys Arg Asp Ala Asp
            140                 145                 150

gac gcg gag cag gcc ttc gag cgc att agc gcc aac ggc cac cag aag      954
Asp Ala Glu Gln Ala Phe Glu Arg Ile Ser Ala Asn Gly His Gln Lys
        155                 160                 165

cag gtg gag aag agt cag aac aaa gcc agg cag tgc aag gac tcg gcc     1002
Gln Val Glu Lys Ser Gln Asn Lys Ala Arg Gln Cys Lys Asp Ser Ala
    170                 175                 180

acc gag gca gag cgg gta tac agg cag agc att gcg cag ctg gag aag     1050
Thr Glu Ala Glu Arg Val Tyr Arg Gln Ser Ile Ala Gln Leu Glu Lys
185                 190                 195                 200

gtc cgg gct gag tgg gag cag gag cac cgg acc acc tgt gag gcc ttt     1098
Val Arg Ala Glu Trp Glu Gln Glu His Arg Thr Thr Cys Glu Ala Phe
                205                 210                 215

cag ctg caa gag ttt gac cgg ctg acc att ctc cgc aac gcc ctg tgg     1146
Gln Leu Gln Glu Phe Asp Arg Leu Thr Ile Leu Arg Asn Ala Leu Trp
            220                 225                 230

gtg cac agc aac cag ctc tcc atg cag tgt gtc aag gat gat gag ctc     1194
Val His Ser Asn Gln Leu Ser Met Gln Cys Val Lys Asp Asp Glu Leu
        235                 240                 245

tac gag gaa gtg cgg ctg acg ctg gaa ggc tgc agc ata gac gcc gac     1242
Tyr Glu Glu Val Arg Leu Thr Leu Glu Gly Cys Ser Ile Asp Ala Asp
    250                 255                 260

atc gac agt ttc atc cag gcc aag agc acg ggc aca gag ccc ccc gct     1290
Ile Asp Ser Phe Ile Gln Ala Lys Ser Thr Gly Thr Glu Pro Pro Ala
265                 270                 275                 280

ccg gtg ccc tac cag aac tat tac gat cgg gag gtc acc ccg ctg acc     1338
Pro Val Pro Tyr Gln Asn Tyr Tyr Asp Arg Glu Val Thr Pro Leu Thr
                285                 290                 295

agc agc cct ggc ata cag ccg tcc tgc ggc atg ata aag agg ttc tct     1386
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Ser Ser Pro Gly Ile Gln Pro Ser Cys Gly Met Ile Lys Arg Phe Ser
            300                 305                 310

gga ctg ctg cac gga agt ccc aag acc act tcg ttg gca gct tct gct     1434
Gly Leu Leu His Gly Ser Pro Lys Thr Thr Ser Leu Ala Ala Ser Ala
        315                 320                 325

gcg tcc aca gag acc ctg acc ccc acc ccc gag cgg aat gag ggt gtc     1482
Ala Ser Thr Glu Thr Leu Thr Pro Thr Pro Glu Arg Asn Glu Gly Val
    330                 335                 340

tac aca gcc atc gca gtg cag gag ata cag gga aac ccg gcc tca cca     1530
Tyr Thr Ala Ile Ala Val Gln Glu Ile Gln Gly Asn Pro Ala Ser Pro
345                 350                 355                 360

gcc cag gag tac cgg gcg ctc tac gat tat aca gcg cag aac cca gat     1578
Ala Gln Glu Tyr Arg Ala Leu Tyr Asp Tyr Thr Ala Gln Asn Pro Asp
                365                 370                 375

gag ctg gac ctg tcc gcg gga gac atc ctg gag gtg atc ctg gaa ggg     1626
Glu Leu Asp Leu Ser Ala Gly Asp Ile Leu Glu Val Ile Leu Glu Gly
            380                 385                 390

gag gat ggc tgg tgg act gtg gag agg aac ggg cag cgt ggc ttc gtc     1674
Glu Asp Gly Trp Trp Thr Val Glu Arg Asn Gly Gln Arg Gly Phe Val
        395                 400                 405

cct ggt tcc tac ctg gag aag ctt tga ggaagggcca ggagcccctt           1721
Pro Gly Ser Tyr Leu Glu Lys Leu
    410                 415

cggacctgcc ctgccagtgg agccagcagt gcccccagca ctgtccccac cttgctaggg   1781

cccagaacca agcgtccccc agccccgaga gggagcctgt cgtctcccag ggaataaagg   1841

agtgcgttct gttcaaaaaa aaaaaaaaa                                     1870


<210> SEQ ID NO 25
<211> LENGTH: 416
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 25

Met Met Pro Gln Leu Gln Phe Lys Asp Ala Phe Trp Cys Arg Asp Phe
1               5                   10                  15

Thr Ala His Thr Gly Tyr Glu Val Leu Leu Gln Arg Leu Leu Asp Gly
            20                  25                  30

Arg Lys Met Cys Lys Asp Met Glu Glu Leu Leu Arg Gln Arg Ala Gln
        35                  40                  45

Ala Glu Glu Arg Tyr Gly Lys Glu Leu Val Gln Ile Ala Arg Lys Ala
    50                  55                  60

Gly Gly Gln Thr Glu Ile Asn Ser Leu Arg Ala Ser Phe Asp Ser Leu
65                  70                  75                  80

Lys Gln Gln Met Glu Asn Val Gly Ser Ser His Ile Gln Leu Ala Leu
                85                  90                  95

Thr Leu Arg Glu Glu Leu Arg Ser Leu Glu Glu Phe Arg Glu Arg Gln
            100                 105                 110

Lys Glu Gln Arg Lys Lys Tyr Glu Ala Val Met Asp Arg Val Gln Lys
        115                 120                 125

Ser Lys Leu Ser Leu Tyr Lys Lys Ala Met Glu Ser Lys Lys Thr Tyr
    130                 135                 140

Glu Gln Lys Cys Arg Asp Ala Asp Asp Ala Glu Gln Ala Phe Glu Arg
145                 150                 155                 160

Ile Ser Ala Asn Gly His Gln Lys Gln Val Glu Lys Ser Gln Asn Lys
                165                 170                 175
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Ala Arg Gln Cys Lys Asp Ser Ala Thr Glu Ala Glu Arg Val Tyr Arg
            180                 185                 190

Gln Ser Ile Ala Gln Leu Glu Lys Val Arg Ala Glu Trp Glu Gln Glu
        195                 200                 205

His Arg Thr Thr Cys Glu Ala Phe Gln Leu Gln Glu Phe Asp Arg Leu
    210                 215                 220

Thr Ile Leu Arg Asn Ala Leu Trp Val His Ser Asn Gln Leu Ser Met
225                 230                 235                 240

Gln Cys Val Lys Asp Asp Glu Leu Tyr Glu Glu Val Arg Leu Thr Leu
                245                 250                 255

Glu Gly Cys Ser Ile Asp Ala Asp Ile Asp Ser Phe Ile Gln Ala Lys
            260                 265                 270

Ser Thr Gly Thr Glu Pro Pro Ala Pro Val Pro Tyr Gln Asn Tyr Tyr
        275                 280                 285

Asp Arg Glu Val Thr Pro Leu Thr Ser Ser Pro Gly Ile Gln Pro Ser
    290                 295                 300

Cys Gly Met Ile Lys Arg Phe Ser Gly Leu Leu His Gly Ser Pro Lys
305                 310                 315                 320

Thr Thr Ser Leu Ala Ala Ser Ala Ala Ser Thr Glu Thr Leu Thr Pro
                325                 330                 335

Thr Pro Glu Arg Asn Glu Gly Val Tyr Thr Ala Ile Ala Val Gln Glu
            340                 345                 350

Ile Gln Gly Asn Pro Ala Ser Pro Ala Gln Glu Tyr Arg Ala Leu Tyr
        355                 360                 365

Asp Tyr Thr Ala Gln Asn Pro Asp Glu Leu Asp Leu Ser Ala Gly Asp
    370                 375                 380

Ile Leu Glu Val Ile Leu Glu Gly Glu Asp Gly Trp Trp Thr Val Glu
385                 390                 395                 400

Arg Asn Gly Gln Arg Gly Phe Val Pro Gly Ser Tyr Leu Glu Lys Leu
                405                 410                 415


<210> SEQ ID NO 26
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe A_44_P1004731

<400> SEQUENCE: 26

ctggcttaca gcttgtttgt tttataactt tacctctctc tgaaaagtct gtaagcaagg     60


<210> SEQ ID NO 27
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe A_42_P592157

<400> SEQUENCE: 27

aaagctttcg gttttgtttt ttaaactgtt tgcagagtgg agaagatcga tcaggaaggg     60


<210> SEQ ID NO 28
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe A_42_P495820
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<400> SEQUENCE: 28

attatgcagg ctatgacgga actactacct tgctatggat gagggttggg caggatttaa 60

<210> SEQ ID NO 29
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe CUST_1_PI195698246

<400> SEQUENCE: 29

gtctcaagaa cagagggcta ccttggggag ccataaagag tgtatttaat aaaacgggct 60

<210> SEQ ID NO 30
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe A_44_P377266

<400> SEQUENCE: 30

aatgaaataa ctaagcatat cttttgagaa ttttattttc ttacatttta aatctgaagg 60

<210> SEQ ID NO 31
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe A_66_P100662

<400> SEQUENCE: 31

tttgtggtcc ctgttcagtc attatgttgt cccttcgctt ctcttgatca gcagaaagca 60

<210> SEQ ID NO 32
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe A_44_P928825

<400> SEQUENCE: 32

gaacgtgtgc acaaagtatc agcagaaatc cagtctgtga aagaagaaca agagcatgtg 60

<210> SEQ ID NO 33
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe A_42_P526140

<400> SEQUENCE: 33

ctcagtgtcc gtgaattggg tatccaagaa catcctgaag ccagaatgtc ttctcagaaa 60

<210> SEQ ID NO 34
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe A_42_P464736

<400> SEQUENCE: 34

aggctgagtt ctccagacca aaagaccatt tggaagttca aagatgtatt tgaggtttgc 60

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<210> SEQ ID NO 35
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe A_43_P20022

<400> SEQUENCE: 35

agctctgagg ctcctgagct cagcacactg gactttggca aaatgactga ccgggaaacg 60

<210> SEQ ID NO 36
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe A_42_P515405

<400> SEQUENCE: 36

atttattcta acttatgcag gggtgcgaga tatgcccccc tgctgtgaca cagatattta 60

<210> SEQ ID NO 37
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe A_43_P21121

<400> SEQUENCE: 37

acctggagac ccactgtcac tggtgatggt gtagccctgc tggtttgggt gatccttgaa 60

<210> SEQ ID NO 38
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe A_44_P180717

<400> SEQUENCE: 38

tggtgtgata aagaggttct ctgggctgct acatggaagt cccaagacca caccttctca 60

<210> SEQ ID NO 39
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe A_42_P602724

<400> SEQUENCE: 39

gtgactacgg gagtggggtg atgagaagct caaaaccgac ttcctttaat caattaacca 60

<210> SEQ ID NO 40
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe A_44_P332606

<400> SEQUENCE: 40

cctggtgagt tggggtcttt ttgacccttg tcacggttcc tccaacaaaa acttgcgcag 60

<210> SEQ ID NO 41
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial

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<220> FEATURE:
<223> OTHER INFORMATION: Probe A_43_P12274

<400> SEQUENCE: 41

aggcagagga gaaggtgaag gcgtaaaaga agacgccagc actgactatg cctgcatcgt 60

<210> SEQ ID NO 42
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe A_44_P421534

<400> SEQUENCE: 42

tttctcagaa tgatgctggg caagagatct gccatcttga gaatgattct gatgtatgag 60

<210> SEQ ID NO 43
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe A_44_P248172

<400> SEQUENCE: 43

ggtttctcct ctatgttgat acagattacc tggattctat atcagaagac gatgagttgt 60

<210> SEQ ID NO 44
<211> LENGTH: 60
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Probe A_43_P13426

<400> SEQUENCE: 44

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<400> SEQUENCE: 47

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<400> SEQUENCE: 48

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<400> SEQUENCE: 56

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<400> SEQUENCE: 58

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<210> SEQ ID NO 59
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<223> OTHER INFORMATION: Primer Ly49i9 R

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<400> SEQUENCE: 75

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<400> SEQUENCE: 76

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<210> SEQ ID NO 77
<211> LENGTH: 24
<212> TYPE: DNA
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1-17. (canceled)

18. A method of predicting the risk of a subject to develop graft versus host reaction (GvHR) or graft versus host disease (GvHD), comprising

(a) determining the expression level of one or more prognostic RNA transcripts, or their corresponding cDNAs, or their expression products, in a sample obtained from said subject, wherein said transcript(s) or expression products is/are the transcript or expression product of one or more genes selected from the group consisting of:

(i) Msr1, Pik3ap1, Pstpip1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Spic, Nfe2, Tnfaip8l2, and Ier3; or

(ii) Msr1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Spic, and Nfe2; or

(iii) Pik3ap1, Pstpip1, Tnfaip8l2, and Ier3;

(b) comparing the expression level of said one or more prognostic RNA transcript, or its corresponding cDNA, or its expression product with a corresponding baseline value; wherein

(i) for every unit of increased expression of Olr1, Msr1, Pik3ap1, and/or Pstpip1; or the corresponding cDNA or expression product, said subject is expected to develop GvHR or GvHD; and

(ii) for every unit of decreased expression of Ctss, Pbx2, Grem1, Ly6g6e, Spr1, Spic, Nfe2, Tnfaip8l2, and/or Ier3; or the corresponding cDNA or expression product, said subject is expected to develop GvHR or GvHD.

19. The method of claim **18**, wherein the expression level is determined by DNA microarray analysis or quantitative PCR and subsequent calculation of the mRNA copy number normalized to the amount of total RNA or to the expression level of one or more housekeeping genes.

20. The method of claim **18**, wherein the expression level of the corresponding expression product(s) is determined by ELISA, Western blotting, protein microarray, immunohistochemistry, flow cytometry or surface plasmon resonance.

21. The method of claim **18**, wherein the sample is a biopsy sample or a sample of Peripheral Blood Mononuclear Cells (PBMC).

22. The method of claim **18**, wherein the subject is a mammal.

23. The method of claim **18**, wherein the subject is a human.

24. The method of claim **18**, wherein the baseline value is the expression level of said at least one gene in at least one healthy subject.

25. The method of claim **18**, further comprising determining the prognostic transcript of one or more genes selected from the group of genes consisting of Ubd, C2, Lst1, Aif1, C1QTNF7, CEACAM4, MME, IGFBP5, Tap1, Ctgf, ANP32A, HCLS1, HTRA1, LGALS7, PTGER2, PTPN7, TGM2, TREM2 and CARD11; or their corresponding cDNAs, or their expression products, wherein

(i) for every unit of increased expression of one or more of Ubd, C2, Aif1, CEACAM4, Tap1, PTGER2, PTPN7, TGM2, TREM2, HCLS1 and/or CARD11; or the corresponding cDNA or expression product, said patient is expected to develop GvHR or GvHD; and

(ii) for every unit of decreased expression of one or more of Lst1, C1QTNF7, MME, Ctgf, ANP32A, HTRA1, LGALS7 and/or IGFBP5; or the corresponding cDNAs or expression product(s), said patient is expected to develop GvHR or GvHD.

26. A method of diagnosing graft versus host reaction (GvHR) or graft versus host disease (GvHD) in a subject following transplantation, comprising:

(a) determining the expression level of one or more prognostic RNA transcripts, or their corresponding cDNAs, or their expression products, in a sample obtained from said subject, wherein said transcript(s) or expression products is/are the transcript or expression product of one or more genes selected from the group consisting of:

(i) Msr1, Pik3ap1, Pstpip1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Spic, Nfe2 Tnfaip8l2, and Ier3; or

(ii) Msr1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Spic, and Nfe2; or

(iii) Pik3ap1, Pstpip1, Tnfaip8l2, and Ier3;

(b) comparing the expression level of said one or more prognostic RNA transcript, or its corresponding cDNA, or its expression product with a corresponding baseline value; wherein

(i) every unit of increased expression of Olr1, Msr1, Pik3ap1, and/or Pstpip1, or the corresponding cDNA or expression product, is indicative of GvHR or GvHD; and

(ii) every unit of decreased expression of Ctss, Pbx2, Grem1, Ly6g6e, Spr1, Spic, Nfe2, Tnfaip8l2, and/or Ier3, or the corresponding cDNA or expression product, is indicative of GvHR or GvHD.

27. The method of claim **26**, wherein the expression level is determined by DNA microarray analysis or quantitative PCR and subsequent calculation of the mRNA copy number normalized to the amount of total RNA or to the expression level of one or more housekeeping genes.

28. The method of claim **26**, wherein the expression level of the corresponding expression product(s) is determined by ELISA, Western blotting, protein microarray, immunohistochemistry, flow cytometry or surface plasmon resonance.

29. The method of claim **26**, wherein the sample is a biopsy sample or a sample of Peripheral Blood Mononuclear Cells (PBMC).

30. The method of claim **26**, wherein the subject is a mammal.

31. The method of claim **26**, wherein the subject is a human.

32. The method of claim **26**, wherein the baseline value is the expression level of said at least one gene in at least one healthy subject.

33. The method of claim **26**, further comprising determining the prognostic transcript of one or more genes selected from the group of genes consisting of Ubd, C2, Lst1, Aif1, C1QTNF7, CEACAM4, MME, IGFBP5, Tap1, Ctgf, ANP32A, HCLS1, HTRA1, LGALS7, PTGER2, PTPN7, TGM2, TREM2 and CARD11; or their corresponding cDNAs, or their expression products, wherein

(i) every unit of increased expression of Ubd, C2, Aif1, CEACAM4, Tap1, PTGER2, PTPN7, TGM2, TREM2, HCLS1 and/or CARD11; or the corresponding cDNA or expression product, is indicative of GvHR or GvHD; and

(ii) every unit of decreased expression of Lst1, C1QTNF7, MME, Ctgf, ANP32A, HTRA1, LGALS7 and/or IGFBP5; or the corresponding cDNA or expression product, is indicative of GvHR or GvHD.

34. The method of claim **26**, wherein the baseline value is the expression level of said at least one gene in said subject prior to said transplantation, or in at least one healthy subject, or in both.

35. A method of monitoring the efficacy of treatment of graft versus host reaction (GvHR) or graft versus host disease (GvHD) in a subject following transplantation, comprising:

(a) determining the expression level of one or more prognostic RNA transcripts, or their corresponding cDNAs, or their expression products, in a sample obtained from said subject at a first time point T1, and a later second time point T2, wherein said transcript(s) or expression products is/are the transcript or expression product of one or more genes selected from the group consisting of:

(i) Msr1, Pik3ap1, Pstpip1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1d, Spr1, Spic, Nfe2, Tnfaip8l2, and Ier3; or

(ii) Msr1, Ctss, Pbx2, Grem1, Ly6g6e, Olr1, Spr1, Spic, and Nfe2; or

(iii) Pik3ap1, Pstpip1, Infaip812, and Ier3;

(b) comparing the expression level of said one or more prognostic RNA transcript, or its corresponding cDNA, or its expression product at time point T1 ($\Delta 1$) and time point T2 ($\Delta 2$) with a corresponding baseline value; wherein

(i) a decline in units of an increased expression of Oki, Msr1, Pik3ap1, and/or Pstpip1; or the corresponding cDNA or expression product at time point T2 in comparison with the increased expression of said at least one gene at the time point T1 ($\Delta\Delta=\Delta 1-\Delta 2$), is indicative of effective treatment of GvHR or GvHD; and

(ii) a decline in units of a decreased expression of Ctss, Pbx2, Grem1, Ly6g6e, Spr1, Spic, Nfe2, Tnfaip8l2, and/or Ier3; or the corresponding cDNA or expression product at time point T2 in comparison with the decreased expression of said at least one gene at the time point T1($\Delta\Delta=\Delta 1-\Delta 2$), is indicative of effective treatment of GvHR or GvHD.

36. The method of claim **35**, wherein the expression level is determined by DNA microarray analysis or quantitative PCR and subsequent calculation of the mRNA copy number normalized to the amount of total RNA or to the expression level of one or more housekeeping genes.

37. The method of claim **35**, wherein the expression level of the corresponding expression product(s) is determined by ELISA, Western blotting, protein microarray, immunohistochemistry, flow cytometry or surface plasmon resonance.

38. The method of claim **35**, wherein the sample is a biopsy sample or a sample of Peripheral Blood Mononuclear Cells (PBMC).

39. The method of claim **35**, wherein the subject is a mammal.

40. The method of claim **35**, wherein the subject is a human.

41. The method of claim **35**, wherein the baseline value is the expression level of said at least one gene in said subject prior to said transplantation, or in at least one healthy subject, or in both.

42. The method of claim **35**, further comprising determining the prognostic transcript of one or more genes selected from the group of genes consisting of Ubd, C2, Lst1, Aif1, C1QTNF7, CEACAM4, MME, IGFBP5, Tap1, Ctgf, ANP32A, HCLS1, HTRA1, LGALS7, PTGER2, PTPN7, TGM2, TREM2 and CARD11; or their corresponding cDNAs, or their expression products, wherein

(i) a decline in units of an increased expression of Ubd, C2, Aif1, CEACAM4, Tap1, PTGER2, PTPN7, TGM2, TREM2, HCLS1 and/or CARD11; or the corresponding cDNA or expression product at time point T2 in comparison with the increased expression of said at least one gene at the time point T1 ($\Delta\Delta=\Delta 1-\Delta 2$), is indicative of effective treatment of GvHR or GvHD; and

(ii) a decline in units of a decreased expression of Lst1, C1QTNF7, MME, Ctgf, ANP32A, HTRA1, LGALS7 and/or IGFBP5; or the corresponding cDNA or expression product at time point T2 in comparison with the decreased expression of said at least one gene at the time point T1($\Delta\Delta=\Delta 1-\Delta 2$), is indicative of effective treatment of GvHR or GvHD.

43. A method of screening for a candidate substance for treatment of graft versus host reaction (GvHR) or graft versus host disease (GvHD), comprising:

(a) monitoring the efficacy of treatment by said candidate substance by using the method according to claim **18** in

(i) a non-human animal model which suffers from GvHR or GvHD and to which the candidate substance has been administered, or

(ii) in an ex vivo model, including but not limited to cell-based and/or tissue-based GvHR or HvHD assay such as the Skin Explant Assay, wherein said cells and/or tissue have been contacted with said candidate substance; and

(b) selecting a candidate substance which shows effective treatment of GvHR or GvHD.

44. The method of predicting the risk of developing graft versus host reaction (GvHR) or graft versus host disease (GvHD) according to claim **18**, or the method of diagnosing GvHR or GvHD according to claim **26**, or a method of monitoring the efficacy of treatment of GvHR or GvHD, comprising the step of using a kit, wherein the kit comprises at least one isolated polynucleotide, wherein each isolated polynucleotide independently comprises

(i) at least 20 contiguous nucleotides of the nucleotide sequence selected from SEQ ID NO: 1, 3, 5, 7, 8, 10, 12, 14, 16, 18, 20, 22, and 24; or SEQ ID NO: 26-47, or

(ii) a nucleotide sequence having at least 90% identity to (i), or

(iii) the coding region of a gene comprising a nucleotide sequence according to (i) or (ii), or

(iv) a nucleotide sequence that can specifically hybridize, under conditions of high stringency, to a polynucleotide having a nucleotide sequence according to (i), (ii) or (iii); and

wherein the kit comprises no more than 9000 isolated polynucleotides in total.

45. The method of claim **44**, wherein the isolated polynucleotides comprise at least 25 contiguous nucleotides.

46. The method of claim **44**, wherein the isolated polynucleotides are arranged in an array.

* * * * *