Microsatellite scanning of the Immunogenome for Associations with Graft-versus-Host Disease following Haematopoietic Stem Cell Transplantation

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(PhD)

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Candidate's Declaration

I, Christian Harkensee, hereby certify that this thesis has been written by me, that it is the record of work carried out by me (unless stated otherwise) and that it has not been submitted in any previous application for a higher degree.

Newcastle, July 2012 Christian Harkensee

Dedicated to the memory of

Akira Sasaki

Without whom this work would never have been undertaken.

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The work described in this thesis is exclusively my own, unless stated otherwise.

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Publications

The work described in this thesis has been published in part.

Peer-reviewed journal publications

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Conference abstracts

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Abstract

Non-HLA gene polymorphisms contribute to the immune response, leading to complications of haematopoietic stem cell transplantation (HSCT). A systematic approach using 4,321 microsatellite (MS) markers typing for 2,909 immune response genes (‘immunogenome’) on pooled DNA of 922 Japanese donors and recipients of HSCT was used to identify recipient and donor risk loci for graft-versus-host disease (GVHD).

Splitting the population into discovery and confirmation cohorts (460/462 pairs), DNA pools were created for a 2-step pooled DNA screening. Fisher’s exact test for 2x2 (each MS allele) and 2xm Chi Square tests were performed, comparing allele frequencies of recipient/donor pools with GVHD grade 0-1 with those of GVHD grade 2-4.

The independent, 2-step pooled DNA screening process has effectively reduced false-positive associations. In the final pooled DNA analysis, 17 (recipient) and 31 (donor) MS loci remained associated with risk or protection from GVHD and were further investigated by individual genotyping in the combined cohorts.

Ten of these loci were confirmed to have consistent associations with GVHD; of these, two associations remained when applying multiple testing correction and multivariate statistics: D6S0035i (MAPK14, *p*=0.00035, OR=0.68) and D1S0818i (ELTD1, *p*=0.000078, OR=1.52).

These findings implicate important new immunoregulatory genes with the process of moderate to severe acute GVHD. These data show that genetic susceptibility to GVHD following HSCT is complex and depends on multiple recipient and donor risk loci. Large-scale genomic screening with microsatellites on pooled DNA, here described for the first time in a HSCT population, is a useful method for the systematic evaluation of multigeneic traits.

List of Contents

Introductory Material

References

Appendices

Supplementary Material

List of Tables

Page

Chapter 1

Chapter 2

Chapter 3

Chapter 4

Chapter 5

List of Figures

Page

Chapter 2

Chapter 4

Chapter 5

Appendices

Page

Chapter 2

Chapter 3

Chapter 4

Supplementary Material

(supplied on a data disk attached to back of thesis)

Chapter 1

Supplementary file 1.1.	**List of 248 gene association studies**

Chapter 2

Supplementary file 2.1.	**JMDP registry analysis and cohort design**
Supplementary file 2.2.	**Statistical Power estimation**
Supplementary file 2.3.	**Construction of final study cohorts and their characteristics**
Supplementary file 2.4.	**Immunogenome gene list**
Supplementary file 2.5.	**Target genes and MS markers**
Supplementary file 2.6.	**Test marker results**

1. INTRODUCTION

1.1. Haematopoietic Stem Cell Transplantation and Graft versus Host Disease

Graft versus Host Disease (GVHD) and its consequences remain the single most important contributor to morbidity and mortality in patients following haematopoietic stem cell transplantation (HSCT). Despite progress made in Human Leukocyte Antigen (HLA) matching, and the use of pharmacologic immunosuppression as GVHD prophylaxis after myeloablative transplantation, moderate to severe acute GVHD (grades II-IV) occured in 25% to 60% of matched related donor transplant recipients, and up to 45% to 70% in unrelated donor recipients (Horowitz, 2004, Andre-Schmutz et al., 2002, Grewal et al., 2003, Laughlin et al., 2001, Morishima et al., 2002). The unpredictability of occurrence and severity of GVHD is the main obstacle today that prevents the wider application of HSCT.

The first successful human bone marrow transplant (BMT) was performed 1959 by Thomas in the US on a patient with leukaemia, using syngeneic bone marrow from his identical twin (Thomas et al., 1959) .

The history of BMT began with the work of Jacobson and Lorenz in the early 1950's, demonstrating that infusion of marrow or spleen cells could 'rescue' mice after a lethal radiation dose (Jacobson et al., 1949, Lorenz et al., 1951).

Later in the 1950's, van Bekkum and De Vries established murine models that provided fundamental knowledge of the biology of marrow transplantation (van Bekkum and De Vries, 1967). Billingham was the first to describe a condition that was initially termed 'Secondary Disease' (because it occurred after successful engraftment), 'runt disease' or 'wasting disease', and later re-named 'Graft-versus-Host Disease', after it became clear that this was an immunological reaction of donor T-cells against host tissues (Billingham and Brent, 1959). In 1957, Uphoff (Uphoff,

1957) was the first to suggest a genetic cause for the graft-versus-host reaction in allogeneic transplants.

In 1958, a first classification of HLA groups as the most important marker of an individuals biological identity was established (van Rood et al., 1958, Dausset, 1958). The capability of the immune system to generate antibodies against antigens on the leukocyte surface was already described in 1954 (Miescher and Fauconnet, 1954). Dausset demonstrated that MHC (Major Histocompatibility Complex) genes (which encode for HLA) were required for the presentation of peptide antigens to T-cell receptors, playing an important role in transplant immunology. In humans, the MHC cluster on chromosome 6 was identified as the coding region for HLA. Further research lead to the detection of the different gene loci (HLA A,B,C,DR, DP, DQ) and a large number of HLA alleles (Shiina et al., 2004). Two main pathways of antigen recognition were detected: A direct response, in which CD8+ cytotoxic T-cells interact with HLA, and an indirect response in which CD4+ T-cells are activated to induce a delayed-type hypersensitivity reaction, cell-mediated toxicity and alloantibody production. Major events were the discovery of the role of lymphocytes and the thymus in the ontogeny of the immune system (1961), the delineation of the human MHC (1963), distinction of B/T-cell subsets (1968) and demonstration of the MHC restricted nature of the adaptive immune response (reviewed in: (Thomas, 1994).

In the 1960’s, studies in canine models laid the foundations for conditioning regimens, GVHD prophylaxis and genetic matching. Observations included that total body irradiation (TBI) did not cure leukaemia nor did it prevent GVHD or bone marrow recovery. HLA mismatch was likely to result in rejection or GVHD, and methotrexate was introduced as an immunosuppressive agent (Thomas et al., 1962). By the end of the 1960’s, the supportive care had also seen significant improvement.

The increasing knowledge of histocompatibility lead to a renewed interest in allogeneic transplantation, using fully or partially matched siblings as donors. While some success was achieved in the transplantation of patients with immunodeficiency (Gatti et al., 1968), the initial results of BMT for leukaemic patients were not encouraging (Thomas et al., 1975a, Thomas et al., 1975b). The reason for this was thought to be patient selection: BMT was seen as a ‘last resort’ for patients with advanced disease, or after multiple chemotherapy failures. A small percentage of patients, however, achieved long-term cure, indicating that BMT had the potential to cure even very advanced disease. Outcome for leukaemic patients improved greatly from the late 1970’s onwards after the introduction of transplantation after first remission, or in early first relapse (Thomas et al., 1979a, Beutler et al., 1979). The increased use of allogeneic bone marrow lead to the first bone marrow donor registries (UK 1975, US 1984).

Transplant conditioning regimens, given as an immunosuppression and for tumour eradication, had come a long way from the early, simple TBI regimen to the reduced intensity conditioning (RIC) regimens of today. Observations with TBI, as well as cyclophosphamide (CY) as single therapies in the 1950’s and 1960’s were such that leukaemia relapsed rapidly after transplantation. The combination of TBI and CY lead to the first observed long term remissions in the mid 1970’s (Thomas et al., 1975a, Thomas et al., 1975b). Introduction of newer chemotherapeutic agents such as busulphan, and fractioned irradiation have reduced toxicity and improved survival. Nevertheless, these myeloablative regimens proved still far too toxic for elderly patients or those with co-morbidities, in which transplant-related mortality (TRM) would reach unacceptable high levels. The last two decades have opened up transplant opportunities for this age and risk group by the development of RIC regimens (Koh and Chao, 2008).

Whilst immunosuppressive regimens achieved far-reaching control of transplant rejection, GVHD and its consequences remained the single most important complication of stem cell transplantation. Studies in animal models and observations in human patients clarified important checkpoints in the pathophysiology of GVHD (Korngold and Sprent, 1978, Shlomchik, 2007). In the 1980’s, even with HLA matched sibling donors up to 50% of recipients developed GVHD. In the 1960's and 1970's, methotrexate and steroids were first used for treatment, later for prevention with only limited effect (Thomas et al., 1979b). The introduction of cyclosporin A, an inhibitor of T-cell activation and proliferation, in 1980, used in combination with a short course of methotrexate, resulted in improved prevention of GVHD (Deeg et al., 1982). T-cell depletion, first described in the early 1980's (Martin et al., 1985), was found to prevent GVHD, however, at the expense of the loss of the GVL (Graft versus Leukaemia) effect, risk of graft failure and delayed immunologic recovery. Newer agents used in prophylaxis include Tacrolimus and Sirolimus, believed to be more potent in blocking T-cell proliferation, and Mycophenolate Mofetil, active against both T-cells and B-cells.

Over the last two decades, improved techniques of molecular genetics replaced the HLA serum typing with genotyping, allowing for matching at individual allele level, further reducing the incidence of GVHD (Little, 2007). Advanced molecular techniques also permitted the identification of minor histocompatibility antigens (mHags), which play an important role in otherwise fully HLA-matched transplants (Goulmy, 2006). The process of GVHD also seemed to be modified by polymorphisms in immunoregulatory genes (Mullighan and Bardy, 2007). Presence of active infection represented a risk factor for GVHD, while in turn GVHD (and its treatment) produced profound immune suppression, increasing the risk of infection.

The concept of the GVL effect was first pointed out in the 1950's (Barnes et al., 1956), and observed in mouse experiments during the 1960's. It was first described in human patients in the mid-1970's when it became apparent that patients with GVHD had a reduced risk of leukaemia relapse (Weiden et al., 1979). Around the same time, animal experiments demonstrated that the GVL effect could be separated from GVHD (Bortin et al., 1979). The introduction of post-transplant donor lymphocyte infusions (DLI) in the second half of the 1980's was the first established method with the aim to enhance the GVL in patients with haematological and other malignancies. The potential of DLI to induce long-lasting remission was demonstrated, however, at the expense of increased GVHD and prolonged bone marrow suppression (Kolb et al., 1990).

Current directions in progress in BMT can be described as four big areas. Firstly, there is continuing improvement in supportive care, anti-infectious therapy, and reduction of toxicity of induction regimens. Secondly, the study of clinical and genetic (HLA and non-HLA) risk factors may lead to a more reliable prediction of transplant complications. Thirdly, separation of GVL from GVHD and fourthly, enhancement of immune reconstitution, could be summarized under the term 'Adoptive Immunotherapy'. Some methods applied, amongst others, include in vivo and in vitro tumor-specific alloimmunization, the use of immunomodulatory cells (T-regulatory cells, dendritic cells, Mesenchymal stem cells), cytokines, growth hormones, non-specific immune regulators and monoclonal antibodies to suppress GVHD, enhance GVL and stimulate the reconstitution of a healthy immune function. With GVHD being the major hurdle of the application of HSCT for other indications, advances in its control are likely to expand the future role of HSCT.

SUMMARY

- **The history of HSCT spans five decades, during which the procedure has become more effective and safe.**
- **Progress in timing, genetic matching, conditioning regimen, GVHD prophylaxis and clinical care has widened the applicability and indications of HSCT**

1.2 Pathophysiology and pathobiology of GVHD

1.2.1. Overview

Pathophysiologically, GVHD involves the recognition of target tissues as being foreign by immunocompetent donor cells, resulting in the induction of an inflammatory response. Acute GVHD has been described in three different phases: (I) presence of a profoundly damaged host milieu prior to contact with donor tissue, characterized by excessive endo- and epithelial damage due to preparing chemotherapy regimes, irradiation, damaged and dying malignant cells and infections, (II) donor T cell activation by host antigen-presenting cells (APC), and (III) the inflammatory response consisting of activation of donor cytotoxic T cells, natural killer cells (NKC) and monocytes. Cytokine toxicity and viral and bacterial infections also contribute to the inflammatory response (Ferrara and Levine, 2006, Ferrara et al., 1999).

1.2.2. GVHD phase 1: Preceding tissue damage, pre-transplant conditioning, and activation of antigen-presenting cells

Preceding local tissue damage

The damage to recipient tissues caused by conditioning regimens and previous chemotherapy or radiation, the underlying malignancy, and concurrent infections had a major impact on the incidence and severity of acute GVHD (Xun et al., 1994, Perez-Simon et al., 2005, Couriel et al., 2004, Gratama et al., 1987). The local micro-environment of inflammatory mediators determined the degree and specificity of APC activation, and subsequently, induction of naïve T-cells. An important mechanism appeared to be the increased cytokine secretion in the local environment, leading to increased expression of adhesion molecules and MHC, increased antigen presentation by APC, increased antigen recognition by T cells, and subsequently increased T cell activation and proliferation. TNF, IL1 and IL6 were the most important cytokines involved in stimulating local tissue inflammation in GVHD (Nestel et al., 1992, Imamura et al., 1994, Remberger et al., 1995, Cooke et al., 1998)

Tissue insults by toxic effects of chemotherapeutics, irradiation, dying diseased cells, or infection with bacterial, viral, fungal or protozoal pathogens, were causing a mixed pattern of cells either weakened by stress, or cell apoptosis and cell necrosis with disruption of tissue architecture. Those tissues which were environmentally exposed, or rapidly dividing and renewing, such as the epithelia of the liver, intestinal tract and skin, were the most vulnerable.

There is evidence that the initial immune response to the tissue damage were triggered by endogenous stress or danger signals, powerful enough to induce activation of local APC in a paracrine fashion (Lotze et al., 2007, Skoberne et al., 2004, Gallucci et al., 1999, Gallucci and Matzinger, 2001). In contrast to pathogen-associated proteins, which induce a specific immune response, endogenous proteins from injured tissue represented a potentially unlimited source of self-antigen. While apoptotic cells were engulfed in quiescence and their antigens presented to T-cells without co-stimulation, hence inducing tolerance; proteins from necrotic cells presented as antigens lead to T-cell activation (Shlomchik, 2007). Nevertheless, a mouse model (Teshima et al., 2002) demonstrated that alloantigen presentation on host epithelium was not a requirement for acute GVHD, but that GVHD could be abrogated by TNFα blockade, supporting the notion of the importance of the cytokine micro-environment.

Activation of host APC

The first circle of augmentation of the pro-inflammatory response occurred still in the injured tissue itself. When local APC became activated, they secreted further pro-inflammatory cytokines like tumour necrosis factor alpha (TNFα), interleukin 1 (IL-1), granulocyte-macrophage stimulating factor (GM-CSF) and Interferon gamma (IFNγ) (Ferrara et al., 1999), which in turn recruited more epithelial cell and APC for cytokine secretion. Increased cytokine concentrations eventually reached systemic circulation, providing a powerful chemoattractant stimulus. Increased cytokine expression stimulates the excretion of chemokines and their receptors, which had an important role in dendrictic cell (DC) activation and maturation, as well as CD8+ T-cell homing to GVHD target tissues (New et al., 2002, Mapara et al., 2006). This micro-climate, in turn, attracted and activated DC and other antigen-presenting cells and broke the ground for mature donor T-cells, which after transplantation recognised increasingly expressed MHC molecules and/or mHags (Matzinger, 2002).

The consequences of tissue damage and subsequent immune system activation were even more imminent in the intestinal mucosal surface. Here, local TNFα secretion negatively affected the surface integrity (Laster et al., 1988), enhancing the potential injuries caused by intramucosal displacement of bacterial endotoxins and lipopolysaccharides (LPS), which could potentiate even further the pro-inflammatory cytokine production by gut-associated macrophages and lymphocytes (Nestel et al., 1992). The intestinal Peyer's Patches (PP) had been identified as a key lymphoid compartment for the development of acute GVHD (Murai et al., 2003) by demonstrating that acute GVHD was abrogated in mice which were PP-deficient or whose T-cell homing had been interrupted by C-chemokine receptor 5 (CCR5) -blockade; suggesting that GVHD induction was determined by the local inflammatory environment, rather than tissue-specific mHags. On the other hand, PP were redundant, hence T-cells primed elsewhere in the body were capable of inducing intestinal GVHD (Welniak et al., 2006).

APC were either tissue-specific and residing (e.g. Langerhans' cell in skin, Kupfer cell in liver) or circulated through the body's blood and lymphoid system in their naïve and immature form. Their key function for the adaptive immune system was their capability of inducing a specific, adaptive immune response by presenting a specific antigen to naïve or memory T-cells through their MHC receptor. DC, the most important APC in GVHD induction, could be activated in a specific (antigen, foreign-recognition) or non-specific (micro-environmental stimuli, danger recognition) manner. The antigen was internalised and processed in endolysosomes to peptide which was loaded onto MHC molecules. Physiologically, immature DC relentlessly sampled endogenous antigen, which was presented to T-cells rendering those tolerant to self-antigen.

Antigen recognised as ‘non-self’, however, lead to DC maturation and antigen presentation to T-cells accompanied by appropriate co-stimulatory signals. DC were able to suppress the response of T-regulatory cells, and control the blood flow to the lymph node into which they home. In the lymph node, the matured DC interacted with naïve or memory CD4 T-cells through the MHC/T-cell receptor (TCR) ‘immunological synapse’, resulting in effective activation and proliferation of an antigen-specific T-cell clone (Lee and Iwasaki, 2007).

It was thought that in early GVHD, tissue antigen was presented to the infused donor T cells by host DC which were critical, and sufficient, to induce a GVHD response (Shlomchik et al., 1999, Duffner et al., 2004). Host Langerhans cells in the skin had been shown to be critical mediators of skin GVHD (Merad et al., 2004). Antigen presentation by host APC to donor T-cells, also called direct recognition, was the predominant mode of allorecognition in the MHC mismatched transplant setting (Ruggeri et al., 2002).

Removal of APC from their specific organ could potentially abrogate GVHD in the same organ (Zhang et al., 2002b). The same authors suggested that host APC localised in specific target organs recruited mature donor T-cells, while DC and macrophages homed to lymph nodes and other secondary lymphoid organs were critical for the activation of a cytotoxic CD8+T-cell response.

Of the different subsets of APC, DC probably was the most critical one in the development of GVHD, supported by its role as the most important ‘professional’ APC, and also by observation in experimental GVHD settings (Duffner et al., 2004, Zhang et al., 2002a).

APC regulation in the context of GVHD is not fully understood. TBI as part of an HSCT conditioning regimen, in combination with G-CSF exacerbated APC activation (Morris et al., 2009), while γδ T-cells, host Natural Killer T-cells (NKT), natural killer (NK) cells and B cells reduced activation (Paczesny et al., 2009a).

1.2.3. GVHD phase 2: Activation of donor T-cells

Activated host APC relocated into secondary lymphoid organs, where following HSCT they met donor T cells. Donor T-cells recognized antigen presented by host APC (foreign antigen or the host MHC receptor itself - direct presentation) or donor APC (recognition of the foreign antigen - indirect presentation) (Shlomchik, 2003, Sayegh and Carpenter, 1996). Donor T-cells required co-stimulation of their T-cell receptor in the binding to the MHC receptor of the APC in order to become activated (Appleman and Boussiotis, 2003), with CD28, ICOS, CD40, OX40 (activation) and CTLA4 (inhibition) being the most important co-stimulatory molecules (Paczesny et al., 2009a).

Different subsets of T-cells had varying roles in induction of GVHD. The two main subsets, CD4+ and CD8+ T cells were both capable of inducing GVHD. In the absence of HLA mismatch, this potency was determined by host mHags which could lead to specific T-cell clones in either CD4+ or CD8+ subset (Goulmy, 2006, Wu and Ritz, 2006). Selective elimination of either subset from grafts did not lead to a reduction in GVHD, and research on selecting specific antigeneic clones for elimination is ongoing (Bondanza et al., 2006).

Naïve donor T-cells (CD62L+ CD44+) also had the potential of inducing GVHD (Anderson et al., 2003). Non-alloreactive donor memory T-cells (CD62L-) did not induce GVHD, but were able to mediate GVL effects through memory transfer (Zheng et al., 2008). Alloreactive donor T-cells, however, were a main cause of GVHD (Zhang et al., 2005).

Regulatory T-cells (Treg) had been the focus of more recent research. Several studies had demonstrated that Treg are capable of suppressing the expansion of activated donor T-cells, and therefore reduce the risk of GVHD, whilst preserving GVL reactions (Yan and Da, 2006, Salomon et al., 2006, Ruggeri et al., 2002). Host and donor NKT also had GVHD-reducing properties (Pillai et al., 2007), by shifting cytokine responses to a T-helper type 2 (Th2) profile (Lowsky et al., 2005), or eliminating host APC (Morris et al., 2005).

In the late 1980's it was discovered that following activation subsets of mainly CD4+ T-cells had antagonistic cytokine excretion profiles, described as Th1 (T-helper type 1) and Th2 (T-helper type 2) cells (Mosmann et al., 1986). Th1 cells secreted pro-inflammatory cytokines like IL2 (interleukin 2), TNF, IFNγ (interferon gamma), while the Th2 (T-helper 2 cell) had anti-inflammatory properties, secreting cytokines like IL4 (interleukin 4) and IL10 (interleukin 10). These phenotypes followed each other over time (in the initial phase of an inflammatory reaction, the response was predominantly pro-inflammatory, followed by an anti-inflammatory response to counteract and prevent excessive inflammation). There is good evidence that genetic polymorphisms resulting in over- or under-expression of certain cytokines could tilt this balance to either a more pro-inflammatory or an anti-inflammatory response (see below). In Phase 2, donor T cells stimulated by APC secrete IL2 and IFNγ (Mosmann et al., 1986), which was central in the control and amplification of the immune reaction against the foreign antigen. IFNγ primed macrophages to produce and secrete IL1 (interleukin 1) and TNF (Nestel et al., 1992), induced the skin and gut pathology of GVHD (Dickinson et al., 1991), and impaired T-lymphocyte function (Huchet et al., 1993). The levels of IFNγ were predictive of GVHD severity (Tanaka et al., 1994). This could be described as a Th1-type response, promoting GVHD. On the other side, Th2-type cytokines like IL4 and IL10 had antagonistic effects on IL2 and IFNγ secretion (Seder and Le Gros, 1995), dampening down reactions leading to acute GVHD and 'shifting' the immune response towards chronic GVHD (Krenger and Ferrara, 1996). Nevertheless, the biology of cytokines in GVHD is likely to be more complex, as opposing effects of the same cytokine (e.g. IL2 or IFNγ) had been observed, depending on factors like timing, concentration and tissue location (Wang et al., 1995, Krenger et al., 1996, Baker et al., 1995, Yang et al., 1998, Brok et al., 1997). Sun et. al. (Sun et al., 2007) postulated that "early Th1 polarization of donor T-cells and Th1 cytokines are critical for GVHD induction, whereas inadequate production could modulate acute GVHD through a breakdown of negative feedback mechanisms for activated T-cells".

IL17 (interleukin 17) Th-cells were a more recently described subset of CD4+ T-cells, characterized by the production of IL17. Their role in GVHD remained controversial (Sun et al., 2007, Paczesny et al., 2009a), as studies had shown that IL17 deficient T- cells enhanced Th1 skewing augmenting acute GVHD, whereas Th17 cells caused severe GVHD *in vitro*.

1.2.4. GVHD Phase 3: Effector phase

Once activated donor T-cells migrate from secondary lymphoid tissue into target organs, where they cause tissue damage. Potentially any organ is capable of expressing alloantigen and therefore to become a target organ for GVHD, however, skin, gut, liver and thymus are the most commonly affected target tissues.

Recent studies have shed some light onto mechanisms that control the ‘homing’ of alloreactive T-cells into their target tissues. Chemokines appeared to be one of the key players. Inflammatory chemokines were expressed by a wide variety of tissues and cells (endothelial cells, fibroblasts, DC, monocytes, NK cells and T-lymphocytes) and regulated trafficking of donor T-cells towards the lymphoid organs where they interacted with APC, as well as target tissues (reviewed in: (Wysocki et al., 2005). Activated T-lymphocytes expressed chemokine receptors which, at least in part, determined their destination by homing to tissues where the according ligands were expressed (e.g.: liver: receptors CXCR3, CCR2, CCR5, ligands: CXCL9/10/11, CCL2/3; gut: receptors CXCR3, CCR9, ligands CXCL9/10/11, CCL25; skin: receptors CXCR3, ligands CXCL9/10/11, CCL2/5/17).

Other mechanisms of T-cell trafficking included selectins and integrins (also reviewed in (Wysocki et al., 2005). E, P and L-selectin were expressed in various tissues including on cells of the myeloid and lymphoid system, and found their ligands, the peripheral node addressins (PNAds) expressed in chronically inflamed tissue. Integrins were transmembrane proteins expressed on immune cells which interacted with molecular structures in tissues that lay exposed due to tissue damage (e.g. collagen, laminin, fibronectin) or specific expressed ligands like adhesion molecules (MADCAM1, VCAM1, ICAM). Expression of MADCAM1 and ICAM1, for example, was critical for induction of acute GVHD in the PP of the intestine and in the liver.

Donor T-cells exerted their deleterious effect on target tissues by direct cytotoxicity (van den Brink and Burakoff, 2002) using different pathways of apoptosis. CD4+ cytotoxic T-lymphocytes (CTL) applied mainly the Fas-FasL (TNF-receptor superfamily member 6) pathway (Via et al., 1996). Fas is widely expressed, its expression is inducible by TNF and IFNγ and therefore enhanced in inflamed tissues. The same cytokines enhanced FasL expression on CTL, hence this mechanism appeared to be a self-augmenting cycle of tissue damage, inflammation, CTL recruitment and apoptosis. CD8+ CTL worked preferentially through the perforine-granzyme pathway. Perforin is secreted by the CTL causing pores in the target cell membrane. This allows granzyme to enter and induce a cell-death sequence. In experimental GVHD, survival was better in peforin/granzyme deficient mice, but the cytotoxic effect was less pronounced than for Fas/FasL (Graubert et al., 1997). Experimental studies for both pathways, by inactivating important components, had shown that GVHD can be abrogated or delayed in onset (reviewed in: (Sun et al., 2007)).
Other apoptosis mechanisms include TRAIL (TNF-related apoptosis-inducing ligand) (Pan et al., 1997), TWEAK (TNF-like weak inducers of apoptosis) and LTβ/LIGHT pathways (Brown et al., 2005).

Much of the tissue damage of the effector phase of GVHD could be attributed to an excessive release of pro-inflammatory cytokines, the so-called ‘cytokine storm’. Local tissue damage, due to conditioning or infection, induced APC activation through TLR and non-TLR pathways, and caused chemoattraction to macrophages, which in response secreted TNF and IL1 (Antin and Ferrara, 1992). These cytokines could significantly augment T-cell activation, which in turn stimulated TNF, IL1 and IFNγ secretion from an array of immune cells. In that sense, the degree of priming of immune cells determined the severity of GVHD. In contrast, tissue damage in itself without the interaction of CTL was capable of inducing GVHD damage (Teshima et al., 2002).

TNF was the most important cytokine in the effector phase (Reddy and Ferrara, 2003). It had synergistic and pleiotrophic effects, causing cachexia, induce APC maturation, recruited T-effector cells, neutrophils and monocytes, and primed homing by chemokine induction. TNF could also cause direct tissue damage by inducing apoptosis and necrosis, and could activate T-cells directly through the receptors TNFR1 (TNF receptor 1) and TNFR2 (TNF receptor 2).

Other effector molecules that had been studied include IL1 and nitric oxide (NO). IL1 had effects very similar to TNF, but might be more organ specific to spleen and skin (Abhyankar et al., 1993). NO is a product of activated macrophages that caused direct tissue insult, and inhibited repair mechanisms. Development of GVHD correlated with levels of oxidation products of NO (Nestel et al., 2000, Weiss et al., 1995).

More recently, larger studies of protein components, genetic expression and genetic polymorphism were aiming to dissect the pathobiology of GVHD further and identifying molecules (biomarkers) that could predict GVHD (Hansen, 2008, Kaiser et al., 2004, Mohty et al., 2007, Paczesny et al., 2008, Srinivasan et al., 2006, Weissinger and Dickinson, 2009).

SUMMARY

- **GVHD is the most important cause of adverse outcome of HSCT and remains largely unpredictable.**
- **Host antigen recognition by donor T-cells is the key step in the induction of GVHD.**
- **However, modulation of this process is very complex and involves pathophysiological events before, during and after T-cell activation.**

1.3. The Genetics of HSCT

1.3.1. Self/non-self genetics

Human Leukocyte Antigens (HLA)

The HLA complex is the strongest known determinant of self/non-self recognition. Six HLA loci are now commonly used for donor/recipient matching: HLA-A, B, C (HLA class I) and HLA-DRB1, DQB1 and DPB1 (HLA class II). Disparity between donor and recipient HLA antigens results in either rejection of the graft (host-versus-graft reaction), or cellular toxicity of the graft against the host (GVHD and GVL).

Well into the 1980’s, HLA matching was based on serologic typing at antigen level. Observations from this time (Kernan et al., 1993) showed that unrelated HSCT had a higher prevalence of GVHD and worse survival, compared to related HSCT.

The introduction of DNA-based high resolution typing since the 1990’s did contribute a great deal to the understanding of HLA matching. More than 2,000 different alleles had been identified within HLA class I and II (Shiina et al., 2009), and large scale registry studies, primarily in the US and Japan, had analysed the effects of different mismatch combinations in unrelated HSCT. For the US registry (Petersdorf et al., 1998), the first high-resolution data showed that in fact 47% of serologically matched HSCT (HLA-A, B, C, DRB1, DQB1) had one allele level mismatch, and 25% had 2 mismatches. Combined mismatches in HLA class I and class II significantly increased the risk of severe GVHD and death. Single class II, but not class I mismatches increased the risk of GVHD. HLA-DRB1 mismatch was the strongest predictor of GVHD. The first data of high-resolution typing from Japan were published in the same year (Sasazuki et al., 1998), coinciding with the US data that combined HLA class I and II mismatches carry the highest risk for GVHD and death. However, single class II mismatches did not increase the GVHD risk, whereas HLA-A mismatch had the strongest association with GVHD and death. HLA-C mismatch was also associated strongly with GVHD, but not with survival risk. These data were expanded in 2002 (Morishima et al., 2002), showing that single mismatches in any of HLA-A, B, C, DRB1 implicated a higher risk of GVHD, with multiple class I mismatches, in particular involving HLA-C, resulting in the highest risk. HLA-A and/or B mismatches increased the risk of death, with combined mismatches of HLA-A or B + HLA-C + HLA-DRB1 or DQB1 showing the poorest survival.

Updates on the US registry confirmed a high GVHD risk for a single or combined HLA-A mismatch, and worse survival with single or combined HLA-A, B, C and DRB1 mismatches (Flomenberg et al., 2004). Conversely, allele-level HLA-A, B, C and DRB1 matching had the best survival, while even a single mismatch of any of those had a measurable effect on survival (Lee et al., 2007). As in previous studies, no effect of HLA-DQB1 and DPB1 was found.

The Japanese registry has recently advanced into identifying individual GVHD high-risk allele mismatch pairs (Kawase et al., 2007), assuming that not all mismatches would actually induce alloreactivity. This study found 29 high-risk allele mismatch combinations in HLA-A, B, C, DRB1 and DPB1. Following on from this work, high risk and low risk mismatch combinations for relapse of haematological malignancies were identified and correlated with high-risk GVHD allele mismatches. Eight mismatch combinations in HLA-DPB1 and HLA-Cw were found that have a very low relapse risk and no increased GVHD risk, elucidating the HLA-basis of the GVL effect (Kawase et al., 2009). The Japanese registry was also the first to describe highly conserved HLA haplotypes and their association with risk or protection from GVHD (Morishima et al., 2010)

Other self/non-self genetics: KIR, LILR, mHags

Killer immunoglobulin-like receptors (KIR) are cell surface receptors on NK cells. Their function is to recognize normal MHC class I receptor expression on cells, hence normal MHC expression leads to inhibition of NK cell activity whereas an abnormal expression (‘missing self’) releases the inhibition and results in killing of the target cell by an apoptotic signal. KIR are highly polymorphic. In mismatched related HSCT for leukaemia, this effect (termed the KIR ligand mismatch) could be exploited for a graft-versus-tumour effect without a higher risk of GVHD (Ruggeri et al., 2007, Leung et al., 2004). However, for the unrelated HSCT setting the data were more controversial. Yabe et. al. (Yabe et al., 2008) and Morishima et.al. (Morishima et al., 2007) had described the effects of HLA and KIR matching for the Japanese registry. These data show that KIR2DL ligand mismatch in the GVHD direction increased the risk for GVHD and mortality, but dependent on HLA matching, underlying malignancy and administration of ATG.

Leukocyte immunoglobulin-like receptors (LILR) have a wider distribution as compared to KIR, but also recognize MHC class I molecules (Sloane et al., 2004). As KIR, LILR are predominantly inhibitory and also highly polymorphic. They had a role in controlling the maturation of DC (Young et al., 2008), and so far unpublished data from the Japanese registry showed associations of LILR with GVHD and survival (verbal communication Toshio Yabe, Kouyuki Hirayasu).

Non-HLA recipient proteins that resulted from gene polymorphisms that were disparate between donor and recipient represented Minor Histocompatibility Antigens (mHags) (Spencer et al., 2010). Donor T-cells recognized such antigens and responded with clonal expansion. If a mHag happened to derive from a malignant protein or cell, the donor T-cell response could exert a strong and specific graft-versus tumour effect, which could be beneficial (Goulmy, 2006). However, if the mHag derived from otherwise healthy tissue, severe GVHD could be the result. In theory, the potential number of mHags could be as vast as the polymorphic disparity between donor and recipient (Brickner, 2006), however, only few mHags induced donor T-cell responses (immunodominance) for reasons that are not fully understood. Experimental matching for known mHags did not result in reduction of GVHD (Warren, 2009). Gene polymorphisms on the Y-chromosome of male recipients of female grafts were potentially a source of many mHags, and several have been identified; female into male HSCT had been recognized as having a higher risk of GVHD and mortality (Randolph et al., 2004).

More recent efforts had attempted to capture mHags with genome-wide approaches (Hansen et al., 2010, Ogawa et al., 2008, Kawase et al., 2008).

1.3.2. Non-HLA genetics

Non-HLA genetics in HSCT is defined as the effect of functional gene polymorphisms that impact on outcome by modulating existing immune or metabolic responses, rather than having direct involvement in self/non-self recognition. HSCT outcomes like acute and chronic GVHD, relapse and survival are not rare events and vary between individuals who may otherwise be genetically similar; possibly comparable to how phenotypes of inflammation, infection and immunity vary in a normal population. It was therefore assumed that the non-HLA genetic effects on HSCT outcome were determined by common genetic variants.

Studies that were aiming at understanding the pathophysiology of GVHD (see above) had identified several immunoregulatory key players, like e.g. cytokines, adhesion molecules, regulators of innate immunity and chemokines. The first such study was published in 1998, implicating TNF and IL10 with GVHD (Middleton et al., 1998).

For this study, a systematic literature search was undertaken that identified 248 gene association studies with outcome of HSCT (list: supplementary file 1.1). At least 105 genes, including cytokines, regulators of innate and adaptive immunity, drug metabolism genes, DNA repair and metabolic genes were found to associate with any HSCT outcome (which included acute and chronic GVHD, relapse, rejection, survival, VOD, infection, drug toxicity). These findings are summarized in table 1.1. Of these, markers for 49 genes associated with acute or chronic GVHD, described in 141 studies.

Analyzing the methodology of these studies, the vast majority (n=238, 96%) were single cohort candidate gene association studies. Only seven studies sought independent confirmation of findings within the same study's setup (Xiao et al., 2010, Chien et al., 2006, Lin et al., 2003, Bochud et al., 2008, Elmaagacli et al., 2009, Mullighan et al., 2004, Espinoza et al., 2011), and only three studies used larger scale approaches. Mullally et. al.

reported a study of 1143 SNP for 220 candidate genes, identifying several chemokines associating with HSCT outcome (Mullally et al., 2008). JMDP had conducted a genome-wide association study with SNP markers, which failed to identify any non-HLA gene association but detected a possible mHag locus (Ogawa et al., 2008). Finally, the NMDP carried out a genome-wide association study (Hansen et al., 2010) the results of which have not been finally reported. Imputation of SNP previously associated, however, confirmed association of IL10 and IL6 with GVHD (Chien et al., 2012).

Given the rapid evolution of HSCT, it had been difficult in the past to build large-scale HSCT study cohorts. Limited availability of study subjects made consideration of demographic or clinical risk factors in study cohort selection difficult, despite the existence of these risks being well established in the literature (e.g. patient and donor age (Kollman et al., 2001, Loren et al., 2006, Wojnar et al., 2006), female donor to male recipient (Randolph et al., 2004, Gahrton, 2007), diagnosis and staging (Chaidos et al., 2007, Wojnar et al., 2006), prior chemotherapy (Hahn et al., 2008), conditioning regimen (Perez-Simon et al., 2005, Hahn et al., 2008), concurrent infections (Hahn et al., 2008, Ljungman, 2007, Young, 2008)). Previous studies often relied on study populations displaying different underlying ethnicities, underlying diagnosis, stem cell sources (related/unrelated), conditioning regimens and GVHD prophylaxis, weakening study power and leading to disparate results. HLA matching and HSCT from sibling donors were the most common measures applied in the study of non-HLA gene polymorphisms, presuming that reducing the ‘noise’ from genetic mismatching would make small effect-size non-HLA association more readily identifiable. Very few studies deliberately chose unrelated or HLA mismatched HSCT, therefore there is a paucity of data on these settings, although these represent the majority of HSCT. Also, earlier serotypical HLA matches may have actually represented mismatches at allele level (Weisdorf et al., 2008), hampering the comparison of results from different studies. Many of the early studies in particular lacked statistical power for the allele/genotype frequency reported; sample sizes <100 were not uncommon.

More recently, the collection of large HSCT cohorts has become reality. Both NMDP and JMDP have now conducted >10,000 unrelated donor HSCT, allowing for future studies with better stratification of genetic, demographic and clinical risk factors. Eventually, the availability of such study populations would allow for study designs that comply with recommendations for the design of genetic association studies (Colhoun et al., 2003, Gambaro et al., 2000, Hirschhorn et al., 2002, McCarthy et al., 2008, Lander and Schork, 1994, Schork, 1997).

Gene	function	gene	function	gene	function	gene	function
ABO	haematopoietic system	**ESR**	innate immunity	IL15RA	cytokine	NOS2A	innate immunity
ACE	other effector	Factor V	haematopoietic system	**IL17A**	cytokine	OGGI	DNA repair
BAFF	haematopoietic system	**Fas**	adaptive immunity	**IL18**	cytokine	P2X7	Drug metabolism
BP1	other effector	**FCGR2A**	adaptive immunity	**IL1RA**	cytokine	PAI1	haematopoietic system
CASP8	adaptive immunity	**FCGR3B**	adaptive immunity	**IL2**	cytokine	**PARP1**	DNA repair
CCL27	chemokines	**FCRL3**	adaptive immunity	**IL23R**	cytokine	**PCAM1**	adhesion
CCL3	chemokines	FOXP3	adaptive immunity	IL4	cytokine	PGP	Drug metabolism
CCL4	chemokines	GRZB	adaptive immunity	IL4R	cytokine	PIR	innate immunity
CCL5	chemokines	**GSTA1**	Drug metabolism	**IL6**	cytokine	Prothrombin	haematopoietic system
CCR5	chemokines	GSTM1	Drug metabolism	IL7R	cytokine	**PTPN22**	haematopoietic system
CCR6	chemokines	GSTP1	Drug metabolism	**IMPDH1**	Drug metabolism	**PTPRC**	haematopoietic system
CCR9	chemokines	GSTT1	Drug metabolism	LCT	metabolic	**RFC1**	DNA repair
CD14	adaptive immunity	HFE	haematopoietic system	LIG3	DNA repair	**TGFB1**	cytokine
CD3EAP	DNA repair	**HLA-E**	adaptive immunity	MADCAM1	adhesion	**TGFB1R**	cytokine
CD86	adaptive immunity	**HLA-G**	adaptive immunity	Mal	adaptive immunity	TLR1	innate immunity
CPS1	metabolic	**HMGB1**	adaptive immunity	**MASP2**	innate immunity	**TLR4**	innate immunity
CTLA4	adaptive immunity	HO1	haematopoietic system	**MBL**	innate immunity	**TLR9**	innate immunity
CXCL12	chemokines	HP	haematopoietic system	**MBL2**	innate immunity	**TNF**	cytokine
CYP2B6	Drug metabolism	HPA5	haematopoietic system	MCP1	innate immunity	TNFRSF1	cytokine
CYP2C19	Drug metabolism	**HPSE**	haematopoietic system	**MDR1**	Drug metabolism	**TNFRSF2**	cytokine
CYP3A4	Drug metabolism	**HSP70**	innate immunity	**MIF**	innate immunity	**VDR**	innate immunity
CYP3A5	Drug metabolism	ICOS	adaptive immunity	**MPO**	innate immunity	VEGF	adhesion
DAAM2	metabolic	**IFNg**	cytokine	MTHFR	Drug metabolism	VLA4	adhesion
DARC	chemokines	**IL1**	cytokine	MUTYH	DNA repair	XRCC3	DNA repair
DECTIN1	innate immunity	**IL10**	cytokine	NKG2D	adaptive immunity		
DNAM1	adaptive immunity	IL12	cytokine	NLRP2	innate immunity		
ERC2	DNA repair	**IL13**	cytokine	**NOD2**	innate immunity		

Table 1.1 (previous page): Genes associated with HSCT outcomes from 248 previous gene association studies. Forty-nine genes (in bold) have been implicated with acute or chronic GVHD.

SUMMARY

- **The genetics of HSCT outcome, including GVHD, involves multiple genetic mechanisms.**
- **Self/non-self recognition strongly predicts GVHD.**
- **Matching of the Human Leukocyte Antigen (HLA) complex reduces the risk of GVHD and is widely applied in clinical practice.**
- **Other self/non-self recognition mechanisms (e.g. KIR, LILR, mHag) also influence the risk of GVHD but are less well understood and not commonly used in clinical practice.**
- **Non-HLA gene polymorphisms modulate innate and adaptive immune responses, >100 genes have been reported to associate with HSCT outcomes.**
- **Results for non-HLA gene polymorphisms are often inconclusive due to limited study quality, therefore findings have been applied little in clinical practice.**

1.4. Summary and conclusion; aim of this study

HSCT has become an ever more important treatment option for an ever wider variety of indications, now moving well beyond malignant and non-malignant conditions of the haematopoietic system. The procedure itself and surrounding medical and nursing care has evolved dramatically, improving cure of the underlying disease and survival, whilst reducing transplant-related mortality and morbidity.

GVHD remains the single major hurdle in wider application of HSCT. Even full HLA matching from sibling donors cannot guarantee its prevention, indicating that other genetic and non-genetic factors are at play which we are just beginning to understand. The research into the KIR and LILR systems are likely to provide a better understanding of self/non-self recognition in the future. A small number of immunodominant minor histocompatibility antigens will probably give explanation for some strong GVHD and GVI effects. Non-HLA gene polymorphisms determine the ‘milieu’ in which self/non-self recognition occurs and may therefore be of important influence on the strength of the immune responses leading to GVHD or GVT.

Despite an abundance of data from >200 previous studies, effects of many non-HLA gene polymorphisms remain inconclusive, which is founded in the generally small effect size of associations of common alleles and genotypes, and issues with study design (heterogeneous study populations, lack of statistical power, lack of validation by confirmatory study on a similar population).

The aim of this study is to elucidate the role of non-HLA gene polymorphisms for the risk of GVHD in a more robust fashion, by applying recommendations for high-quality gene association study design. Key elements of the study include:

- Study population: genetically homogeneous background, control of clinical confounders, clinically relevant population, adequate sample size

- Gene targets: More indiscriminate approach (genome-wide/targeted), rather than a candidate gene approach
- More stringent study design: screening and independent confirmation cohorts

1.5 Outline of study plan/brief history of the project

The idea of this study was conceived in 2004. The author's plan was to conduct a high-quality association study in the field of immunogenetics; the search for an adequate study population led to co-operation with institutions in Japan.

In 2005, the author spent six months at the Division of Molecular Life Sciences at Tokai University, Kanagawa, Japan, at the invitation of Professor Hidetoshi Inoko, a renowned expert in the field of HLA genetics. Tokai University hosts the DNA sample collection of JMDP and is involved in many of the registry research projects. During these six months, the author finalised a proposal for a genome-wide association study into the non-HLA genetics of GVHD using microsatellite markers, a methodology also pioneered at Tokai University. Dr Peter Middleton and Dr Andrew Gennery would act as supervisors for a PhD thesis with Newcastle University, whilst Professor Inoko would provide local supervision.

After funding for this work was obtained (JSPS post-doctoral fellowship, Kay-Kendall Leukaemia Fund international fellowship), the work started in Japan in March 2007. An initial assessment of the availability of DNA samples (March-June 2007), however, showed that a genome-wide association study would be unfeasible due to the lack of samples with a sufficient amounts of DNA. The study plan was adjusted to a targeted genomic screening focusing on the immune system.

The selection of an appropriate study population received particular attention in order to control confounding variables (see chapter 2), and a small-scale pilot study (October-December 2007) using 41 candidate SNP markers was conducted to ensure that a study based on the selected study population would be capable of demonstrating small effect-size non-HLA gene polymorphisms. After this was achieved, the large-scale approach was carried out. Main steps included the identification of the genes of the immunogenome and allocation of microsatellite markers (July-December 2007), pooling of DNA samples (January-March 2008 and December-February 2009), and genotyping of pooled DNA in a screening (April-

December 2008) and confirmatory cohort (March-August 2009), followed by data analysis and evaluation (until February 2010).

2. METHODOLOGY

2.1 Aim and purpose

2.2 Objectives

2.3 Study question and hypothesis

2.4 Overview of Study design

2.5 Selection of the study population

2.6 Selection of genes and markers

2.7 Preparation of DNA

2.8 Construction of DNA pools

2.9 Procedure of individual sample DNA PCR

2.10 Procedure of pooled DNA PCR

2.11 DNA genotyping

2.12 Data retrieval and processing

2.13 Data analysis

2.1 Aim and purpose of the study

The aim of this study was to improve health, survival and quality of life of recipients of matched unrelated donor HSCT for acute leukaemia by identifying genetic risk factors that increase or decrease risk of GVHD. This study aimed to identify ‘risk’ and ‘protection’ recipient and donor non-HLA genetic polymorphisms that contribute to the severity of acute GVHD, enabling clinicians to stratify the risk of GVHD prospectively.

Findings were expected to be applicable to future patient care:

- identified “risk” alleles in donors/recipients that predict the occurrence and severity of acute GVHD
- identification of ‘risk’ donors or recipients as a guide for planning conditioning and GVHD prophylaxis regimens
- identified “risk” genes in donors aid donor selection for reducing acute GVHD

Potential broader future scope of results:

- contribution to the understanding of genetic pathology of acute GVHD
- facilitating the development of new, specific prophylaxis and treatment options for GVHD (monoclonal antibodies, gene therapy)
- impact on research and management of similar or related inflammatory disorders

2.2 Objectives

2.2.1. Objective

The objective of this study was to investigate allele frequency differences of microsatellite markers between cases of absent or mild acute GVHD (grade 0-1, controls) and moderate to severe acute GVHD (grade 2-4, cases). As cases we considered HSCT recipients (‚intrinsic' risk of GVHD) as well as donors (‚graft' risk of GVHD).

2.2.2 Key objective elements

Variables

Genetic polymorphisms presenting in the form of microsatellite allele frequency differences between the study groups of different severity of acute GVHD (grade 0-1 versus 2-4) separately for donors and recipients.

Outcome parameters

Pooled DNA genotyping outcomes:
Moderate to severe acute GVHD (grade 2-4) was the single outcome of the two-step pooled DNA screening (discovery and confirmatory cohorts).
Standard definitions and classifications were used to clinically define acute GVHD - the modified Glucksberg criteria according to international consensus (Glucksberg et al., 1974, Rowlings et al., 1997, Przepiorka et al., 1995).
From a clinician's perspective, acute GVHD grade 2 was seen as a cut-off point for starting active and aggressive intervention to stop progress of acute GVHD (Hara et al., 2007). Acute GVHD grade 2 or more severe

was associated with increased morbidity and mortality, and reduced quality of life (Pasquini, 2008, Kanda et al., 2012, Kodera et al., 1999, Morishima et al., 2007, Sasazuki et al., 1998, Yano et al., 2000).

Individual genotyping: outcomes

- Degree of severity of acute GVHD (grade 0 versus 1-4, grade 0-1 versus 2-4, grade 0-2 versus grade 3-4, grade 0-3 versus 4)
- Degree of severity of chronic GVHD (absent chronic GVHD versus limited and extensive disease, absent and limited disease versus extensive disease)
- 100 day/one year/three years/five years survival rate, log rank test for survival
- Relapse rate

2.3 Study Question and Hypothesis

2.3.1. Study Question

“Are non-HLA microsatellite polymorphisms in unrelated HSCT donor and/or recipient immune system genes associated with graft versus host disease?”

2.3.2. Hypothesis

The hypothesis was based on the concept that genetic susceptibility to GVHD is the result of a complex genetic trait, involving multiple loci:

- GVHD has in part a complex genetic trait, and that common allele polymorphism of non-HLA genes in the patient and donor genomes contribute to the development of GVHD; these risk alleles may be detectable with a systematic genome scanning approach.

- Such non-HLA risk alleles can have an effect size that reaches that of certain HLA mismatches, hence can be consistent despite variation in clinical and genetic risk factors over time. Such risk alleles can be useful for prediction of acute GVHD risk in clinical practice.

Hypothesis:
“Allele frequency differences of microsatellite markers are associated with moderate-severe acute GVHD.”

Null hypothesis:
“Allele frequency differences of microsatellite markers are **not** associated with moderate-severe acute GVHD.”

2.4. Overview of study design

2.4.1. Key features of a robust genetic association study design

Considering the above methodological issues about genetic association studies, as discussed in the introduction part of this thesis, a more robust design should entail:

- Study and control cohorts should stem from a genetically homogenous population
- Confounding variables needed to be well controlled
- Cases and controls needed to be well defined, phenotypes well established and graded
- Environmental factors that influence gene function well established
- Genes and markers selected that are biologically meaningful
- Outcomes well defined, consistently reported
- Study design addressing error by chance, multiple testing issues: Design with at least a discovery and independent confirmation cohort, appropriate rigorous statistics
- Sufficiently powered cohorts – adequate sample size
- Systematic rather than random/candidate marker approach

2.4.2. Measures to achieve a more robust study design

This study has taken measures to address the above issues by:

- Identifying of a study population from a more homogeneous background
- Control of confounding parameters: All known genetic, demographic and clinical risk factors were carefully analyzed.
- 'Modelling' of hypothetic cohorts were used to design a study cohort with ideally minimal confounders and maximum statistical power.

- Definition of phenotypes: Ensuring that GVHD in all subjects of this study was defined using the modified Glucksberg criteria (Przepiorka et al., 1995)
- Estimating impact of environmental factors
- Defining the scope of approach: Weighing the advantages and disadvantages of different options: candidate gene approach, targeted screening, whole genome screening.
- Addressing type I (incorrectly rejecting the null hypothesis) and type II (false acceptance of the null hypothesis) errors by considering issues of statistical power, reproducibility, multiple testing.

2.4.3. Outline of the study design

- Modification of a whole-genome scanning approach with microsatellite markers (Tamiya et al., 2005).
- Descriptive, retrospective case-control study with two nested cohorts (discovery/confirmatory) of pooled DNA screening, followed by individual genotyping of the combined cohorts for confirmation.
- Selection of a genetically and clinically homogenous cohort of approximately n=1000 donor-recipient pairs (see power calculation) from the JMDP registry
- Microsatellite markers as screening tool – indiscriminate approach (i.e. large scale rather than candidate gene approach)
- Focus on immune system genes would be expected to yield targets with a higher positive predictive value than a more indiscriminate approach. A review of genome-wide association studies on immune system disorders had shown that genetic associations are more likely to be located in immunoregulatory genes (Zhernakova et al., 2009)
- Estimating impact of environmental factors by dividing the cohort into two subsequent time frames (1993-2000, 2001-2005). HSCT practice was likely to have changed during these time periods, not all of these changes may have been recorded in the dataset.

- Introduction of a two-step independent screening, estimate of statistical power, use of statistical correction for multiple testing.
- A phased, 2-step pooled DNA screening: Splitting of cohort of n=1000 pairs into two groups of approximately n=500 pairs each. Within each group, construction of four DNA pools (Donors GVHD 0-1, Donors GVHD 2-4, Recipients GVHD 0-1 and Recipients GVHD 2-4) using an established, highly accurate DNA pooling method. Pooled typing of the full MS marker set in the 1st screening step, followed by retyping of positively associated MS markers only in the confirmatory step, to eliminate pseudo-positive markers.
- Individual genotyping of remaining associated MS markers on the combined cohort of approximately n=1000 pairs, to eliminate artefacts introduced by DNA pooling.
- Analyses planned for pooled genotyping: two directions of analysis:
    - Donors GVHD 0-1 with Donors GVHD 2-4 ('intrinsic risk of donor to induce severe GVHD in recipient')
    - Recipients GVHD 0-1 with Recipients GVHD 2-4 ('intrinsic risk of recipient to develop severe GVHD')
- Significance of allele frequency differences would be determined by Fisher's Exact Test for each individual marker allele (2x2 test) and for alleles of a marker (2xm test).

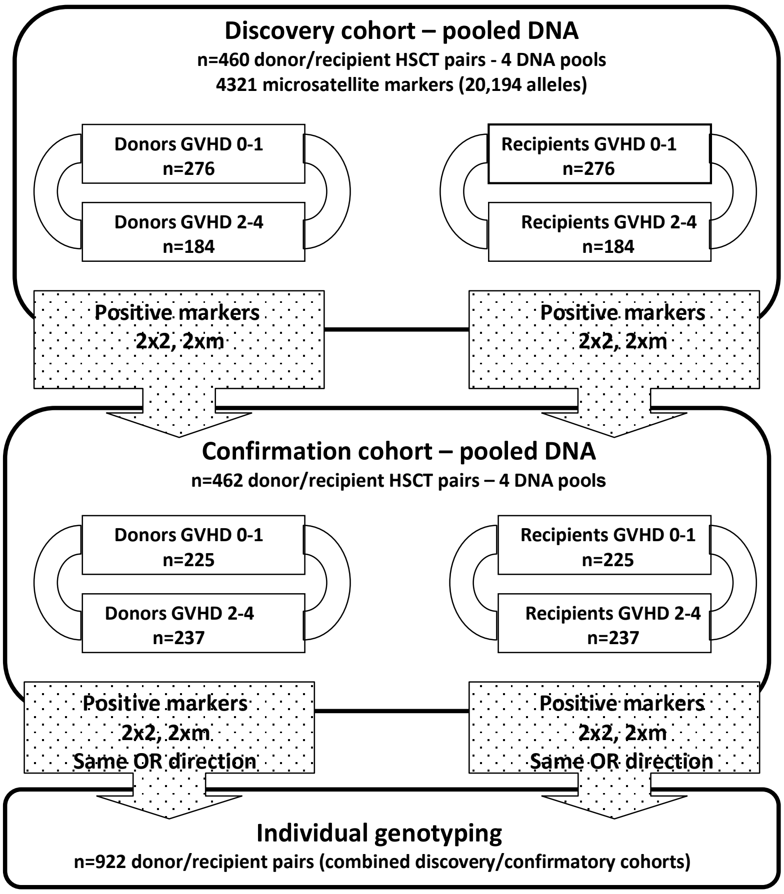


Figure 2.1: Overview of the design of this study. In a first screening step (Discovery Cohort), microsatellite markers representing the entire immunogenome are typed on pooled DNA of 460 HSCT recipients and their donors; aiming to detect allele frequency differences between those recipients and donors of no or low grade GVHD (grade 0-1) and those of moderate to severe grade GVHD (grade 2-4). Positive markers only will be taken over to a second screening step (Confirmation Cohort) with an identical setup. Markers still remaining associated with GVHD will then be typed on all individuals of the combined discovery and confirmation cohorts.

2.4.4. Ethical approval

Ethical approval to this study was granted by the Ethics Committee of the School of Medicine of Tokai University, approval number No 02-4-1, 9 June 2006.

This study was also approved by a meeting of the Research Committee of the Japan Marrow Donor Programme (JMDP). Use of DNA samples and clinical data was explicitly granted. Donors and recipients have given written informed consent at the time of graft harvesting or transplantation for DNA samples and data to be used for research purposes, according to the declaration of Helsinki.

Summary – study design

- **Study cohort from a genetically homogenous population with little/no admixture, controlled confounding parameters, well defined phenotypes and outcomes**
- **Sample size with adequate statistical power**
- **Confirmatory testing of identified associations in two independent cohorts**
- **Targeted genome scanning approach, focusing on biologically meaningful genes**
- **Using microsatellite markers in a pooled DNA typing approach**

2.5. Selection of the study population

2.5.1. Analysis of JMDP registry population and cohort selection

The JMDP registry confirmed that all selected HSCT pairs were of Japanese origin – hence there was no genetic admixture other than that of the overall Japanese population.

For the purpose of selection of study cohorts, an opportunity was given to analyze data from the JMDP registry of unrelated donor HSCT performed between 1993 and 2000 (n=2469 HSCT pairs) for risk factors of acute GVHD grade 0-1 versus grade 2-4. This was followed by 'modelling' of potential study cohorts according to the identified risk factors, aiming for a clinically meaningful study population with an optimal control of confounding variables. Given here is a brief summary; the details of the analysis are available in supplementary file 2.1.

Univariate and backward multivariate logistic regression analyses were performed on the registry population. Univariate analysis showed that T-cell depletion, antithymoglobulin (ATG), HLA matching, GVHD prophylaxis with a tacrolimus-based regimen, standard dose cyclophosphamide/total body irradiation (Cy/TBI) conditioning regimen, donor age ≤30 years, and underlying diagnosis other than acute lymphoblastic leukaemia (ALL) or chronic myeloid leukaemia (CML) are all protective of acute GVHD grade 2-4. Multivariate analysis was performed by stepwise logistic regression, including all the variables showing associations in univariate analysis. ATG administration, HLA matching, GVHD prophylaxis with tacrolimus, donor age ≤30 years and Cy/TBI standard regimen were upheld in the final step of multivariate analysis.

Based on these findings, four model cohorts were devised, by selecting out for the established risk factors in a step-wise fashion. Decision criteria included the results of multivariate analyses of the models, clinical meaningfulness of the model, and available sample size. Eventually, the most suitable model for the discovery cohort was a selection by diagnosis (acute leukaemia: ALL and acute non-lymphoblastic leukaemia (ANLL)), recipient age (≥4 years, ≤40 years) and no T-cell depletion; resulting in a cohort of approximately 1000 sample pairs. This selection would include all degrees of HLA matching and mismatching, and therefore somehow reflect a population as typically seen in HSCT practice.

2.5.2. Power estimation

A statistical power estimation (conducted by Dr Hirofumi Nakaoka, details in supplementary file 2.2) showed that a sample size of approximately 500 pairs per cohort would be required to provide sufficient statistical power (0.8) to demonstrate effect sizes of an Odd's ratio of 1.5 at allele frequencies of 0.3-0.6. Larger effect sizes would detect lower frequency allele associations (approximately allele frequency of 0.1 for OR=2.0; allele frequency of 0.05 for OR=2.5). Associations with an OR between 1.3-1.5 represented the lower limit of detection for the screening and confirmatory cohorts.

2.5.3. Construction of the actual study cohorts

The next step in constructing the actual study cohorts was an assessment of DNA sample availability (supplementary file 2.3). This assessment showed that of the initial n=1000 sample pairs, n=112 were depleted of DNA, and a further n=345 sample pairs were transferred for use for another study. The DNA content of each available sample was determined by DNA quantification and multiplication by volume. This revealed that a genome-wide study would have been unfeasible because the vast majority of samples would not provide sufficient DNA. However, for a targeted genome scanning or a candidate gene approach enough samples would have been available. The options were discussed amongst all contributors and decided to opt for a targeted genomic scanning (of immune system genes) in a two-step pooled DNA screening design. For the first step, samples of the 1993-2000 registry cohort would be included, for a second step samples from a later cohort (2001-2005) would be made available by JMDP.

Based on the estimates made of DNA amount required (see section 2.7.2. below), sample pairs were selected on the basis of DNA amount availability for both samples per pair (supplementary file 2.3). N=460 pairs were chosen from the 1993-2000 registry cohort for the discovery cohort (first screening step), following the criteria: Diagnosis (acute leukaemia: ALL and acute non-lymphoblastic leukaemia (ANLL)), recipient age (≥4 years, ≤40 years), full bone marrow as stem cell source and no T-cell depletion.

The same criteria were used for selection of the confirmatory cohort, this time incorporating HSCT pairs from the time period 2001-2005. The HLA matching of the confirmatory cohort were to be ‘adjusted’ to that of the discovery cohort by pairing of each sample pair for HLA matches and mismatches at the same HLA locus, or combination of loci.

The characteristics of this population are shown in supplementary file 2.3.

SUMMARY - cohort construction

- **Careful univariate and multivariate analysis of a large stem population (here: JMDP HSCT registry 1993-2000, n=2469 HSCT) can provide a good understanding of demographic, clinical and genetic risk factors for the intended outcome (here: GVHD grade 2-4).**
- **Designing of hypothetical cohorts with repeat univariate and multivariate analysis can optimize control of confounding variables whilst maintaining adequate sample size for good statistical power.**
- **The heterogeneous nature of HSCT, lack of large numbers of study subjects, and variability of HSCT management over time makes control of confounding variables difficult.**
- **The cohort construction of this study faced challenges over the availability of DNA samples, demanding a flexible approach to cohort and study design.**
- **The process resulted in devising of two study cohorts with well established confounders (i.e. diagnosis, HLA mismatch as the most consistent), and a strategy for a study design (confirmation by independent cohort).**

2.6. Selection of genes and markers

2.6.1 Systematic identification of genes

As outlined above, it was decided to adopt an approach of a targeted genome scanning, focusing on genes that are biologically meaningful in the context of GVHD. The pathobiology has been studied in some detail (Ferrara et al., 2003, Duran-Struuck and Reddy, 2008, Sun et al., 2007). Key pathophysiological pathways are located within the immune system, or are driven by immune responses:

- Development and maturation of immune cells
- Innate immunity
- Adaptive immunity
- Lymphocyte receptor repertoires, MHC, tyrosine kinases, protein kinases
- Pattern recognition – Toll/like Receptors
- Effector pathways of lymphocytes – apoptosis
- Intracellular mechanisms
- Extracellular mechanisms (cytokines, complement, chemokines)
- Modifiers of immune responses

The approach was inclusive of genes for which some involvement with the immune system was described, rather than exclusive of genes without described immune system involvement; because such a role may not yet have been investigated for many genes. Exclusion on the basis of absent evidence would be more arbitrary then inclusion of genes for which such evidence exists; recognizing, however, that such an approach had its limitations as potentially relevant genes may not have been included. The minimum inclusion criteria for admission into the immunogenome panel were a functional role of the gene in immunoregulation (i.e. function of the transcribed gene product or a genetic variation of the gene) and belonging to the same gene family of such a gene. Genes that would not fulfil these criteria would not be included in this study. As the search approach was inclusive and aimed at identifying those genes that were eligible rather than those that were not, there was no active process of exclusion. A literature search was carried out using defined search terms with the objective to compile a complete ‘Immunogenome’. This literature search included general textbooks (Janeway et al., 2005, Mak and Saunders, 2006) and used a wide variety of databases to broaden and deepen the search, as well as to include the very latest information from recently published journal papers. Overall information on candidate genes were extracted from >2000 journal papers.

In addition, genes specifically linked to GVHD and other HSCT outcomes were traced and categorised:

- Genes associated with GVHD and other HSCT outcomes in previous studies
- Genes whose expression has been associated with GVHD and other HSCT outcomes
- Genes that have been associated, by identification of polymorphism or gene expression, with immune processes that are highly relevant also in the GVHD pathophysiology
- Genetic susceptibility loci of acute leukaemia (as potential confounders as these have an impact on survival)
- Genes that may have implications for GVHD or transplant outcomes in a broader sense, e.g. enzymes and other metabolic genes influencing immune responses, drug metabolism genes, DNA repair genes, etc.

Gene names were initially compiled in a list, which was standardised to current nomenclature by identifying the official gene symbol from the GeneCard and NCBI databases. Additional information, such as the exact genomic location, was retrieved. Literature searches were ongoing throughout the duration of the project until completion of genotyping work (February 2010) to include cutting-edge research and new associations. The compiled ‘HSCT-specific Immunogenome’ included eventually n=3093 genes (see supplementary file 2.4). Finally, this ‘immunogenome’ was compared with a similar collation reported in the previous literature (Ortutay and Vihinen, 2006), finding that genes from this previous study were included, but that this study’s gene inclusion was far more comprehensive than that of the previous one.

2.6.2. Selection of MS markers

With regards to larger scale and genome wide studies Lander et.al. pointed out that genetically younger, isolated populations have larger haplotype blocks with wider linkage desequilibrium, requiring fewer markers, and predicatively less disease alleles (Lander and Schork, 1994).

MS markers for this study were selected from the existing panel of approximately 30,000 markers routinely used for whole genome association studies.

This marker panel was collated over several years by a research team at Tokai University devoloping the above mentioned genome wide scanning methodology (Tamiya et al., 2005) with MS markers. Almost 70,000 markers were typed on different East-Asian populations (Japanese, Mongolian, Korean), and eventually 30,000 markers selected that were highly polymorphic, had a limited average number of alleles (6.4+/-3.1) and an average heterozygosity of 0.67+0.16. According to haplotype block structure of East-Asian populations, which was well preserved in Japanese in particular, an average marker linkage disequilibrium (LD) of 100 kB was estimated. Markers were also selected by position, aiming to chart the entire euchromatic genome at regular 100 kB intervals, thus providing overlapping/double coverage for each LD region. For 95% of the genome marker coverage with inter-marker distance of <200kB was achieved.

For this study, markers from this panel were selected that would flank the candidate gene to provide overlapping cover within the range of LD, estimated to be approximately 100 kb. Hence, if the two flanking markers would be no more than 100 kb apart, full overlapping coverage for the locus would have been provided.

In this study, of the n=3,093 target genes, n=184 (6%) had to be excluded because these were located in regions lacking appropriate microsatellites or their exact genomic location was unclear. For n=34 further genes not represented by the marker panel we identified suitable microsatellites and designed primers accordingly (appendix 2.2).

The final selection included n=2,909 genes. Because many of these genes were located in clusters at close proximity, n=2,297 target genes were selected as representative for the n=2,909 genes (table 2.1). These gene loci were tagged with n=4,321 microsatellite markers (supplementary file 2.5). When measuring the distance between the centre of the gene and the marker start point, for 88% of target genes full overlapping coverage within a 100 kb range was identified. A further 8% of genes had partial coverage within estimated LD, with one or two flanking markers at >100 kb but <200 kb range. For 3% of target genes the range of one or two microsatellite markers was >200 kb (table 2.2).

Each target gene locus was tagged with an average of 1.8 microsatellite markers. There was a broad variation in the number of markers covering a gene locus, between a single flanking marker pair covering several candidate genes in regions of high gene density, and up to ten markers covering a single, very large gene. It was estimated that the total LD range of the selected markers taken together may cover up to 15% of the genome (table 2.3), hence cover substantially more genes than the selected target genes. From the number of genes within the LD range of 65 microsatellites (associated at an interim step in pooled screening) we extrapolated that our selection of microsatellite markers may have covered up to a third of all human genes.

	N=	%
Selected immunogenome genes	**3,093**	**100**
Unknown gene location/no marker	184	6
Immunogenome genes included in this study	2,909	94
Target genes selected to represent immunogenome of 3,093 genes	**2,481**	**100**
Included: genes covered with markers from MS panel	2,263	91.2
Included: genes for which markers were designed	34	1.4
excluded: unknown gene location	-35	-1.4
excluded: no MS marker available	-149	-6.0
Total target genes included in study, representing 2,909 immunogenome genes	**2,297**	**92.6**

Table 2.1: Gene and marker selection. As many MS markers had several genes within their LD range, one 'target gene' was selected for each such MS marker. For 7.6% of gene loci appropriate marker cover could not be established.

Markers	markers	%
Total markers selected:	4,321	
Total genes selected:	,2297	
Markers per gene average:	1.88	
Markers intronic:	1,320	30.55
Markers outside genes:	3,001	69.45
markers/genes covered with 2 flanking markers within 100 kb range	3,801	87.97
markers/genes not covered with 2 flanking markers within 100 kb range	516	11.94
markers exact location unknown	4	0.09
	4,321	100

Table 2.2: Specification of the degree of LD coverage of genes provided by the selected MS markers

	n=	%
Base pairs human genome	3,164,700,000	100
LD cover 4321 MS markers	432,100,000	13.7
Total number of genes human genome	30,000	100
Estimated genes covered by 4321 MS markers	10,301	34.3

Table 2.3: Estimation of total gene coverage of the selection of MS markers for this study. Data on the number of base pairs and genes of the genome are from the Human Genome Project website. LD of MS markers assumes 100kb, and the estimated number of genes covered by this selection is an extrapolation from the number of genes within the 100 kb LD range of 65 MS markers from this study.

Summary – genes and markers

- **As GVHD is a disorder of immunoregulation, associated polymorphic genes are more likely to be located in the immune system. Targeting functional and structural genes of the immune system would be expected to yield a higher positive predictive value for such associations than a more indiscriminate approach.**
- **A genomic screening of the immunogenome is feasible at high density with gene-flanking microsatellite markers.**
- **Due to their long range linkage disequilibrium, microsatellite markers cover large genomic areas around the target genes.**

2.7. Preparation of DNA

2.7.1 Provision of DNA samples

All DNA samples for this study were provided by JMDP, DNA preparation was not part of this study. In brief, samples were obtained from patients and donors at the time of HLA matching confirmation and stored for research purposes with appropriate consent. Tokai University is hosting the sample collection for JMDP.

Fresh samples were centrifuged and the buffy coat removed, from which the DNA of nucleated cells was extracted using commercial DNA extraction sets (QIAmp DNA blood extraction kit®, QIAGEN).

2.7.2 Estimation of DNA requirements for this study

The requirement of DNA amount was determined mainly by two factors: The number of planned reactions (i.e. the number of microsatellite markers, approximately n=4,000), and the DNA concentration of the DNA pool aimed for. The latter one depended on the DNA samples with the lowest DNA concentration to be included, and had its limitation in the composition of the PCR mixture. The standard PCR mixture for this experiment had a total volume of 20 μl, of which 8 μl was dedicated for the DNA. Dilution of the DNA sample was limited by the need for a restricted use of TE buffer (as >10 μl buffer per well is known to inhibit the PCR reaction). In addition, if the total amount of DNA in the reaction was <40 ng, PCR might become more unstable and the capability to detect small allele frequency differences of MS markers decreases (observations by Dr Akira Oka of his own experiments).

As the lowest sample concentrations was approximately 10 ng/μl, the estimated final DNA pool concentration would be approximately 6-8 ng/μl, therefore total amount of DNA per reaction well is 48-64 ng. Thus, the amount of DNA required from each sample varied with the total number of individual samples in the pool – the higher the number of individual samples, the lower the amount of DNA required from each individual as the total amount of DNA per marker plate well was constant. Based on the measurements of DNA concentrations, estimates of total amount per sample, and a preliminary estimate of total DNA requirements for the study, only samples with a total DNA amount of >4 µg were 'shortlisted' for the first pooled screening, and samples with an amount of >2.5 µg for the second pooled screening (details of the estimation of DNA amounts required: appendix 2.3).

2.7.3 Measurement of DNA concentration

Amount of DNA available was likely to be limited, given the age of DNA samples, the large number of previous studies performed on this collection, and the large amount of DNA required for this study.
In order to preserve the collection for future work, it was agreed with JMDP that the total DNA amount of each selected sample would be assessed by measurements of concentration and volume. DNA concentration of each selected sample would be determined by an established standardized method for measurement of DNA concentration (PICO Green®), and volume would be estimated by visual comparison with a standard volume set (identical sample tubes with volumes in steps of 50 µl, ranging from 50 - 1000 µl).

For the DNA concentration measurement with PICO green® dsDNA quantification kit (Molecular Probes, P-7589) a DNA dilution of 1:200 was used according to the maker's instructions. In preparation, 5 µl of original DNA was diluted in 995 µl of 1/10 TE buffer pH 7.5. Of this solution, 100 µl was pipetted onto the measurement plate and incubated for 3 min with a 100 µl of a 1/200 solution of PICO green fluorescent reactant. For quality control, a set of different concentrations of a standard DNA of a known concentration was divised: 1/1000, 1/300, 1/100, 1/30, 1/10 dilutions as well as a control well containing buffer with no DNA. Three independent measurements were then obtained using a Flouroskan Ascent CF (Thermo Labsystems) photometer, with settings: Integration time 20 ms, filter pair: Excitation 485nm, Emission 527nm, normal beam, single measurement. A customized excel worksheet was used for quality control and calculation of concentrations.

2.7.4. Estimation of total DNA amount of sample, allocation of pairs to screening steps

Availability of DNA concentrations and sample volumes were allowing for a more exact estimation of total available DNA amount per sample.
The total content of a DNA per sample in ng/µl was estimated by a simple formula:

Total amount of DNA/sample in ng **=** *DNA concentration in ng/µl* ***x*** *sample volume in µl*

Sample pairs were then ranked according to DNA amount in both partners in descending order, grouping them in three distinct groups:

- Total amount >4,000 ng: For inclusion into 1st pooled screening
- Total amount >2,500 ng: For inclusion into 2nd pooled screening
- Total amount >500 ng: For inclusion into individual typing
- Total amount <500 ng: exclusion from the study

Decision on inclusion and exclusion from the study, and allocation to pools were based on the estimated requirements, the total amount of DNA available per sample, and the original sample concentration.
Agreement with JMDP on sample handling, in- and exclusion criteria:

- At least a minimum of 500 ng of DNA should remain in each sample, hence samples with an amount of DNA of 500 ng or less were excluded from the study.
- Samples with a total amount of 4,000 ng or more were included into the first screening, pipetting 3,500 ng
- Samples with a total amount between 2,500 and 4,000 ng were included into the second screening, pipetting 2000 ng
- From samples with a total amount between 1000 and 2500 ng, 500 ng were pipetted to store for inclusion into individual MS or SNP typing.

2.8 Construction of DNA pools

2.8.1. Considerations for definition of DNA pools

At the outset, decisions had to be made on defining the pools ('which samples to pool together?') and how large the intended pool was going to be. Key aspects here are:

- Sufficient statistical power of individual pool: The power calculation (see above) suggested that a minimum pool size should be in the range n=200-250 samples (at a cohort size of 400-500).
- The definition of pools should be clinically meaningful

Although it would have been desirable to pool different degrees of GVHD (e.g. grades 0, 1-2 combined, 3-4 combined) separately, resulting pool sizes would not have provided a sufficient statistical power. From the sample numbers available, separating degrees of GVHD into two groups seemed the only feasible option. Donors and Recipients were pooled separately but accordingly.
Three scenarios were considered:

- Grade 0 GVHD versus Grade 1-4 GVHD. This approach would have separated samples at a ~50:50 proportion, in view of statistical power the strongest option. Drawback: Would not have distinguished between degrees of GVHD, but only presence of GVHD yes/no.
- Grade 0-1 GVHD versus Grade 2-4 GVHD: Would have separated samples at a ~2/3: 1/3 proportion. Resulting in acceptable power, and would have distinguished groups with a survival advantage from groups with survival disadvantage, also marking the stage of clinical intervention. Drawback: May not have distinguished risk genes for severe GVHD very clearly.
- Grade 0-2 GVHD versus Grade 3-4 GVHD: Would have separated samples at a ~3/4:1/4 proportion. Advantage: Clearly would have

distinguished severe GVHD. Disadvantages: Reduced statistical power for severe GVHD group, would have ignored distinction by survival and point of clinical intervention.

The decision to choose the Grade 0-1 GVHD versus Grade 2-4 GVHD was based on:

- The aim of the study to provide a risk predicting tool for clinical decision making – determining which genetic risks separated recipients with favourable and poor survival perspective, and which genetic risks separated recipients requiring treatment intervention from those who did not.
- The acceptable statistical power for this option.

2.8.2. Existing methods of DNA pooling

Methods of DNA pooling and their accuracy compared to individual typing and family typing for the study of complex genetic diseases had been described previously (Shaw et al., 1998, Barcellos et al., 1997, Craig et al., 2005, Hoffjan et al., 2006).
Here a high-accuracy pooling method was applied that was a standard procedure for genome wide association studies (GWAS) in the same department (Tamiya et al., 2005, Oka et al., 2003, Collins et al., 2000, Daniels et al., 1998), which had been modified further to increase accuracy (unpublished, internal validation data available).

In some aspects the application of the pooling method differed from the application to WGA studies:

- This study cohort consisted of paired samples – therefore inclusion of both partners was essential to reflect allele frequency differences.

- Genome wide association studies (GWAS) with microsatellites rarely used pool sizes >200 samples – there were no data on pooling accuracy for such a pool size.
- DNA amount, concentration and quality was very variable – compared to previous studies, samples of this study had rather low DNA concentrations.

The initial preparation of samples consisted of measuring sample DNA concentration measured by the PICO green® method (described above).

Key features to ensure a high accuracy of DNA pooling were:

- The use of calibrated pipettes for all pipetting
- Repeat measurements with PICO green®, acceptance of a narrow variation margin (<5%) only for DNA pooling

2.8.3. Practical procedure of DNA pooling

Sequential steps were involved in the pooling process. The pooling process was divided into four phases.

Phase 1 – Individual sample measurement

- Pipette testing (procedure described in appendix 2.4)
- Dividing samples into groups of the intended pools (see above)
- Ranking of samples by DNA concentration in decreasing order
- Dividing of the sample group into sub-groups of 96-well plate format size
- Choosing a target concentration for each group. To pool equal amounts of DNA at equal concentration, by definition the final pool concentration was determined by the lowest sample concentration, towards which the pooling process aimed. The limitation of this

approach lay within a minimum concentration of 6 ng/µl required for pooled DNA PCR. Thus, any samples with a lower concentration had to be excluded; and caution had to be applied not to dilute low concentration samples too much to render them unsuitable. As higher concentrations ranged from ~30 – 200 ng/µl, a step-wise approach in dilution was applied, diluting the first group of samples to a target concentration of ~25 ng/µl.

- Dilution to this initial target concentration (using non-calibrated pipettes) and measurement of sample concentration by PICO green (the PICO green assay set up by using calibrated pipettes) using 1/10 TE Buffer pH 8.0. Three measurements were performed on the same plate, and an average concentration calculated.
- Ranking of tested samples in decreasing order of concentration. Exporting result file into excel to identify subgroups of samples that lie within a +/- 2.5% range of concentration – separation of these samples for small pool construction.
- The remaining samples of all subgroups combined were again ranked in decreasing order of concentration. A new subgroup of plate format size is identified, a new target concentration chosen, dilution and concentration measurements performed. Again this subgroup was ranked by sample concentration, groups for intermediate pool construction identified and separated.
- This procedure was repeated until all samples were allocated to intermediate pools. This procedure required 3-5 rounds until all or most samples were resolved. Concentration of the last small pools often approached required minimum concentration of the final DNA pool. Occasionally, a very few samples with borderline-low concentration were allocated into the final DNA pool, rather than one of the intermediate pools.

Phase 2 – Construction of intermediate pools

- Using the calibrated pipettes, between 5 and 13 intermediate pools were created from each group of samples representing a DNA pool. The average concentration of samples considered for each intermediate was calculated as a fixed volume to be pipetted into the intermediate pool. The volume depended on the intended DNA amount for the final DNA pool.

Phase 3 – Construction of final DNA pool

- The concentration of intermediate pools was assessed by PICO green measurements (each pool in three independent wells, three measurements per well, calculation of average)
- Careful, stepwise dilution of intermediate pools was applied to adjust these pools to an equal concentration within a range of +/- 2.5%
- Intermediate pools were then pooled together using calibrated pipettes to achieve a final DNA pool

Phase 4 – Adjusting final DNA pool concentrations

- In order to ensure comparable conditions among all pools (i.e. measurement of true allele frequencies), final DNA pools in each screening step were also adjusted to an equal concentration, amount and volume.
- DNA pools were assessed in the same way as intermediate pools by multiple, repeat concentration measurement.
- Concentration was adjusted by a cautious stepwise dilution (2-3 steps) towards the pool with the lowest concentration, accepting a range of no more than +/- 2.5%.

DNA pooling represented the most technically difficult step of this project. To keep a consistently high standard and avoid human error, these considerations were applied:

- Use of calibrated pipettes for all pipetting actions (except the initial sample dilution, see appendix 2.4). All calculations of DNA amount and sample volumes were based on the actual volumes measured in pipette testing, rather than the nominal volume on the pipette.
- Careful tracking of all pipetted volumes, correcting at each step for volumes abstracted for concentration measurements.
- DNA protection by aseptic working conditions, light protection
- Adequate mixing at spinning at each handling step
- DNA-saving approach: Dilution to low concentration, early pooling into intermediate pools to avoid DNA-consuming repeat measurements (the Tokai standard protocol dilutes all samples to a relatively low concentration within a narrow margin of variation +/- 5%) before constructing intermediate pools of equal sample numbers). To compensate for the possibly induced increased variation, we decreased the margin of variation to +/- 2.5%.
- The pooling strategy resulted in a number of intermediate pools with a wider range of concentrations – again, we compensated by applying a more narrow margin for concentration variation (+/-2.5% for intermediate and large pools)
- Requirement for DNA top-up of low concentration samples for inclusion – for a small number of samples, top-up with highly concentrated original DNA was necessary to increase concentration to a level suitable for inclusion.

Results of the pooling process

Due to the requirement of highest attainable accuracy, pooling of DNA was a time consuming process. Construction of each DNA pool took between 3 and 6 weeks.

Table 2.4 summarizes the eight DNA pools constructed, and Figure 2.2 illustrates a typical process of pool building.

1st Screen

Pool	average concentration ng/µl	No. individuals	Pool volume (ml)	DNA amount pool (ng)	DNA amount per individual (ng)
D01	6.78688	276	82382.57	559120.6	2025.799
D24	6.6247	184	90477.92	599389.1	3257.549
P01	6.426204	276	83366.22	535728.4	1941.045
P24	6.487866	184	83667.12	542821.1	2950.115

Average all 6.581412

2nd screen

Pool	Average concentration ng/µl	No. individuals	Pool volume (ml)	DNA amount pool (ng)	DNA amount per individual (ng)
D01	20.10275	225	18115.88	364179	1618.573
D24	19.78577	237	18992.85	375788.2	1585.604
P01	20.40206	225	18231.22	371954.4	1653.131
P24	20.48707	237	19979.93	409330.3	1727.132

Average all 20.19441

Table 2.4: Constructed DNA pools for 1st and 2nd screening. Concentration variation for each screening step is within a 2.5% margin of the average concentration. Note that samples of the first screening step were diluted previously and had therefore a lower initial concentration than samples of the 2nd screening, explaining the difference in concentration.

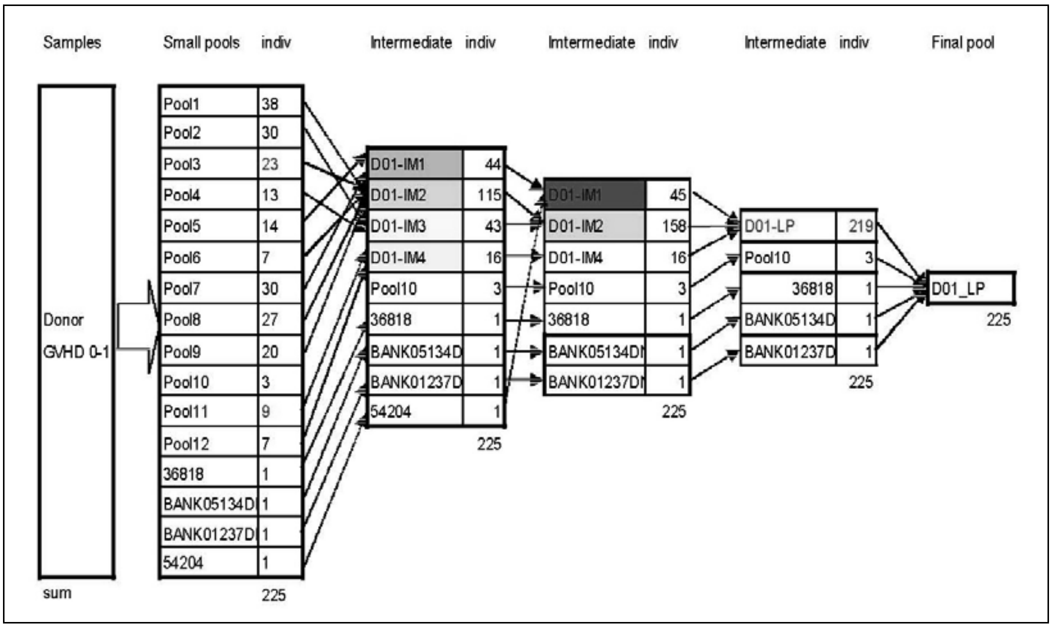


Fig 2.2: Example of a 'pooling tree', summarising the pooling process (here for the Donor GVHD grade 0-1 pool of the 2nd screening). Individual samples are concentration-adjusted and then pooled into small pools (here: 12 small pools). These small pools are then concentration-adjusted again and pooled together into intermediate pools. In a stepwise process one large pool results. Some individual samples of low initial concentration have to run alongside to be added to intermediate pools or even the final large pool.

2.8.4. Quality control of pooled DNA

Test marker for pooled/individual PCR and genotyping

Prior to embarking on pooled genotyping, individual DNA samples and pooled DNA were tested for accuracy with the applied methods by typing of a microsatellite test marker.

Objectives of test marker typing:

- To ensure appropriate PCR conditions
- To investigate if the different amounts of DNA lead to appropriate PCR results
- To define the optimal typing dilution
- To investigate whether the results of pooled PCR typing reflect results of individual typing (= quality check of DNA pooling process)

Microsatellite marker 066B03 was a standard test marker that had been used in most previous microsatellite genome-wide association studies from this laboratory to study the quality of DNA pools. It amplified well under standard pooled PCR conditions, and typed well under standard typing conditions. It had six major alleles, and reflected therefore an ‘average’ microsatellite.

Important variables of the PCR and genotyping process (details see below) were the amount of DNA used in the PCR mixture, and the dilution of resulting DNA product used for the genotyping process. Both of these factors could influence the fluorescent signal in genotyping, which determined the allele frequency in the pool. For this experiment, a high, medium and low level DNA setup was chosen (appendix 2.5) for the PCR procedure, and the PCR product diluted for each of these x10, x20 and x40. This was performed separately for each of the DNA pools, and then compared with results from typing all 922 HSCT pairs individually.

The results of the test marker typing were summarized in the supplementary file 2.6.

Comparison of allele frequencies between pooled and individual genotyping showed a very high concordance between pooled DNA and individual sample typing. Using a high amount of DNA gave results most accurately reflecting allele frequencies seen in the individual typing. Dilution of the PCR product had relatively little influence on results, although we saw increasing inaccuracies with using the higher dilution.
Using high amount DNA and a PCR product dilution x20, the mean difference in allele frequency for the test marker in the discovery cohort was 0.45% (standard deviation (SD): -2.61 – 0.942%, range -5.42-6.3%); for the confirmatory cohort -0.08% (SD: -0.62 – 0.26%, range -1.16 – 0.82%). The pooled genotyping was able to pick up allele frequencies as low as 0.02. There were no significant differences in allele numbers for frequencies of 0.05 and above, which we therefore used as a lower cut off value for reporting allele frequency in this study.

For the process of pooled DNA PCR and genotyping, a high amount of DNA (93 ng/reaction) for PCR and a PCR product dilution x20 was chosen.

2.9. Procedure of individual sample PCR

As a first step, two sets of individual typing master plates of individual samples were created. Using concentration data from DNA pooling, the volume required was calculated to pipet an amount of 100 ng of DNA (an amount estimated to cover all individual genotyping needs of this study). Matching volumes of dH_2O were added manually to achieve a concentration of 1ng/ μl.
Using a Beckman MultiMek pipetting robot (Beckman Coulter Inc), 50 μl/well of this solution was separated onto yet another set of plates. As a final step, again using MultiMek, both sets of plate were diluted by pipetting 50 μl/well of dH_2O to a final concentration of 0.5 ng/ μl.

Sequence of Individual PCR and genotyping:

- A set of reaction plates was prepared in accordance with the individual typing DNA masterplates
- Using Beckman MultiMek, 2 μl of DNA were transferred from the master plate onto the reaction plate
- A PCR reaction mixture for individual typing was prepared in a tube at -30°C:

dH2O	5.45 μl/well
ABI 10x Buffer	1.00 μl/well
ABI 2.0 M dNTP	1.00 μl/well
Roche AmpliTaq Gold 5U/ μl	0.05 μl/well
Primer Mix 10 μM each	0.5 μl/well

- Using a reservoir, 8 μl/well of this solution was pipetted into each well using MultiMek.
- PCR conditions on an ABI gene amplification system (Applied Biosystems) were used as described in the protocol (figure 5); here 56°C were applied as annealing temperature for both markers.

- Individual genotyping was identical to the protocol for pooled genotyping (see above), a dilution of x20 was used for individual plates.

Individual DNA Typing (PCR)

Marker:

Basic Mixture

Ingredient	per well	Total (x1030)	Lot
dH2O	5.45	5613.5	
10x Buffer	1	1030	
2.0 mM dNTP	1	1030	
Ampli Taq Gold 5U/ul	0.05	51.5	
Primer mix 10 uM each	0.5		
DNA (0.5ng/ul)	2		
sum	10	7725	

Main Marker Mixture

Ingredient	x1000 wells
Basic mixture	7500
dH2O	400
primer F- 100uM	50
primer R- 100uM	50
sum	8000

- 8ul/well

Control Marker Mixture

Marker 1:
Marker 2:

Ingredient	x12 wells
Basic mixture	90
dH2O	3
Primer mix 20M each)	3
	96

x2

- 8ul/well

PCR settings

95 C	9 min	
*	1 min	hold
72 C	1 min	
96 C	45 sec	
*	45 sec	40 cycles
72 C	1 min	
72 C	5 min	
4 C	∞	hold

Figure 2.3: Protocol and worksheet for individual MS PCR

2.10. Procedure of pooled DNA PCR

2.10.1. Primer preparation

Primers for microsatellite markers (Sigma-Genosys, Japan) were extracted manually from master plates of the MS marker collection for genome-wide association studies onto plates specific for this study. 15 μl of 10μMol primer mix were pipetted into each well. A set of 44 marker plates was created for the first screening. On the original master plates, markers were located in order of chromosomes and known typing requirements (PCR product dilution x10, x20,x40) to reduce typing error. This order was disrupted when creating plates for this study, resulting in a higher rate of typing error as compared to the previous studies.

2.10.2. Steps of PCR procedure

- For each marker plate, a set of four reaction plates representing the four pools was created.
- Onto each reaction plate, 2 μl of primer mix was pipetted into each well using a multi-channel pipette.
- A PCR mix of sufficient volume for all four plates was prepared in a bottle kept at -20°C. Volumes per well:

AB 10x PCR Buffer 15mM	2.0 μl
AB Gene Amp dNTP mix 2mM	2.5 μl
Roche AmpliTaq Gold 5U/ul	0.1 μl

- Prepared reaction plates were set onto frozen metal block trays.
- PCR mix and pooled DNA (13.4 μl/well) were mixed manually in a sample tray after appropriate mixing and spinning down of the ingredients.

- 18 µl/well of the PCR mix/DNA mixture was then pipetted onto the reaction plate under intense manual mixing with the primer in the bottom of the well.
- Plates were sealed, spun down and immediately amplified on a ABI DNA amplification system using a standard amplification protocol.
- Following amplification, PCR products were sealed and stored at -30°C for further processing, usually the following day.

PCR Procedure for Pooled DNA

1. Preparations

Get reagents (dNTP, buffer) and marker plates out of freezer
Switch on PCR Thermocyclers (AB GeneAmp PCR System 9700)
PCR PE plates: Label/ clearly distinguish by colour
Get 2 large ice boxes
25 ml tube for PCR mix – into ice box
X1 pipetting tray on frozen block – into ice box
Pipettes and pipette tips for corresponding volumes

AB Gene Amp dNTP mix 2mM lot:
AB 10x PCR Buffer 15mM lot:
Roche AmpliTaq Gold 5U/ul lot:

2. Preparation of mixture

Mix and spin down reagents.
Prepare PCR mixture according to number of plates:

Marker plates		1 plate	2 plates	3 plates	4 plates	
Total pool plates	1 well	4 plates	8 plates	12 plates	16 plates	1 plate
Ingredient	vol ul/well	x410 wells	x820 wells	x1230 wells	x1640 wells	x100 wells
10x buffer	2	820	1640	2460	3280	200
2.0 mM dNTP	2.5	1025	2050	3075	4100	250
AmpliTaq Gold	0.1	41	82	123	164	10
Total PCR mix all pools	**4.6**	**1886**	**3772**	**5658**	**7544**	**460**
DNA/each pool	**13.4**	**1340**	**2680**	**4020**	**5360**	**1340**
Primer Mix	2	NA	NA	NA	NA	NA
PCR mix/each pool	NA	460	920	1380	1840	460
Total each pool mix	**20**	**1800**	**3600**	**5400**	**7200**	**1800**

3. Preparation of plates

Get ice trays for plates from freezer – put plates on trays.
First step: divide marker plate into the four plates of each set of pools. Pipet marker into the bottom of each well. Use same pipette tips for each row for all four plates. Cover with strong sticky sheet.
Second step: Add PCR mix by rows, mix well using one set of pipette tips per row. Cover with clear rubber sheets. Spin down.

vol mix/DNA per well:		18 ul
Vol primer per well:		2 ul
Total per well:		20 ul

PCR Run (Applied Biosystems GeneAmp PCR System 9700)

96°C	9 min	
57°C	1 min	hold
72°C	1 min	
96°C	45 sec	
57°C	45 sec	30 cycles
72°C	1 min	
72°C	5 min	
4°C	∞	hold

Figure 2.4: Pooled DNA PCR protocol and worksheet

2.11. DNA Genotyping

2.11.1. Protocol for individual and pooled DNA genotyping

Pooled and individual DNA genotyping followed the same protocol. A stored PCR product was diluted, dried up and denatured before a run on a DNA analyzer.

Sequence of pooled DNA genotyping:

- Set up of ABI 3730 DNA analyzer (Applied Biosystems)– fresh reagents (AB 3730 Buffer (10x), Polymer, dH_2O) for each typing lot
- Preparation of a typing plate for each PCR product plate
- Dilution of PCR product x20/x40 (reasoning see below) with dH_2O using the Beckman MultiMek pipetting robot. Briefly, the robot prepared an intermediate mixing solution of a variable amount of dH_2O and 2µl of PCR product; and pipetted an aliquot of 2µl (representing the desired target dilution) of that solution onto the prepared typing plate
- Dry up of diluted DNA in a SpeedVac vacuum centrifuge for 10 min at 45°C
- Preparation of a mixture of 1 ml of standard Formamide with 5 µl AB GeneScan 500LIZ Size Standard per plate
- Pipetting 10 µl of this solution by Eppendorf Multi-pipette into each well, sealing of plate
- Denature of plate for 3 min at 95°C on a ABI DNA amplification system, followed by 5 min cooling on an ice tray
- Running of plates on an ABI 3730 DNA analyzer in gene mapper modus (protocol: GM_in2kV10sec_RV7_RT3500). Usually, two DNA analyzers were run in parallel, one running donor plates and one running recipient plates, swapping over donors and recipients on a daily base to randomise technical artefacts introduced by the individual machine.

At laboratory peak times, part of the pooled DNA genotyping work (overall <10%) was carried out by Ms Yamaguchi and Miss Matsushita, two laboratory technicians at Tokai University, following the protocols established by the author and under his supervision, using PCR products created by the author. Approximately one third of the individual microsatellite marker genotyping was undertaken by Ms Higuchi, a further laboratory technician at Tokai University, mostly in summer 2010 (following the return of the author to the UK), using the established protocols, under guidance from the author and direct supervision by Dr Akira Oka.

Pooled Genotyping – Run on ABI 3730 DNA analyser

Preparations

- Get PCR products, Formamide, 500 LIZ out of freezer/fridge
- Switch on RTV400
- Switch on L,R pumps
- Switch on Speed vac, open valve, check rubber ring, set temp 45°C, t=10min
- Switch on multimek, set up: water, trays
- Switch on x4 PCR Thermocyclers, set for heat 95°C
- Prepare ABI 3730 DNA analyser:

1. remove and clean water/wast/buffer plates
2. Mix new buffer: 15 ml of 3730 buffer plus 135 ml aqua dest (total 150)
3. Replace water/waste/buffer trays – ensure buffer tray cable secured
4. Fill glass bottle with buffer
5. Check polymer
6. Close, buffer tray back in to place
7. Insert sample sheets: Run 3730 data Collection – Tree: Plate Manager – connect USB – Import – Mark All – open – ok. Tree: Run Scheduler – advanced search (put in plate date) – search – add all – done

PCR Product Dilution **Dilution Factor :x10 x20 x40**

- Spin down PCR product plates
- Prepare a set of PCR PE plates – label
- Prepare a set of NUNC plates – no label
- Prepare plate covers – strong for PCR prod, tissue for new plates
- Make dilution on multimek according to plan
- Cover new plates/PCR product plates, discard NUNC plates

Dry up

- Speed Vac temp 45°C, t=10min

Add Size Standard, Formamide

- Preparation: Get 1 bottle of Formamide (1 ml) for each plate
- To each 1 ml of Formamide add 5 ul of 500LIZ
- Mix well and spin down
- Use multipipette to pipette 10 ul of Formamide/500LIZ into each well
- Cover with strong cover
- Spin down

Denature

- Get 2 Ice boxes
- Switch on PCR thermocylers
- Denature for 3 min at 95°C, Ice cooling for 5 min

Prepare 3730 run:

- Spin down
- Remove strong plate cover
- Put into 3730 plate tray, grey rubber cover
- Slot in according to order
- Start run – green arrow

Machine No 1:
Machine No 2:
Machine No 3:
AB 2730 Buffer (10x) lot:
AB GeneScan 500LIZ Size Standard lot:
Formamide:

Figure 2.5: Protocol/worksheet for Pooled PCR genotyping

2.12. Data input, retrieval and processing

2.12.1. Data input to 3730 DNA analyzer (Applied Biosystems):

- A Java-based application (SampleSheetMaker v1.0, Applied Biosystems) was used for data input for the genotyping process. This application produced a text file (.txt) that contained, besides the technical information for the run, details such as the marker name, amplicon size and allele size to facilitate further processing with the GeneMapper and MultiTyper softwares (see below).

2.12.2. Raw typing data retrieval and processing

- Peak signal quality was initially assessed using the ‘capillary viewer’ function in the Run 3730 Data Collection v2.0 software (Applied Biosystems®).
- Electrophoretic runs were analysed using the GeneMapper v3.5 software (Applied Biosystems®). In particular, peak signal and size standard quality were assessed. Settings for the analysis methods were such that the optimum analysis quality was achieved for peak height between 2000 and 11,000 fu (fluorescent units), with lowest recognition level at 200 fu and highest at 30,000 fu.
- Raw data were retrieved from GeneMapper in the form of ‘fsa’ (per well) and ‘ser’ file (containing the data analysis per plate)
- These data were combined using a Java-based application from ABI, called ‘Fsa2Fsb’.

2.12.3. Assessing peak heights

- Fsa2Fsb files were imported into the MultiPeaks software (Applied Biosystems®), a further Java-based application. This application could visually display allele size and peak heights of MS markers, based on the data input information, and allowed selection and logging of marker peaks.

- Within Multipeaks, peaks were selected manually in a simultaneous display of all four pools for each screening step. Information provided included the peak height (fu), the allele size (in base pairs), and the allele frequency (in %). As markers names were coded by their plate location in the institutes primer stock (e.g. '136A04'), there was a blinding to the analyzer as to which candidate gene he was assessing.
- All markers were assessed by the same analyzer in at least triplicate at different time intervals, in order to reduce intra-observer variability.
- As a general rule, alleles with a frequency <5% in all pools were excluded as such frequencies represent the limits of technical resolution and statistical power of this study. Allele frequencies <5% were occasionally selected if the other three pools had a consistent frequency of this allele >5%, and if the quality of the allele signal was appropriate (>200fu).
- Microsatellite allele selection involved an element of judgment, consisting in recognition of a particular microsatellite pattern (size of repeat units) and certain known microsatellite artifacts. The repeated microsatellite analysis lead to a 'training effect' in the observer, with the result that almost all microsatellite patterns were recognized and alleles determined. The strategy for resolving unclear typing results involved:
    - re-analysis by the same observer at a different time
    - retrieval of repeat size information of the marker and attempt to identify the microsatellite pattern
    - re-analysis by a different observer experienced in microsatellite analysis
    - re-typing/re-PCR of the same marker and re-analysis

  - exclusion of marker if no meaningful analysis can be obtained
  - Using a source reference of MS graphs from previous studies, as archived in the laboratory.

- In almost all cases it was possible to identify the MS by its typical peak pattern and by the base pair distance between peaks. If the MS identification was unclear, one or more independent opinions from other experienced researchers in the team were sought.
- For individual genotyping, the software Multityper (Applied Biosystems®) presented peak height data in a similar way for single datasets only.
- Results of chosen peaks were stored in a text file. Text files had to be manually edited (elimination of null and error well) before statistical analysis.

2.12.4. Genotyping artefacts

Microsatellite genotyping has a number of inherent artefacts which could affect the number of alleles, or allele allocation measured (Olejniczak and Krzyzosiak, 2006, Matsumoto et al., 2004, Miller and Yuan, 1997).

- Stutter alleles: these are artificial peaks that derive from product amplification one to two repeat units shorter than the correct sized PCR product or allele. The reason for this effect is slippage of Taq polymerase on the repeated sequence. In pooled typing, these stutter peaks are included with the correct sized alleles one or two units shorter, and therefore not identifiable. Stutter is more prevalent in dinucleotide repeats. Identification of stutter alleles requires at least some individual typing to identify and quantify the stutter effect. A number of mathematical methods have been devised to analyze stutter alleles. The stutter effect is usually marker specific, very consistent and reproducible between pools, therefore it is not thought to influence consistency of pooled DNA typing by e.g. mimicking allele frequency differences. Nevertheless, it can lead to a wrong estimate of allele frequencies in pooled as well as individual genotyping.

- “+A peaks”: An artificial fragment created by DNA polymerase adding a non-templated nucleotide at the 3’ end of the DNA fragment. This results in artefacts one base pair longer than the true allele for each peak, true or stutter allele. These artefacts are often recognisable as a parallel pattern ‘shifted’ from the true microsatellite pattern by one base pair, and would become apparent on visual inspection of the peak graph.
- Differential amplification: Preferential amplification of a shorter allele or PCR product. Reason: larger alleles reanneal at a faster rate because of more repeat units), resulting in reduced PCR efficiency. Short sized PCR products, artefacts (“starter peaks”) as well as short-sized alleles, can be grossly over-estimated and lead to false-positive results. This is not a consistent effect and tends to vary with each genotyping – hence the repeated independent typing (eight pools, if a marker passed through both screenings) is likely to have reduced a large proportion of such artefacts.
- Compound/interrupted microsatellite repeats, areas of gene copy number variation: As our marker panel is highly selected for informative markers, such microsatellites have largely been excluded previously.

Individual genotyping of markers that would remain associated with GVHD outcome would reveal the majority of such artefacts.

2.13. Data Analysis

3.13.1. Preparation of data

Data from text files, specifying the marker name, the allele positions and peak heights, were fused together at the level of the individual pools.

For the analysis a custom-made data analysis tool was used that had been applied in genome-wide microsatellite studies previously (Tamiya et al., 2005). The functions of this tool were:

- Conversion of peak height signals into allele frequencies by a mathematical algorithm on the basis of numbers of pool size and numbers of cases and controls
- Calculation of allele frequency differences
- Calculation of p-values using two types of Fisher's exact test for the 2x2 contingency tables for each individual allele and the 2x*m* contingency tables for each locus, where *m* referred to the number of marker alleles observed in a population. The Markov chain/Monte Carlo simulation method was employed to execute the Fisher's exact test for the 2x*m* contingency table (Tamiya et al., 2005).

After the first screening a large number of false positive markers and alleles was expected (each marker has 2-20 alleles – statistically there is a 1:20 by-chance association of each allele). There was a deliberate non-application of multiple testing statistics at this point to retain a high sensitivity for small effect-size association. Measures for identifying those markers and alleles that have a consistent association with GVHD included:

- Direct comparison of associations between the first and second screening by p-value and direction of Odds Ratio (protective or risk in both screens consistent)
- Careful inspection of peak graphs of the remaining consistently associated markers to identify typing errors and artifacts
- Individual genotyping of those markers showing the highest technical quality and statistical consistency. Test-typing on a small number of samples in the first instance may identify errors relating to the pooled genotyping process and artifacts.

Analysis of individual genotyping would be conducted in SPSS for Windows v 17.0 (IBM®), including:

- Ensuring Hardy-Weinberg Equilibrium (http://genepop.curtin.edu.au/help_input.html)
- Significance tests: 2-sided Fisher's Exact test, Kaplan-Meyer Analysis for alleles and genotypes
- Application of Bonferroni's correction for multiple testing
- Multivariate analysis (multiple logistic regression, Cox regression) in SPSS

3. Exploration study

3.1. Introduction
3.2. Aims, hypotheses, objectives and study design
3.3. Materials and methods
3.4. Results
3.5. Discussion

3.1. Introduction

Evidence from a large number of previous studies showed that non-HLA gene polymorphisms had an impact on the risk of HSCT outcomes, such as acute and chronic GVHD, relapse and survival. However, the review of the literature also showed that very few of these associations were of larger effect size or consistent amongst studies in different ethnic populations or clinical settings.

Examining quality criteria of genetic association studies it emerged that a more stringent design, involving a discovery or screening cohort and an independent confirmation cohort, was necessary.

Having analyzed a large cohort of HSCT donor and recipient pairs, which encompasses almost all unrelated donor HSCT through JMDP in Japan between 1993 and 2000, an understanding of demographic, clinical and genetic risk factors within this population permitted the construction of a study cohort with improved control of confounding variables (supplementary file 2.2).

Before embarking on a larger scale scanning of the extended genomic areas, which committed large resources, it was useful to test the study cohort with known determinants of HSCT outcome, such as SNP and MS markers that showed strong results in previous studies.

3.2. Aims, hypotheses, objectives and study design

3.2.1. Aims

This exploratory study had the aim to confirm or refute previously identified SNP associations with HSCT outcomes, which include acute GVHD, chronic GVHD, relapse and survival.

3.2.2. Hypotheses

A study population exists that allowed the identification of non-HLA genetic associations in a consistent fashion across two independent cohorts, even if the effect size of the association was low.

Polymorphisms in non-HLA genes are associated with HSCT outcomes like acute GVHD, chronic GVHD, relapse and survival.

3.2.3. Objectives

The objectives of this study were:

- Testing of a panel of SNP and MS markers previously associated with HSCT outcome, as a confirm/refute approach in a Japanese population
- Variables: Genotypes of polymorphic SNP and MS markers
- Outcomes: acute GVHD (grade 0 versus grade 1-4, grade 0-1 versus grade 2-4, grade 0-2 versus grade 3-4, grade 0-3 versus grade 4), chronic GVHD (no cGVHD versus limited and extensive disease, no cGVHD and limited disease versus extensive disease), relapse (yes versus no), survival (Kaplan-Meyer analysis)

3.2.4. Study design

This was a case-control study with a two-step screening/confirmation approach. A population was defined by modelling hypothetical cohorts with different risk factors and assessing them by multivariate analysis, and the model with the least clinical confounding chosen (supplementary file 2.2). Selected markers were identified from the previous literature. Standardised laboratory methods were applied to PCR and genotyping. Statistical methods include Bonferroni's correction for the number of included markers, and an additional measure of effect size (previous studies showed that associations with an OR<0.5 or >2.0 have a higher likelihood of being consistent, regardless of p-value).

3.3 Materials and Methods

3.3.1. Population

Donor and recipient HSCT pairs were selected from the JMDP registry of unrelated HSCT. We chose pairs with a diagnosis of acute leukaemia. These form the largest subgroup within HSCT. Cohorts represented 2 samplings of the same national pool, taken from two distinct timeframes (1993-2000, 2001-2005). Inclusion criteria were diagnosis (acute lymphoblastic leukaemia, ALL; acute non-lymphoblastic leukaemia, ANLL), age (4-40 years), conditioning (myeloablative), and stem cell source (bone marrow). All transplants were T-cell replete and received GVHD prophylaxis with either cyclosporin A or tacrolimus with methotrexate and corticosteroids. Analysis of the source as well as the selected HSCT population showed that HLA mismatching, donor age and GVHD prophylaxis regimen (cyclosporin A versus tacrolimus) were the only confounders remaining significant in multivariate analysis (data not shown here).

All donor-recipient pairs were HLA-typed retrospectively to allele level at six loci (HLA-A, HLA-B, HLA-C, HLA-DRB1, HLA-DQB1, and HLA-DPB1). The distribution of HLA matching of the confirmatory cohort was adjusted to that of the screening cohort by matching each sample of the screening cohort with a confirmatory cohort sample of the same HLA class or HLA class combination according to the previous literature (Sasazuki et al., 1998, Morishima et al., 2002) and our own analyses of risk matches/mismatches within this study population (data not shown).

Table 4 in supplementary file 2.3 shows the demographic and clinical characteristics of the selected cohorts. There was no statistically significant difference between the cohorts in the baseline demographic criteria. Tables 5 and 6 in supplementary file 2.3 specify the degree of HLA matching and mismatching. For reasons of comparison, we have used the NMDP/CIBMTR classification of HLA matching (Weisdorf et al., 2008). According to this classification, 357 HSCT pairs have a 8/8 (HLA A, B, C, DRB1) high-resolution allele match, 331 (35.9%) are partially matched (1 mismatch within these HLA loci), and 234 (25.4%) are mismatched (two or more mismatches within these HLA loci). Considering the HLA DQ and DP loci also, only 78 HSCT pairs (8.5%) had a 12/12 allele match. In Japanese, HLA A, B, and C mismatches are associated with risk of acute GVHD. HLA C mismatches, however, have a protective effect on relapse (whilst HLA A, C and B mismatches associate with a risk of death) (Sasazuki et al., 1998, Morishima et al., 2002, Morishima et al., 2007). More recent research has focused on specific allele mismatches, rather than mismatches in loci, aiming to identify non-permissive mismatches for acute GVHD (Kawase et al., 2007) or protective mismatches against relapse (Kawase et al., 2009), as well as risk HLA haplotypes for GVHD (Morishima et al., 2010).

3.3.2. Gene and SNP marker selection

Selection of candidate markers was based on a search of the published literature on genetic associations with HSCT outcomes. As the TaqMan® SNP genotyping platform was used, selection was limited to markers for which standard assays were available for this system.

For some genetic loci the same markers that were associated in other populations were non-polymorphic in Japanese (NOD2, TGFB1). The HapMap data base (www.hapmap.org) was used to identify haploTag SNP for these loci. The SNP markers included in this study are detailed in table 3.1.

3.3.3. Genotyping

Assay information of the used genotyping assays below is supplied in appendix 3.1.

TaqMan genotyping

TaqMan® SNP genotyping assays (Applied Biosystems, Branchburg, USA) were applied for 38 selected SNP according to the maker’s instructions.

Individual genomic DNA (2.1 ng/well) was arranged onto 384-well plates (EDR-384 SII) and samples dried up at 45°C in vacuum over 90 minutes. A 40x reaction mixture, consisting of 2µl/well of TaqMan Universal Master Mix, No Amp Erase® UNG (Applied Biosystems, Branchburg, USA), 0.05µl/well of 40x TaqMan® SNP genotyping assay mix, and 1.95µl/well of purified water, was pipetted robotically directly onto the dried-up 384 well plates. Plates were covered with Micro Amp Optical Adhesive Film 4311971 (Applied Biosystems, Branchburg, USA) before running a polymerase chain reaction (PCR) on a Gene Amp PCR System 9700. PCR conditions consisted of an initial cycle of 95°C (10 min), 40 cycles of 92°C (15 sec) and 60°C (1 min), and a final cooling to 4°C.

Runs were analysed on a 7900HT Sequence Detection System (Applied Biosystems) using the SDS 2.1 (Applied Biosystems) software. Results were exported as txt files into Microsoft office excel for compilation and further processing. Genotypes were allocated considering the forward/reverse direction of the primer, and checked against the genotype distribution of each SNP for a Japanese population in HapMap (www.hapmap.org). Hardy-Weinberg Tests were carried out using the genepop tool (http://genepop.curtin.edu.au/genepop_op1.html).

Luminex genotyping of IL10 SNP

The IL-10 promoter SNPs rs1800872 (-592A/C), rs1800871(-819T/C), and rs1800896 (-1082A/G) were genotyped by PCR-SSO using Luminex Multi-Analyte Profiling system (xMAP) (Luminex Corp., Austin, TX).A fragment of IL-10 promoter region, containing SNPs, -592, -819, and -1082, was amplified by PCR using 5' biotinylated primers (supplementary table 1). The PCR product was denatured and hybridized with the mixture of the six oligonucleotide probes, specific for each base of the corresponding biallelic SNP, immobilized on fluorescent coded microsphere beads. The hybridization mixture containing the PCR product, hybridization buffer (Wakunaga Pharmaceuticals, Hiroshima, Japan), beads mixture and SAPE (Wakunaga Pharmaceuticals, Hiroshima, Japan) were incubated at 55 ºC for 30 minutes. After washing, the hybridized product was analyzed on the Luminex 100.

3.3.4. Statistical analysis

Genotype results were imported into SPSS Statistics v 17.0 (SPSS Inc). Because little is known about effects of non-HLA polymorphisms in HLA-mismatched populations, we used three analytic approaches in order to identify significant associations: 2-sided Fisher's Exact Test (95% confidence intervals) with Bonferroni's correction for significance testing, Odd's Ratio (95% confidence intervals) as a measure of effect size, and independent testing in a confirmatory cohort (without application of multiple testing correction). Variables were the three individual genotypes, and mismatch between donor and recipient genotypes. Outcomes were acute GVHD (0-4), acute GVHD grades 2-4, acute GVHD grades 3-4, acute GVHD grade 4, chronic GVHD, extensive chronic GVHD, relapse, death (overall, at 100 days/1 year/3 years) and survival (as log rank test in Kaplan Meier analysis). For the screening cohort we considered as significant a *p*-value of p=0.05 with Bonferroni's correction for the number of SNP markers tested. As the *p*-value is not a good surrogate marker for effect size, and often small in HSCT-outcome association studies, associations showing Odd's Ratios of ≤0.5 and ≥2.0 (this follows observations of OR's of significant markers in previous studies) were included separately.

Screening and confirmatory cohort data were analysed on the overall cohort in the first instance. In order to reduce confounding by HLA mismatching, we conducted identical analyses on a subgroup with a higher degree of HLA matching (8/8 allele matching at the HLA A, B, C, DRB1 loci, with additional exclusion of combined HLA-DQB1 and DPB1 mismatches; allowing for either a HLA-DQB1 or a HLA-DPB1 mismatch only), similar to previous reports from JMDP(Ogawa et al., 2008), resulting in cohorts of 160 (discovery) and 166 (confirmatory) pairs.

For the screening cohort, we would genotype all 41 chosen SNP markers (table 1) on both donor and recipient cohorts, and conduct overall and subgroup analyses. Markers only that show a corrected *p*-value of <0.05 and/or an OR of ≤0.5 and ≥2.0 in either the overall or the subgroup analyses would be selected for confirmatory typing. If a marker that showed an association that was persisting applying when Bonferroni's correction, we tested other associations of the same marker in the confirmatory cohort even if these would not reach the multiple testing thresholds, in order to capture borderline significance or effect size of genotypes, building on the strength of testing in an independent confirmatory cohort.

Given the high degree of linkage between the CTLA4 as well as the IL10 SNPs in the study, unambiguous haplotypes could be determined directly without recourse to computational methods.

As the distribution of acute GVHD degrees of severity was significantly different between the screening and confirmation cohort, all associations with acute GVHD as outcome were re-analysed after randomising the study population into two different cohorts (using an online based tool for random assignment: http://www1.assumption.edu/users/avadum/applets/RandAssign/GroupGen.html).

Multivariate analysis was performed on the combined cohorts using STATA v 11.0. Odds ratio (OR) of acute GVHD for the selected SNP in multivariate analysis was estimated by a multivariate logistic regression analysis with the adjustment for recipient and donor ages, underlying diagnosis, the use of TBI, ATG, female donor into male transplant, GVHD prophylaxis (tacrolimus versus cyclosporin A), relapse and HLA mismatch to address possible confounding.

Target gene	SNP	Target gene	SNP
CCL4	rs2634508	*NOD2*	rs1077861
CD86	rs1129055		rs1861757
CTLA4	rs231777		rs1861759
	rs231775 (CTLA4-49)		rs6500328
	rs3087243 (CTLA-CT60)		rs2111234
FAS	rs1800682 (FAS-670)		rs2111235
FCGR2A	rs1801274		rs7203344
HLA-E	rs1264457 (HLA-E R128G)		rs17313265
	rs1800795	*TGFB1*	rs1800469 (TGFB1-509)
HSP70/hom	rs2075800		rs2241715
IFNg	rs2069705		rs2241716
IL1A	rs1800587 (IL1A-889)		rs4803455
IL1B	rs16944 (IL1B-511)	*TLR4*	rs12377632
IL2	rs2069762 (IL2-330)		rs1927907
IL10	rs1800896 (IL10-1082)	*TNF*	rs361525 (TNF-238)
	rs1800871 (IL10-819)		rs1799964 (TNF-1031)
	rs1800872 (IL10-592)		rs1800629 (TNF-308)
IL15RA	rs2228059 (IL15RA N182T)		rs1799724 (TNF-857)
IL23R	rs6687620	*TNFRSF1B*	rs1061622 (TNFR2 codon 196)
MIF	rs755622	*VDR*	rs731236
MTHFR	rs1801133 (MTHFR C677T)		

Table 3.1: Selected candidate SNP markers of this study.

3.4. Results

3.4.1. Screening cohort

All transplants (n=460 pairs)

In the screening cohort, involving 460 bone marrow transplants performed between 1993 and 2000, 41 single nucleotide SNP markers were typed in both patient and donor cohorts. Of these, six markers were excluded from analysis, for technical (multiple clusters: rs1927907, rs4803455) and statistical reasons (minor allele frequency <5%: rs1800795, rs6687620, rs361525, rs1800629). All 35 markers included in the analysis were in Hardy-Weinberg equilibrium (defined as p value >0.05, with statistical correction for the number of tested markers).

Thirteen markers, plus the IL10 and CTLA4 haplotypes, showed an association with a HSCT outcome in the donor screening cohort (table 3.2). By significance testing applying Bonferroni's correction, only the marker IL10-1082 and the CTLA4 haplotype showed significant association, while three further markers were selected for confirmatory typing by their effect size (marker CTLA4 rs231775 also showed relevant effect size individually; marker CTLA4 rs231777, which showed no individual association, was included in the confirmatory cohort as part of the CTLA4 haplotype (not listed in table 3.2)). The recipient cohort (table 3.3) revealed 15 markers, plus the CTLA4 haplotype, that were associated with a HSCT outcome. The IL2-330 SNP and the CTLA4 haplotype revealed significant associations above the multiple testing thresholds, while five SNP markers had ORs ≤0.5 and ≥2.0.

HLA-matched subgroup (n=160 pairs)

When analyzing the HLA-matched subgroups of these cohorts, 7 markers and the CTLA4 and IL10 haplotypes in the donor cohort (table 3.4) showed outcome associations, of which 5 markers and the CTLA4 haplotype were included for confirmatory typing. Only the CTLA4 haplotype had a p-value significant when multiple testing correction was applied. In the HLA matched recipient subgroup, three markers showed an association with HSCT outcome, of which one was selected for the confirmation cohort by strength of OR (table 3.5).

3.4.2. Confirmatory cohort

All transplants (n=462 pairs)

Seven markers for the donor cohort (CTLA4: rs231775, rs231777, rs3087243(included for forming the CTLA4 haplotype, only rs231775 and rs3087243 showed an association in the screening cohort); FAS: rs1800682; IL10: rs1800896; NOD2: rs2111235, rs6500328) and ten markers for the recipient cohort (CTLA4: rs231775, rs231777, rs3087243(part of CTLA4 haplotype, only rs231775 and rs231777 showed were associated in the screening cohort) ; FAS: rs1800682; IL2: rs2069762 ; NOD2: 17313265; TGFB1: rs2241716; TNF: rs1799964; TNFRSF1B: rs1061622) were selected for typing in the confirmatory cohort. Firstly; the aim was to confirm associations from the screening cohorts that had significant p-values after multiple testing correction (high significance), then associations that had ORs ≤0.5 or ≥2.0 (large effect size), and thirdly associations within these selected markers that were consistent in both screening and confirmatory cohort (independent cohort confirmation), regardless of multiple testing correction or effect size.

There were no consistent findings in the overall donor confirmatory cohort (table 3.2). In the overall recipient confirmatory cohort (table 3.3), the donor-recipient genotype mismatch of the TNF-1031 SNP (rs1799964) was consistently associated in both screening and confirmatory cohorts with a higher risk of severe acute GVHD (grade 4). The CC genotype of the same marker was associated with acute GVHD grade 4 in the screening cohort, and just escaped significance level in the confirmatory cohort (p=0.06).

HLA-matched subgroups (166 pairs)

In the donor HLA-matched subgroup (table 3.4), none of the markers typed in the confirmatory cohort showed any association. The HLA matched recipient cohort (table 5) revealed a consistent association between risk of chronic GVHD and the GT genotype of rs2069762 (IL2-330).

Table 3.6 summarises the consistent associations of this study, comprising the IL2-330 and TNF-1031 SNP.

Donor - All

Gene	Marker	Discovery cohort – genotype & association	Confirmatory cohort – genotype & association
CTLA4	rs231775	**AA aGVHD** (*p*=0.0043, **OR:=0.049**, CI: 0.028-0.083 GG aGVHD (*p*=0.0071, OR=1.90, CI: 1.19-3.03	n/s
CTLA4	rs3087243	GG aGVHD (*p*=0.0086, OR=1.81, CI:1.18-2.78)	n/s
CTLA4	haplotype	CAA aGVHD (*p*=0.0025, OR=0.59, CI: 0.42-0.82) **CGG aGVHD** (***p*=0.00057**, OR=1.72, CI: 1.27-2.34)	n/s
FAS	rs1800682	**CC aGVHD4** (*p*=0.023, **OR=0.21**, CI:0.37-0.96**)**	n/s
IFNg	rs2069705	CC ext cGVHD (*p*=0.035, OR=0.57, CI: 0.33-0.96) CC relapse (*p*=0.04, OR=0.60, CI:0.37-0.96)	n/t
IL10	rs1800896	**AA survival (*p*=0.001) protective**	n/s
IL10	haplotype	CCA survival (*p*=0.032) protective	n/t
MTHFR	rs1801133	CT cGVHD (*p*=0.03, OR=0.63, CI=0.42-0.96)	n/t
NOD2	rs17313265	CT survival (*p*=0.012) risk CC survival (*p*=0.008) protective	n/t n/t
NOD2	rs2111235	**TT aGVHD4** (*p*=0.016, **OR=0.33**, CI: 0.14-0.80)	n/s
NOD2	rs6500328	**GG ext cGVHD** (*p*=0.011, **OR=0.17**, CI: 0.023-0.78)	n/s
TGFB1	rs1800469	CC aGVHD2-4 (*p*=0.035, OR=1.69, CI: 1.09-2.61) CT aGVHD2-4 (*p*=0.036, OR=0.66, CI: 0.45-0.96)	n/t n/t
TGFB1	rs2241715	GG aGVHD2-4 (*p*=0.047, OR=1.64, CI: 1.06-2.53 GT survival (*p*=0.03) protective GT ext cGVHD (*p*=0.032, OR=0.57, CI:0.34-0.94) GT aGVHD2-4 (*p*=0.037, OR=0.67, CI: 0.46-0.98)	n/t n/t n/t n/t
TNF	rs1799964	TT relapse (*p*=0.041, OR=1.71, CI: 1.04-2.82)	n/t
TNF	rs1799724	CC survival (*p*=0.014) protective	n/t

Table 3.2 (previous page): Results of SNP genotyping on all donor samples. Explanation of abbreviations (apply also to the the donor HLA matched and recipient results tables): aGVHD= acute GVHD, aGVHD4= acute GVHD grade 4, aGVHD 2-4= acute GVHD grade 2-4, cGVHD= chronic GVHD, ext cGVHD= extensive chronic GVHD, survival= p-value for log rank test as explored by Kaplan-Meyer analysis, mismatch= genotype mismatch between donor and recipient, *p*= *p*-value by 2-sided Fisher's Exact Test, OR= Odds Ratio, CI= 95% confidence intervals for OR, n/s= non-significant, n/t= not tested. Bold: Withstanding Bonferroni's multiple testing corrections or have OR ≤0.5 or ≥2, italic: consistent associations. Marker rs231777 had no individual association and is therefore not included in this table, but was included into the confirmatory cohort as part of the CTLA4 haplotype.

Recipient - All

Gene	Marker	Discovery cohort – genotype & association	Confirmatory cohort – genotype & association
CTLA4	rs231775	AA cGVHD (*p*=0.046, OR=1.83, CI: 1.02-3.28)	n/s
CTLA4	rs231777	mismatch aGVHD (*p*=0.004, OR=1.91, CI: 1.24-2.96)	n/s
CTLA4	haplotype	CAA cGVHD (*p*=0.011, OR=1.5, CI=1.11-2.03);	n/s
		CGG cGVHD (***p*=0.0013**, OR=0.62, CI: 0.47-0.83)	n/s
		CGG aGVHD2-4 (*p*=0.019, OR=0.70, CI: 0.52-0.94)	n/s
		TAG aGVHD4 (*p*=0.0071, **OR=3.71**, CI: 1.56-8.86)	n/s
FAS	rs1800682	CC relapse (*p*=0.017, OR=1.68, CI: 1.03-2.74)	n/s
		CT relapse (*p*=0.0025, **OR=0.50**, CI: 0.33-0.78),	n/s
		CT aGVHD (*p*=0.009, OR=1.79, CI: 1.15-2.77)	n/s
		TT cGVHD (*p*=0.024, OR=1.75, CI: 1.03-2.82)	n/s
		TT ext cGVHD (*p*=0.014. OR=1.74, CI: 1.03-2.94)	n/s
HLA-E	rs1264457	mismatch survival (*p*=0.023) risk	n/t
IL1A	rs1800578	mismatch aGVHD2-4 (*p*=0.026, OR=1.69, CI: 1.11-2.56)	n/t
IL1B	rs16944	AA aGVHD (*p*=0.048, OR=0.63, CI: 0.39-0.99)	n/t
		GG aGVHD (*p*=0.032, OR=1.75, CI:1.08-2.82)	n/t
IL15RA	rs2228059	AC survival (*p*=0.024) risk	n/t
IL2	rs2069762	**GG aGVHD4** (***p*=0.0014, OR=4.51**, CI:1.91-10.6)	n/s
		GT survival (*p*=0.0021) protective,	n/s
		TT survival (*p*=0.0061) risk	n/s
NOD2	rs17313265	**CC aGVHD2-4** (*p*=0.036, **OR=2.15**, CI: 1.06-4.37)	n/s
TGFB1	rs1800469	mismatch aGVHD2-4 (*p*=0.02, OR=1.63, CI:1.1-6.4)	n/t
TGFB1	rs2241715	mismatch aGVHD2-4 (*p*=0.015, OR=1.61, CI: 1.09-2.39)	n/t
		mismatch cGVHD (*p*=0.035, OR=1.58, CI: 1.04-2.41)	n/t
TGFB1	rs2241716	**AA ext cGVHD** (*p*=0.0041, **OR=2.58**, CI:1.36-4.87)	n/s
TNF	rs1799964	***mismatch aGVHD4*** *(p=0.022,* ***OR=2.53****, CI:1.16-5.53)*	***mismatch aGVHD4*** *(p=0.0053**,** **OR=3.40**, CI:1.48-7.81)*
		CC aGVHD4 (*p*=0.041, **OR=4.92**, CI:1.27-19.02***)***	CC aGVHD4 trend (*p*=0.06)
TNF	rs1799724	CC survival (*p*=0.02) protective,	n/t
		CT survival (*p*=0.02) risk	n/t
TNFRSF1B	rs1061622	**TT aGVHD4** (*p*=0.023, **OR=4.69**, CI: 1.1-20.11)	n/s

Table 3.3 (previous page): Significant Results of SNP genotyping on all recipient samples. Explanations of abbreviations please see table 2. The marker rs3087243 was not associated individually with chronic or acute GVHD and is not listed here, but was included in the confirmatory cohort forming part of the CTLA4 haplotype.

Donor - HLA

Gene	Marker	Discovery cohort – genotype & association	Confirmatory cohort – genotype & association
CTLA4	rs231775	**GG aGVHD** (p=0.026, **OR=2.02**, CI: 1.09-3.75)	n/s
CTLA4	rs3087243	GG aGVHD (p=0.021, OR=1.97, CI: 1.11-3.50)	n/s
CTLA4	haplotype	CAA aGVHD (p=0.012, OR=0.55, CI: 0.35-0.87) **CGG aGVHD** (**p=0.00097, OR=2.06**, CI: 1.22-5.94)	n/s n/s
IFNg	rs2069705	**CC ext cGVHD (**p=0.036, **OR=0.42**, CI:0.20-0.93) **CT ext cGVHD** (p=0.017, **OR=2.69**, CI: 1.22-5.94)	n/s n/s
IL10	rs1800896	**AA aGVHD** (p=0.038, **OR=0.21**, CI:0.04-0.96)	n/s
IL10	haplotype	**CCG aGVHD** (p=0.027, **OR=4.70**, CI:1.08-20.54)	n/s
MTHFR	rs1801133	**TT aGVHD** (p=0.0016, **OR=12.13**, CI: 2.73-53.90)	n/t
NOD2	rs17313265	**CT relapse** (p=0.013, **OR=2.68**, CI:1.02-7.09)	n/s
TNF	rs1799724	CC survival (p=0.006) protective	n/t

Table 3.4: Results of SNP genotyping on HLA-matched donor samples. Explanations of abbreviations please see table 2.

Recipient - HLA

Gene	Marker	Discovery cohort – genotype & association	Confirmatory cohort – genotype & association
FAS	rs1800682	**CT aGVHD** (*p*=0.0024, **OR=0.39**, CI=0.22-0.71)	n/s
IL1B	rs16944	AA aGVHD (*p*=0.043, OR=0.51, CI:0.27-0.97)	n/t
IL2	rs2069762	GT survival (*p*=0.037) protective *GT cGVHD (p=0.039, OR=1.97, CI=1.05-3.71)* TT survival (*p*=0.039) risk	n/s ***GT cGVHD** (**p=0.00041, OR=3.24**, CI: 1.69-6.20)* n/s

Table 3.5: Results of SNP genotyping on HLA-matched recipient samples. Explanations of abbreviations please see table 2.

marker	genotype	cohort	outcome	*p*=	total	cases all	controls all	cases pos	cases neg	controls pos	controls neg	Odds ratio	OR CI (95%)
***TNF*-1031** **rs1799964** **recipients (all)**	mismatch	Screening	aGVHD 4	0.022	448	28	420	12	16	96	324	2.53	1.16-5.53
	mismatch	Confirmation	aGVHD 4	0.0053	460	24	436	12	12	99	337	3.40	1.48-7.81
***IL2*-330** **rs2069762** **recipients (HLA matched)**	GT	Screening	cGVHD	0.039	160	72	88	39	33	33	55	1.97	1.05-3.71
	GT	Confirmation	cGVHD	0.00041	166	75	92	40	35	23	68	3.24	1.70-6.20
***CTLA4*-CT60** **rs3087243** **donors (HLA matched)**	GG	random 1	aGVHD	0.022	159	58	101	20	38	54	47	0.46	0.27-0.78
	GG	random 2	aGVHD	0.045	166	53	11	22	31	67	46	0.49	0.29-0.83

Table 3.6: SNP markers showing significant association in recipient screening and cohorts.

3.4.3. Further analyses

To understand the mechanism of the associated genotype, the analysis was extended to all IL2-330 genotypes and chronic GVHD outcomes in the confirmatory cohort, and it was found that GT also associated with extensive chronic GVHD (p=0.00022, OR: 5.18, CI: 2.37-11.39). The TT genotype exerts a protective effect against extensive chronic GVHD (p=0.0029, OR: 0.3, CI: 0.13-0.67). This finding was replicated when combining screening and confirmatory cohorts (GT and extensive chronic GVHD: p=0.00055, OR: 2.90, CI: 1.74-5.08; TT and extensive chronic GVHD: p=0.001, OR: 0.40, CI: 0.23-0.71), suggesting that the GG genotype is likely to be the higher risk genotype. No significant association was found with the GG genotype, which was likely due to limited statistical power of this low frequency genotype. Mirroring the analysis by MacMillan et. al. (MacMillan et al., 2003) in the combined cohorts, the G allele showed a trend with risk of extensive chronic GVHD (p=0.07), but not with acute GVHD.

The extended analysis of the TNF-1031 CC genotype in the confirmatory cohort showed that it was also associated with acute GVHD grade 2-4 (p=0.029, OR=3.41, CI: 1.99-5.82). The TNF-1031 donor-recipient genotype mismatch was found to be a risk factor for acute GVHD grade 2-4 (p=0.003, OR=1.93, CI: 1.13-3.30) and grade 3-4 (p=0.002, OR=2.21, CI: 1.13-3.80) in the confirmatory cohort.

The stratification applied in ‘matching’ the degree of HLA mismatch of the confirmatory cohort to that of the screening cohort may have introduced a bias (significantly different distribution of acute GVHD grades, see supplementary table 1). In order to address this, samples were randomly assigned to two cohorts, resolving any significant difference between time frames, and acute GVHD as an outcome measure. Re-analysis of the data for acute GVHD outcomes showed that the genotype mismatch of the TNF-1031 SNP as a risk factor for acute GVHD grade 4 would still hold up as significant (p=0.005, OR=3.26, CI: 1.91-5.58; p=0.021, OR=2.60, CI: 1.52-4.45). The CTLA4-CT60 (rs3087243) SNP showed a consistent association of the GG genotype as protective against acute GVHD (p=0.022, OR=0.46, CI: 0.27-0.78; p=0.045, OR=0.49, CI: 0.29-0.83) in the random cohort analysis of the HLA-matched subgroup.

3.4.4. Multivariate analyses

Multivariate analyses (tables 3.7-3.9) were performed on the combined (screening and confirmatory) cohorts and showed that the TNF-1031 donor-recipient genotype mismatch (acute GVHD grade 4), the CC genotype (acute GVHD grade 4), and the IL2-330 GT genotype (chronic GVHD) are independent risk factors, while the CTLA4-CT60 GG genotype is independently protective against acute GVHD.

***IL2*-330: chronic GVHD**	Univariate		Multivariate	
Variable	OR (95% CI)	*P*-value	OR (95% CI)	*P*-value
Recipient age	1.008 (0.99-1.03)	0.481	1.008 (0.98-1.03)	0.528
Donor age	1.024 (0.99-1.05)	0.106	1.020 (0.99-1.05)	0.195
Female to male transplant	0.900 (0.52-1.57)	0.71	0.876 (0.48-1.60)	0.664
Diagnosis ANLL vs ALL	1.087 (0.70-1.69)	0.711	1.022 (0.63-1.67)	0.929
Total body irradiation (TBI)	1.419 (0.72-2.80)	0.313	1.284 (0.62-2.67)	0.502
Cyclosporine vs tacrolimus	1.024 (0.66-1.59)	0.916	0.996 (0.61-1.62)	0.987
Relapse	0.526 (0.32-0.86)	0.011	0.573 (0.34-0.96)	0.033
Genotype GT	**2.507 (1.60-3.93)**	**0.000066**	**2.273 (1.42-3.63)**	**0.0006**

Table 3.7: Multivariate analysis of the IL2-330 GT genotype as risk factor for chronic GVHD in the HLA-matched subgroup. The genotype is an independent risk factor.

***CTLA4*-CT60: acute GVHD**	Univariate		Multivariate	
Variable	OR (95% CI)	*P*-value	OR (95% CI)	*P*-value
Recipient age	1.017 (0.99-1.04)	0.146	1.020 (0.99-1.05)	0.121
Donor age	0.995 (0.97-1.03)	0.763	0.997 (0.97-1.03)	0.854
Female to male transplant	1.644 (0.93-2.89)	0.085	1.630 (0.89-2.97)	0.111
Diagnosis ANLL vs ALL	1.280 (0.81-2.03)	0.296	1.129 (0.69-1.85)	0.631
Total body irradiation (TBI)	0.847 (0.43-1.68)	0.634	0.916 (0.45-1.86)	0.809
Relapse	1.255 (0.77-2.06)	0.369	1.330 (0.80-2.24)	0.273
Genotype GG	**0.468 (0.29-0.75)**	**0.002**	**0.497 (0.31-0.80)**	**0.004**

Table 3.8: Multivariate analysis of the CTLA4-CT60 GG genotype for acute GVHD (grade 1-4 versus no GVHD) in the HLA-matched subgroup, confirming this genotype as an independent risk factor.

***TNF*-1031: acute grade 4 GVHD** Variable	Univariate OR (95% CI)	*P*-value	Multivariate OR (95% CI)	*P*-value
Recipient age	0.978 (0.95-1.01)	0.109	0.975 (0.94-1.01)	0.112
Donor age	1.038 (1.00-1.08)	0.044	1.033 (0.99-1.07)	0.105
Female to male transplant	0.610 (0.27-1.38)	0.235	0.582 (0.24-1.42)	0.236
Diagnosis ANLL vs ALL	1.001 (0.57-1.76)	0.996	1.148 (0.60-2.18)	0.673
Total body irradiation (TBI)	0.909 (0.40-2.07)	0.819	0.992 (0.39-2.51)	0.987
Anti-thymoglobulin (ATG)	3.562 (0.99-12.73)	0.051	2.246 (0.45-11.15)	0.322
Cyclosporine vs tacrolimus	1.336 (0.75-2.37)	0.321	1.516 (0.80-2.86)	0.198
Relapse	0.115 (0.03-0.48)	0.003	0.154 (0.04-0.65)	0.011
HLA match	0.465 (0.24-0.92)	0.027	0.765 (0.35-1.67)	0.502
Genotype CC	**4.336 (1.7-11.1)**	**0.002**	**3.888 (1.39-10.90)**	**0.010**
Genotype mismatch	**2.905 (1.65-5.1)**	**0.00023**	**2.307 (1.18-4.52)**	**0.015**

Table 3.9: Multivariate analysis of TNF-1031 genotype mismatch and CC genotype as a risk factors for acute GVHD grade 4 in the overall (HLA matched and mismatched) cohort. Both are independent risk factors, with competing effects from HLA matching and relapse.

3.5. Discussion

The exploration study has identified three non-HLA SNP associations with HSCT outcome: The TNF-1031 donor-recipient genotype mismatch with severe GVHD (grade 4, in the overall cohort), the recipient IL2-330 GT genotype with risk of chronic GVHD, and the CTLA4-CT60 GG genotype protective against acute GVHD (grade 1-4; the latter two associations were found in the HLA-matched subgroup only).

TNFα is a cytokine that has been associated with severity of acute GVHD in several previous genetic, gene expression and animal model studies. Teshima et. al. (Teshima et al., 2002) have demonstrated in an animal model that TNF is essential in the development of acute GVHD. Previous data from a Japanese population have shown that the TNF haplotype including TNF-1031 was associated with severe GVHD(Ishikawa et al., 2002), and the TNF-1031C allele was associated with higher TNF expression(Higuchi et al., 1998). A more recent study (Goyal et al., 2010) describes the C allele as a risk factor for grade 3-4 acute GVHD. Therefore an association of the TNF-1031 CC genotype with severe acute GVHD, as seen in this study, albeit showing only a trend in the confirmation cohort, would be biologically meaningful and replicate previous findings. However, the TNF-1031 CC genotype displays strong linkage disequilibrium with HLA, in particular with HLA-B61(Higuchi et al., 1998). This may explain our finding of the strong association between donor-recipient genotype mismatch and acute GVHD grade 4 in the overall cohort only, but not in the HLA matched subgroup. Our study did not have the power to elucidate if any particular TNF-1031 genotype mismatch combinations carry a higher risk. As the group affected with acute GVHD grade 4 is small (just above 5%), further studies should confirm this result independently. The finding that genotype mismatch was also associated with grade 2-4 as well as grade 3-4 acute GVHD (which are larger groups) in the confirmatory cohort gives further indication that the genotype mismatch is likely to be a risk factor for acute GVHD. Nevertheless, the strength and consistency of this association mean that it is potentially a strong discriminator for prediction of the most severe form of acute GVHD (grade 4), which could be exploited in clinical practice.

The IL2-330 (rs2069762) SNP has an almost identical genotype distribution between Caucasian and Japanese populations (Caucasian: TT: 0.536, GT: 0.464, GG: 0; Japanese (this study): TT: 0.450, GT: 0.440, GG: 0.110). The G allele is the known high-expressing allele, and high levels of IL2 have been described to correlate with severity of acute GVHD (Das et al., 2001, MacMillan et al., 2003). A previous study from North America on a cohort of similar time frame to our screening cohort (MacMillan et al., 2003) reported an association between the recipient IL2-330 G allele and acute GVHD; and a trend towards risk of chronic GVHD. In our study, we found an association of the GT genotype with risk of chronic GVHD. More detailed analysis showed that the low frequency GG genotype is likely to be the highest risk genotype for chronic GVHD, whilst GT associated with risk, and TT with protection. Our findings therefore confirm those of the previous study even across different ethnic populations, qualifying this marker as a predictor of chronic GVHD risk.

The effect of the CTLA4-CT60 polymorphism on HSCT outcomes was studied previously, in settings of HLA matched sibling donors(Perez-Garcia et al., 2007, Murase et al., 2011) and matched unrelated donors (Vannucchi et al., 2007) in Caucasian populations. In HLA matched sibling transplants, the donor G allele was associated with increase of relapse and worse survival, while the AA genotype was linked to risk of acute GVHD. The findings in matched unrelated donor HSCT were similar, with the donor AA genotype associating with severe acute GVHD (grade 3-4), but risk of G allele or GG genotype with relapse or survival was not observed. Our findings are in accordance with these results, identifying the GG genotype as protective against acute GVHD (remarkably, the screening cohort result indicated a risk of the GG genotype with acute GVHD (see table 4) – a finding completely reversed by the randomisation). We could not establish any risk of the GG genotype with relapse or survival, or the AA genotype with acute GVHD. This may be explained by the fact that in the Japanese population, the GG genotype is more prominent than in Caucasians, while the AA genotype is more rare (HapMap data of genotypes: Caucasians: AA: 0.208, AG: 0.513, GG: 0.283; Japanese: AA: 0.047, AG: 0.389, GG: 0.542). The risk of acute

GVHD, relapse or survival associated with this marker may therefore be lower in the Japanese population, compared to Caucasians.

The results raise also some methodological questions which are beyond the scope of this study:

- By incorporating a measure of effect size into the statistical analysis, this study extends beyond previous approaches focussing on significance and correction for multiple testing. Our results suggest that this approach may be more sensitive, but because of limited power and small number of identified associations no conclusions could be made about the impact on sensitivity and specificity, and statistical multiple testing burden.
- Despite the effort to control variability of study population characteristics, reproducibility of associations remains low and appeared to be dependent on distribution of these characteristics amongst the cohorts. This may be due to the overall small effect size of the associations, confounders in the study cohort, or both. A more comprehensive typing (full typing of all markers on both screening and confirmation cohort) and analysis would be required.

Clinical and population characteristics of study cohorts may explain some of the contradictory results observed in previous studies, therefore careful design of study cohorts and control of confounders should receive more attention. The growing number of HSCT may facilitate in the future the availability of larger, genetically and clinically more homogeneous study cohorts; however, the changing and expanding indications of HSCT are likely to prove a challenge.

In conclusion, this study demonstrates that non-HLA genetic association with HSCT outcomes do exist and can be detected even in the HLA-mismatched setting. Such associations could be useful for application in future clinical practice in this clinically highly relevant population. These findings should be verified by larger studies also on populations of different ethnicities.

4. RESULTS

4.1. Pooled DNA PCR and genotyping – 1st and 2nd screening steps

4.2. Individual Genotyping

4.3. Further exploration of a susceptibility region by SNP typing

4.4. Genetic susceptibility regions for moderate-severe acute GVHD

4.1. Pooled DNA PCR and genotyping – 1st and 2nd screening steps

4.1.1. Technical quality aspects

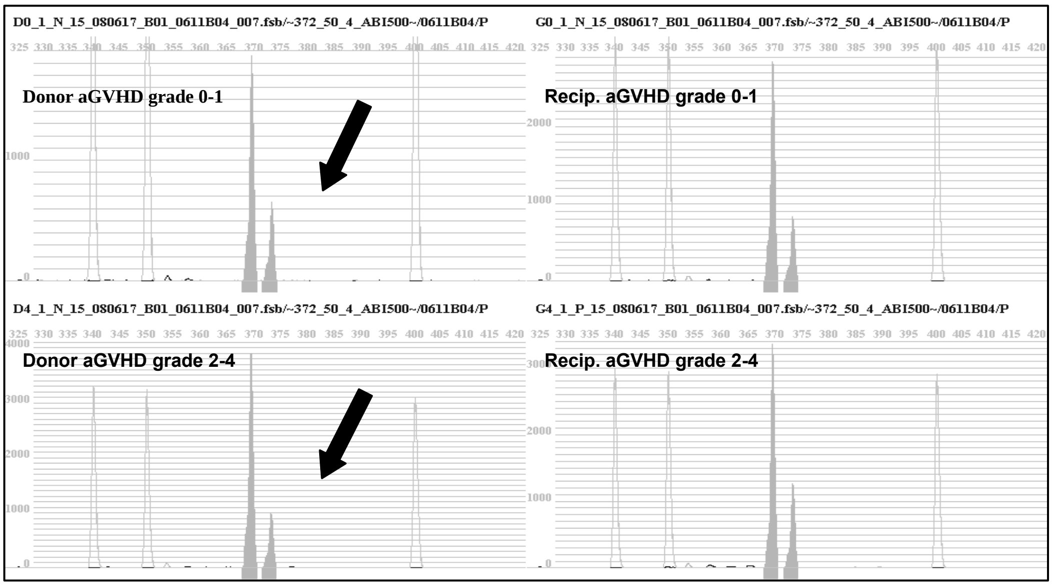
In the first instance, the full set of marker plates for the first screening, involving 4,321 MS markers, was typed in all four pools. The quality of peak signals was assessed within the Run 3730 Data Collection version 2.0 software (Applied Biosystems). The Capillary Viewer would indicate peak signals that were excessively high, adequate or absent.

Following import and analysis of typing data in GeneMapper version 3.5 (Applied Biosystems), peak sizes and quality of size standardisation were analysed. In particular peak sizes that were off-scale, and samples with inadequate size standard became apparent.

Finally, peak signal quality was evaluated in MultiPeaks version 0.21.1 (a Java- application also supplied by Applied Biosystems). For pooled DNA genotyping, consistency of peak sizes and quality amongst pools was of particular importance. Peak sizes >30,000 and <200 flourescence units (fu) were classified as typing error. For the purpose of consistency, however, stricter quality criteria were applied: A minimum peak height of 1000 fu for higher frequency alleles (>15%) and 500 fu for lower frequency alleles (<15%), absence of noise at the baseline, and no more than 50% peak height variation between the four pools. The overall peak pattern would be consistent amongst pools. Figure 4.1 shows a typical four-pool graph of a marker with a significant association.

The initial error rate was 11.36%, the majority of these were high or low signal errors. With re-typing applying different DNA dilutions, and re-PCR, the error rate was reduced to 0.8% (details see appendix 4.1).

First Screen



Second Screen

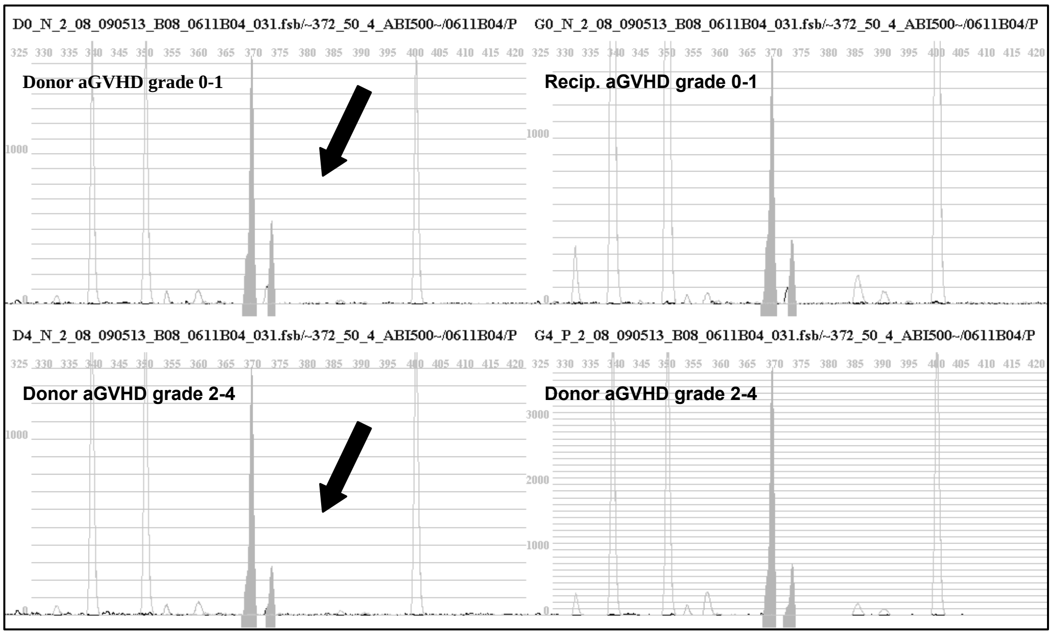


Figure 4.1: Example of a peak height graph of marker D6S0035i as displayed by the MultiTyper (Applied Biosystems®) software. The images show the results of the four pools (top image: first screening, bottom image: second screening). Allele 2 has a higher peak height in the donor GVHD 0-1 group, suggesting a protective effect. This is replicated in the 2nd screen.

4.1.2. Results of pooled DNA screening

First pooled DNA screening (Discovery Cohort)

In the 1st pooled DNA screening, 4,321 microsatellite markers were typed in four DNA pools (donors of recipients with GVHD grade 0 and 1, donors of recipients with GVHD grade 2-4, recipients with GVHD grade 0 and 1, and recipients with GVHD grade 2-4).

Allele frequency differences were analysed in two directions, separately for each individual allele (Fisher's exact test for 2x2 Chi Square test) and for each marker as a whole (Fisher's exact test for 2xm Chi Square test):

- Between donors of recipients with GVHD grade 0 and 1 and donors of recipients with GVHD grade 2-4
- Between recipients with GVHD grade 0 and 1, and recipients with GVHD grade 2-4.

The results were collated using a custom-built analysis and database system. Peak height data were translated into allele frequencies, and significance tests performed as described in the methodology section.

This system automatically extracted the strongest associated allele for each marker (2x2), and all markers associated by 2xm analysis (result details see table). While all markers positive by 2xm analysis also had at least one allele associated by 2x2 analyses; not all markers who carried an associated allele were also positive by 2xm analysis.

In first screening analysis (tables 3.1, 3.2), 34 (0.79%, donor) and 35 (0.81%, recipient) markers were excluded because of technical failure in PCR or genotyping.

103 (2.38%, donor) and 105 (2.43%, recipient) markers were non-polymorphic. This is an expected result as the microsatellite marker panel

used in this study contains microsatellites that are polymorphic for some, but not all populations.

1^{st} pooled DNA screening results:

In the donor pools analysis, 1016 alleles (2x2 test) and 624 MS markers (2xm test) showed an association with acute GVHD grade 2-4, either as a risk or protective. In the recipient analysis, 931 alleles and 543 MS markers were associated.

All markers that were positive by 2xm or 2x2 analyses were typed again in the 2^{nd} screening step (tables 4.1, 4.2). Inclusion of markers positive only for 2x2 but not for 2xm analysis was a measure of additional sensitivity for the second screening step. Naturally, the first screening step contained many false positive associations:

- Statistically false positives, estimated as 5% of 4,321 markers (that would equal 216 markers in the 2xm analysis) or 5% of 20,197 (donor analysis) or 20,132 (recipient analysis) alleles (which would lead to 1010 (donor analysis) and 1007 (recipient analysis) false positives in the 2x2 analyses).
- Errors introduced by DNA pooling process (e.g. variation in number of DNA copies per pool).
- Inherent artefacts of microsatellite typing (e.g. +A alleles, preferential amplification).

Second pooled DNA screening (Confirmation Cohort)

The main purpose of the secons pooled DNA screening step was to eliminate false positive associations by independent confirmation. Following 2nd pooled screening, identification of true and false positives was much more specific as the independent typing, in addition to p-value, introduces criteria which could be used to distinguish true and false positive associations:

- Association of the same allele within a marker
- Consistency of the odd's ratio ('risk', 'protective') of the same allele between the two screening steps
- Consistency of the microsatellite pattern and typing quality (as assessed by the peak image).

Tables 4.1 and 4.2 give the details of the 1st and 2nd screening steps separate for the donor GVHD 0-1 versus donor GVHD 2-4 analysis, and the recipient results accordingly. Results for 2x2 and 2xm analysis were also separated.
All markers that showed a positive 2xm or 2x2 result in first screening (1016 (23.51%, donor analysis) and 931 (21.54%, recipient analysis) were typed again in second screening, but analysed separately for 2x2 and 2xm Chi-Square tests.

In second screening, 6 (donor analysis) and 10 (recipient analysis) markers showed a non-polymorphic results. These markers were typed again in all screening pools of 1st and 2nd result, using a new primer set. The non-polymorphic result was confirmed (hence, the initial polymorphic result in 1st screening represented a false positive association). We also excluded 17 (donor analysis) and 13 (recipient analysis) markers for which we technically could not reproduce the positive association in first screening despite repeated attempts of PCR and typing (as described above). Except for those markers displaying non-polymorphism or PCR failure, all markers had satisfactory allele allocations as described in section 2.12.3.

2nd pooled DNA screening results:

In the donor analysis, 335 alleles (6.44%) had a significant result by p-value (<0.05), while in the 2xm analysis 178 markers (27.73%) were significant. In recipients, 314 alleles (6.32%) and 141 markers (25.97%) were confirmed.

Determining consistency of associations across the two screenings

In the next step, false positive markers in the 2x2 analysis were excluded by identifying and selecting those markers that shared the same associated allele, and had an Odd's ratio that consistently pointed in the same direction (towards risk/protection).

When inspecting the results of positive markers that did not share the same most strongly associated allele within the marker, we noticed that many markers had several positive alleles. On inspection of the peak image we found that occasionally presumed artefacts represent the strongest allele, with a 'true' allele, which showed strongest allele association in the other screening, 'obscured'. Therefore we decided to determine all associated alleles in markers positive for 2x2 analysis and 2xm analysis (as we assumed that if 2x2 associations of the strongest allele within a marker would not result in 2xm-positivity, it would be unlikely that an allele with an even weaker association would have had a significant effect on risk/protection). Markers that would have a shared associated allele and be 2xm positive were entered into the odd's ratio analysis.

Pooled DNA screening results – same allele and Odd's ratio direction:

Eventually, 97 (donor analysis) and 74 (recipient analysis) alleles would remain with a p-value of <0.05 for 2x2 analysis in both screenings, a shared allele and consistent odd's ratio direction; with 57 (donor) and 40 (recipient) markers by 2xm analysis, accordingly.

Donors		markers overall	%	alleles 2x2	%	markers 2x2	%
1st screen	tested	4321	100	20197	100	4321	100
	positive	1016	23.51	1016	5.03	642	14.86
	negative	3175	73.32	19181	94.97	3548	82.11
	non-polymorph	103	2.38	N/A		97	2.24
	failed	34	0.79	N/A		34	0.79
	expected false pos 2xm	216	5	1009	5	216	5
	difference pos-false pos 2xm	800	18.51	7	0.03	425	9.86
2nd screen	tested	1016	100	5205	100	642	100
	positive	335	32.97	335	6.44	178	27.73
	negative	658	64.77	4870	93.56	442	68.69
	non-polymorph	6	0.59			6	0.93
	failed	17	1.67			17	2.65
	same allele as 1st screen allele			125			
	not same allele			210			
	- 2xm pos AND 2nd allele			47			
	sum same allele			172			
	same OR direction			**97**	10.42	**57**	10.50
	expected false pos 2xm			51	5	32	5
	difference pos-false pos 2xm			46		25	

Table 4.1: Results of the pooled donor GVHD 0-1 v donor GVHD 2-4 analysis

Recipient		markers overall	%	alleles 2x2	%	markers 2x2	%
1st screen	tested	4321	100	20132	100	4321	100
	positive	931	21.54	931	4.62	543	12.57
	negative	3252	75.22	19201	95.38	3641	84.26
	non-polymorph	105	2.43	103	0.51	105	2.43
	failed	35	0.81	35	0.17	32	0.74
	expected false pos	216	5	1006	5	216	5
	difference pos-false pos	715	16.55	-75	-0.38	327	7.57
2nd screen	tested	931	100	4969	100	543	100
	positive	314	33.73	314	6.32	141	25.97
	negative	594	63.80	4655	93.68	386	71.09
	non-polymorph	10	1.07	N/A		10	1.84
	failed	13	1.40	N/A		6	1.10
	same allele as 1st screen allele			136			
	not same allele			208			
	- 2xm pos AND 2nd allele			27			
	sum same allele			163			
	same OR direction			**74**	7.95	**40**	7.37
	expected false pos 2xm			46.55	5	27.15	5
	difference pos-false pos 2xm			27.45		12.85	

Table 4.2: Results of the pooled recipient GVHD 0-1 v recipient GVHD 2-4 analysis

Further steps of selecting associated microsatellite markers

The confirmation of the first screening results by independent did reduce, but not completely eliminate false positive associations. The number of associations found after analysis of the second screening step would still exceed the number of expected true positives (as compared to previous GWAS using this approach) as well as the resources allocated to individual genotyping. Therefore, within the 2x2 datasets we used a two-step selection system to identify strong association and high quality typing markers for preferential selection for individual genotyping, aiming to eliminate markers falsely positive for lower quality genotyping.

1st step:

- Selection by allele frequency (=frequency of a certain allele in the pool): Alleles with a consistent allele frequency of >0.10 higher were selected. Low frequency alleles had a lower fluorescent signal peak height (as peak signal height correlates with allele frequency in the pool; a low signal at the border of technical resolution and/or a low allele frequency at the border of statistical power were more likely to represent artefacts), and may represent new mutations within the microsatellite; and/or:
- 2xm positive: An allele association also resulted in the marker being positive in the 2xm analysis. This was more likely to the case in markers with smaller number of alleles (=number o alleles of a marker), increasing the statistical power of each allele.

2nd step:

- The fluorescent signal height was determined. The signal height depends on the number of allele copies in the sample, hence on the effectiveness of PCR. The genotyping process is calibrated to give accurate readings of fluorescent signals between 500-30,000 fu, i.e. the allele frequency distribution within one marker could expected to be proportionally accurate, even with a variation of amount of DNA in the sample. Signals below or above this range are prone to distort the distribution of allele frequencies (i.e. an overall low signal may miss or misread low frequency alleles, while a very high signal may exaggerate the reading for high frequency alleles). A signal of 1000 fu or above (but <30,000 fu) of the associated allele was regarded as of highest quality.

- Inspection of the microsatellite pattern: Consistency in the microsatellite pattern in all eight pools (allele number, sequence, peak height).

Associated markers remaining following genotyping quality assessment:

This process resulted in a 'shortlist' of 48 ms markers (31 in the donor analysis, 17 in the recipient analysis) selected for individual genotyping (table 3.3).

4.2. Individual genotyping

4.2.1. Individual genotyping of the alleles found associated with GVHD grade 2-4 in the pooled screenings

Most artefacts introduced by pooled PCR and genotyping (as described above in methodology section) were readily identifiable by ‘test-typing’ on a small number of individual samples, therefore all remaining 48 markers were subjected to typing on 14 samples each that stem from a healthy Japanese control population, unrelated to this study. This step eliminated 9 (donor) and 2 ms markers (recipient) from further analysis due to pooling artefacts, copy number variation error or discovered non-polymorphism.

Eventually 19 (donor) and 11 (recipient) markers underwent individual genotyping on the full sample set (922 donors or recipients). Three (donors) and 4 (recipient) markers with weaker associations, despite passing the criteria for individual genotyping, were eventually not individually typed due to resource restrictions. The overview results of the individual genotyping are presented in table 4.3.

After applying Hardy-Weinberg Equilibrium tests for genotyping quality control, 10 MS markers were confirmed to have an association with Grade 2-4 acute GVHD that was consistent in both pooled DNA screenings and individual genotyping (tables 4.4-4.6) in univariate analyses. Associations with *p*-values that would withstand application of Bonferroni’s correction for the total number of alleles in individual genotyping (n=123, 2x2 analysis: corrected threshold for *p*=0.05 association: *p*=0.0004065; *p*=0.1 trend: *p*=0.0008131) and markers (n=30, 2xm analysis: corrected threshold for *p*=0.05 association: *p*=0.00166, *p*=0.1 trend: *p*=0.00333), as well as those showing a trend with correction, were indicated.

Five further markers (D16S0452i, D5S1173i, D3S1225i, D14S0499i and AJ133269.1_180046) showed significant associations but failed the HWE for both case and control cohorts. From a genotyping quality control perspective these markers were therefore excluded from further analysis. Nevertheless, from a biological perspective failed HWE does not necessarily imply an invalid result. Due to the underlying malignant disease which is in part genetically determined, both the recipient as well as the HLA-matched donor population cannot be expected to reflect an allele distribution that would be expected in a 'healthy' population.

Results after applying multiple testing correction statistics

Four markers (recipient D5S424, donor D6S0035i, D1S0818i, D17S0219i), demonstrated associations by 2xm and/or 2x2 analyses that had *p*-values that held up against statistics for multiple testing correction, while one further marker (D6S0330i) showed a trend when Bonferroni's correction was applied.
When including markers that failed the HWE test, one further marker (D16S04521i) would show an association.

Target gene	MS identifier 2	Donor/ Recipient	Test typing	Full individual typing Yes/No	outcome individual typing
SNRPN	D15S122	D	passed	Y	not confirmed
AGPAT4	D6S0330i	D	passed	Y	confirmed
PDE4B	D1S0716i	D	passed	N	Not tested
ALKBH1	D14S594	D	failed	N	-
TRAF7	D16S0452i	D	passed	Y	failed HWE
NFKBIZ	DISO7_10001184	D	failed	N	-
TIAF1	D17S0406i	D	passed	Y	artefact
ELTD1	D1S0818i	D	passed	Y	confirmed
ITPKB	D1S1143i	D	passed	Y	not confirmed
MCM2	D3S3607	D	passed	Y	not confirmed
SMARCAL1	D2S0809i	D	passed	Y	artefact
EDAR	D2S1281i	D	failed	N	-
CD86	D3S1225i	D	passed	Y	failed HWE
FBXW7	D4S0270i	D	passed	Y	not confirmed
C1QTNF2	D5S403	D	failed	N	-
MAPK14	D6S0035i	D	passed	Y	confirmed
ETV1	D7S0119i	D	passed	Y	not confirmed
HSPB1	D7S1218i	D	passed	Y	not confirmed
DLG5	D10S0603i	D	passed	N	not tested
TCF8	D10S565	D	passed	Y	not confirmed
CAV1	AJ133269.1_180046	D	passed	Y	failed HWE
C1QBP	D17S0113i	D	failed	N	-
EIF4A3	D17S0294i	D	passed	N	Not tested
DSCAM	D21S0184i	D	failed	N	-
ATF4	D22S428	D	failed	N	-
BTK	DXS0923i	D	failed	N	-
IL1RAPL2	DXS0629i	D	passed	Y	confirmed
IL1RAPL2	DXS0151i	D	passed	Y	confirmed
TGM3	AL031678.2_90137	D	failed	N	-
SOCS3	D17S0219i	D	passed	Y	confirmed
LTB	TNF C	D	passed	Y	trend only
F2RL1/S100Z	D5S424	R	passed	Y	confirmed
HRK	D12S0781i	R	passed	Y	multiple alleles
MAP3K7	D6S0738i	R	passed	N	not tested
NFKBIZ	DISO7_10001184	R	failed	N	-
C1QA	D1S1655i	R	passed	Y	not confirmed
AKT3	D1S1335i	R	passed	Y	confirmed
NMI	D2S1334i	R	passed	Y	not confirmed
EDAR	D2S1281i	R	failed	N	-
CSF2	D5S1174i	R	passed	Y	non-polymorphic
IL7R	D5S1173i	R	passed	Y	failed HWE
RNASE6	D14S0499i	R	passed	Y	failed HWE
MMP25	D16S3082	R	passed	Y	not confirmed
DDX42	D17S0271i	R	passed	Y	confirmed
TRIM26		R	passed	N	not tested
TBL1X	DXS0324i	R	passed	Y	confirmed
SSTR2	chr17.fa.O7frz.78835314	R	passed	N	Not tested
ISG20	D15S0049i	R	passed	N	Not tested

Table 4.3 : overview results of individual genotyping

Target Gene	Marker name (internal)	Database name	Donor/Patient	allele size	allele no	1st screen 2xm	1st screen 2x2 p-value	1st screen OR	2nd screen 2xm	2nd screen 2x2 p-value	2nd screen OR
F2RL1/S100Z	0507E03	D5S424	P	117.7	05	0.00465911	0.00123516	1.581714	2.37636E-09	5.88101E-10	2.29902
MAPK14	0611B04	D6S0035i	D	373.2	02	0.0331471	0.0331471	0.688211	0.00163933	0.00163933	0.595028
ELTD1	0111F11	D1S0818i	D	172	01	0.000310432	3.58175E-05	1.902177	0.0167968	0.0167968	1.470116
IL1RAPL2	2310B01	DXS0151i	D	466.6	04	0.000451	0.000451	1.783574	0.000105178	0.000105	1.864524
SOCS3	T002C05	D17S0219i	D	206	03	0.000157143	4.3431E-05	0.42191	0.0111833	0.00396346	0.471879
IL1RAPL2	2309D05	DXS0629i	D	393.4	03	0.151619	0.030286	1.45962	0.0201712	0.006152	1.568938
TBL1X	2309A04	DXS0324i	P	385.1	01	0.001843	0.001843	0.604196	0.0259134	0.025913	0.693579
DDX42	1704G02	D17S0271i	P	222	01	0.0360375	0.0128895	0.676094	0.0397464	0.0397464	0.743281
AGPAT4	0606E02	D6S0330i	D	166.6	07	0.000453657	0.000453657	1.616777	0.0123369	0.0123369	1.40784
AKT3	0109C12	D1S1335i	P	90.3	03	0.00030278	0.000182015	1.637257	0.0111414	0.00302767	1.488903
TRAF7	1601E07	D16S04521i	D	271	12	0.00002303	0.00002303	0.331837	0.0008224	0.00035560	0.535539
CD86	0310G01	D3S1225i	D	97.4	03	0.000021968	0.000021968	0.370631	0.0268393	0.0268393	0.647246
CAV1	137G11	AJ133269.1_180046	D	384.1	05	0	0.000000087	4.635323	0.002575	0.0041277	2.163354
RNASE6	1406B07	D14S0499i	P	359.9	02	0.00121386	0.000101171	1.760132	0.00000002	0.000000001	2.354878
IL7R	0508H03	D5S1173i	P	146.7	04	0.001375	0.00007793	0.634464	0.00000013	0.000000116	0.529155

Table 4.4: Genotyping results from both pooled screening steps of 15 microsatellite markers that showed an association in the individual genotyping.

TargetGene	Marker name (internal)	Database name	Donor/Patient	allele size (bp)	Associated allele no	aGVHD 01-24 2xm *p*=	aGVHD 01-24 2x2 *p*=	2x2 Odds ratio	95% CI lower	95% CI higher	HWE decision
F2RL1/S100Z	0507E03	D5S424	P	117.7	05	0.0004*	0.002017	1.338207	1.113486	1.608281	**ok**
MAPK14	0611B04	D6S0035i	D	373.2	02	0.0004*	0.00035*	0.685984	0.558405	0.84271	**ok**
ELTD1	0111F11	D1S0818i	D	172	01	0.0007*	0.0000783*	1.519239	1.242103	1.858208	**ok**
IL1RAPL2	2310B01	DXS0151i	D	466.6	04	0.0066	0.007038	1.41669	1.125021	1.783976	**ok**
SOCS3	T002C05	D17S0219i	D	206	03	0.005	0.000275*	0.418673	0.259705	0.674948	**ok**
IL1RAPL2	2309D05	DXS0629i	D	393.4	03	0.016	0.001315	0.7778	2.698158	4.312269	**ok**
TBL1X	2309A04	DXS0324i	P	385.1	01	0.021	0.013253	0.753511	0.603937	0.940129	**ok**
DDX42	1704G02	D17S0271i	P	222	01	0.0404	0.008597	0.71826	0.563124	0.916134	**ok**
AGPAT4	0606E02	D6S0330i	D	166.6	07	0.071	0.00074†	1.38941	1.150105	1.678508	**ok**
AKT3	0109C12	D1S1335i	P	90.3	03	0.195	0.032222	1.226761	1.017861	1.478534	**ok**
TRAF7	1601E07	D16S04521i	D	271	12	0*	0.0002735*	0.672402	0.54339	0.83204	**failed**
CD86	0310G01	D3S1225i	D	97.4	03	0.029	0.0080907	0.75196	0.60978	0.92729	**failed**
CAV1	137G11	AJ133269.1_180046	D	384.1	05	0.354	0.0279587	1.391733	1.04506	1.85340	**failed**
RNASE6	1406B07	D14S0499i	P	359.9	02	0.137	0.0076539	1.337914	1.08112	1.65570	**failed**
IL7R	0508H03	D5S1173i	P	146.7	04	0.0056	0.0122439	0.7072632	0.427571	0.98156	**failed**

Table 4.5: individual genotyping associations of microsatellite markers (2xm) and alleles (2x2) with aGVHD grade 2-4. *P*-values shaded dark (*) are significant against multiple testing correction; *p*-values shaded bright (†) show a trend. Included in this table are the five markers failing HWE testing, one of these showing an association.

Target Gene	Marker	allele no	aGVHD 01-24 *p*=	total	cases all	controls all	cases pos	cases neg	controls pos	controls neg	Odds ratio	lower CI (95%)	higher CI (95%)
F2RL1/S100Z	D5S424	05	0.00202	1842	842	1000	446	396	457	543	1.338	1.1135	1.60828
MAPK14	D6S0035i	02	0.00035	1824	832	992	207	625	323	669	0.686	0.5584	0.84271
ELTD1	D1S0818i	01	0.000078	1832	842	990	619	223	634	347	1.519	1.2421	1.85821
IL1RAPL2	DXS0151i	04	0.00704	1297	595	702	228	367	214	488	1.417	1.125	1.78398
SOCS3	D17S0219i	03	0.00028	1826	838	988	24	814	65	923	0.419	0.2597	0.67495
IL1RAPL2	DXS0629i	03	0.00132	1291	591	700	307	284	426	274	0.778	0.6234	0.97071
TBL1X	DXS0324i	01	0.01325	1271	585	686	264	321	358	328	0.754	0.6039	0.94013
DDX42	D17S0271i	01	0.0086	1824	834	990	129	705	201	789	0.718	0.5631	0.91613
AGPAT4	D6S0330i	07	0.00074	1828	838	990	360	478	348	642	1.389	1.1501	1.67851
AKT3	D1S1335i	03	0.03222	1842	842	1000	364	478	383	617	1.227	1.0179	1.47853

Table 4.6: Allele numbers and Odds Ratio calculation for associated alleles from individual genotyping, illustrating the effect sizes of the associations.

4.2.2. HLA subgroup analysis of alleles

Mirroring the analysis of SNP markers in the pilot study, the effects of the alleles were also analysed in a subgroup of higher HLA matching. HLA matching was defined as high-resolution (allele level) match for HLA-A, B, C, DRB1 (i.e. 8/8 matching), with allowing for either a HLA-DQB1 or DPB1 only, and including 12/12 matches. Results of this subgroup analysis are presented in table 4.7. While some of the associations were limited to the HLA mismatched group only, others showed an effect on both degrees of matching, and some associations appeared to have a larger effect on the HLA-matched subgroup than on the mismatched one. Two markers had other alleles than the one identified by pooled screening associated with acute GVHD grade 2-4. In both cases, the markers had two main alleles only, hence could be analysed like a single nucleotide polymorphism (SNP) marker. While one allele of these markers indicated a GVHD risk, the corresponding ‘opposite’ allele would have a protective effect, as the OR of the associations showed (table 4.8.)

4.2.3. Genotype analysis with HLA subgroup analysis

An analysis of genotypes was also conducted where possible. As MS have many alleles, and therefore a large number of possible allele combinations forming a genotype, such analyses would have only be useful with a reasonable frequency of the genotype in question. A limit of an allele frequency of 0.1 or above was applied. Primarily the homozygosity and heterozygosity of the associated allele versus the remaining genotypes was investigated; and then all other genotypes that had a frequency of 10% or more were analysed.

Five markers showed an association with acute GVHD grade 2-4 of the homozygous genotype of the same associated allele (table 4.10); while four further markers showed associations of other genotypes with acute GVHD grade 2-4 (tables 4.11, 4.12). All of the latter four markers had only two or three major alleles accounting for >90% of the total allele frequency; the genotypic analysis showed that the genotype of the ‘oppositional’ allele had a stronger (and opposite) effect as compared to the allelic effect of the originally identified allele. One example was the above mentioned marker 0611B04 (D6S0035i): Whilst the allelic screening suggested that the minor allele 02 had a protective effect, it is in fact the major homozygous allele 01 genotype that constituted a risk of moderate-severe acute GVHD.

marker info		all alleleic association					HLA mismatched			HLA matched		
TargetGene	**Marker name**	**Donor/Patient**	**allele no**	**aGVHD 01-24 2xm *p*=**	**aGVHD 01-24 2x2 *p*=**	**2x2 Odds ratio**	**aGVHD 01-24 *p*=**	**Odds ratio**	**95% CI**	**aGVHD 01-24 *p*=**	**Odds ratio**	**95% CI**
F2RL1/S100Z	D5S424	P	05	0.0004	0.002017	1.338207	**0.0107**	1.349883	1.1-1.7	**0.066**	1.347273	0.9-1.8
MAPK14	D6S0035i	D	02	0.0004	0.00035	0.685984	**0.02457**	0.74731	0.6-0.9	**0.00273**	0.579385	0.4-0.8
ELTD1	D1S0818i	D	01	0.0007	0.0000783	1.519239	**0.0011**	1.52398	1.2-2.0	**0.051**	1.404808	1.0-2.0
IL1RAPL2	DXS0151i	D	04	0.0066	0.007038	1.41669	**0.071**	1.30469	0.98-1.70	**0.019**	1.628809	1.1-2.4
SOCS3	D17S0219i	D	03	0.005	0.000275	0.418673	**0.000872**	0.384298	0.2-0.7	**0.115**	0.480896	0.2-1.1
IL1RAPL2	DXS0629i	D	03	0.016	0.001315	0.7778	**0.06**	0.768652	0.6-1.1	**0.005**	0.575585	0.4-0.85
TBL1X	DXS0324i	P	01	0.021	0.013253	0.753511	**0.298**	0.85887	0.7-1.1	**0.009**	0.598058	0.4-0.9
DDX42	D17S0271i	P	01	0.0404	0.008597	0.71826	**0.0316**	0.713717	0.5-0.9	**0.155**	0.739331	0.5-1.1
AGPAT4	D6S0330i	D	07	0.071	0.00074	1.38941	**0.027**	1.304192	1.0-1.6	**0.00669**	1.571115	1.1-2.1
AKT3	D1S1335i	P	03	0.195	0.032222	1.226761	**0.01824**	1.323822	1.1-1.7	**0.685**	1.068627	0.8-1.5

Table 4.7: Association of alleles separated by degree of HLA matching. The effect of polymorphisms is either visible mainly in the HLA-matched subgroup (MAPK14, AGPAT4), or mainly in the HLA-mismatched subgroup (F2RL1, ELTD1, SOCS3, DDX42, AKT3).

marker info		all alleleic association					HLA mismatched				HLA matched		
TargetGene	**Marker name**	**Donor/Patient**	**allele no**	**aGVHD 01-24 2xm *p*=**	**aGVHD 01-24 2x2 *p*=**	**2x2 Odds ratio**	**allele**	**aGVHD 01-24 *p*=**	Odds ratio	lower CI (95%)	**aGVHD 01-24 *p*=**	Odds ratio	95% CI
F2RL1/S100Z	D5S424	P	05	0.0004	0.002017	1.338207	04	**0.03319**	0.76	0.6-1.0	**0.000696**	0.54	0.4-0.8
MAPK14	D6S0035i	D	02	0.0004	0.00035	0.685984	01	**0.0344**	1.31	1.0-1.7	**0.0066**	1.64	1.2-2.3
ELTD1	D1S0818i	D	01	0.0007	0.0000783	1.519239							
IL1RAPL2	DXS0151i	D	04	0.0066	0.007038	1.41669							
SOCS3	D17S0219i	D	03	0.005	0.000275	0.418673							
IL1RAPL2	DXS0629i	D	03	0.016	0.001315	0.7778							
TBL1X	DXS0324i	P	01	0.021	0.013253	0.753511							
DDX42	D17S0271i	P	01	0.0404	0.008597	0.71826							
AGPAT4	D6S0330i	D	07	0.071	0.00074	1.38941							
AKT3	D1S1335i	P	03	0.195	0.032222	1.226761							

Table 4.8: Association of alleles other than those identified by pooled DNA genotyping, with HLA matching subgroup analysis

Target Gene	DS name	allele position	allele ID	P value aGVHD 01-24 association *p*=	total	cases all	controls all	cases pos	cases neg	controls pos	controls neg	Odds ratio	lower CI (95%)	higher CI (95%)
ELTD1	D1S0818i	172	01	0.0006	916	421	495	228	193	211	284	1.59	1.224	2.066
IL1RAPL2	DXS0151i	466.6	04	0.0313	918	420	498	117	303	108	390	1.39	1.031	1.885
TBL1X	DXS0324i	385.1	01	0.0053	914	420	494	145	275	216	278	0.68	0.519	0.888
AGPAT4	D6S0330i	166.6	07	0.0003	914	419	495	90	329	55	440	2.19	1.52	3.151
AKT3	D1S1335i	90.3	03	0.0197	921	421	500	82	339	68	432	1.54	1.081	2.184

Table 4.9: Associations with moderate-to severe acute GVHD (grade 2-4) of homozygous genotypes of the same alleles as identified in the pooled and individual genotyping.

marker info		all homozygous genotypes				HLA mismatched homozygous genotypes			HLA matched homozygous genotypes		
TargetGene	**Marker name**	**homozyg genotype**	**aGVHD 01-24 *p*=**	**Odds ratio**	**95% CI**	**aGVHD 01-24 *p*=**	**Odds ratio**	**95% CI**	**aGVHD 01-24 *p*=**	**Odds ratio**	**95% CI**
F2RL1/S100Z	D5S424	0505	0.101	1.3	0.9-1.8	0.0817	1.41	0.9-2.1	0.69	1.12	0.7-1.9
MAPK14	D6S0035i	0202	0.099	0.64	0.3-1.1	0.0737	0.52	0.3-1.0	1	0.93	0.4-2.1
ELTD1	D1S0818i	0101	0.0005	1.59	1.2-2.1	0.0031	1.63	1.2-2.3	0.14	1.44	0.9-2.2
IL1RAPL2	DXS0151i	0404	0.031	1.39	1.0-1.9						
SOCS3	D17S0219i	0303	0.52	0.59	0.1-2.4	0.22	0.21	0.1-1.8	1	0.74	0.1-8.2
IL1RAPL2	DXS0629i	0303	0.02	0.73	0.6-0.9						
TBL1X	DXS0324i	0101	0.0053	0.68	0.5-0.9						
DDX42	D17S0271i	0101	0.14	0.55	0.3-1.2						
AGPAT4	D6S0330i	0707	0.00025	2.19	1.5-3.2	0.0059	1.94	1.2-3.1	0.0008	2.77	1.5-5.1
AKT3	D1S1335i	0303	0.019	1.54	1.1-2.2	0.0233	1.7	1.1-2.6	0.56	0.83	0.5-1.5

Table 4.10: homozygous genotype associations of the same allelic associations identified by pooled DNA genotyping, with analysis separate for HLA matched/mismatched subgroups.

marker info		all homozygous genotypes				HLA mismatched homozygous genotypes			HLA matched homozygous genotypes		
TargetGene	**Marker name**	**homozyg genotype**	**aGVHD 01-24 *p*=**	**Odds ratio**	**95% CI**	**aGVHD 01-24 *p*=**	**Odds ratio**	**95% CI**	**aGVHD 01-24 *p*=**	**Odds ratio**	**95% CI**
F2RL1/S100Z	D5S424	0404	0.000059	0.36	0.2-0.6	0.0067	0.44	0.2-0.8	0.00149	0.18	0.1-0.6
MAPK14	D6S0035i	0101	0.00053	1.6	1.2-2.1	0.069	1.36	1.0-1.9	0.00093	2.18	1.4-3.4
ELTD1	D1S0818i										
IL1RAPL2	DXS0151i										
SOCS3	D17S0219i										
IL1RAPL2	DXS0629i										
TBL1X	DXS0324i										
DDX42	D17S0271i										
AGPAT4	D6S0330i										
AKT3	D1S1335i										

Table 4.11: Genotypic associations other than those allelic associations identified by pooled DNA genotyping, with subgroup analysis for HLA matched/mismatched subgroup

Target Gene	**Marker name**	**allele position**	**allele ID**	**P value aGVHD 01-24 Association *p=***	**total**	**cases all**	**controls all**	**cases pos**	**cases neg**	**controls pos**	**controls neg**	**Odds ratio**	**lower CI (95%)**	**higher CI (95%)**
F2RL1/ S100Z	D5S424	116	04	6E-05	921	421	500	20	401	61	439	0.36	0.21	0.605
MAPK14	D6S0035i	369	01	5E-04	912	416	496	229	187	215	281	1.6	1.23	2.081
IL1RAPL2	DXS0629i	397	04	0.001	916	419	497	159	260	139	358	1.58	1.19	2.08
LTB	TNFC	160	05	0.003	915	419	496	23	396	9	487	3.14	1.44	6.869

Table 4.12: Associated genotypes of other alleles than those identified through pooled screening and individual genotyping.

4.2.4. Analysis of MS marker associations on Chromosome X

Alleles from three MS markers (DXS0629i, DXS0324i, DXS0151i) were found to be associated with grade 2-4 acute GVHD. Analysis in the pooled screening was by counting overall alleles within the pool, correcting for the overall number of alleles (i.e. for males only one allele was counted, for females two). The analysis of individual genotyping was mirroring this approach in order to confirm the findings from pooled DNA screening.

Two of the alleles had a protective effect, while one indicated a risk for GVHD. One allele was recipient-intrinsic with a protective effect, whereas the two others derived from the donor, exerting a protective or risk effect. Two markers of these alleles were intronic to the same, very large gene IL1RAPL2.

An analysis separating the gender effects did show that the markers in the IL1RAPL2 gene had very similar effects on the recipient when coming from a female or male donor. The effect of the marker in TBL1X appeared to be mainly on the male recipient.

In the context of transplantation, many polymorphisms on chromosome X have been described as minor histocompatibility antigens (mHag). These are antigens outside the major histocompatibility complex (MHC) that can induce strong immunological responses leading to either graft rejection, GVHD or graft-versus-leukaemia effects. The analysis of markers on chromosome X in this respect is complex and beyond the scope of this study. Such analysis would require careful evaluation of confounding variables relating to donor/recipient sex, rejection and chronic GVHD as outcomes, subgroup analysis of the different female/male combinations of donor and recipient, as well as consideration of HLA matching.

			All				Female				Male			
Gene	**Marker**	**allele no**	**p for aGVHD 01-24 *p*=**	**Odds ratio**	**lower CI (95%)**	**higher CI (95%)**	**p for aGVHD 01-24 *p*=**	**Odds ratio**	**lower CI (95%)**	**higher CI (95%)**	**p for aGVHD 01-24 *p*=**	**Odds ratio**	**lower CI (95%)**	**higher CI (95%)**
IL1RAPL2	DXS0151i	04 D	0.00704	1.417	1.125	1.7839764	0.021	1.428118	1.05609	1.9311997	0.082	1.395542	0.9754874	1.9964762
IL1RAPL2	DXS0629i	03 D	0.00132	0.778	0.623	0.970705	0.018	0.70393	0.5264287	0.9412825	0.036	0.683761	0.4851211	0.9637359
TBL1X	DXS0324i	01 R	0.01325	0.754	0.604	0.9401294	0.232	0.829365	0.618453	1.1122049	0.022	0.672497	0.4805425	0.9411286

Table 4.13: X-chromosomal markers associated with acute GVHD grade 2-4

4.2.5. Multivariate analysis

In order to understand which of the identified associations would be consistent when compared to other major variables in the dataset which we identified previously, multivariate analysis was conducted in STATA v 11 (performed by Dr Hirofumi Nakaoka). This was undertaken as backward multiple logistic regression, i.e. all variables showing a significant association in univariate analysis were include and eliminated in a stepwise fashion until no further improvement to the model could be achieved.

Variables included were recipient age, donor age, female into male transplant, diagnosis, use of total body irradiation, use of antithymoglobulin, use of cyclosporine A versus tacrolimus for GVHD prophylaxis, relapse and HLA matching (HLA-DQB1 or DPB1 mismatch and fully matched pairs only, versus all other grades of mismatching).

A single dataset containing all clinical variables and genotyping results was constructed. Samples for which we did not have all variable information or genotyping results were excluded (53 samples), therefore p-values for univariate analysis differ slightly from those reported in the tables above. Markers on the X-chromosome were not included.

Diagnosis (ALL > ANLL), donor age (older) and HLA mismatch were the strongest competing variables in multivariate analysis.

Results of the multivariate analysis

Five markers (D6S0035i D17S0219i D1S0818i D6S0330i D5S424) showed associations in multivariate analysis that had effect sizes larger than any of the clinical variables, and are therefore independent predictors of moderate-severe GVHD.

	Univariate			Multivariate		
	OR	95% CI	*P* value	OR	95% CI	*P* value
Recipient age	0.984	0.972-0.997	0.015	0.987	0.973-1.001	0.06
Donor age	1.018	1.000-1.035	0.045	1.021	1.003-1.040	0.023
F-M transplant	1.181	0.856-1.629	0.311	1.15	0.818-1.616	0.421
Diagnosis (ANLL vs ALL)	0.628	0.482-0.818	5.6×10^{-4}	0.644	0.485-0.857	2.5×10^{-3}
TBI	0.751	0.506-1.115	0.155	0.687	0.449-1.053	0.085
ATG	1.186	0.467-3.016	0.72	0.788	0.292-2.126	0.638
Cya vs tac	1.109	0.854-1.440	0.439	1.067	0.810-1.406	0.644
Relapse	0.69	0.508-0.939	0.018	0.727	0.528-1.001	0.051
HLA match	0.705	0.536-0.928	0.013	0.727	0.544-0.972	0.031
D6S0035i (MAPK14) allele 2	0.67	0.541-0.829	2.3×10^{-4}	0.672	0.538-0.839	4.5×10^{-4}
D17S0219i (SOCS3) allele 3	0.456	0.289-0.721	7.5×10^{-4}	0.426	0.264-0.685	4.3×10^{-4}
D1S0818i (ELTD1) allele 1	1.49	1.218-1.822	1.0×10^{-4}	1.46	1.185-1.799	3.9×10^{-4}
D6S0330i (AGPAT4) allele 7	1.376	1.141-1.659	8.4×10^{-4}	1.435	1.180-1.745	2.9×10^{-4}
D5S424 (F2RL1) allele 5	1.495	1.212-1.838	1.4×10^{-4}	1.497	1.206-1.859	2.5×10^{-4}
D17S0271i (DDX42) allele 1	0.719	0.564-0.918	8.0×10^{-3}	0.731	0.566-0.944	0.016
D1S1335i (AKT3) allele 3	1.229	1.018-1.483	0.032	1.221	1.005-1.484	0.045
TNFC Allele 5	1.238	0.977-1.568	0.077	-	-	-

Table 4.14: Multivariate analysis of microsatellite alleles associated with grade 2-4 acute GVHD.

4.3 Further exploration of a susceptibility region by SNP typing

Microsatellites as applied in this study ‘represented’ and identified a region of linkage disequilibrium to disease-associated genetic features like e.g. functional polymorphisms, assuming an average length of linkage disequilibrium of approximately 100 kb. Further work of investigation was therefore needed aiming to limit down in size the disease-associated locus, or even identify the underlying genetic variation that causes the disease association (see the more detailed discussion on this Topic in the discussion section).

As an example, a small exploration was undertaken into the MAPK14 locus (marker D6S0035i) using tag SNP identified through the HapMap project. The region on Chr 6 was searched for 50 kb on each side of the microsatellite (6:36,100.000 – 6:36,200.000), identifying 159 SNP in 6 haplotype blocks, of which 25 SNP were tag SNP. Focussing on the largest of the haplotype blocks, five SNP (rs6934216, rs851020, rs16884919, rs12530381, rs7760405) were selected and genotyped using TaqMan methodology. As not all of the 25 tag SNP were available for this platform, not all haplotypes would be captured, but haplotype analysis was attempted.

Three of these SNP markers showed association with grade 2-4 acute GVHD:

- rs851020 and rs12530381 (the latter is the closest to the microsatellite, and the coding region of MAPK14) both associated with allelic and genotypic risk (table 4.15). These markers had an almost identical allele and genotype distribution, and may have been linked.

- rs6934216 and rs851020 showed a protective allelic and genotypic trend towards association (table 4.15).

Due to the limited capture no haplotypes were derivable from these data. Further work with either SNP or microsatellites would be required to investigate associations at this locus.

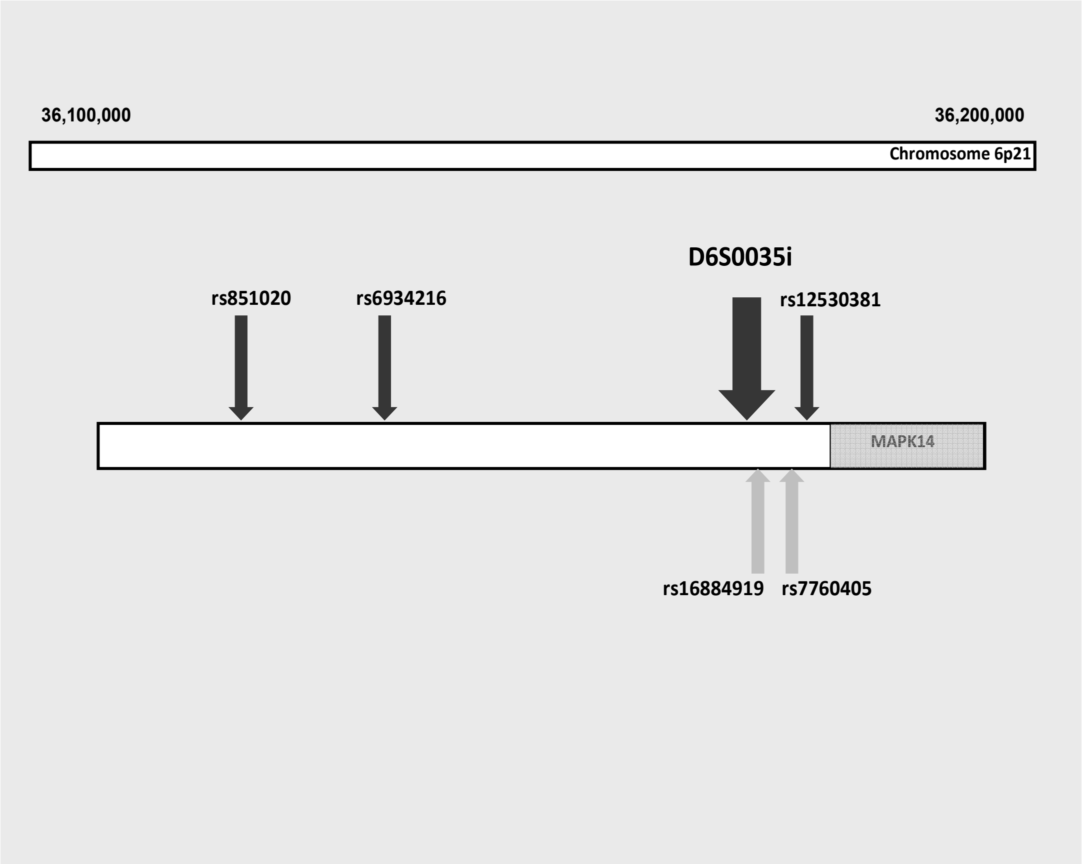


Figure 4.2: Map of microsatellite and tagSNP positions in the intronic region of the MAPK14 gene. The shaded area of the gene indicates the exon. The large arrow indicates the position of the microsatellite, the small arrows show the position of selected SNP. Dark arrows indicate association of the marker with acute GVHD grade 2-4.

marker	allele freq	allele freq	assoc allele	p=	OR	OR 95% CI
rs12530381	A (73%)	G (27%)	A	0.0013	1.407493	1.1-1.8
rs6934216	A (9%)	G (91%)	G	0.287	0.831325	0.6-1.1
rs851020	C (72%)	G (28%)	C	0.0035	1.362699	1.1-1.7

marker	genotype freq	genotype freq	genotype freq	assoc genotype	p=	OR	OR 95% CI
rs12530381	GG (0.08)	AA (0.53)	AG (0.39)	AA	0.0043	1.584844	1.2-2.1
rs6934216	GG (0.82)	AA (0.07)	AG (0.16)	GG	0.08	0.732426	0.5-1.1
rs851020	GG (0.10)	CC (0.53)	CG (0.37)	CC	0.00014	1.667178	1.3-2.2

Table 4.15: SNP allele and genotype associations of markers close to microsatellite D6S0035i

4.4. Genetic susceptibility regions for moderate-severe acute GVHD

4.4.1. Introduction

Each of the identified alleles or markers represented a region of approximately 100 kb of linkage disequilibrium (LD) with an associated genetic variation. Microsatellites in themselves are rarely directly disease causative, but linked to such a variation which could be a polymorphism, a mutation, deletion or duplication, or epigenetic trait.

The specific LD for any of the associated genetic loci in this study was not immediately known. The HapMap database gave information about the LD of SNP markers but not microsatellites. Previous studies have used well known association loci, placing a variety of SNP and MS markers around it (Koch et al., 2000, Ohashi and Tokunaga, 2003) or well characterized populations (Varilo et al., 2003), or mathematical models (Terwilliger et al., 2002, Shifman et al., 2003) to determine LD of MS markers. These studies found that the LD of MS markers extended beyond that of SNP markers (up to 400 kb, compared to up to 30 kb for SNP). Also, LD decreased with distance from the marker, even on the same haplotype block.

Therefore it was reasonable to assume a LD of 100 kb as a starting point for locus analysis, until detailed exploration of each locus by higher density typing with more MS or SNP markers indicated its specific LD.

Obviously, intronic MS markers with no other genes within a 100 kb range were prime candidates genes for further association testing. Six loci (AKT3, ELTD1, AGPAT4, MAPK14, IL1RAPL2 with 2 loci) fulfilled these criteria. All of these had been target genes, and two of these (ELTD1 and MAPK14) had marker as well as allele associations that were consistent even with application of multiple testing correction and in multivariate analysis. Two loci had intronic markers that were not within the target gene, but coincidentally within other genes within 100 kb distance from the target gene (TBL1X→SHROOM2; SOCS3→DNEL2), both had further genes within LD range. Finally, the loci F2RL1 and DDX42 were intronic in the target gene but had several other, non-targeted genes at close range. The following sections will describe each locus in turn. Information has been obtained from the gene cards website (http://www.genecards.org/) and additional sources, as referenced.

4.4.2. AKT3 locus

Chr 1:241718158- 242080053
MS marker D1S1335i location: Chr1:241980312-241980412

The AKT3 (Protein Kinase B isoform 3, PKB) gene is a large gene, more than 360 kb long. In the pooled screening it was covered by 5 MS markers, of which only this one, which was also closest to the coding region, showed an association (Figure 4.3).

AKT3 has a broad effect on cell function, it is an important regulator of cell signalling in response to insulin and growth factors, it has a role in cell proliferation, differentiation, apoptosis, tumorigenesis as well as glycogen synthesis and glucose uptake (Somanath et al., 2006). AKT dysregulation, mainly studied in mice, leads to diseases like diabetes, cancer, cardiovascular and neurological disease (Hers et al., 2011). In T-lymphocytes, AKT3 has in important role in cell development and proliferation. AKT3 regulates glucose uptake, protein synthesis, and stimulates the E2F and forkhead transcription factors (Matthews and Cantrell, 2006). In a genome-wide gene expression study of GVHD, PKB expression was repressed in donor CD4 T-cells in chronic GVHD (Baron et al., 2007).

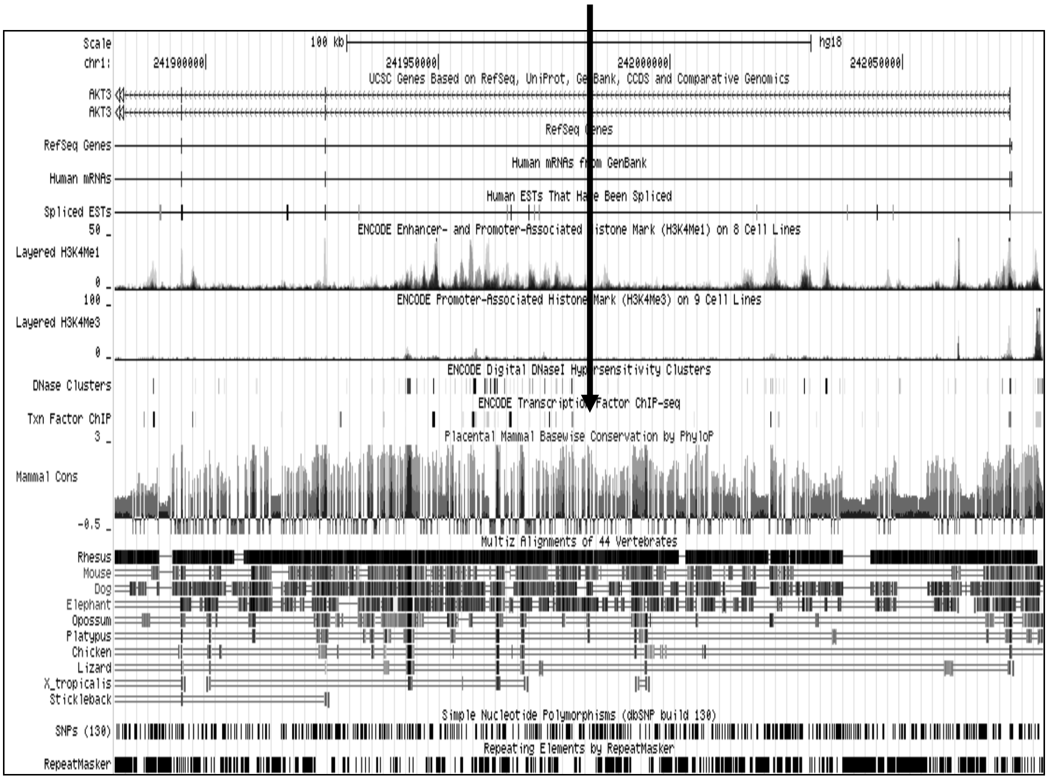


Figure 4.3: Genomic map of the AKT 3 gene and position of the associated microsatellite

4.4.3. ELTD1 locus

Chr 1:79128037-79279105
MS marker D1S0818i location: Chr 1:79149764-79149943

ELTD1 (EGF latrophillin and seven transmembrane containing 1) is part of the EGF-TM7 (Epidermal Growth Factor seven transmembrane) family. It has important funcions in leukocyte adhesion and neutrophil migration, and defects in this gene had consequences for innate and adaptive immunity (Yona and Stacey, 2010, Leemans et al., 2004). Genetic variation in this gene had been associated with parasitic susceptibility in cattle (Porto Neto et al., 2011) and subcutaneous fat thickness in humans (Lee et al., 2011).

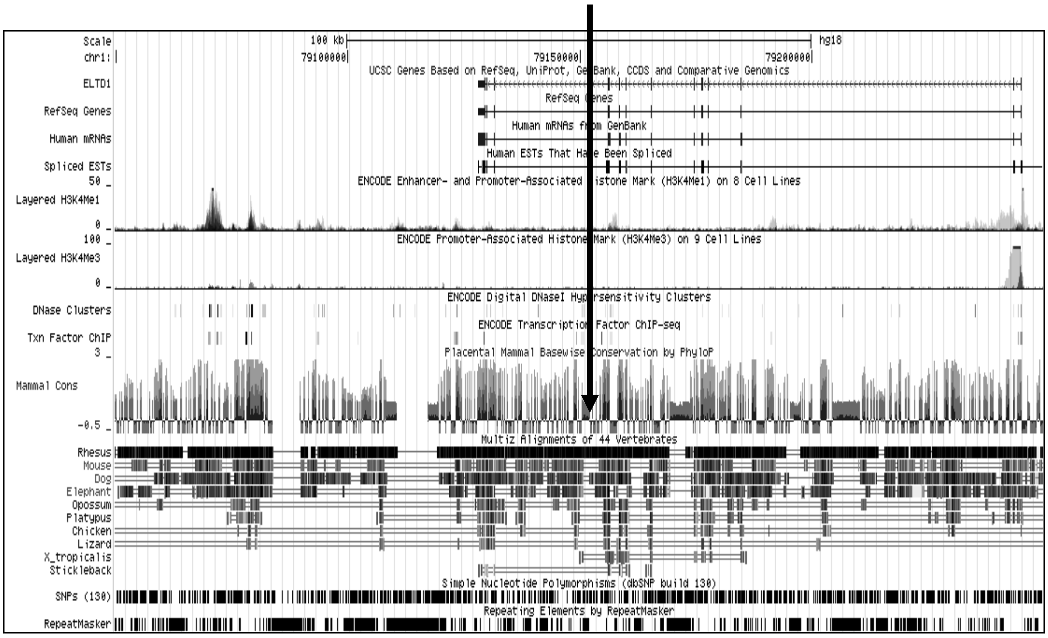


Figure 4.4: Genomic map of the ELTD1 gene and position of the associated microsatellite

4.4.4. AGPAT4 locus

Chr 6: 161332749-161458407

MS marker D1S0818i location: Chr 6: 161511402-161511576

AGPAT4 (1-acylglycerol-3-phosphate O-acyltransferase 4) is a membrane enzyme that is involved in de novo phospholipid biosynthesis. The wider function of this protein is not known. Variations in this gene, however, had been associated with acute as well as chronic GVHD in a population from Finland (Turpeinen et al., 2009). This study found the donor SNP rs749013 associating with risk of acute as well as chronic GVHD, mirroring the finding of this study (donor allele of MS associated with risk of acute GVHD). The SNP marker is located approximately 50 kb upstream towards the exon, and in contrast to the Finnish population is non-polymorphic in Japanese.

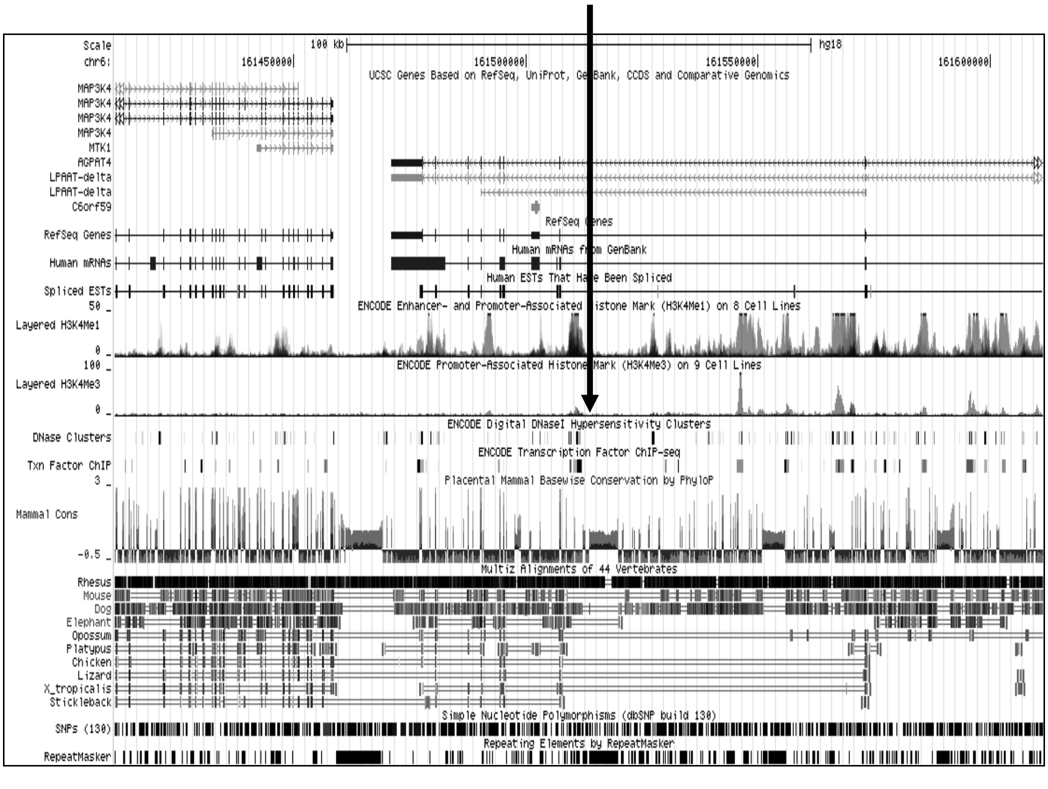


Figure 4.5: Genomic map of the AGPAT4 gene and position of the associated microsatellite

4.4.5. MAPK14 locus

Chr 6: 36129769-36215820
MS marker D6S0035i location: Chr 6: 36178949-36179320

The gene for MAPK14 (Mitogen-activated Protein Kinase 14) is located on chromosome 6 close to, but outside the HLA region. The function of this gene has been explored extensively. MAPK14 responded to activation by environmental stress, pro-inflammatory cytokines, HSP70 and lipopolysaccharides (as part of the TLR pathway) (Kang et al., 2008, Lissauer et al., 2009, Mackay and Sallusto, 2006). It was a regulator of chronic inflammation in rheumatoid arthritis (Korb et al., 2006) and inflammatory bowel disease (Waetzig et al., 2002). MAPK14 had effects on the recruitment of immune cells to the colonic mucosa (Kang et al., 2010) and epithelia of the skin (Eckert et al., 2003). MAPK14 was a key element in the activation of the glucocorticoid kinase, which decreased susceptibility to cytotoxic drugs and promotes cell survival (Meng et al., 2005).

On the basis of the largely pro-inflammatory effects of MAPK14, inhibitors have been developed for the treatment of rheumatoid arthritis and other inflammatory conditions. While in vitro and animal models did show very promising results, a recent randomized controlled clinical trial had failed to show any long term benefit for patients with rheumatoid arthritis (Genovese et al., 2011), indicating that the role of MAPK14 is complex.

MAPK13, a splicing variant of MAPK14, is located close to this gene.

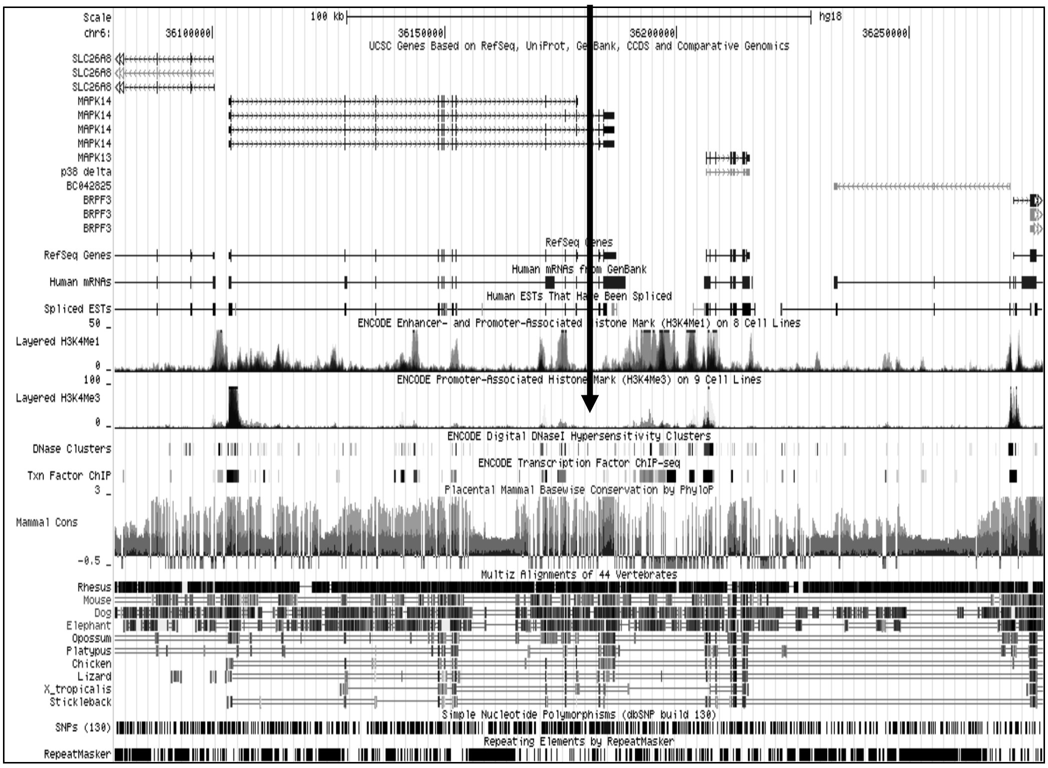


Figure 4.6: Genomic map of the MAPK14 gene and position of the associated microsatellite

4.4.6. IL1RAPL2 loci

Chr X: 103697652-104898478

MS marker DXS0629i location: Chr X: 103769044-103769435 (intronic)

MS marker DXS0151i location: Chr X: 103689786-103690263

The IL1RAPL2 (interleukin 1 receptor accessory protein-like 2) gene is very large, more than 1000kb, it was covered for this study by 10 MS markers. Only these two markers, which closely flank the coding region of IL1RAPL2, showed association (albeit in opposite directions).

This gene is part of the IL1 receptor family, which was the reason for inclusion in this study. It has, however, so far no documented role in the immune system. There is extensive literature of the association of IL1RAPL2 with cognitive impairment and mental retardation (Valnegri et al., 2011).

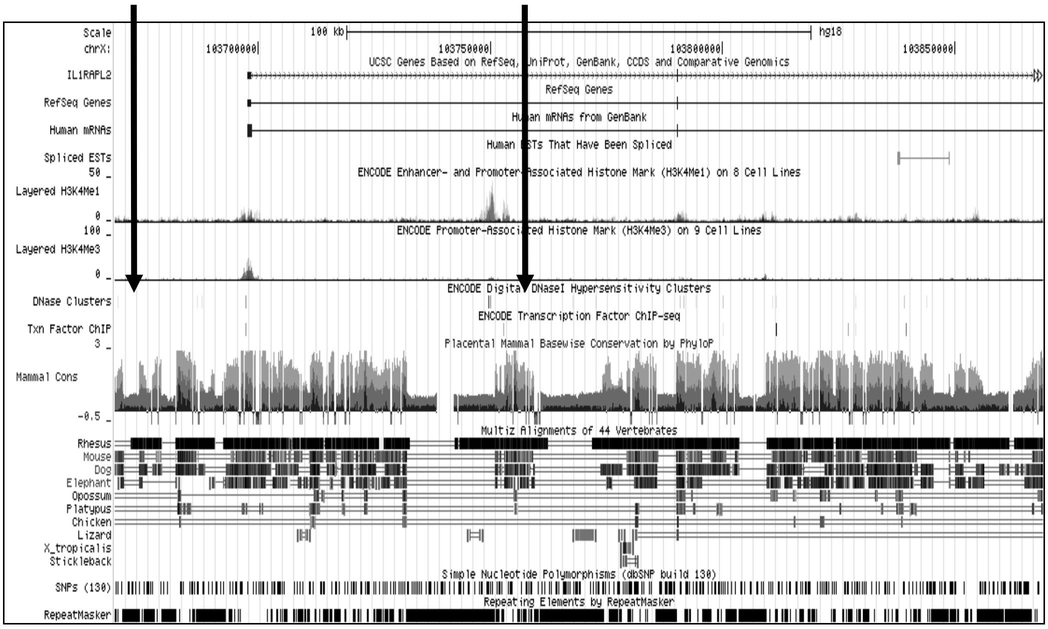


Figure 4.7: IL1RAPL2 gene locus on chromosome X with two MS markers (left: DXS0151i, right: DXS0629i), flanking the coding region of the gene.

4.4.7. TBL1X locus

Chr X: 9391369-9647778
MS marker DXS0324i location: Chr X: 9722847-9723231

The target gene TBL1X (transducin (beta)-like 1 X-linked) is a further large X-chromosome gene. The marker flanked the coding region at a distance of ~80 kb, and was co-incidentally located intronically within the gene SHROOM2. A further gene, GPR143, was located within a 100 kb LD range of the marker between SHROOM2 and TBL1X (see Figure 4.8).

Little knowledge exists about the function of TBL1X. It had an essential role in transcription activation mediated by nuclear receptors (Glass and Ogawa, 2006). It recruited NFkB to its target for gene transcription and had a potential role in tumorigenesis (Ramadoss et al., 2011), and also regulated MYC gene expression, which is important for growth and expansion of somatic cells (Toropainen et al., 2010). Genetic polymorphisms in TBL1X had recently been linked to autism in males (Chung et al., 2011), but the mechanism remained unclear.

SHROOM2 (shroom family member 2) had a broad role in the morphogenesis of thickened epithelial shields during embryonal development (Lee et al., 2009), and regulated epithelial proliferation and angiogenesis (Farber et al., 2011).

GPR143 (G-protein coupled receptor 143) was involved in intracellular signal transduction, in particular the transfer of melanin. Mutations in GPR143 lead to variant forms of albinism and mental retardation. The protein expressed by GPR143 also represented a self or tumour antigen (Touloukian et al., 2003).

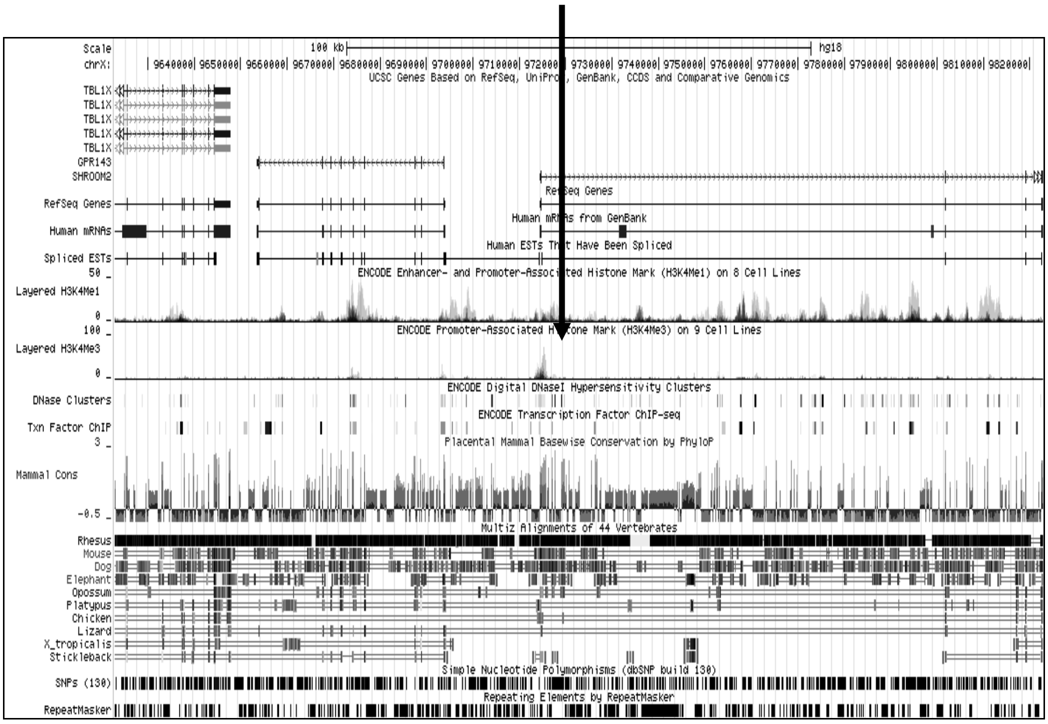


Figure 4.8: TBL1X gene locus on chromosome X. The marker is intronic to SHROOM2.The MS position is located outside TBL1X, but LD of the marker includes the coding regions of TBL1X and GPR143.

4.4.8. F2RL1 locus

Chr 5:76150610- 76166896
MS marker D5S424 location: Chr 5: 76193683- 76193804

F2RL1 (coagulation factor II (thrombin) receptor-like 1) was implicated in chronic responses associated with vessel inflammation and wound healing; stimulated activation of T-cells and neutrophils, promoted leukocyte rolling, adhesion and extravasation, increased capillary permeability and enhances production of cytokines. High F2RL1 expression in experimental intestinal radiation injury promoted inflammation and fibrosis. F2RL1 has been demonstrated on T-cells, where it triggered in an essential manner the IL6-secretion induced by thrombin, trypsin and tryptase (Li and He, 2006)

The location of the MS marker was intronic of the S100Z gene, the function of which is unclear. A genome-wide association study has found SNP polymorphism in this gene to associate with severity of ulcerative colitis (Festen et al., 2010). The S100 gene family was described to have wide-ranging roles in tumorigenesis, autoimmunity and innate immunity.

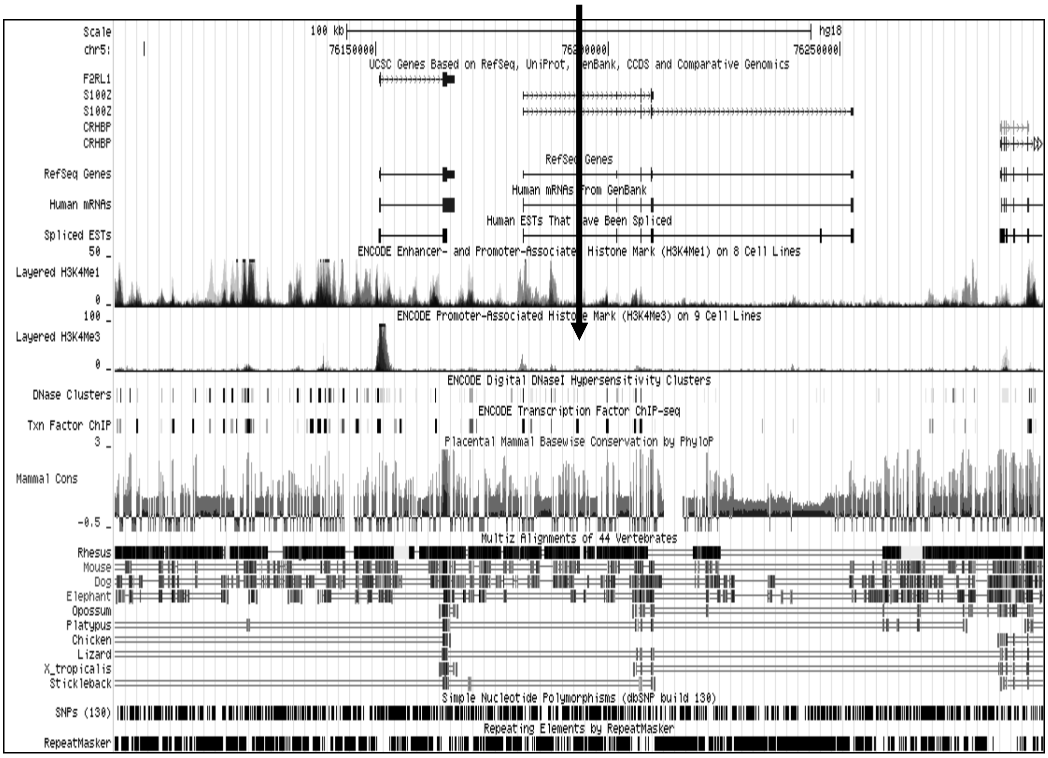


Figure 4.9: F2RL1 gene locus. The MS marker is located within S100Z, but its LD range includes F2RL1.

4.4.9. DDX42 locus

Chr 17: 59205299-59250409

MS marker D17S0271i location: Chr 17: 59224879-59225107

This marker was intronic of DDX42 (DEAD (Asp-Glu-Ala-Asp) box polypeptide 42) in a very gene dense region. Other genes within 100 kb LD region included CCDC47 (coiled-coil domain containing 47) which had an unknown function, FTSJ3 (FtsJ homolog 3 (E.coli)), PSMC5 (proteasome (prosome, macropain) 26S subunit, ATPase 5) and SMARCD2 (SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2).

DDX42 was involved in the survival of cells, counteracting the apoptotic effect of TP53BP2 (Uhlmann-Schiffler et al., 2009), while FTSJ3 was involved in ribosome synthesis (Morello et al., 2011).

PSMC5 is a functional element of the proteasome. An essential function of a modified proteasome, the immunoproteasome, was the processing of class I MHC peptides. It participated in transcriptional regulation since it has been shown to interact with the thyroid hormone receptor and retinoid X receptor-alpha.

SMARCD2 was involved in transcriptional activation and repression of selected genes by chromatin remodelling.

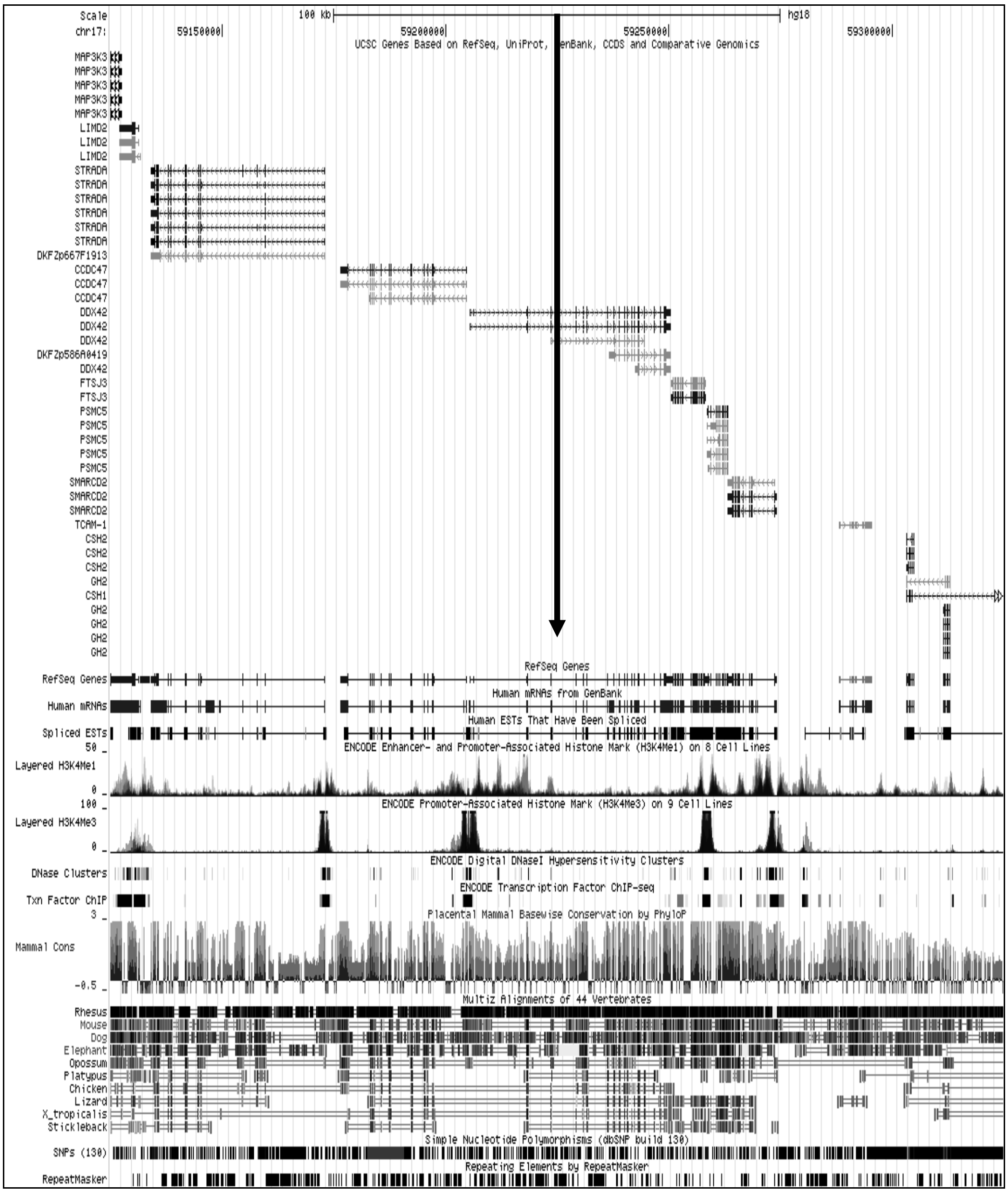


Figure 4.10: DDX42 gene locus. The marker is located in DDX42, but the genes CCDC47 and FTSJ3 are also within in LD range.

4.4.9. SOCS3 locus

Chr 17: 73864454- 73867753
MS marker D17S0219i location: Chr 17: 73941484-73941691

This locus has a high gene density. The target gene, SOCS3 (suppressor of cytokine signalling 3) was just within LD range of the marker, which was intronic to DNEL2, also known as DNAH17 (dynein, axonemal, heavy chain 17). The other gene within range was PGS1 (phosphatidylglycerophosphate synthase 1).

DNAH17 is the force generating protein of respiratory tract ciliae and sperm flagellates. The function of PGS1 is unclear. SOCS3 is an important negative regulator of the janus kinase pathway, which is used by most cytokines for transcription activation (Tamiya et al., 2011), hence it had an important anti-inflammatory effect (Alexander and Hilton, 2004). In the animal model, SOCS3 had a suppressing role on the severity of GVHD (Hill et al., 2010).

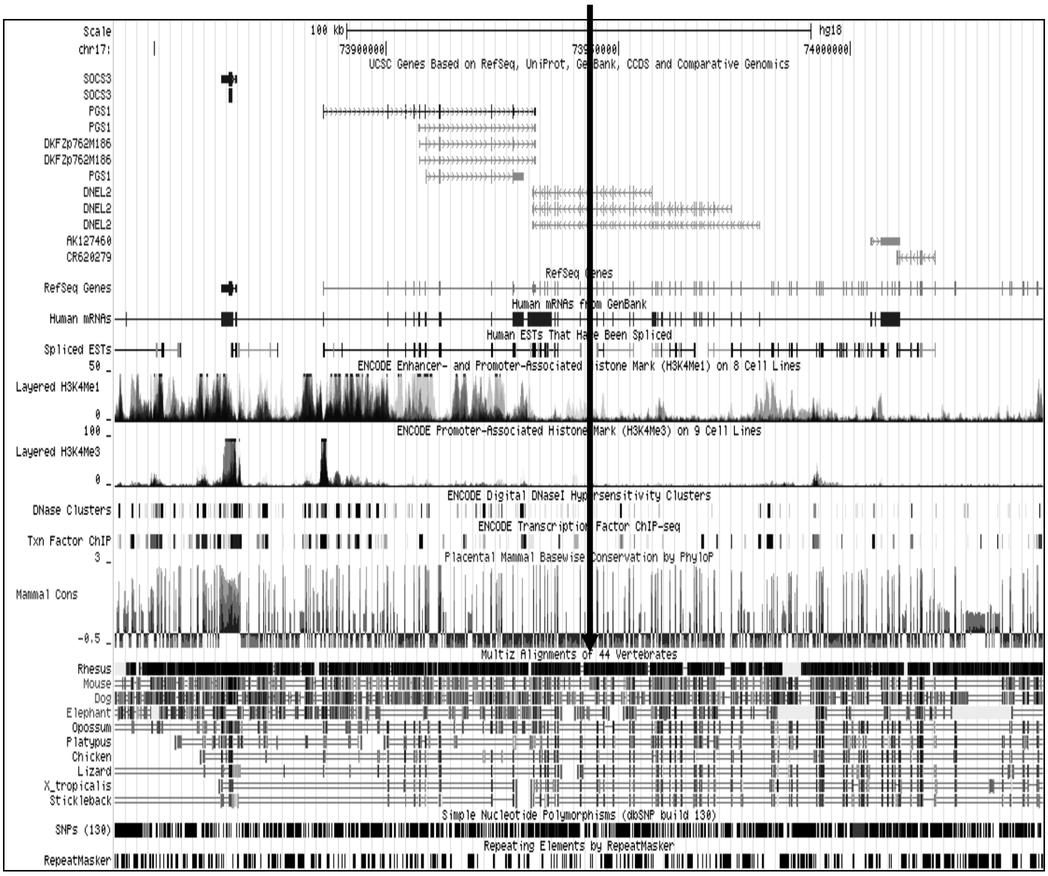


Figure 4.11: The SOCS3 gene locus. SOCS3 is just at the border of the LD range of the marker, which locates to DNAH17 (DNEL2). PGS lies between SOCS3 and DNAH17.

5. DISCUSSION AND CONCLUSION

5.1. Strengths and limitations of the methodology

5.1.1. Introduction: Towards a high-quality gene association study

In the introduction to this study, existing literature on non-HLA gene polymorphisms associating with HSCT outcome was reviewed in a systematic way; the finding was that the majority of these studies have methodological quality issues, relating to study populations (small, heterogeneous), target gene loci (candidate gene selection) and statistical analysis (statistical power, application of multiple testing correction). There is now quite clear guidance on the design of high-quality genetic association studies(Colhoun et al., 2003, Gambaro et al., 2000, Lander and Schork, 1994, Schork, 1997, Rannala, 2001). The question is:

To what extent did this study fulfil criteria of a high quality genetic association study?

The main areas pointed out by these authors include:

- Population: Genetic structure, confounding variables, case and control definitions, phenotype heterogeneity, outcome classification
- Statistics: Requirement for a pathophysiological link between gene and disease, failure to attribute results to chance (type I/II error), sample size, statistical power, independent confirmation, multiple testing
- Selection of target genes and markers

More recently, a review (McCarthy et al., 2008) of the methodology of several very large scale genome-wide association studies with SNP markers for common variant genetic traits highlighted the need for careful definitions of cases and controls, large sample sizes and replication study in order to achieve robust results. Replication, even when using robust methodology, had often not being consistent; not necessarily indicating spurious results but the varying impact of clinical or environmental variables on a small effect size polymorphism. This phenomenon had been termed ‘informative heterogeneity’.

5.1.2. Population

Did the study population stem from a homogeneous genetic background?

It was pointed out that the studied population should stem from a homogenous genetic background without genetic admixture. All HSCT pairs entered into this study were genetically of Japanese origin. We knew from data of the HapMap Consortium (Consortium, 2005, Stranger et al., 2005) that genetic variation varies enormously between different populations. The Japanese population had a genetic structure of less, and better preserved haplotype blocks than Caucasians or Africans (Conrad et al., 2006, Gabriel et al., 2002). This was advantageous for the power of the study, as less MS markers were required for gene coverage (details of the genetic background were described in more detail in supplementary file 2.1).

As this approach was expected to yield robust results for a Japanese population, findings may be less applicable to other populations and would require confirmation. Allele frequencies and genotypes of MS as well as SNP markers, and associated genetic disease risks, vary amongst populations, some markers may be polymorphic and disease associated in one population and non-polymorphic in another. Nevertheless, there is substantial concordance of genetic variation across populations also, allowing for comparison of risk and large scale studies.

How well did this study address demographic or clinical confounders that affect acute GVHD severity?

Clear definition of cases, controls, risk factors and outcomes were essential. In Japan, since 1992 the consensus on the modified Glucksberg criteria for the diagnosis of GVHD (Glucksberg et al., 1974, Przepiorka et al., 1995, Rowlings et al., 1997) was used. As these contained subjective elements, and as several independent centres across Japan were applying these criteria, there were likely elements of intra- and inter-observer variability, which were not quantifiable for this population.

The criteria for selection of this study population did reduce confounding variables to some degree:

- Selection by diagnosis: Different underlying diagnoses carried variable risks for GVHD. CML and ALL in particular had an intrinsic GVHD risk, compared to other malignancies. Focusing on ALL and ANLL had reduced this variability. However, ALL and ANLL in itself had significantly different risks for GVHD, remaining a confounder.
- Recipient age: Recipient age >40 years per se was a risk factor for GVHD, and exclusion of patients above this age removed the effect of older age. Infants and young children with leukaemia also have a higher risk of GVHD, therefore exclusion of this age group reduced confounding. However, a minor effect towards GVHD risk remained in the age group below 10 years.
- Selection of unrelated bone marrow as graft source and myeloablative conditioning: These measures avoided effects on GVHD as an outcome by donor source (reduced GVHD risk with related donors), other stem cell source (higher, or lower GVHD risk with e.g. peripheral blood stem cell transplantation (PBSCT) or cord blood), conditioning (lower GVHD risk with reduced-intensity conditioning).
- The selection by diagnosis and age ‘streamlined’ some of the clinical confounders. Treatment for leukaemia was largely protocol-

driven, compared to other indications, hence variables such as previous chemotherapy, conditioning regimen and GVHD prophylaxis were very similar.

As previous data and sample collections were often small, there was little room for considering clinical risk factors for GVHD or other HSCT outcomes, although these were well established (Loren et al., 2006, Randolph et al., 2004, Perez-Simon et al., 2005, Kollman et al., 2001). In this situation, multivariate analysis was applied to correct for the clinical confounders. Despite the selection criteria applied, this study had remaining confounding variables that required multivariate analysis:

- Donor age >30 years
- HLA mismatching
- GVHD prophylaxis with Cyclosporin A or tacrolimus
- Minor effects of recipient age, conditioning regimen

The prevention, diagnosis and management of GVHD had changed over this time period. Although all patients had myeloablative conditioning, this varied with underlying disease and staging. While the prophylactic regimen in Japan consisted initially of cyclosporine A, methotrexate and steroids, a change from cyclosporine A to tacrolimus reduced the incidence of GVHD (Hara et al., 2007). The JMDP database did not provide detailed information on dosage of methotrexate and steroids in the earlier HSCT.
ATG and T-cell depletion, in contrast to Europe or North America, had little role in Japan as it was found to dramatically increase the relapse rate of leukaemia. A few of the more recent transplants in this study cohort used in addition newer agents such as mycophenolate mofetil. Similarly, the management of GVHD over these 12 years had evolved – improved diagnostics, better control of immunosuppression, better control of concurrent infections through improved diagnostic tests and newer

antibiotics, better nursing care and monitoring, and new, more powerful treatments of GVHD had gradually changed the characteristics of GVHD. Most of these characteristics were not captured in the dataset as such information was not prospectively collected at the time.

The application of two separate time frames by this study was likely to provide some correction for this type of confounding, but may also have had effects on the sensitivity of the study:

- Associations consistent across both subsequent time frames would indicate some degree of independence from the effects that changes in supportive transplant practice, factors that were not recorded in the dataset, over time would have had on outcome.
- The disadvantage of this approach was that it ruled out all associations that did not have that degree of consistency, i.e. associations that evolved in the cohort of the second screening alone would have went undetected. This was likely to have a negative effect on sensitivity of the study. The findings indicate associations that were valid consistently over a long period of time, but may not necessarily represent the strongest effects on GVHD
- Despite the effort of correcting for genetic and clinical confounders, significant variables affect outcome, as the multivariate analysis demonstrated.
- The effects of HLA matching and mismatching could not effectively been adjusted between the cohorts. This study was able to adjust HLA match or mismatch by pairing of samples from the first screening cohort with those from the second cohort at the HLA locus or locus combination, but not by serogroups or even alleles. More recent research from the Japanese registry has shown that different allele mismatches at the same HLA locus may have risk as well as protection effects, depending on the specific allele (see below).

What was the effect of HLA matching and mismatching on GVHD?

Because HLA matching was known as a significant risk factor for GVHD (Morishima et al., 2002, Morishima et al., 2007, Kawase et al., 2009, Oh et al., 2005, Sasazuki et al., 1998, Kawase et al., 2007), and possible to control in a study setting, most previous studies in the 1990's and 2000's used higher HLA-matched HSCT pairs (e.g. 8/8, or even 12/12 matched) or related HSCT for genetic association studies. This measure was thought to reduce genetic confounding caused by HLA mismatching. The disadvantage of this approach was that data from these studies were meaningful to only a small subset of the HSCT population in clinical practice, and that other clinical confounders could not be addressed due to sample size issues.

Consequences for this study of the decision not to select samples by HLA matching or mismatching:

- Not restricting inclusion for degree of HLA matching made this study population more representative of a HSCT population seen in clinical practice.
- The large proportion of HLA mismatched pairs would allow for an analysis of the effects of non-HLA gene polymorphisms in an HLA mismatched population.
- The proportion of HLA matched HSCT pairs was large enough to permit subgroup analysis.
- The adjustment of the degree of HLA matching of the confirmatory cohort (2nd screening) to that of the discovery cohort (1st screening), in order to achieve a similar degree of genetic confounding, has introduced stratification. The JMDP registry population between 2001 and 2005 had an overall higher degree of HLA matching than the population from 1993-2000. Hence, the HLA matching of the confirmatory cohort was not representative of the degree of HLA matching of the Japanese registry cohort during that time; mismatching was over-represented. This was reflected in the GVHD

prevalence, which was higher in the confirmatory cohort than in the discovery cohort.

How could the selection study be modified to minimize confounding and stratification?

As HSCT is rapidly expanding, larger registry cohorts may become available for research in the near future. Important steps to reduce clinical and genetic confounding would include:

- Reducing the time frame of sampling (e.g. 5 years), to reduce confounding that stems from development in supportive therapy.
- Use of most recent transplants – reflect more the current clinical practice
- Aim for higher cohort size to increase statistical power
- Focus on single large diagnostic groups (eg. ALL, AML separate) rather than combined, as these carry in themselves different risks for outcomes
- Rather than by time frames, the study cohort could be divided by other important variables, such as degree of HLA matching. This requires more detailed understanding of the risk of HLA mismatching by e.g. high-risk allele mismatches or HLA haplotypes. Such analysis would be very valuable in directly comparing the competing risks of HLA mismatch and non-HLA gene polymorphisms. In addition, this analysis would give an insight into the non-HLA immunogenetics of HLA mismatched HSCT, an area that it under-researched.
- As SNP gene-chip GWAS typing is becoming more readily available, it would be useful to conduct this approach in a parallel study mirroring the same set up. This would provide a complementary perspective on the genetic variation in the same study population, and facilitate the fine-mapping of associated microsatellite loci (SNP or SNP haplotype associations within LD

range of associated MS could limit down the area requiring sequencing).

SUMMARY: Study population

- **The study population stemmed from a genetically relatively homogeneous background**
- **Case and control definition followed standard practice of GVHD classification.**
- **Extensive efforts were made to identify and address confounding variables. The effect of confounding variables could be reduced by careful evaluation in a larger stem population and selection of a study population.**
- **Nevertheless, substantial clinical confounding remained and required multivariate analyses.**
- **Selection carried a risk of stratification for new confounders, which needed to be identified (e.g. HLA matching, see above).**
- **Limited availability of large study cohorts and rapid evolution of the field of HSCT made effective control of confounding variables difficult.**
- **Careful selection of a population that would be relevant in clinical practice rather than just of research interest (e.g. understanding pathobiology) may facilitate clinical application of study findings (e.g. risk stratification).**

5.1.3. Reasoning for choice of scale of approach

Which genes to focus on in relation to GVHD – all, some, or few?

The findings from the literature appraisal indicated that a larger scale, more systematic approach to candidate gene and marker selection was required to better understand the effect of non-HLA gene polymorphisms on GVHD. The initial decision was on the extent of cover of the genome - ranging from a selected candidate gene approach to whole genome scanning. Table 5.1 lays out the advantages and disadvantages of three approaches to gene selection, representing three degrees of indiscrimination: A candidate gene approach, where a small number of genes believed to have a high likelihood of being involved in the pathogenesis of acute GVHD (highly discriminate); a targeted genomic approach (e.g. focusing on the immune system as a whole, less discriminatory), and a genome wide scanning approach (indiscriminate).

The decision for a targeted genome scanning approach, which includes the genes of the entire immune system in a broader sense (‘Immunogenome’), supplemented by genes relevant for GVHD (previously associated genes and other strong candidates) and leukaemia (e.g. susceptibility genes, drug metabolism genes), was based on aspects of feasibility and study quality:

- Previous data from genome-wide association studies indicated that immune response associated conditions tend to have genetic associations within the immune system genes (Zhernakova et al., 2009) – as GVHD is a result of immune system dysregulation, focusing on immune system genes should have yielded a higher positive predictive value for associations.
- Reduced number of markers reduced the need for multiple testing statistics - resulting in higher power
- Feasible in the available time (3 years) and with available resources

- Reasonable trade-off between number of available samples, resulting statistical power of cohorts, multiple testing statistics

	Candidate approach	Targeted genome scanning	Whole genome scanning
Advantages	• Simple to perform • Simple statistics • Cheap • Powerful with small sample size	• Systematic approach to biological meaningful selection of genes • Statistically robust with reasonable sample size, positive predictive value	• Indiscriminate approach to genes • Reflects full genetic contribution to disease
Disadvantages	• Likely to miss important associations	• May miss important associations outside targeted system	• Requires large sample size • Issues with statistical power, multiple testing • Expensive • Time consuming

Table 5.1: Advantages and disadvantages of different approaches to gene selection

SUMMARY – Scale of approach

- **A targeted genome scanning (indiscriminate selection of all immune system genes, ‘immunogenome’) provided the best trade-off between the competing factors of gene selection, statistical power and available resources.**
- **Main disadvantage was that important associations outside the selected panel may not be detected.**

5.1.4. Reasoning for choice of marker type and marker number, and pooled/individual typing approach

Single Nucleotide Polymorphisms or microsatellite markers?
What were the consequences for study design by choosing microsatellite markers?

Modern high-throughput genetic screening approaches mainly use two different types of genetic markers:

- Single Nucleotide Polymorphisms (SNP): A SNP is a genetic variation where a single nucleotide within the genome sequence is altered. SNP in coding sequences may alter gene expression and cause a change in biology, or may link to a causative variant.
- Microsatellites (MS): MS are short sequence repeats, commonly as a variable number of di, tri, or tetra tandem base repeats. Microsatellite markers often, but not always stand in linkage desequilibrium (LD) with SNP on the same haplotype block.

SNP and MS both have their specific advantages and disadvantages (see table 5.2) (Bahram and Inoko, 2007, Jorgenson and Witte, 2007).

At the time this study was developed (2005-2006), new miniaturized, standardised and automated genome-wide SNP typing platforms were evolving, using hundreds of thousands of SNP markers on a single sample. During this time there was still an ongoing debate about which markers to include in these assays, sample size and statistical power, typing quality, and processing of the vast amount of data. In addition, these systems were still very expensive, especially for larger scale studies (table 5.3 shows a cost comparison of a SNP based and MS based approach for 2007). The advantages of such an approach were obvious: The methodology became technically ever simpler, reproducible, faster and cheaper, individual sample data were retained and allowed for multiple outcome measures. Initial studies had limited numbers of samples (in the hundreds), and statistical power was limited, due to the enormous multiple testing burden. In order to detect the small effect sizes of common variants, now sample sizes of tens of thousands have been used (Vercelli and Martinez, 2006, Anonymus, 2007). Such large numbers still remained a challenge for many conditions, including HSCT where the largest collections of data and sample have just reached (CIBMTR/NMDP) or are approaching (JMDP) the 10,000' mark. Providing consistent case, control and phenotype definition was still a major problem.

There were clearly advantages of the MS approach in this setting. The method of genome-wide scanning with MS markers was pioneered and brought to a high standard by a Japanese group (Prof Inoko, Tokai University), with the first study published in 2005 (Tamiya et al., 2005) (summarised in Figure 5.1). This approach used almost 30,000 MS markers spread throughout the genome at high density (charting at 100 kb with overlap), and sequential screening in three steps on pooled DNA. More than ten genome wide studies using this approach have since been published.

MS markers have a larger LD range – therefore less markers were required to provide genome coverage, as compared to SNP, which gave MS an advantage with regards to power, sample size and multiple testing correction. The haplotype block structure of the Japanese population was highly preserved – allowing the full exploitation of the large LD of MS markers. Our selection of markers achieved a very high density of coverage for the target genes – 97% of target genes had either two flanking MS markers, or at least one, within the projected LD range of 100 kb. (the genome-wide MS panel would provide cover to ~90% of the euchromatic region of the genome). On the other hand, true LD range of MS markers was not known, therefore the LD may have been shorter or longer, creating either gaps or extended coverage. In contrast to SNP arrays, which were so densely packed that individual markers could not have been regarded as independent, MS loci could be regarded as independent and gave a clearer distinction of haplotype blocks.

By evolution, SNP and MS were often closely linked, with a MS indicating mutation or causative SNP polymorphism within its LD. By mathematical models, SNP markers, which have only two alleles, were more resistant to mutations as compared to MS, which could have 2-20 or even more alleles. A MS marker therefore may have ‘mutated away’ and lost its linkage; while on the other hand it may have indicated an evolutionary more recent genetic risk variation that SNP may not had captured (Oka et al., 2012, Hiruma et al., 2011). From this model, MS and SNP approaches were complimentary to each other by having a large area of overlap, and each additional aspects of genomic variation which the other approach did not cover.

Limitations of using a microsatellite-based approach include existing gaps in cover, and the fact that the pooled approach would allow for allelic, rather than genotypic association.

- This study had a very good cover of target genes (almost 90% full cover, and a further 7% partial cover. However, there are gene regions within the genome which have no suitable natural microsatellites, or have genetic variation (e.g. gene duplication) that make microsatellite typing inherently difficult.
- High-throughput MS typing required pooling of DNA, which lead to loss of individual genotypic information in the screening stages, relying on allele frequency differences between pools alone. Allele frequency differences often but not always reflect genotypic risks, and important associations may have been missed that way. Additionally, at individual level a pooled allele frequency difference indicating a protective effect may translate at individual genotypic analysis into a risk, and vice versa. Hence, at the individual genotyping stage the finding of an associated allele should ideally

backed by identifying a genotypic association. This, however, is not always possible given the large number of genotypes for microsatellites resulting from the large number of alleles. For some markers, nevertheless, this study was able to confirm the association of homozygous genotypes.

	SNP	MS
Advantages	• Allows for individual genotyping and data analysis • High-throughput platforms available • Technically more simple • Lower mutation rate – more stable over time, but misses recently evolved genetic variation	• Wider linkage desequilibrium • Requires less markers than SNP for same coverage (~30,000 for whole genome) • Statistically more powerful – allows for lower sample size with same coverage • more alleles – more informative • Clear definition of haplotypes • Cheaper to perform than SNP
Disadvantages	• Short LD range – many gaps, may miss epigentic variation • Unclear definition of haplotype blocks ('virtual' haplotype definition) – may miss important associations • Large number of markers required for coverage (>500,000 for whole genome) • Multiple testing requires large sample size for sufficient power • Expensive • Time consuming • Requires high-density SNP typing of candidate regions	• Higher mutation rate – may miss older SNP associations • No high-throughput platform available – requires pooled DNA approach • Technically more demanding • Requires high-density SNP typing of candidate regions • Artifacts introduced by DNA pooling • DNA pooling allows for single outcome measure only at screening stage

Table 5.2: Advantages and disadvantages of large scale genomic approaches using SNP and MS

	SNP	MS (individual)	MS (pooled)*
Estimated no of markers	70,000	4,000	4,000
Estimated assay costs	$ 600,000	$ 8,000,000	$ 70,000
Estimated time	3 years	>10 years	3 years

Table 5.3: Estimation of assay costs and time requirements for a targeted immunogenome scanning study, based on n=1000 sample pairs (time point March 2007) in US $

***this includes costs for 3 pooled screening steps and individual genotyping of identified candidate gene regions with approximately 100 SNP.**

Approach to genome-wide scanning (Tamiya et.al.)

- A simple case-control study design of a cohort of n=375 patients and an equal number of controls
- Highly accurate DNA pooling, constructing 3 pools each for cases and controls, each containing n=125 individuals
- A phased three-step genomic screening on pooled DNA. A panel of 27,039 MS markers was tested on the first set of case and control pools, markers found associated (n=2,748) were tested on the second pool set. Markers still remaining positive (n=372) were subjected to typing in the third screening step, which still left n=133 MS markers associated. Chi Square and Fisher's exact test for 2x2 and 2xm tables, with a significance level of p=0,05 were used to establish the association after each screen
- The remaining n=133 markers were individually genotyped on the combined set of n=375 cases and control pairs, to eliminate errors potentially caused by the pooling process. Of these, n=47 still remained associated.
- Of these n=47 associated gene regions, n=7 regions were selected for fine mapping with SNP, based on high allele frequency and high degree of significance. Fine mapping was performed on a further independent cohort of n=565 cases and control pairs.
- Statistical power estimation indicated that the power to detect allele frequencies <0.25 is limited given the sample size per pool (n=125)
- Based on data on the pooling method, and data from test markers typed individually and in the created pools, difference in allele frequency was calculated to be <4%.
- As the number of multiple comparisons in this screening is n+1, pseudo-positive markers were calculated as n=1352 (first screening), n=257 (second screening) and n=25 (third screening).
- Pritchard's method was used on a set of 69 randomly selected markers to verify the absence of stratification.

Figure 5.1: Methodological summary of a genome-wide scanning approach with MS markers

SUMMARY – marker choice and consequences for study design

Microsatellite markers have inherent advantages over SNP markers:

- **They are more polymorphic and therefore more informative.**
- **Because their LD range is wider, for a given genomic region less MS markers are required than SNP to provide the same cover, giving the MS approach a statistical advantage.**

Choosing a MS marker based approach has consequences for study design:

- **The variability in PCR and typing requirements means that there are no commercial high-throughput platforms available.**
- **High throughput can be achieved by DNA pooling, which is technically complex.**

5.1.5. Technical aspects

What were the technical challenges of the study design, and how were they addressed?

The microsatellite approach, however, had some drawbacks, mainly for technical reasons, some of which were discussed in the first reported genome-wide association study using this approach (Tamiya et al., 2005). This study was derived from this approach and shared its methodology, marker set and analysis tools.

Due to their larger variability and resulting variable length of the marker amplicon, MS markers did require variable PCR conditions which hinder automatization. The genome wide study approach mentioned above (Tamiya et al., 2005) had therefore selected preferentially those markers that had similar amplicon sizes and PCR conditions. However, 3-5% of markers frequently failed in genome-wide scanning, requiring re-processing in order to keep the fail rate below 2%. These circumstances made the development of standardized, fast and cheap assays difficult, and ruled out a large-scale, high throughput approach on individual samples.

There was a focus on MS markers that had 3-6 major alleles, which was a trade-off between technical conditions, LD, statistical power and controlling the false-positive error rate. Smaller numbers of alleles (e.g. 2) reduced the informative content, while markers with larger numbers of alleles could be highly informative and indicate rarer variants but had a poor statistical power.

Another source of technical difficulties was the requirement for a high-throughput platform, as the individual sample PCR and typing of several thousand MS markers would have been prohibitive from a time and cost perspective. Pooling of DNA was applied, and the method for this was refined to a degree that the SD for allele frequency differences between pools and individual genotyping could be kept near +/- 1%. However, the pooling process required expertise and time, had size limitations (the volume of the PCR reaction limits the maximal pool size to ~1000 individuals) and produced some inherent artefacts that required individual inspection and allele selection of each set of pools per marker. Some algorithms were developed to semi-automate this inspection step and take the element of judgement out of this process (Schnack et al., 2004, Perlin et al., 1995, Miller and Yuan, 1997, Matsumoto et al., 2004, Olejniczak and Krzyzosiak, 2006). A further disadvantage of DNA pooling was that the capability to analyze individual information was lost. Samples had to be pooled towards a single outcome, which restricted the extent of the analysis.

SUMMARY – technical challenges of genomic screening with microsatellites

- **Due to their high polymorphism, MS markers have varying PCR and typing conditions.**
- **Markers with 3-6 alleles are preferentially selected, representing a trade-off between marker informative content and statistical power.**
- **DNA pooling requires time and expertise, and has drawbacks such as PCR and typing errors, and the loss of individual data and analysis.**

What was the technical validity of this study?

Typing errors

It was already mentioned in the results section that the MS marker panel for this study was re-plated from the genome-wide marker panel plates which were sorted according to PCR typing conditions; therefore the higher number of initial PCR and typing error was expected, and corrected successfully (overall 1.1% (donor) and 1.0% (recipient) of the 4,321 MS markers eventually failed PCR and typing over the two screening steps.

Was the pooled DNA representative of the true allele frequencies?

The quality of the DNA pools, as assessed by a test marker, was in keeping with the previously reported studies, with no significant allele frequency differences between pools and individual typing. The mean allele frequency difference was below 1% in all pools (which was lower than the 2% reported previously (Tamiya et al., 2005)).

This marker, however, represented only a spot measure of an 'ideal' marker under optimal PCR and typing conditions. To gain a better understanding of the consistency of DNA pool quality the pooled and individual allele frequencies for the 30 MS markers that were typed individually were reviewed (data not shown). Again, a very high concordance was found between pooled and individual typing.

How were pooling/typing artefacts identified and addressed?

The methodology was successful in identifying spurious associations due to artefacts. Of the eight MS markers that were not confirmed in individual typing, six had additional low frequency alleles that were not detected in pooled typing, and rendered the pooled allele association non-significant. Only two markers had an over-estimation of the associated allele in the pool resulting in an association that could not be confirmed in individual typing. This represented a known MS PCR error (preferential amplification of the shorter-repeat alleles) which was exaggerated through the pooling process. Other artefacts that became apparent only in individual genotyping resulting in non-confirmation of the pooled association included mistaking a starter peak for an allele, non-polymorphism, and multiple alleles due to copy number variation.

How were false positive associations addressed?

The two screening steps of this study had, compared to the initial publication of this methodology, a higher rate of false positive association (table 5.4). This table shows also a projection of this study based on the data of Tamiya et.al.(Tamiya et al., 2005) Tamiya et.al.'s study had seen a reduction in marker number by approximately 90% in the first and second pooled screening step, and around 60% in the third pooled screening. In this study a reduction by approximately 75% and 65% was observed in the pooled screenings. Only the third screening step (which was not a pooled screening in this study, but a selection by allele identity and OR direction) reduced the number of associations close to the number projected.

There were differences between the study by Tamiya et.al. and this study that could explain these findings. Tamiya et.al. had a smaller pool size (n=125 cases/controls), so the statistical power to detect low frequency alleles was much reduced, and the investigators would consequently not include alleles of a frequency of 20% or lower. The pool sizes of this study were larger, which increased statistical power and sensitivity of low frequency allele detection. In addition, in order to capture all potential associations even if of low frequency, alleles of a frequency of 5% and above were included. This allele frequency was within the technical resolution of the pooled DNA approach, but at the border or below the statistical power for the sample size. Analysis of the 2nd pooled screening showed indeed that 48% (donor) and 51% (recipient) of associations had allele frequencies below 15%.

Tamiya et.al. did conduct the three pooled screening steps with selection of identified alleles and markers by *p*-value only (without correction for multiple testing), and selected by OR direction only after the third screening. This study has shown that using a reduced number of MS markers for a targeted screening, a two-step pooled screening approach was sufficient.

	Tamiya (2005)			This study projected			This study Donors			This study Recipients		
	Markers total	Markers positive	%	Markers total	Markers positive	%	Markers total	Markers positive	%	Markers total	Markers positive	%
1st screen	27039	2847	10.53	4321	455	10.53	4321	1016	23.51	4321	931	21.55
2nd screen	2847	372	1.38	455	60	1.4	1016	335	7.75	931	314	7.27
3rd screen	372	133	0.49	60	22	0.5	335	31	0.72	314	17	0.39
Indiv typing	133	47	0.17	22	7	0.17	31	6	0.14	17	4	0.09

Table 5.4: Comparison of rates of positive association between the original genome-wide study (Tamiya 2005), the projection for and the actual results for this study. The rate of positives in the first and second screens is higher than in the genome-wide study and the projection, but reaches very similar rates at the entry and after individual genotyping.

SUMMARY - Internal quality controls point to a high degree of technical validity of this study:

- **PCR and genotyping errors were followed up and largely eliminated**
- **Artefacts were actively sought and resolved/excluded**
- **Prospective typing of a test marker showed a high degree of concordance between allele frequencies in the pools and by individual genotyping, in keeping with previous studies using the same approach.**
- **Retrospective analysis of individually typed associated markers confirmed the high concordance**
- **A larger number than expected of false positive associations was anticipated and effective measures taken to separate false positives from true positives**

5.1.6. Data analysis

Statistical aspects: Are the analyses valid?

The targeted genomic approach had advantages over genome-wide approaches with regards to statistical power. Investigation of the immune system was achieved with around 15% of the number of markers needed for a genome-wide scan. The selection of disease-relevant genes provided a higher positive predictive value and immediately gave a pathophysiological link between gene and disease, thus increasing the likelihood that the association were true.

Aspects of type I and II errors were already discussed in the previous section ‘technical aspects’. Knowing that non-HLA associations with GVHD were likely to be of small effect size, for this study a high degree of sensitivity was deliberately chosen for the two pooled DNA screening steps (by including allele frequencies at the level of technical resolution, rather than at the level of statistical power; and non-application of multiple testing correction), accepting a large number of false positive associations. Independent confirmation in a second screening cohort was sought to confirm or refute the associations of the first screening cohort, and provided a powerful tool for further selection (allele identification, OR in the same direction). This approach did indeed reduce the number of false positive associations efficiently to levels that were projected, and identified a number of consistent associations. Most of these associations had effect sizes close to the limit of detection given the statistical power of this study; hence this was a successful strategy. It was, nevertheless, not possible to establish which falsely negative associations may have been missed, as a validation study of the approach was beyond the remit of this project. On the other hand, several publications of studies having used the pooled DNA microsatellite based approach have been successful in identifying new associations, and most of these studies confirmed the findings of previous SNP studies, i.e. on rheumatoid arthritis (Tamiya et al., 2005), hypertension (Yatsu et al., 2007), Asthma (Hui et al., 2008), adult height (Kimura et al., 2008), anorexia nervosa (Nakabayashi et al., 2009), complications after radiotherapy for cancer (Michikawa et al., 2010), psoriasis (Hiruma et al., 2011) and macular degeneration (Meguro et al., 2012). The genetic risk for Behçet's disease was explored using the identical genome-wide marker set independently in two populations (Japanese, Korean), resulting in the identification of HLA-B51 as a genetic risk (Meguro et al., 2010, Horie et al., 2012). Multiple correction statistics (Bonferroni's correction) were applied for the individual genotyping step only, still resulting in four MS markers being associated with grade 2-4 acute GVHD.

Nevertheless, detection of effect sizes much below an OR=1.5 was very limited due to the small number of samples (for a genomic screening approach). Low frequency alleles caused a large number of false positive association, hence these were not replicated very well which may have statistical power as well as technical reasons.

SUMMARY – data analyses

This study's approach was deliberately sensitive by:

- **using technical resolution of the scan (rather than statistical power resolution)**
- **non-application of multiple testing correction through a two-step screening process.**
- **Provision of specificity by independent confirmation of associations that were true but had a low effect size.**

Ten such loci were identified, while the number of false positive associations were effectively reduced.

The statistical power given the pool and cohort sizes, allele frequencies and number of tests was moderate – associations of alleles with an OR <1.3-1.5 may not be reliably detected.

SUMMARY – methodological strengths and limitations I

Strengths:

This study fulfilled criteria for a high-quality genetic association study:

- **Population of genetically homogeneous background**
- **Attempt to control genetic, demographic and clinical confounders**
- **Discovery/independent confirmation study design**
- **Large scale, indiscriminate gene targets**

Technical strengths:

- **Microsatellite markers – wide LD, informative**
- **control of typing errors**
- **high quality DNA pooling**
- **Control of artefacts**
- **Control of false positive associations**

Statistical strengths:

- **Sensitive and specific for small effect size associations**

SUMMARY – methodological strengths and limitations II

Limitations:

The design of study cohorts for genetic association studies with HSCT outcomes is difficult:

- **Control of confounding variables still requires multivariate analyses**
- **Cohort design by selection may induce stratification and new confounders**
- **HLA matching adjusted between cohorts, but not representative of registry**

Technical limitations:

- **Targeted genomic approach may miss important associations**
- **MS markers may not capture all genetic variation at a locus**
- **MS requires pooled DNA approach – loss of individual information, potential of typing errors**
- **Lack of validation study for this approach – scope of false negative markers unknown**

Statistical limitations:

- **Sample size provides limited statistical power – associations with Odd's ratio <1.5 not well represented, HLA subgroup analysis not very powerful**

5.2 Discussion of results

5.2.1. Hypothesis and objectives

The hypothesis of this study stated: “Allele frequency differences of microsatellite markers are associated with moderate-severe acute GVHD”.
The finding of 10 microsatellite loci associated with moderate-severe acute GVHD through a methodology that complied with many requirements for a high-quality genetic association study, with valid technical and statistical results, confirmed this hypothesis; rejecting the null hypothesis: “Allele frequency differences of microsatellite markers are **not** associated with moderate-severe acute GVHD.”

The assumption for this hypothesis was that GVHD is in part a complex genetic trait, and that common allele polymorphism of non-HLA genes in the patient and donor genomes contributed to the development of GVHD. It was also assumed that such non-HLA risk alleles had an effect size that reached that of certain HLA mismatches, hence could be consistent despite variation in clinical and genetic risk factors over time. The objective of this study, the demonstration of the existence of such polymorphisms through a targeted genome scanning with MS markers, was therefore achieved.

4.2.2. Roles and functions of identified associations

Exploratory study

Before embarking on a large scale genomic approach, the study population was explored by a smaller scale pilot study in order to establish whether identification of small size non-HLA polymorphism would be feasible in this population. For this purpose 41 SNP markers, all of these stemming from previous candidate gene studies, were genotyped using TaqMan® (Applied Biosystems) assays in a confirm/refute approach (Harkensee et al., 2012).

The study was capable of confirming previously reported SNP associations: IL2-330 as a risk for development of chronic GVHD, TNF-1031 as a risk for severe acute GVHD, and CTLA4-CT60 as protective against acute GVHD. These findings add credibility to the previous results, and confirmed the capability of the study population to demonstrate such non-HLA polymorphisms in a consistent manner. The associated IL2 and TNF genotypes represent high-producer variants of these cytokines that have been extensively studied in the context of GVHD. Both have essential roles in inducing and maintaining GVHD (see introduction section above). CTLA4 is an important second signal for T-cell activation, and the findings of these studies are in keeping with previous results.

Pooled DNA screening and confirmation with MS markers

The identified genomic loci associated with a MS marker represented an area of LD within which presumably a genetic variant that had a causative role in grade 2-4 acute GVHD is located. Further work, using a variety of methods that include higher density mapping with MS or SNP, or sequencing, would be required to determine the true LD and detect such genetic variants. The following description of roles and functions of genes within the LD ranges of the associated markers is therefore assumptive; the causative genetic variants still remained to be found.

The findings from this work underline the notion that modulation of the antigen recognition and subsequent T-cell activation by non-HLA genes may occur during any of the three stages in the pathophysiology of GVHD. The microsatellite loci identified by this study put new pathways onto the map of GVHD pathobiology. Presuming that LD is strongest close to the MS location, genes that are in close range or are an isolated gene within the LD range have a higher likelihood to be a player in GVHD.

In this study, the MAPK14 (key player of proinflammatory response within the TLR pathway) and ELTD1 (a membrane protein closely involved in leukocyte adhesion and migration through endothelia) loci not only clearly have important roles in immune function, but also strong associations withstanding Bonferroni' correction. AGPAT4, another isolated gene within the MS markers LD, has an unknown function but SNP polymorphisms had been associated with GVHD severity before (Turpeinen et al., 2009). Strikingly, that study found a donor risk associated with a genetic variant, as did the microsatellite in this study. The associated SNP in the study by Turpeinen et.al. is polymorphic in the Finnish as well as Caucasian population, however, not in the Japanese. AGPAT4 is a transcriptional variant of the AGPAT1 locus which is situated in the MHC Class III region on chromosome 6, and is expressed uniformly in most tissues. AGPAT4 is highly polymorphic, and the linkage it may have to other MHC genes has not been studied sufficiently. However, ectopic expression of AGPAT in cytokine responsive cell lines may lead to enhanced expression of TNF when stimulated with IL1β, suggesting the gene could have a role in immunoregulation (Leung, 2001). The finding that the AGPAT4 locus shows association in a consistent pattern across two genetically very diverse population makes this gene a very strong candidate for further exploration and, hopefully, clinical application.

Some loci have more than one gene within the LD range. Target gene F2RL1 is a clotting factor with well known immunomodulatory properties, like regulation of chronic inflammation in blood vessels, leukocyte rolling, adhesion and extravasation, and activation of T cells and neutrophils. The other gene at this locus, S100Z, is a known risk gene for inflammatory bowel disease. SOCS3 is attributed with an important negative feedback loop of cytokine secretion, which is a potent driver of GVHD.

Other loci implicate apoptosis pathways (DDX42) or broader metabolic and regulatory pathways (e.g. SHROOM2 – epithelial generation and regeneration, TBL1X – NFkB recruitment for gene transcription, PSMC5 – proteasome function, SMARCD2 – transcriptional activator).

The loci on the X-chromosome (IL1RAPL2 and TBL1X) are of particular interest, as they could represent potential minor histocompatibility antigens (mHag). In fact, the MS DXS0151i showed a protective effect for non-female to male HSCT (p=0.03) with regards to acute GVHD grade 2-4. The prevalence of rejection was too small (n=20) to yield robust results, hence further study is required to clarify the role of this marker.

How should the results of these studies be followed up?
How can the findings from these studies be applied in clinical practice?

Exploratory study (further details see supplementary file 5.1):

- A confirmatory study on a larger cohort with more clearly defined HLA matching and clinical subgroups (this study, with participation of the author, of SNP markers associated with HSCT outcomes from previous studies in Japan, is currently under way).
- A full typing of all SNP in both screening and confirmation cohort would be desirable to understand the issue of reproducibility better (there are no plans to conduct this at present).
- Functional data: the possibility of correlating gene expression (e.g. of IL2 and TNF) with clinical phenotypes should be explored, prospective observation of recipients with genotype, expression profiles and clinical phenotype
- If this would show a difference in GVHD outcome between cases and controls (i.e. confirm that these genotypes would indeed predict risk), an interventional clinical trial could be undertaken.

MS-based pooled DNA scanning study:

- Confirmation of all MS markers in a separate cohort would be desirable

- Associated MS loci should be explored further in order to identify underlying causative genetic variants. This requires fine mapping with SNP and MS markers in the first instance to limit the size of the susceptibility area (practically, mapping the haplotype block of the MS marker). Sequencing can then be applied to identify functional gene variations. (JMDP and Tokai University have agreed to perform this investigation for the MAPK14 locus lead by the author using newly designed MS markers, tagSNP and next generation sequencing).
- All identified causative genetic variants should be confirmed independently, functional data gained and prospective clinical application sought, as described for the exploratory study.
- The microsatellite locus in the MAPK14 gene could be a treatment target: This gene is known to promote inflammatory responses, and specific MAPK14 inhibitors have been developed and trialled in conditions like rheumatoid arthritis. The effects were short lasting with no overall benefit after a 6 month treatment period. The reasons for the short duration of the effect and how to overcome this are not currently known, nevertheless, MAPK14 inhibitors potentially could have a future role in prevention or treatment of acute GVHD.
- It would be conceivable that the information of genetic risk/protective loci gained by this study could be used to intensify or relax GVHD prophylaxis regimen, based on a predictive score. This information could also serve in the selection of donors, should there be a choice available and should GVHD be a particular risk to be avoided. It would be essential to test such hypotheses in a prospective manner on a contemporaneous HSCT population.
- The identified MS loci suggest many pathways not implicated with GVHD before – there is a wide scope for further genetic and functional studies.
- Further study of the X-chromosome loci – could these associations represent mHags?

SUMMARY – Discussion of results

- **Demonstrating the existence of non-HLA MS susceptibility regions for acute GVHD risk confirms the hypothesis of this study**
- **These susceptibility regions contain genes that implicate several new pathways with the pathophysiology of acute GVHD**
- **All findings should be confirmed in a further independent cohort**
- **Further exploration of MS loci include fine mapping or sequencing**
- **Prospective clinical evaluation of risk genotype, gene expression profiling and clinical phenotype is required before application in clinical practice**
- **The TNF-1031 and IL2-330 SNP could be applicable for prospective clinical observation**
- **The MAPK14 locus brings potentially a clinical application. The pathophysiological role in inflammatory diseases is reasonably well understood, a treatment exists and has been used in a clinical trial. MAPK14/p38 inhibitors could have a future role in GVHD prophylaxis and treatment.**

5.2.3. Implication of the results for study design and methodology

In the SNP-based pilot study and the MS-based immunogenome screening alike, results pointed to themes that had so far not been well addressed in previous studies:

- The effect size of associated markers remained small
- Reproducibility of previous associations was low
- Construction of appropriate study cohorts remained a challenge

The objectives of the design of these two studies were to apply stringent methodology that would eliminate spurious results, but also allow a high degree of sensitivity in order to pick up low effect size associations. These studies were two of few who considered control of confounding variables by actively selecting cases to provide more homogeneity.

The screening step of the exploration study identified several SNP genotypes associating with HSCT outcomes, some of these confirming previous reports, with appropriate significance level and effect size. It was surprising that only a very small number of these replicated independently in the confirmatory cohort. The observation was that associations disappeared or even reversed.

These findings were mirrored in the MS-based study. This study included all genes that were reported as being associated with acute GVHD in the literature. Forty MS markers linking to 25 previously associated gene loci were positive in the first screening (table 5.5). None of these, with the exception of the TNF locus which showed a trend, was replicated.

What could have been the reasons for this lack of replication?

- Despite the effort of reducing confounders, such as demographic (recipient age), clinical (diagnosis, HSCT source, conditioning) and genetic (homogeneous ethnic background, subgroup analysis of HLA matching) ones, this study population had still known confounders which were significant in multivariate analysis (donor age, HLA matching). There were probably unknown confounders which may not have been captured in the dataset.

- The adjustment of the degree of HLA matching of the confirmatory cohort to that of the screening cohort. As the HSCT's of the earlier time frame (1993-2000) were more mismatched due to lack of better donors, the confirmation cohort represented the same degree of mismatching, although the overall HSCT population in Japan already experienced better HLA matching. As a result, prevalence of GVHD in the confirmatory cohort was slightly higher than in the overall HSCT population in Japan from the same time frame.
- Allocating HSCT into two distinct time frames (1993-2000 versus 2001-2005). This was introduced as an additional measure to make consistency more robust, by making associations independent of changes that occurred over the 13 years of development of HSCT. To some degree it could be expected that this measure reduced unknown confounding variables, but it was likely to have reduced the power of confirming associations from the screening cohort. This means that some of the positive associations in the screening step of both studies may well not have been spurious, but not confirmed because of competing confounders.
- Statistical power of these studies was limited – if the effect size in the confirmatory cohort was below the level of adequate statistical power, it may have escaped detection.

Most of the previous studies in the field of non-HLA genetics tried to control genetic confounding by selecting HSCT pairs that were either HLA matched related or unrelated HSCT. The thinking behind this strategy was that HLA mismatching had strong effects on HSCT outcome while non-HLA genetic variants had small effects. In order to show these small effects, HLA mismatching would have to be reduced, otherwise smaller effect size associations could not be detected because these would not be visible in the 'noise' of genetic confounding.

These studies have observed that indeed some non-HLA polymorphisms showed effects mainly or only in the HLA-matched subgroup (e.g. IL2-330 and CTLA4-CT60 SNP in the exploratory study; F2RL1, AGPAT4 loci in the MS-based study). However, it was remarkable that some effects were clearly stronger in the HLA mismatched subgroups, with weak or absent effects in the HLA matched subgroups (e.g. TNF-1031 SNP in the exploratory study, ELTD1, SOCS3, DDX42 and AKT3 loci in the MS-based study). As the statistical power was only moderate, future confirmatory studies are certainly required to confirm this finding.

If confirmed, the finding that different degrees of HLA matching or mismatching involves different genetic risk loci, could expand the current knowledge of the pathophysiology of GVHD. Although the T-cell mediated alloreaction remained in the centre of the pathophysiological process, modulating mechanisms that were responsible for the severity of GVHD could be very different depending on the degree of HLA matching. It could be postulated that GVHD in fact involves very diverse pathomechanisms according to the HSCT setting (e.g. related/unrelated donor, cord HSCT, presence of minor histocompatibility antigens, preceding tissue damage through infection or chemotherapy, etc.), and therefore would require diverse strategies of prevention and treatment.

The literature review undertaken for these studies showed that small effect sizes and poor reproducibility are notorious for non-HLA polymorphisms associating with HSCT outcome. This study tried to overcome these problems by using stricter criteria for cohort inclusion and independent confirmation, thus improving the study quality. Despite this, low effect sizes and poor reproducibility persisted.

What are the methodological lessons learned from this study?
What should future genetic association studies in the field of HSCT consider?

- Studies should be adequately powered: Most associations are expected to be of low effect (i.e. OR <2), therefore the size of the cohorts should be able to provide statistical power within this range.
- An independent confirmatory cohort from the same ethnic and clinical background would be essential.
- Construction of cohorts with careful exploration and measures of control for demographic, clinical and confounders. Such confounders include: Age of donor and recipient, sex of donor and recipient (demographic), type and source of transplant, conditioning regimen, GVHD prophylaxis, etc (clinical), ethnic background, HLA matching, KIR, mHag (genetic). The expanding registries and application of HSCT may soon be able to provide adequate numbers of subjects for such approaches.
- Expanding the scope of investigated populations – ‘from the bench to the bedside’. The research question should not just focus on understanding the mechanisms of GVHD, but translate into clinical practice (i.e. studying small subgroups like HLA-matched HSCT may have helped clarifying some of the non-HLA genetic risk, but was of little relevance in clinical practice because the results refer to a small and diverse population). Selecting cohorts that share clinical characteristics like diagnosis, type of HSCT etc. makes results more relevant to clinical practice and facilitates translation.

Genetic loci previously associated – positive in 1^{st} screening		Within ‘top 100’ associations by p-value
ABCB1	IL6	IFNG
CCL2	IL7R	
CCR5	ITGA4	
CTLA4	KIR	
CXCR3	MTHFR	
ESR	PTPN22	
FCGR3	TGFB	
GSST1	TGFBR	
HSPA1L	TLR3	
IFNG	TLR4	
IL1	TNF	
IL1RN	TNFRSF1B	
IL2		

Table 5.5: Gene loci associated with GVHD in previous studies showing an association in the 1st screening step. None of these were replicated in the 2nd screening step, except TNF which showed a trend.

SUMMARY – methodological implications for future studies

- **Although study power and cohort selection had an impact on results, lack of reproducibility and small effect sizes of associated genotypes is a common theme in non-HLA gene association studies**
- **Associations differ between HLA-matched and HLA-mismatched subgroups, indicating that non-HLA gene polymorphisms may have variable effects in different HSCT settings**
- **Future genetic association studies need to consider adequate statistical power, stringent study designs and careful cohort construction.**
- **The perspective, aim and objectives of future studies should also be on clinical questions**

5.3. Future

Despite the plethora of data from genome-wide association studies, very few of these, SNP or MS based alike, have actually been able to identify causative genetic variants. The epigenetic function of the genome just has begun of being understood, projects such as ENCODE provide a deeper insight on how genes are regulated (Consortium, 2007). According to this research, gene function could be regulated by structural (mutations, polymorphisms, etc) or functional (epigenetic) elements, the latter ones may not necessarily comply with the limitations of haplotype blocks or LD. For example, remote regulatory elements may cause an association signal, but the regulated gene could be far away outside the LD range (Consortium, 2007).

The scope of genetic disease association research is rapidly expanding. Genome-wide, high-throughput approaches with SNP or MS markers have rapidly advanced knowledge about the influence of genetic polymorphisms on health and disease, and have enhanced understanding of underlying pathomechanisms.

Despite these advances, common genetic variables only explain a very small fraction of the total genetic risk (2-3%), the missing proportion has been referred to as the ‘dark matter’ of genetic risk (Maher, 2008). SNP-based genome-wide association studies of common genetic variants may not be best suited to explore missing genetic risk due to the high threshold of significance, which makes small effect size association escape detection. The MS approach using a multi-step confirmation design without application of multiple testing correction statistics at this stage, maybe somewhat more sensitive, but no direct comparison studies have been performed. Apart from small effect size, there are several reasons for this lack of detecting larger proportions of genetic risk (Maher, 2008):

- Associated marker in LD with causative variant - loss of effect size

- Rare alleles that may not be captured by scanning for common variants
- Copy Number Variations (CNV) – which are not picked up well by current genome-wide approaches (Stefansson et al., 2008, Consortium, 2008)
- Transcriptional control of a gene locus by several other genes which are not necessarily in LD (Brem et al., 2002)
- Epigenetic effects (Waterland and Jirtle, 2003)

There are several ways how more knowledge about the 'dark matter' could be established. Fine mapping of regions within LD of associated markers, using SNP, MS or sequencing, could reveal causative variations. Most recently, sequencing of selected genomic regions or the whole genome came within reach of broad application with the advent of faster and cheaper sequencing technology (next generation sequencing). Next generation sequencing (NGS) works by high-throughput, parallel sequencing of overlapping short stretches of genome (100-250 bp), which are annotated by computational methods (Bentley et al., 2009). NGS is capable of detecting rare variants that escape detection by genome-wide studies using SNP or MS markers; and is very effective in detecting new microsatellites fur further investigation (Santana et al., 2009, Zalapa et al., 2012).

Future efforts are aiming to integrate data from large scale genomic and gene transcription or expression research (Hansen, 2008). A few microarray studies have already been undertaken measuring protein signatures of GVHD in urine (Weissinger and Dickinson, 2009, Kaiser et al., 2004) or gene transcription in blood (Buzzeo et al., 2008, Krijanovski et al., 2007, Paczesny et al., 2009b). These studies, especially if capable of discriminating profiles in different HSCT settings, could greatly contribute to the understanding of GVHD pathophysiology.

The future of genetic research into the causes of GVHD is likely see new approaches:

- **larger scale marker-based genomic studies, using SNP or MS markers**
- **integration of genetic and functional data, dissection of GVHD pathophysiology**
- **Whole genome sequencing approaches is likely to identify further, and rarer genetic variants associating with GVHD, but have not yet been conducted.**

5.4. Conclusions

This study has demonstrated that a MS-based, pooled DNA scanning methodology, derived from a genome-wide scanning approach and for the first time applied in an HSCT setting, was capable of identifying non-HLA genetic risk loci for the development of moderate-severe acute GVHD.

The expected low effect size of associations suggested an approach that was robust, powerful and sensitive. This study did show that a microsatellite-based approach had some inherent advantages (i.e. more informative markers, a study design of a multi-step screening) over similar SNP-based approaches, but also some disadvantages (e.g. the requirement for DNA pools, lack of high-throughput platforms).

With regards to translating the study design, overall this study went much further to control confounding variables than previous studies, but some confounders remained. Due to the nature of rapidly evolving progress in this field, robust cohort design is difficult. The choice of genetic marker type, study design with independent confirmation, and selection of a population from an ethnically homogeneous background with attempt of controlling confounders complied with well laid out requirements for a high-quality genetic association study. A larger number of subjects, providing the study with a stronger statistical power, could potentially have led to a larger number of susceptibility loci identified. From a technical perspective, extensive quality controls had ensured adequate quality of pooled DNA and interpretation of typing signals. False positive markers had effectively been eliminated, despite a deliberately ‘sensitive’ approach by using technical resolution of DNA pools as a threshold for inclusion, and non-application of multiple testing correction whilst building on confirmation in an independent cohort to rule out false positives.

This approach confirmed three previous SNP associations (IL2-330, TNF-1031 and CTLA4-CT60) in an exploration study, and ten new target gene microsatellite loci (F2RL1, MAPK14, ELTD1, IL1RAPL2 (x2), SOCS3, TBL1X, DDX42, AGPAT4 and AKT3) in MS-based pooled DNA approach. All of these loci should be confirmed in a further independent cohort. Some of these loci, e.g. the SNP from the exploration study which have known high-expression genotypes, are close to potential prospective observation and application in clinical practice as predictors of risk. The MAPK14 locus was confirmed in this study by SNP typing, was already one of the better understood with regards to pathophysiology (it was involved in pro-inflammatory responses). A specific treatment (p38 inhibitor) already exists that has been trialled in humans. Hence, the way to clinical application could be promising. An associated MS in the AGPAT4 locus has confirmed the finding of association in this locus in a genetically diverse population, rendering this locus a strong candidate for further exploration.

Some observations in these studies raised new questions and hypotheses. This study demonstrated that small effect size associations with HSCT outcome did exist and could be consistent, but most associations from the screening step were not reproducible, even with this more stringent study design. Heterogeneity of confounders, hence cohort construction, was a likely cause for the lack of reproducibility. Future studies should consider more the issues of statistical power, study and cohort design.

Another important observation was the discrepancy of effect markers had in HLA matched or mismatched subgroups. With the focus mainly on HLA-matched study cohorts, previous studies may have missed associations that are predominant in HLA-mismatched subgroups only. It may be possible that the pathogenesis of GVHD involves different genes in different degrees of HLA matching – a hypothesis that would have to be proven by future studies.

The availability of ever larger HSCT registries for research is likely to facilitate larger scale investigations that are likely to overcome the methodological problems of previous studies (i.e. statistical power), including this one. The future will probably see larger scale genomic approaches (e.g. SNP, MS or sequencing based) and integration with gene expression, elucidating the pathophysiology of GVHD and identifying new targets for clinical application.

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APPENDICES

Appendix 2.1: Characteristics of the study population

Appendix 2.2: Procedure for custom-design of MS markers

Appendix 2.3: Estimation of DNA requirements for
the pooled screening steps

Appendix 2.4: Calibration of pipettes for DNA pooling

Appendix 2.5: PCR mixtures for test typing

Appendix 3.1: Information of SNP assays
used in the exploration study

Appendix 4.1: Genotyping errors and their resolution

Appendix 2.1

Characteristics of the study population

	Screening	Confirmation	*Difference p=*
Demographic			
Recipients	460	462	
Recipient gender Male	269 (58.48%)	289 (62.55%)	n/s
Recipient gender Female	191 (41.52%)	173 (37.45%)	n/s
Donor gender Male	267 (58.04%)	278 (60.17%)	n/s
Donor gender Female	193 (41.96%)	182 (39.39%)	n/s
Female donor to Male recipient transplant	102 (22.17%)	84 (18.18%)	n/s
Recipient age range	4-40 y	4-40 y	n/s
Recipient age mean	21.7 y	24.1 y	n/s
Donor age range	20-70y	19-51 y	n/s
Donor age mean	34 y	34.3 y	n/s
Clinical			
Diagnosis Acute lymphoblastic leukaemia	260 (56.52%)	254 (54.98%)	n/s
Diagnosis Acute non-ALL	200 (43.48%)	208 (45.02%)	n/s
High risk leukaemia	279 (60.65%)	246 (53.25%)	<0.1
HLA matching – 12/12 loci	41 (8.91%)	37 (8%)	n/s
HLA matching – 12/12 and 10/10 loci	160 (34.78%)	166 (35.93%)	n/s
HLA matching - GVHD risk mismatches	220 (47.83%)	229 (49.57%)	n/s
Conditioning – Cyclophosphamide + total body irradiation (TBI)	334 (72.61%)	322 (69.67%)	n/s
Conditioning – Busulphan/Cyclophosphamide or Busulphan based	53 (11.52%)	47 (10.17%)	n/s
Conditioning - TBI based	73 (15.87%)	83 (17.97%)	n/s
Conditioning - other	0	10 (2.16%)	n/s
GVHD prophylaxis – Cyclosporin A based	279 (60.65%)	154 (33.33%)	<0.05
GVHD prophylaxis - Tacrolimus based	177 (34.48%)	305 (66.02%)	<0.05
GVHD prophylaxis - other	4 (0.87%)	3 (0.65%)	n/s
Outcome			
Acute GVHD grade 0	124 (26.96%)	124 (26.84%)	n/s
Acute GVHD grade 1	153 (33.26%)	99 (21.42%)	<0.05
Acute GVHD grade 2	105 (22.83%)	143 (30.95%)	<0.05
Acute GVHD grade 3	50 (10.87%)	72 (15.58%)	<0.05
Acute GVHD grade 4	28 (6.09%)	24 (5.19%)	n/s
Chronic GVHD - none	244 (53.04%)	242 (52.38%)	n/s
Chronic GVHD - limited disease	71 (15.43%)	63 (13.64%)	n/s
Chronic GVHD - extensive disease	95 (20.65%)	106 (22.94%)	n/s
Chronic GVHD - unknown	50 (10.86%)	49 (10.6%)	n/s
Relapse	115 (25%)	110 (23.81%)	n/s
Survival – 100 days	395 (86.9%)	403 (87.23%)	n/s
Survival – 1 year	306 (66.52%)	312 (67.53%)	n/s
Survival – 3 years	245 (53.26%)	258 (55.84%)	n/s

Appendix 2.1: Population characteristics. *p* refers to statistically significant differences between the screening and confirmation cohorts.

Appendix 2.2:

Procedure for custom-design of MS markers

1. Procedure for custom-design of MS markers

Some target genes were located in gene regions that did not have adequate cover with MS markers from the genome-wide panel. Therefore, for 59 genes MS markers had to be custom-designed following the procedure below:

- Identification of target gene genomic location on the NCBI or GeneCard databases
- Retrieving the genomic sequence, plus an additional sequence of 50 kb to both sides of the target gene, from the UCSC genome browser website (http://genome.ucsc.edu/), using the 'Gene Sorter' function
- Importing the retrieved sequence into the 'Blat' function of the same website, checking for multiple sequence locations, applying settings to identify SNP and possible amplicons
- Importing the same sequence into Sputnik (http://cbi.labri.u-bordeaux.fr/outils/Pise/sputnik.html) to identify microsatellite repeats within the obtained ~100kb sequence.
- Selection of an appropriate candidate microsatellite, criteria: as many repeats as possible, preferably 3-4 base repeats, uninterrupted repeat sequence.
- Importing the same sequence into geneview, location of the identified microsatellite, cut and paste the microsatellite with 1000 base pairs flanking on each side.
- Import of obtained sequence into primer express, primer search using the settings: Melting temperature (Tm) 56-58°C, amplicon length max 400 base pairs.
- If suitable primer pairs not found: Trying of a different microsatellite from the Sputnik output

- If suitable primer pair found: Checking of primer pair with the ‘In silico PCR’ function on the UCSC website to ensure uniqueness of primer pair for the intended target.
- For n=8 loci it was not possible to design appropriate primers. Reasons were either a complete absence of suitable microsatellites within the target regions, or extensive duplication of highly similar sequence (e.g. within the FCGR gene cluster) disabling identification of a unique sequence.

Appendix 2.3:

Estimation of DNA requirements for the pooled screening steps

1. Estimation of DNA amounts required for single genotyping

The essential DNA requirements for conducting pooled DNA genotyping are as outlined in table 1.

Screen	Cohort	No. markers	Amount for conc 6 ng/µl	Amount for conc 8 ng/µl	No. samples	Total DNA at 6 ng/µl	Total DNA at 8 ng/µl
1	Pat 0-1	4000	48	64	281	683.27	911.03
1	Pat 2-4	4000	48	64	195	984.61	1312.82
1	Don 0-1	4000	48	64	281	683.27	911.03
1	Don 2-4	4000	48	64	195	984.61	1312.82
2	Pat 0-1	500	48	64	128	187.50	250.00
2	Pat 2-4	500	48	64	111	216.21	288.28
2	Don 0-1	500	48	64	128	187.50	250.00
2	Don 2-4	500	48	64	111	216.21	288.28

Table 1: Basic DNA requirement estimates

2. Additional DNA amounts required for processing, further typing

To calculate the total amount required for the first screening step, an extra one third for possibly necessary repeat experiments was added, and, depending on sample concentration, an extra 100-500 ng of DNA required for the pooling process (repeated concentration measurements). Therefore final requirements for the first and second pooled screenings were as outlined in table 2.

Screen	Cohort	High conc	Low conc
1	Pat 0-1	1714	1314
1	Pat 2-4	2249	1849
1	Don 0-1	1714	1314
1	Don 2-4	2249	1849
2	Pat 0-1	833	433
2	Pat 2-4	884	484
2	Don 0-1	833	433
2	Don 2-4	884	484

Table 2: Corrected DNA requirements including allocations for pipetting/pooling, in ng amount.

Following the first and second pooled screening steps, around 100 markers were expected to show a significant association. These markers would then be individually genotyped on the entire cohort. As the amount of DNA required for one MS marker typing was 1-2 ng/sample, this would require a further 200 ng of DNA, plus a 15% margin for repeat experiments.

Only the markers which showed a consistently significant association after the two pooled screenings and the individual genotyping confirmation step would be subjected to SNP ‘scanning’ of the 100 kb region, with approximately 50 SNP. Using a TaqMan® assay, this required 1-2 ng of DNA per SNP studied (hence, 100 ng), plus a margin of 15% - approximately 120 ng of DNA.

Separately, the plan was to study all SNP associated with HSCT outcomes by individual genotyping using a TaqMan® assay. These were approximately 150 SNP, including a margin of 15% requiring 350 ng of DNA.

After summing up all these requirements, a further 15% of DNA amount was added for pipetting and measurement variability.

In summary, maximum DNA requirements for the entire study were as in table 3.

Usage	Entry 1st Screen, ng	Entry 2nd Screen, ng
First Screen	2250	N/A
Second Screen	N/A	890
Individ MS typing	230	230
SNP screen	120	120
SNP previous	350	350
Intermed sum	2950	1590
Add for pipet/measure	450	260
Total	3400	1850

Table 3: Estimated total DNA amounts required for entire study

Appendix 2.4:
Calibration of pipettes for DNA pooling

The process of pooling requires a very high degree of accuracy. Therefore for all pipetting of pools only calibrated pipettes with a fixed volume are used (i.e. the pipette is dedicated to this process for the duration of the study, the volume on the pipette is not changed). For calibration, a set of at least 3 pipettes is tested, and the one is chosen that has the lowest volume variation (which has to be <1%). Only original pipette tips of the maker are used. The aim was to have fixed pipette volumes for all standard procedure volumes. Volumes of individual samples had to be pipetted with multiple fixed pipettes if necessary. For all pooling into intermediate or large pools fixed volume pipettes with the exact volume required were 'custom-calibrated'.

Procedure of pipette calibration

Preparation

- A set of five 2ml plastic flipcap tubes is prepared for each pipette
- Each tube is weighed three times on a high sensitivity scale (nanograms, Mettler® Toledo) at standard conditions (stable lab table and temperature)

Practical procedure

- Each of the five tubes is pipetted with the target volume by a standard technique:
- Attachment of the tip by a single, firm but gentle movement in vertical direction
- Gentle, slow aspiration with 1-2 seconds wait after completion of aspiration

- Keeping pipette vertical at all times of aspiration, transfer, dispensing
- Slow dispensing of sample into tube, wait for 1-2 seconds with tip inside fluid before removing
- Each filled tube is then weighed three times
- Calculation of mean, standard deviation, standard error and variance on an excel template spreadsheet.

Pipette volume range	Nominal volume	Pipetted volume	SD	Variance	Upper error %	Lower error %
2-20	20	19.7	0.00006	0.00000003	0.4	-0.44
10-100	100	98.9	0.0001	0.00000002	0.12	-0.24
100-1000	380	378	0.0009	0.0000009	0.35	-0.22
20-200	95	94.5	0.0001	0.00000003	0.24	-0.28
20-200	87	86.8	0.00007	0.000000005	0.09	-0.06

Table 1: Examples of pipette tests. The pipette that delivered the volume closest to the aimed volume was chosen, if the error was within a range of +/- 1%.

Appendix 2.5:

PCR mixtures for test typing

High amount DNA

DNA amt/well ng	93.18677
Marker typing capacity	6000

Medium amount DNA

DNA amt/well ng	62.12451
Marker typing capacity	9000

Low amount DNA

DNA amt/well ng	46.59338
Marker typing capacity	12,000

ingredient	**vol µl/well**
dH2O	0
10xbuffer	2
2.0mM dNTP	2.5
Primer mix	2
AmpliTaqG	0.1
DNA	13.4
total vol (µl)	**20**

ingredient	**vol µl/well**
dH2O	4.2
10xbuffer	2
2.0mM dNTP	2.5
Primer mix	2
AmpliTaqG	0.1
DNA	9.2
total vol (µl)	**20**

ingredient	**vol µl/well**
dH2O	6.5
10xbuffer	2
2.0mM dNTP	2.5
Primer mix	2
AmpliTaqG	0.1
DNA	6.9
total vol (µl)	**20**

Table 3.11: PCR mixtures for three options of DNA amount in the PCR procedure, as applied for MS marker testing

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Appendix 3.1:

Information of SNP assays used in the exploration study

Primers for Luminex Genotyping of *IL10* SNP

PROBE	oligonucleotide name	sequence (5'--> 3')
IL10P common probe	IL10CR-2	TTTTTTTTTTTTTTTTTTTTCAGACTACTCTTACCCA
-1082A probe	1082AS-4	TTTTTTTTTTTTTTTTTTTTCTGTTCCCCTTCCCAAAGA
-1082G probe	1082GS-3	TTTTTTTTTTTTTTTTTTTTTTCCCCCTCCCAAAG
-819C probe	819CR-2	TTTTTTTTTTTTTTTTTTTTAGGTGATGTAACATCTCTGTGC
-819T probe	819TS-2	TTTTTTTTTTTTTTTTTTTTGCACAGAGATATTACATCACCT
-592A probe	592AR-8	TTTTTTTTTTTTTTTTTTTTCCGCCTGTACTGTAGG
-592C probe	592CR-2	TTTTTTTTTTTTTTTTTTTTCGCCTGTCCTGTAGGAA

PRIMER	oligonucleotide name	sequence (5'--> 3')
IL10P forward primer	IL10-F2	CAAATCCAAGACAACACTACTAAGGC
IL10P reverse primer	IL10-R2	GGCTAAATATCCTCAAAGTTCCCAAG

TaqMan Assays

Assay ID	Context Sequence	Design Strand	Category ID	Group ID	Gene Symbol	NCBI Gene Reference	Cytogenetic Band	SNP Type	Location on NCBI Assembly
C__15944115_20	TATCTAGCTATATGATTGTGAGTTA[A/G]CTTCTTAAATCTTCTATGACTCAGT	Forward	Chr12	D12S313	*IFNG*		12q15a	INTERGENIC/UNKNOWN	66841278
C__15820717_10	GTCAGCCTGTGGGGTAACTTGGTCC[A/G]TGGGATTTCCCCTAAAAAGGTAGCC	Forward	Chr16	D16S3136	*NOD2*	NM_022162.1	16q12.1c	INTRON	49291470
C___7514871_10	GGAAGCAAAGGAGAAGCTGAGAAGA[C/T]GAAGGAAAAGTCAGGGTCTGGAGGG	Reverse	Chr6	D6S276	*TNF;LTA;LTB*		6p21.33a	INTERGENIC/UNKNOWN	31650287
C___9077561_20	AATGGAAAATCCCAGAAATTCTCCC[A/G]TTTGGATCCCACCTTCTCCATCCCA	Forward	Chr1	D1S484	*FCGR2A*	NM_021642.2	1q23.3a	MIS-SENSE MUTATION	159746369
C__25651063_10	CATTGCATTCTTGACAGATTCTCTT[A/G]TTGCCTTAAAAAGAATCACTGGCCT	Forward	Chr16	D16S3136	*NOD2*	NM_022162.1	16q12.1c	INTRON	49322877
C___9546481_20	GATTTTTACATATGAGCCTTCAATG[A/G]TGTTGCCTGGTTACTATTATTAAAG	Reverse	Chr2	D2S160	*IL1A*	NM_000575.3	2q13d	UTR 5	113259431
C__34029672_10	GAGCTTCTGCAAAGTGGAAGAATAC[C/T]GCTTGGCCCTAACTCCTCACCCCAA	Reverse	Chr16	D16S3136	*NOD2*	NM_022162.1	16q12.1c	INTRON	49305205
C___1384440_10	GTGCCACCCATTTATTGGGGAAAAG[C/T]CCTAAAAGGGGAAGTGGGGAAGGGA	Reverse	Chr16	D16S3136	*NOD2*	NM_022162.1	16q12.1c	INTRON	49310316
C___8861232_20	GTGGCCATCCCTGGGAATGCAAGCA[G/T]GGATGCAGTCTGCACGTCCACGTCC	Forward	Chr1	D1S2667	*TNFRSF1B*	NM_001066.2	1p36.22a	MIS-SENSE MUTATION	12175542
C__16049347_10	TTGCTGTGTTTGTAATTCAGGTAAA[C/T]CTATTTTCTGTAAAGCAGGCATGAT	Reverse	Chr8	D8S285	*CCL4*		8q12.1c	INTERGENIC/UNKNOWN	59833385
C__15859930_10	AGTAACTCAGAAAATTTTCTTTGTC[C/A]TAAAACTACACTGAACATGTGAATA	Forward	Chr4	D4S402	*IL2*		4q27d	INTERGENIC/UNKNOWN	123597430
C___1839943_10	TACCTTGGGTGCTGTTCTCTGCCTC[G/A]GGAGCTCTCTGTCAATTGCAGGAGC	Forward	Chr2	D2S160	*IL1B*		2q13d	INTERGENIC/UNKNOWN	113311338

C___1202883_20	GAAAAGCTGCGTGATGATGAAATCG[G/A]CTCCCGCAGACACCTTCTCCTTCAA	Forward	Chr1	D1S2667	*CLCN6;MTHFR;C1orf167*	NM_005957.3	1p36.22a	MIS-SENSE MUTATION	11778965
C___8708473_10	GAGGAGGGGGCAACAGGACACCTGA[A/G]GGATGGAAGGGTCAGGAGGCAGACA	Forward	Chr19	D19S220	*TMEM91;TGFB1;B9D2*		19q13.2c	INTERGENIC/UNKNOWN	46552136
C___9578811_10	TCATATGGTTAACTGTCCATTCCAG[A/G]AACGTCTGTGAGCCTCTCATGTTGC	Forward	Chr10	D10S1765	*FAS*		10q23.31b	INTERGENIC/UNKNOWN	90739943
C__15820716_10	TTGCTCTTGACTCTTGGCAGGAAAC[A/G]TACAACTCTTTCTTTCTTCTTTTCT	Reverse	Chr16	D16S3136	*NOD2*	NM_022162.1	16q12.1c	INTRON	49291534
C___3296043_10	TCTTCACCACTATTTGGGATATAAC[A/G]TGGGTTAACACAGACATAGCAGTCC	Reverse	Chr2	D2S117	*CTLA4*		2q33.2a	INTERGENIC/UNKNOWN	204447164
C__11722137_10	TTTTCAAACAAGAAGTAGTTTTTCA[C/T]CAAACAATGTCTCTTATGTAATTCA	Reverse	Chr9	D9S1776	*TLR4*	NM_138554.2	9q33.1c	INTRON	119512585
C__15873886_20	ATGTCAGAGACGGAGACGAGGCAAC[A/C]GGACCGTGGAGGAGAAAAATAGAAA	Forward	Chr19	D19S220	*B9D2;TGFB1*	NM_000660.3	19q13.2c	INTRON	46548726
C___1882528_10	GGAGGCGGATGCTGTGAGTTCCCAG[G/T]TCTTGGCTGTTGTCTGAGAGGGGGT	Forward	Chr10	D10S591	*IL15RA*	NM_002189.2,NM_172200.1	10p15.1b	MIS-SENSE MUTATION	6042374
C___2213785_10	TTTCTAGCCGCCAAGTGGAGAACAG[C/G]TTGGAGCGGTGCGCCGGGCTTAGCG	Forward	Chr22	D22S539	*SLC2A11;MIF*		22q11.23a	INTERGENIC/UNKNOWN	22566392
C___1272348_10	CTGTTCCTATTCAGCCATCTTGGCT[C/T]GGGACCAGAGAACTTCGTATTTCTT	Reverse	Chr1	D1S198	*IL23R*		1p31.3a	INTERGENIC/UNKNOWN	67421048
C___7504226_10	CCATATACCTGAAAGATCTGATGAA[A/G]CCCAGCGTGTTTTTAAAAGTTCGAA	Forward	Chr3	D3S1558	*CD86*	NM_006889.3,NM_175862.3	3q13.33c	MIS-SENSE MUTATION	123321009
C___3052613_1_	GTGATGATAGGGTTACACATCTGCT[C/T]CAATTCCTTTCTCTTATGATCAAAC	Forward	Chr6	D6S276	*HSPA1A;HSPA1L;LSM2*	NM_005527.3	6p21.33a	MIS-SENSE MUTATION	31885925
C___2215707_10	GGCCCAGAAGACCCCCCTCGGAATC[A/G]GAGCAGGGAGGATGGGGAGTGTGAG	Reverse	Chr6	D6S276	*LTB;LTA;TNF*		6p21.33a	INTERGENIC/UNKNOWN	31651080
C___1384434_10	TGGCCTTTGGAAGGGGCATTTCTGA[A/T]TAAGATCTGGGCCGCTCTCCGCTGG	Reverse	Chr16	D16S3136	*NOD2*	NM_022162.1	16q12.1c	INTRON	49317048
C___3017467_10	TGTTTTATTTAAGCCTCACAAGGGT[A/G]TAGTGTGACTACACTGTTTCTTAAC	Forward	Chr16	D16S3136	*NOD2*	NM_022162.1	16q12.1c	INTRON	49294157

C__15873887_10	ATTGTATGGTTTGTGTTCTTCTATC[C/T]TTCAGGGACCATCTAGGTGGACCTT	Reverse	Chr19	D19S220	*TGFB1;B9D2*	NM_000660.3	19q13.2c	INTRON	46545926
C___7514879_10	GAGGCAATAGGTTTTGAGGGGCATG[A/G]GGACGGGGTTCAGCCTCCAGGGTCC	Reverse	Chr6	D6S276	*LTB;LTA;TNF*		6p21.33a	INTERGENIC/UNKNOWN	31651010
C___2404008_10	TGGACAGGCGGTCCTGGATGGCCTC[A/G]ATCAGCGCGGCGTCCTGCACCCCAG	Forward	Chr12	D12S85	*VDR*	NM_000376.2,NM_001017535.1	12q13.11c	SILENT MUTATION	46525024
C___2415786_20	GCACAAGGCTCAGCTGAACCTGGCT[A/G]CCAGGACCTGGCCCTGCACTCTCCT	Reverse	Chr2	D2S117	*CTLA4*	NM_001037631.1,NM_005214.3	2q33.2a	MIS-SENSE MUTATION	204440959
C__11918223_10	GTCGAGTATGGGGACCCCCCCTTAA[C/T]GAAGACAGGGCCATGTAGAGGGCCC	Reverse	Chr6	D6S276	*LTB;LTA;TNF*		6p21.33a	INTERGENIC/UNKNOWN	31650461
C___3017459_20	ACATTTCTCTTGGCTTCCTGGTGCG[G/T]GCCAAAGGTGTCGTGCCAGGGAGTA	Forward	Chr16	D16S3136	*NOD2*	NM_022162.1	16q12.1c	SILENT MUTATION	49303084
C__31784020_10	TCTATTAAGGTAGACCACCTCTCCC[C/T]TTTTTTTTTTTTCAAACAAGAAGTA	Forward	Chr9	D9S1776	*TLR4*	NM_138554.2	9q33.1c	INTRON	119512551
C___2415784_10	CTTATCTCTCTCTAGACCTTCTTGG[C/T]TAAGAAACCATGTAGTTTGTATGAA	Forward	Chr2	D2S117	*CTLA4*	NM_001037631.1,NM_005214.3	2q33.2a	INTRON	204441833
C__30031638_10	CCTGAATTCTCAGTAACTTAGAAGT[A/C]ATTTCTAATGATTCCGGCTGGGCAC	Forward	Chr19	D19S220	*TGFB1;B9D2*	NM_000660.3	19q13.2c	INTRON	46543349
RS1264457-GA		Forward			*HLA-E*				
RS1800795-GC		Reverse			*HLA-E*				

Appendix 4.1:

Genotyping errors and their resolution

1. 1st screening PCR and genotyping – technical results (all pools combined)

The initial round of PCR and genotyping had an error rate of 11.36%. This was expected as there is some variation in PCR conditions of markers on the panel for the genome-wide association studies. In that set-up, these variations were addressed by grouping markers requiring the same conditions on the same plate. As the selection of markers for this study disrupted this order, markers with different typing conditions were on the same plate. The main causes of error were absence of peak signal (4.34%) and low peak signal (5.08%), indicating either PCR failure or high dilution/low concentration of PCR product. High peak signal, size standard errors, data collection failure and mechanical errors of PCR and genotyping accounted for the remaining 2.06% of errors.

1.1. Strategy for resolving error samples (1st step):

- Samples with an absent peak signal were re-typed using a x10 dilution.
- Samples with a low peak signal were re-typed using a x20 dilution.
- Samples with size standard errors, data collection failure or mechanical errors were re-typed using a x40 dilution.
- Samples with high peak signals were subjected to a dilution sequence of x80, x200, x400 and x800

Results of the 1st step of error sample resolution:
All of the high peak/size standard/data collection/mechanical error samples had adequate results. Most of the low peak signal and some of the absent

peak signal sample errors were resolved, but 5.20% of samples remained with absent/low peak signal error. We presumed that the reason is primary PCR failure.

1.2. Strategy for resolving error samples (2nd step):

- Repeat PCR of all samples with absent/low peak signal
- DNA purification of PCR product in persisting low peak signal samples

Results of the 2nd step of error sample resolution:
A further 2.53% of samples were resolved, remaining 2.67% with persistently absent/low peak signal. Possible reasons include degradation of primers (primers for studies in this institution stem from a master primer set on plates which are defrosted and re-frozen each time a primer aliquot is taken) or inadequate PCR conditions.

1.3. Strategy for resolving error samples (3rd step):

- Re-PCR with primers from a separate primer stock
- If error persists: purchase of fresh primer, modification of PCR conditions (extension to 35 cycles, increasing concentration of dNTP, change of annealing temperature), re-typing after PCR product purification

Results of the 3rd step of error sample resolution:
Only 0.8% of samples remained as error. At this point, no further attempts of resolution were undertaken - the additional information gained would not have stood in relation to the time and effort to achieve it.

2. Error resolution for the second pooled DNA screening

Error resolution of the second pooled screening followed the same principles. Eventually, 1.55% of markers were not reproducible and excluded (1.67% in the donor screen, 1.3% in the recipient screen).

Supplementary Material

A data disc containing the supplementary material is attached to the back of this page.

Supplementary File 1.1

List of 248 gene association studies: Associations of non-HLA gene polymorphisms with HSCT outcomes

Last updated: 15 April 2012

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Supplementary file 2.1:

JMDP registry analysis and study cohort design

1. Genetic background of the Japanese population

It has been pointed out that the studied population should stem from a homogenous genetic background without genetic admixture. It was known from data of the HapMap Consortium (Consortium, 2005, Stranger et al., 2005) that genetic variation varies enormously between different populations, more so the closer the population was to the evolutionary African population, and less so the further the population had moved away from Africa. The Japanese, as the furthest East of all Asian populations, had a genetic structure of less, and better preserved haplotype blocks than Caucasians or Africans (Conrad et al., 2006, Gabriel et al., 2002). While the European and North American History was characterized by large shifts and admixing of populations (e.g. migration within Europe, immigration and displacement of Caucasians, Africans and Asians to North America); due its geography Japan had experienced fewer admixtures. The Japanese population is genetically closely related to that of South East and North East Asia, areas on the Asian mainland from which the Japanese archipelago was initially and repeatedly colonised, and to which it maintained close relations through history (Omoto and Saitou, 1997, Nanta, 2008, Hanihara, 1991).

According to their records, all HSCT donors and recipients in this study were of Japanese origin, hence genetic admixture is very low. As this population had larger size and a smaller number of preserved haplotype blocks, with fewer haplotypes per block, the linkage disequilibrium range of a selected marker could expected to be wider as compared to other populations, therefore less markers would be required to give the same LD range coverage as for a more genetically diverse population. This had implications for statistical power (potentially, the population size required could be set lower, and a smaller number of markers required less statistical correction for multiple testing).

Difference of genetic variation between populations has been an area of intense research in the HSCT field. For example, the lower incidence of GVHD in the Japanese population could be attributed in part to differences in HLA alleles amongst the Japanese and other population, and subsequent HLA matching for HSCT (Petersdorf et al., 2007, Morishima et al., 2007a). With growing HSCT registries, there has been a move towards studying populations from a more homogenous ethnic background. Non-HLA gene polymorphisms previously associated with GVHD also showed considerable variation of allele and genotype distribution (e.g. IL10 (Middleton et al.), IL6 (Visentainer et al., 2008), NOD2 (Tanabe et al., 2011)).

2. Cohort Selection

2.1. Analysis of clinical and genetic risk factors in a large, unselected HSCT population

Clinical risk factors for acute GVHD have been documented in studies from the JMDP registries or other unrelated HSCT studies in Japan. These included donor-recipient gender mismatch, patient age, donor age, diagnosis (acute lymphoblastic leukaemia(ALL) versus chronic myeloid leukaemia (CML)), GVHD prophylaxis (cyclosporine versus tacrolimus), relapse risk, antithymoglobulin (ATG), conditioning regimen (total body irradiation (TBI) versus non-TBI), stem cell source (bone marrow transplant (BMT) versus peripheral blood stem cell transplant (PBSCT)) and blood group (ABO) mismatch (Kawase et al., 2007, Morishima et al., 2007a, Hara et al., 2007, Kimura et al., 2008). Multivariate analyses in Japanese genetic association studies had confirmed the significance of these risk factors. Studies in other populations identified Donor and recipient cytomegaly virus (CMV) status, intensity of conditioning regimens, malignant disease stage, diagnosis, unrelated versus related HSCT, early transplants (before 2000), older donor age, older patient age, high nucleated cell count, stem cell source, ethnicity, gender mismatch, donor parity and ABO mismatch as further clinical risk factors (Hill et al., 1997, Socie et al., 2001, Aschan, 2007, Chaidos et al., 2007, Wojnar et al., 2006, Svennilson et al., 2003, Nash et al., 1992). For the Japanese population, more recent work identified KIR and KIRL mismatches, HLA haplotypes and minor histocompatibility antigens (mHag) as genetic risk factors.(Yabe et al., 2008, Morishima et al., 2010, Kawase et al., 2008, Ogawa et al., 2008). Eventually, it had to be assumed that many more clinical and genetic risk factors exist of which we have little evidence, owed to the restricted nature of data collections.

In order to identify risk factors for moderate-severe GVHD (grade 2-4), a large cohort (n=2469 HSCT pairs) from the JMDP registry, representing a majority of unrelated donor HSCT in Japan between 1993-2000, was investigated for significant associations by both log rank test and Fisher’s exact test, and binary logistic regression.

The baseline characteristics of this population were summarised in table 1.

Risk factors for grade 2-4 GVHD considered included recipient age, recipient gender, donor age, donor gender, donor-recipient gender mismatch (female donor to male recipient), diagnosis, AB0 mismatch, conditioning regimen, cyclophosphamide dose, total body irradiation dose, number of nucleated cells in graft, GVHD prophylaxis, antithymocyte globulin, T-cell depletion and HLA matching.

Table 2 shows the associations of clinical risk factors with grade 2-4 acute GVHD in univariate analysis, using Fisher’s Exact Test with 95% confidence intervals for Odds Ratio. Donor T-cell depletion (TcD) and the use of anti-thymocyte globulin (ATG) to eradicate recipient T-cells and 5-locus HLA matching confered the strongest effects on the prevention of acute GVHD. Certain diagnosis in itself, or by their population and treatment characteristics, carried a higher risk of acute GVHD. Donor age >30 years almost matched the effect size of HLA mismatch. A conditioning regimen consisting of standard dose cyclophosphamide and total body irradiation had the lowest risk of acute GVHD. Cyclophosphamide in itself modulated the recipient immune response in a GVHD protective way, even at high dose. TBI at standard doses has the lowest GVHD risk, but as part of conditioning (TBI versus no TBI) had no impact on GVHD risk. No significant effect on GVHD risk was found with recipient or donor gender, female into male mismatch, AB0 matching, graft nucleated cell count, or recipient age. Recipient age >40 years, however, showed a tendency towards a higher risk of grade 2-4 GVHD.

The multivariate analysis for this unselected population is shown in table 3. Taken all risk factors from the univariate analysis into account, seven of these remained significant, relating to demographics (donor age >30y, high risk diagnosis (ALL, CML)), conditioning (other conditioning regimen than CyTBI, cyclophosphamide dose none/low versus standard/high) and GVHD prophylaxis (cyclosporine A versus tacrolimus, no ATG versus ATG, HLA mismatching).

Category	Factor	Frequency	Percent
Recipient age	0-10y	406	16.4
	11-20y	542	22.0
	21-30y	600	24.3
	31-40y	453	18.3
	41-50y	421	17.1
	51-60y	47	1.9
Recipient gender	Female	994	40.3
	Male	1475	59.7
Donor age	0-10y	0	.0
	11-20y	20	.8
	21-30y	895	36.2
	31-40y	941	38.1
	41-50y	602	24.4
	51-60y	9	.4
	61-70y	1	.0
	unknown	1	.0
Donor gender	Female	974	39.4
	Male	1495	60.6
Female-male gender mismatch	no F-M mismatch	1950	79.0
	F-M mismatch	518	21.0
Diagnosis	unknown	7	.3
	ALL (acute lymphoblastic leukaemia)	653	26.4
	ANLL (acute non-lymphoblastic leukaemia)	617	25.0
	CML (chronic myeloid leukaemia)	643	26.0
	HD (Hodgkin’s disease)	52	2.1
	ID (primary immunodeficiency)	17	.7
	LPD (lymphoproliferative disease)	1	.0
	MDS (myelodysplastic syndrome)	201	8.1
	MF (myelofibosis)	2	.1
	MM (multiple myeloma)	2	.1
	NHL (non-Hodgkin lymphoma)	96	3.9
	SAA (severe aplastic anaemia)	178	7.2
ABO matching	matched	1248	50.5
	minor mismatch	526	21.3
	major mismatch	620	25.1
	minor & major mismatch	55	2.2
	unknown	20	.8
Conditioning	No of different regimens	86	
	Busulphan+Cyclophosphamide	241	9.8
	Busulphan+Cyclophosphamide+other	145	5.9
	Cyclophosphamide+other	53	2.1
	Cyclophosphamide+total body irradiation	639	25.9

	Cyclophosphamide+total body irradiation+other	90	3.6
	Cyclophosphamide+total body irradiation+busulphan	251	10.2
	Cyclophosphamide+total body irradiation+Ara-C	504	20.4
	Cyclophosphamide+total body irradiation+VP16-213	220	8.9
	other	59	2.4
	Total body irradiation+other	267	10.8
Cyclophosphamide dose	none	295	11.9
	<120	576	23.3
	120 (standard)	1262	51.1
	>120	312	12.6
	unknown	24	1.0
Total Body Irradiation	none	486	19.7
	<1200	336	13.6
	1200	1485	60.1
	>1200	149	6.0
	unknown	13	.5
No of nucleated cells	<251	509	20.6
	251-400	1437	58.2
	>400	503	20.4
	unknown	20	.8
GVHD prophylaxis	No of different regimens	21	
	Cyclosporin A - based	1818	73.6
	Tacrolimus - based	641	26.0
	Other	10	.4
Antithymoglobulin	unknown	4	.2
	no ATG	2279	92.3
	ATG	186	7.5
T-cell depletion	unknown	4	.2
	no T-cell depletion	2448	99.1
	T-cell depletion	17	.7
HLA matching	5-locus matched	925	37.5
	mismatched	1544	62.5

Table 1: Baseline characteristics of an unselected HSCT population (n=2469) from the JMDP registry

Category	comparison	p-value	case all no	control all no	case pos	case neg	control pos	control neg	Odds Ratio	Confidence interval	confidence interval	comment
GVHD prophylaxis	**No TcD v TcD**	0.039	1444	968	13	1431	3	965	2.9222	0.83051	10.282	No TcD higher risk
GVHD prophylaxis	**No ATG v ATG**	0.002	1447	968	128	1316	54	914	1.64629	1.18468	2.28777	ATG protective
HLA matching	**mismatch v 5 locus match**	<0.0001	968	1447	653	315	837	610	1.5108	1.27436	1.79111	HLA mismatch higher risk
Diagnosis	**high risk (ALL+CML) v low risk (other)**	<0.0001	968	1447	566	402	703	744	1.49007	1.2644	1.75603	ALL, CML risk
GVHD prophylaxis	**Cyclosporin v tacrolimus**	<0.0001	968	1447	751	214	1032	411	1.39762	1.15566	1.69023	CyA higher risk
Donor age	**>30y v <30y**	<0.0001	968	1447	652	316	863	584	1.39625	1.17735	1.65585	higher age-higher risk
Conditioning	**Other v CyTBI**	0.002	968	1447	218	750	408	1039	1.35098	1.11792	1.63263	Non-CyTBI higher risk
Conditioning	**Cy no/low dose v standard/high dose**	0.001	956	1436	964	472	576	380	1.3474	1.13674	1.59709	no/low have higher risk
Conditioning	**TBI standard dose v lower/higher dose**	0.023	964	1438	797	167	1135	303	1.27406	1.03325	1.57098	standard dose protective
Donor age	**>40y v <40y**	0.021	968	1447	265	703	335	1112	1.25127	1.03809	1.50822	higher age-higher risk
Recipient gender	**Male v Female**	0.062	968	1447	600	368	842	605	1.17151	0.99173	1.38388	
Donor gender	**Male v Female**	0.14	968	1447	605	363	856	590	1.14875	0.97195	1.35772	
ABO matching	**matched v mismatched**	0.156	962	1434	474	488	749	685	0.88832	0.75437	1.04604	
No of nucleated cells	**high v low**	0.215	954	1441	85	869	108	1333	1.20727	0.89727	1.62438	
Donor-Recipient gender mismatch	**Female into Male v other**	0.495	968	1446	197	771	311	1135	0.9325	0.76304	1.13958	
Recipient age	**>40y v <40y**	1	968	1447	179	789	267	1180	1.00264	0.81297	1.23657	
Conditioning	**TBI v non-TBI**	1	964	1438	774	190	1155	283	0.99814	0.81302	1.22542	

Table 2: Univariate analysis of clinical risk factors in an unselected cohort of Japanese HSCT from the JMDP register (1993-2000)

							95.0% CI for Exp(B)	
	B	SE	Wald	df	Sig.	Exp(B)	Lower	Upper
No ATG v ATG	-.500	.147	11.604	1	.001	1.648	1.236	2.197
HLA mismatch v 5-locus match	-.413	.071	34.048	1	.000	1.511	1.315	1.736
Cyclosporin A v Tacrolimus	.347	.080	18.812	1	.000	1.415	1.210	1.656
No CyTBI v CyTBI	-.241	.084	8.244	1	.004	1.271	1.079	1.498
High risk diagnosis (ALL+CML) v other	.236	.068	12.080	1	.001	1.266	1.108	1.447
Donor age >30y v <30y	.009	.003	6.862	1	.009	1.009	1.002	1.016
Cyclophosphamide non/low v standard/high	-.007	.003	4.992	1	.025	1.007	1.001	1.013
TBI v no TBI	.152	.092	2.769	1	.096	1.164	.973	1.393
Donor age >40y v <40y	.004	.003	1.870	1	.172	1.004	.998	1.009
TBI dose low/high v standard	-.009	.008	1.546	1	.214	.991	.976	1.005
TcD v no TCD	-.672	.581	1.339	1	.247	.511	.164	1.594
ABO matched v mismatched	.072	.066	1.190	1	.275	1.075	.944	1.225
Nucleated cell count low v high	.122	.117	1.086	1	.297	1.129	.898	1.419
Female into male gender mismatch	-.110	.139	.625	1	.429	.896	.682	1.177
Recipient gender	-.061	.088	.474	1	.491	.941	.792	1.119
Donor gender	-.072	.107	.455	1	.500	.930	.754	1.147
Recipient age >40y v <40y	-.001	.002	.135	1	.713	.999	.995	1.003

Table 3: Multivariate analysis (Cox regression) of clinical risk factors in an unselected Japanese HSCT cohort from the JMDP registry, 1993-2000

2.2. Designing a study cohort accounting for clinical risk factors

A large proportion of HSCT in Japan by JMDP between 1993 and 2000 included one or more statistically significant risk factors for moderate-severe acute GVHD (grade 2-4), (see table 4). This outcome was chosen because GVHD was one of the most commonly reported HSCT outcomes in the literature. The challenge was to devise a model for cohort selection that eliminated the strongest effects of these clinical risk factors, while preserving a sample size that would provide adequate statistical power. Knowing that the effect of HLA mismatching has an OR of approximately 1.5, it was aimed for a sample size that would undercut this OR with regards to statistical power. It was estimated that for a single outcome a sample size of approximately n=500 in each of the two screening steps (or 1000 altogether) would be required to achieve an OR of 1.3 for an allele frequency of 0.2.

I order to reduce the effect of HLA mismatching, a higher degree HLA-matched subgroup was analysed as a comparison (mismatched only for either one HLA-DQB1 or HLA-DPB1 locus, largely representing an 8/8 match of HLA A, B, C, DR) and non- ATG group as a control to compare variability and significance of the clinical risk factors in the different models.

GVHD prophylaxis with either cyclosporine A or tacrolimus was not applied for cohort selection as this would have introduced a strong time bias (cyclosporine A was largely replaced by tacrolimus in the late 1990's when registry studies showed that this measure significantly reduced the incidence of acute GVHD). Donor age >30 years has a strong effect, but such limitation would have been practically unrealistic with regards to sample size and power. These data showed that a standard dose Cyclophosphamide/TBI regimen carried the lowest risk of acute GVHD, but this regimen was in practice not suitable for all patients, especially high-risk ones. TBI in itself was known to induce a higher risk for acute GVHD; however, in this analysis TBI showed only a trend in this direction. In summary, the data on the different conditioning regimen and their dosages indicate that a TBI versus non-TBI analysis carried a large number of confounders.

Table 5 gives an overview of the models devised. Model 1 followed strictly the order of the effect size of the multivariate analysis. The second selection step (ATG given – HLA mismatched removed) already reduced the sample size below target (870 HSCT pairs). This is the model used as a control to study variability, significance and effect sizes of risk factors in the other models.

In Model 2, the focus was on the conditioning regimen (ATG given – conditioning other than Cyclophosphamide/TBI), reaching a sample size of 609 HSCT pairs, which would have been unfeasible.

Model 3 concentrated on the underlying diagnosis (excluding ALL and CML – ATG given included), resulting in a sample size of 1054 HSCT pairs. A diagnosis-driven approach appeared the most feasible. However, concerns about this approach included the bundling of a multitude of diagnoses in the low-risk group (including malignancies and non-malignancies), versus two very different diagnoses in the high risk group (ALL, and CML – the latter one almost abandoned as a HSCT indication). Hence, a cohort selecting the two large, relevant acute leukaemia groups (ALL, ANLL) was included in the following comparison (Model 4).

In model 1, donor age >30, cyclosporine-based GVHD prophylaxis, non-Cy/TBI conditioning regimens and TBI remained the most important clinical confounders (table 6), despite high degree of HLA matching. Model 3 (table 7) favoured a multitude of low-risk diagnosis over full HLA matching, resulting in a wider variety of clinical confounders, which amongst donor age >30 years and cyclosporine-based GVHD prophylaxis also included non-cyclophosphamide/TBI conditioning regimens, cyclophosphamide dose, TBI dose and HLA mismatching.

In contrast, model 4 (table 8) displayed cyclosporine GVHD prophylaxis, donor age and HLA mismatching as the strongest confounders, while aspects of conditioning regimens and AB0 mismatch had a borderline significant role. As this model provided a sample size of adequate statistical power, it was chosen as the preferred model for cohort design. At this point, it was chosen to exclude HSCT pairs of a recipient age <4 years and >40 years. Leukaemia in infants and small children had very different causes and outcomes compared to the leukaemia of older children and adults. Also, an analysis of age groups (5 year intervals) showed a significant increase in risk of acute

GVHD grade 2-4 with recipient age >40 (data not shown here). This reduced the number of eligible sample pairs to n=1000.

risk factor	frequency unselected
No ATG	92.50%
HLA mismatch	62.50%
CyA GVHd prophylaxis	73.60%
Non-CyTBI regimen	74.10%
High risk diagnosis	54.40%
Donor age >30y	63%
Cy dose none/low	36.30%
TBI	80.30%

Table 4: Proportion of clinical risk factors in unselected HSCT population from the JMDP registry, 1993-2000

Model	1	ATG given removed	HLA mismatched removed	high risk diagnosis removed	donor age >30y removed	Cy dose none/low removed	TBI removed
Remaining no	2469	2279	870	416	170	107	25
Model	2	ATG given removed	Non-CyTBI removed	high risk diagnosis removed	donor age >30y removed	Cy dose none/low removed	TBI removed
Remaining no	2469	2279	609	311	118	93	0
Model	3	high risk diagnosis removed	ATG given removed	Non-CyTBI removed	donor age >30y removed	Cy dose none/low removed	TBI removed
Remaining no	2469	1173	1054	311	118	93	0
Model	4	ALL/ANLL selected	ATG given removed	Non-CyTBI removed	donor age >30y removed	Cy dose none/low removed	TBI removed
	2469	1270	1209	273	99	82	0

Table 5: Modelling of hypothetic study cohorts. Model 1 represents a 5-locus HLA matched and ATG removed cohort, Model 2 is selected for homogeneity of conditioning regimens, while models 3 and 4 were selected by diagnosis (model 3: non-high risk diagnosis, model 4: ALL and ANLL selected). Model 4 was chosen for cohort design, as it provides the best statistical power.

Variables in the Equation

	log rank univariate	B	SE	Wald	df	Sig.	Exp(B)	95.0% CI for Exp(B)	
								Lower	Upper
Cyclosporin v tacrolimus	0.003	.468	.148	10.047	1	.002	1.597	1.196	2.134
Donor age <30 v >30	0.001	.016	.006	6.912	1	.009	1.016	1.004	1.029
Cyclophosphamide+TBI v other	0.021	-.387	.151	6.586	1	.010	.679	.505	.913
TBI v noTBI	0.778	.319	.162	3.884	1	.049	1.375	1.002	1.889
Cyclophosphamide no/low v standard/high dose	0.104	-.008	.006	2.045	1	.153	.992	.981	1.003
recipient age <40 v >40	0.368	.003	.003	.843	1	.359	1.003	.996	1.010
donor age <40 v >40	0.06	.003	.004	.473	1	.492	1.003	.994	1.012
abo matched v mismatched	0.62	.068	.119	.330	1	.566	1.071	.848	1.353
Female donor into male recip v other	0.977	-.082	.148	.309	1	.578	.921	.689	1.231
high risk doagnosis v other	0.148	.040	.119	.113	1	.737	1.041	.824	1.315
T-cell depletion v no T cell depletion	0.94	-.178	1.012	.031	1	.860	.837	.115	6.083
ATG given v no ATG	NA			.	0[a]	.			
5-locus HLA match v mismatch	NA			.	0[a]	.			

Table 6: Multivariate analysis (binary logistic regression) of model 1

Variables in the Equation

	log rank univariate	B	SE	Wald	df	Sig.	Exp(B)	95.0% CI for Exp(B)	
								Lower	Upper
Donor age <30 v >30	0.0001	.021	.006	14.678	1	.000	1.021	1.010	1.032
Cyclosporin v tacrolimus	0.00001	.483	.126	14.631	1	.000	1.621	1.265	2.075
Cyclophosphamide+TBI v other	0.001	-.343	.135	6.467	1	.011	.710	.545	.924
5-locus HLA match v mismatch	0.013	-.254	.111	5.192	1	.023	.776	.624	.965
Cyclophosphamide no/low v standard/high dose	0.001	.248	.113	4.842	1	.028	1.282	1.027	1.599
TBI dose standard v none/high	0.009	-.024	.012	4.095	1	.043	.976	.954	.999
TBI v noTBI	0.798	.218	.142	2.350	1	.125	1.244	.941	1.645
Female donor into male recip v other	0.376	.098	.137	.507	1	.476	1.103	.842	1.444
recipient age <40 v >40	0.575	-.001	.003	.166	1	.684	.999	.993	1.005
donor age <40 v >40	0.029	.001	.004	.084	1	.772	1.001	.993	1.009
T-cell depletion v no T cell depletion	0.846	-.147	1.011	.021	1	.885	.863	.119	6.265
abo matched v mismatched	0.621	.009	.107	.008	1	.929	1.010	.819	1.245
high risk doagnosis v other	NA			.	0[a]	.			
ATG given v no ATG	NA			.	0[a]	.			

Table 7: multivariate analysis (binary logistic regression) of model 3

	log rank univariate	B	SE	Wald	df	Sig.	Exp(B)	95.0% CI for Exp(B)	
								Lower	Upper
5-locus HLA match v mismatch	0.0001	-3.879 x10-1	.099	15.224	1	.000	.678	.558	.824
Cyclosporin v tacrolimus	0.01	.308	.111	7.694	1	.006	1.361	1.095	1.691
Donor age <30 v >30	0.0001	.013	.005	7.309	1	.007	1.013	1.004	1.023
Cyclophosphamide no/low v standard/high dose	0.009	-8.952 x10-3	.004	4.135	1	.042	.991	.983	1.000
abo matched v mismatched	0.024	.192	.095	4.119	1	.042	1.212	1.007	1.460
donor age <40 v >40	0.0001	.007	.004	3.944	1	.047	1.007	1.000	1.014
high risk doagnosis v other	0.042	.167	.097	2.950	1	.086	1.181	.977	1.428
Cyclophosphamide+TBI v other	0.046	-2.150 x10-1	.126	2.906	1	.088	.807	.630	1.033
Female donor into male recip v other	0.6	-6.642 x10-2	.118	.320	1	.572	.936	.743	1.178
recipient age <40 v >40	0.382	-1.168 x10-3	.003	.132	1	.717	.999	.993	1.005
TBI v noTBI	0.785	-2.637 x10-2	.147	.032	1	.858	.974	.730	1.299
T-cell depletion v no T cell depletion	0.188	-1.009 x10-1	117.788	.007	1	.932	.000	2.269 x10-105	7.551 x10+95
TBI dose standard v none/high	0.976	.000	.011	.000	1	.986	1.000	.979	1.022
ATG given v no ATG	NA			.	0[a]	.			

Table 8: multivariate analysis (binary logisitc regression) of model 4. This model was chosen as the preferred model for cohort design.

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Power calculation

The power of association testing was calculated based on following 2x2 contingency tables.
Given a microsatellite loci with k alleles, we created 2x2 contingency tables (table 3.1) for each indiv
chi-squared test or Fisher's exact test.
Power for each pool was calculated, changing combinations of following parameters:

- Odds ratio: 1.5, 2.0, and 2.5
- Marker allele frequency: 0.03, 0.05, 0.10, and 0.30
- Type I error rate: 0.05

Power was calculated by using the software 'PS: Power and Sample Size Calculation'.
The statistical power was calculated in the total cells as the power to detect association in successiv
association tests in pool 1 and pool 2 are significant ($p<0.05$). Therefore,
Power (Total) = Power(Pool 1) * Power(Pool 2)
The reason why we calculated the total power described above is that we select microsatellite mark
successive pools 1 and 2 as candidates for next screening.

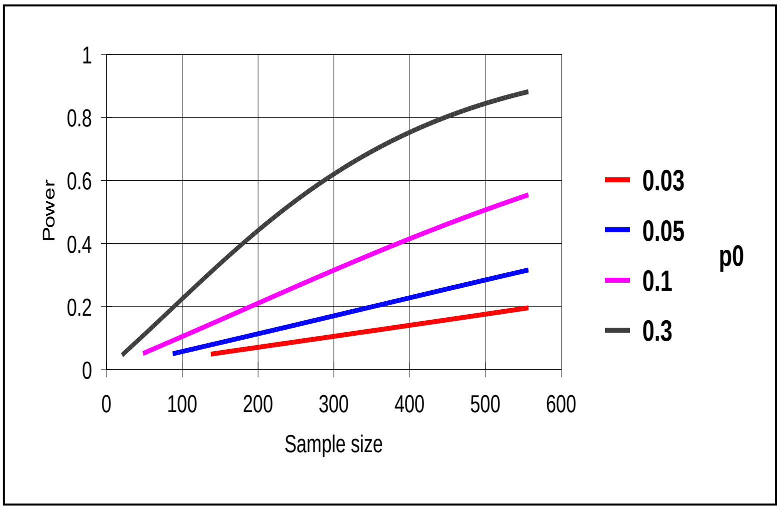


Fig 1: Statistical power for OR=1.5

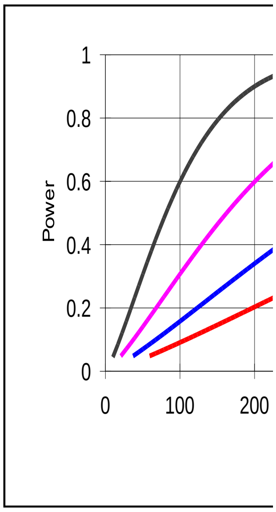


Fig 2: Statistical powe

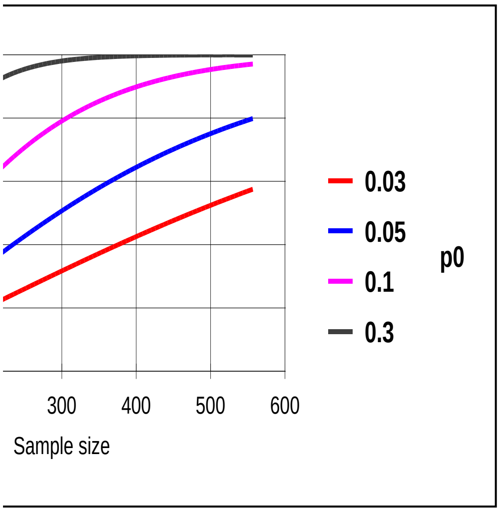
vidual allele, which can be analyzed using a

ve pools 1 and 2. In other words, both of the

kers that confer statistical significance in

	Marker allele	
	M_1	$M_2 \sim M_k$
Grade 2-4 GVDH	a	b
Grade 0-1 GVDH	c	d

Chi Square table for power calculation.



er for OR=2.0

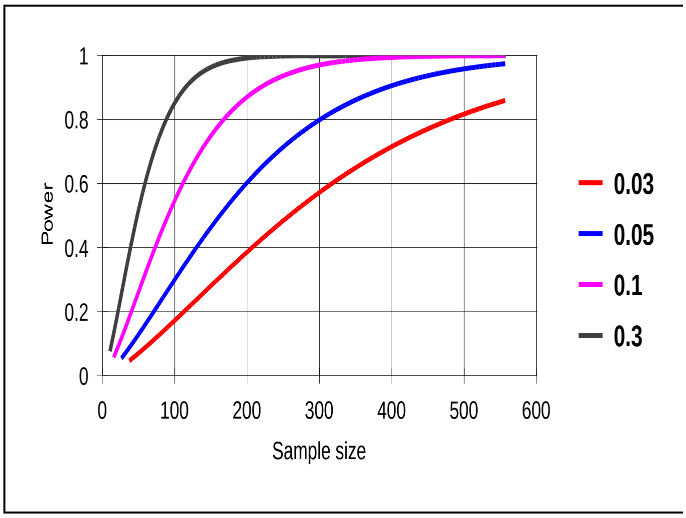
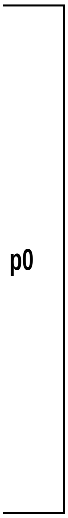


Fig 3: Statistical power for OR=2.5

a~d: Allele counts



Supplementary file 2.3:

Construction of final study cohorts and their characteristics

1. Initial assessment of DNA sample number, quantity and concentration

At this point it was decided to assess the actual availability of DNA samples for the chosen cohort model. The first step was the identification of selected samples from the database and the sample collection, stored in different freezers at -70°C.

The Japan marrow Donor Programme (JMDP) provided two large data files: One contained the clinical data, with a unique pair number (UPN) and a DNA sample number as identifiers. The second file contained the UPN, the DNA sample number, and a new DNA Bank number for each sample which was established recently when the JMDP DNA collections from different time periods were integrated into one system. Samples were in cardboard boxes in simple numerical order, representing the timely order of the transplantations.

As an initial step, a data file of the intended cohort linking all sample information and clinical information together was created. From this data file lists were extracted to enable the identification of the targeted samples in the boxes. Original DNA samples of the intended cohorts were then obtained from the original collection and sorted into a separate set of boxes. Samples were separated into donors/recipients, ALL/ANLL, grades of GVHD 0-4, and finally in numerical order.

At the same instance, the total volume of each sample was estimated by comparing its volume to standard test volumes pipetted in 50 µl intervals (50-800 µl) into a set of identical test tubes. This later enabled an estimation of the total amount of DNA per original sample tube in ng/µg (see below).

Missing and depleted samples were identified by simple visual inspection, and listed accordingly. Of the initial n=1000 pairs, n=112 were completely (both pair partners) or partially (one pair partner) depleted and therefore excluded. N=543 pairs had at least some DNA and were therefore extracted from the collection for further exploration. N=345 pairs had been transferred to Tokyo University (Research Group Professor Ogawa) to be included in a separate study. These samples were mostly fully HLA matched. Enquiries with Professor Ogawa's team revealed that of the n=345 sample pairs, n=74 pairs were also depleted and excluded.

This meaned that a maximum of only n=814 samples would be available for this study, with at that point an unknown amount of DNA, and at that point uncertainty when a larger proportion of fully HLA matched pairs would become available from Tokyo University.

As time was constraint, a feasibility report explored the available options.

1.1. Sample Availability and Study Scenario Feasibility

Three different study scenarios, reflecting a spectrum between a genome wide scanning study and an individual genotyping study have been assessed for feasibility from a sample availability point of view (table 1). From the experience of previous microsatellite and SNP studies in the Tokai University laboratory, the required amount of DNA was estimated for these scenarios (table 2).

1	Genome wide scanning using approximately 30.000 MS markers
2	Limited genome scanning of immune regulatory genes, approximately 3000 MS markers
3	Individual genotyping study using approximately 100 MS and SNP markers

Table 1: Scenarios for feasibility assessment

Study type	**Minimum DNA in microgr**
Genome wide, 30.000 MS	30
Limited scanning, 3000 MS	5
Individual genotyping, 100 MS/SNP	1

Table 2: Estimates of DNA amount required

1.2. Sample Concentration and volumes

Samples available at Tokai University. All available samples of pairs from the initial ALL and ANLL cohorts (age stratified 4-40 years) were identified from different freezers at Tokai University. Available and unavailable samples were marked in a list, and the volume of the available samples was estimated using a simple model.

The DNA concentration of 1086 (543 pairs) available samples was measured using the PICO Green method (described in the methods section). Total amount was calculated multiplying concentration with estimated volume.

Tokyo University samples. Professor Ogawa kindly provided a table with concentration and quality data of all samples from this cohort he used in his study. These data did not contain any total volume estimations, therefore at this stage these have been estimated applying data available from the samples at Tokai University. We estimated samples with a concentration >5ng/µl to correspond with a total amount of >1µ, a concentration of >10ng/µg with a total amount of >5µg, and a concentration of >50ng/µl with a total amount of >30µ, accordingly.

Summary of sample availability: Table 3 summarises the sample availability for the different study scenarios. The data for Tokai University samples are accurate, while the Tokyo University data are estimates for the reasons explained above.

Scenario	**Samples available at Tokai**	**HLA matched 8/8**	**Samples available at Tokyo**	**HLA matched 8/8**	**Total** (HLA matched)	**Pairs required for scenario**	**+ / -**
Genome wide	44	15 (34%)	41	27 (66%)	**85** (42, 49%)	900+	**-815**
Limited genome	407	81 (19.9%)	271	195 (72%)	**678** (276, 40%)	600+ / 900+	**+78/ -222**
Individual typing	543	120 (22%)	271	195 (72%)	**814** (315, 38%)	500+	**+314**

Table 3: Summary of expected sample availability for different study approaches

1.3. Conclusions

Genome wide scanning. This scenario was not feasible given the very limited number of pairs having a sufficient amount of DNA. Even extrapolated to the entire study population (2469 pairs), which would be completely unselected, no more than 330 pairs would have had a sufficient amount of DNA.

Limited genome scanning. This approach was a feasible option if samples from Tokyo University were included, and if the study would only implicate two screening steps. Application to JMDP for further sample access was required.

Individual Genotyping. This was also a feasible option. The cohort size of over 800 may even allow for some further selection. Although even with the samples available at Tokai University this could be feasible, the proportion of 8/8 HLA matched pairs is low for a Japanese population (20%). A better approach would be to include the matched pairs from Tokyo University.

The options were discussed between the team at Tokai University and JMDP in October 2007. All partners were keen on undertaking a genomic screening study, rather than a candidate gene association study. It was agreed to combine samples from Tokai and Tokyo Universities for a first screening step on pooled DNA, using microsatellite markers, on the selected cohort that was proposed. Access to further samples was approved, and samples and dataset prepared. The first screening would encompass HSCT between 1993 and 2000, while the second cohort would include those between 2001 and 2005.

2. Application of selection criteria for construction of a discovery and a confirmatory cohort

HSCT pairs for the first cohort (time frame 1993-2000, n=460) were selected on the basis of criteria for model 4, and DNA availability. Criteria included:

- Acute leukaemia (ALL or ANLL)
- Myeloablative conditioning
- T-cell replete
- Full bone marrow HSCT
- Recipient age 4-40 years
- DNA availability for both donor and recipient sample of 5 µg.

The second cohort (n=462) was selected by the same criteria. In order to reduce confounding by different grades of HLA mismatching, samples were paired for HLA matching between first and second cohort. In practice, for each of the 48 allele mismatch combinations, an equivalent was chosen from the 2001-2005 stem population.

All donor-recipient pairs were HLA-typed retrospectively to allele level at six loci (HLA-A, HLA-B, HLA-C, HLA-DRB1, HLA-DQB1, HLA-DPB1). The distribution of HLA matching of the confirmatory cohort was adjusted to that of the screening cohort by matching each sample of the screening cohort with a confirmatory cohort sample of the same HLA class or HLA class combination according to the previous literature (Sasazuki et al., 1998, Morishima et al., 2002) and our own analyses of risk matches/mismatches within this study population (data not shown).

Table 4 shows the demographic and clinical characteristics of the selected cohorts. There was no statistically significant difference between the cohorts in the baseline demographic criteria. Tables 5 and 6 specify the degree of HLA matching and mismatching. For reasons of comparison, we have used the NMDP/CIBMTR classification of HLA matching (Weisdorf et al., 2008). According to this classification, 357 HSCT pairs had an 8/8 (HLA A, B, C, DRB1) high-resolution allele match, 331 (35.9%) were partially matched (1 mismatch within these HLA loci), and 234 (25.4%) were mismatched (two or more mismatches within these HLA loci). Considering the HLA DQ and DP loci also, only 78 HSCT pairs (8.5%) had a 12/12 allele match. In Japanese, HLA A, B, and C mismatches were associated with risk of acute GVHD. HLA C mismatches, however, had a protective effect on relapse (whilst HLA A, C and B mismatches associate with a risk of death) (Sasazuki et al., 1998, Morishima et al., 2002, Morishima et al., 2007b). More recent research had focused on specific allele mismatches, rather than mismatches in loci, aiming to identify non-permissive mismatches for acute GVHD (Kawase et al., 2007) or protective mismatches against relapse (Kawase et al., 2009), as well as risk HLA haplotypes for GVHD(Morishima et al., 2010).

Multivariate analysis of the finally selected combined cohorts (n=922 HSCT pairs, table 7) showed that diagnosis, recipient age and HLA mismatch remain the most significant confounding variables. ALL had a higher risk for moderate-severe acute GVHD than ANLL. Recipient age below 10 years was carrying a higher GVHD risk. 8/8 loci HLA match is protective against GVHD. Relapse and major ABO mismatch still showed trends towards risk.

	Screening	Confirmation	*Difference p=*
Demographic			
Recipients	460	462	
Recipient gender Male	269 (58.48%)	289 (62.55%)	n/s
Recipient gender Female	191 (41.52%)	173 (37.45%)	n/s
Donor gender Male	267 (58.04%)	278 (60.17%)	n/s
Donor gender Female	193 (41.96%)	182 (39.39%)	n/s
Female donor to Male recipient transplant	102 (22.17%)	84 (18.18%)	n/s
Recipient age range	4-40 y	4-40 y	n/s
Recipient age mean	21.7 y	24.1 y	n/s
Donor age range	20-70y	19-51 y	n/s
Donor age mean	34 y	34.3 y	n/s
Clinical			
Diagnosis Acute lymphoblastic leukaemia	260 (56.52%)	254 (54.98%)	n/s
Diagnosis Acute non-ALL	200 (43.48%)	208 (45.02%)	n/s
High risk leukaemia	279 (60.65%)	246 (53.25%)	<0.1
HLA matching – 12/12 loci	41 (8.91%)	37 (8%)	n/s
HLA matching – 12/12 and 10/10 loci	160 (34.78%)	166 (35.93%)	n/s
HLA matching - GVHD risk mismatches	220 (47.83%)	229 (49.57%)	n/s
Conditioning – Cyclophosphamide + total body irradiation (TBI)	334 (72.61%)	322 (69.67%)	n/s
Conditioning – Busulphan/Cyclophosphamide or Busulphan based	53 (11.52%)	47 (10.17%)	n/s
Conditioning - TBI based	73 (15.87%)	83 (17.97%)	n/s
Conditioning - other	0	10 (2.16%)	n/s
GVHD prophylaxis – Cyclosporin A based	279 (60.65%)	154 (33.33%)	<0.05
GVHD prophylaxis - Tacrolimus based	177 (34.48%)	305 (66.02%)	<0.05
GVHD prophylaxis - other	4 (0.87%)	3 (0.65%)	n/s
Outcome			
Acute GVHD grade 0	124 (26.96%)	124 (26.84%)	n/s
Acute GVHD grade 1	153 (33.26%)	99 (21.42%)	<0.05
Acute GVHD grade 2	105 (22.83%)	143 (30.95%)	<0.05
Acute GVHD grade 3	50 (10.87%)	72 (15.58%)	<0.05
Acute GVHD grade 4	28 (6.09%)	24 (5.19%)	n/s
Chronic GVHD - none	244 (53.04%)	242 (52.38%)	n/s
Chronic GVHD - limited disease	71 (15.43%)	63 (13.64%)	n/s
Chronic GVHD - extensive disease	95 (20.65%)	106 (22.94%)	n/s
Chronic GVHD - unknown	50 (10.86%)	49 (10.6%)	n/s
Relapse	115 (25%)	110 (23.81%)	n/s
Survival – 100 days	395 (86.9%)	403 (87.23%)	n/s
Survival – 1 year	306 (66.52%)	312 (67.53%)	n/s
Survival – 3 years	245 (53.26%)	258 (55.84%)	n/s

Table 4: Population characteristics. *p* refers to statistically significant differences between the screening and confirmation cohorts.

	alleles mismatched	n=	%
Matched 8/8 n=357 (38.7%)	HLA-DQ-DP	30	3.3
	HLA-DQ	6	0.7
	HLA-DP	243	26.4
	Fully matched	78	8.5
Partially mismatched n=331 (35.9%)	HLA-DR	1	0.1
	HLA-C-DQ	3	0.3
	HLA-C-DP	92	10
	HLA-A	11	1.2
	HLA-C	25	2.7
	HLA-DR-DQ-DP	104	11.3
	HLA-DR-DQ	18	2
	HLA-DR-DP	17	1.8
	HLA-A-DQ	1	0.1
	HLA-A-DP	41	4.4
	HLA-B-DQ	1	0.1
	HLA-B-DP	3	0.3
	HLA-C-DQ-DP	11	1.2
	HLA-B-DQ-DP	2	0.2
	HLA-A-DQ-DP	1	0.1
Mismatched n=234 (25.4%)	HLA-C-DR	6	0.7
	HLA-A-DR	2	0.2
	HLA-C-DR-DQ	11	1.2
	HLA-C-DR-DP	14	1.5
	HLA-B-DR-DQ	1	0.1
	HLA-A-B-C-DR-DQ-DP	4	0.4
	HLA-A-B-C-DQ-DP	2	0.2
	HLA-A-B-C-DP	8	0.9
	HLA-A-B-C	2	0.2
	HLA-A-B-DR-DQ-DP	2	0.2
	HLA-A-C-DR-DQ-DP	22	2.4
	HLA-B-C-DR-DQ-DP	2	0.2
	HLA-A-C-DR-DQ	3	0.3
	HLA-A-C-DR-DP	5	0.5
	HLA-A-C-DQ-DP	3	0.3
	HLA-B-C-DR-DP	1	0.1
	HLA-B-C-DQ-DP	1	0.1
	HLA-A-B-DP	1	0.1
	HLA-A-C-DQ	2	0.2
	HLA-A-C-DP	22	2.4
	HLA-B-C-DP	21	2.3
	HLA-A-B	1	0.1
	HLA-A-C	10	1.1
	HLA-B-C	2	0.2
	HLA-A-DR-DQ-DP	9	1
	HLA-B-DR_DQ_DP	6	0.7
	HLA-C-DR-DQ-DP	68	7.4
	HLA-A-DR-DQ	2	0.2
	HLA-A-DR-DP	1	0.1
Total		922	100

Table 5: Detailed HLA mismatch. All matches and mismatches are based on high-resolution allele typing of the HLA A, B, C, DRB1, DQB1 and DPB1 loci. The classification as outlined by NMDP/CIBMTR (Weisdorf et al., 2008), which focuses on the HLA A, B, C and DRB1 loci only, without consideration of HLA DQB1 or DPB1. Matched 8/8 refers to allele match at the loci HLA A, B, C and DRB1. Partially matched HSCT allows for one allele mismatch within this group, whereas mismatched HSCT has two or more allele mismatches within HLA A, B, C and DRB1. 340 HSCT pairs (36.9%) had an HLA C mismatch.

mismatch group	group total n=	%
3 HLA I +3 HLA II	4	0.433839
3 HLA I +2 HLA II	2	0.21692
3 HLA I +1 HLA II	8	0.867679
3 HLA I + 0 HLA II	2	0.21692
2 HLA I +3 HLA II	26	2.819957
2 HLA I +2 HLA II	13	1.409978
2 HLA I +1 HLA II	46	4.989154
2 HLA I +0 HLA II	13	1.409978
1 HLA I +3 HLA II	83	9.002169
1 HLA I +2 HLA II	43	4.663774
1 HLA I +1 HLA II	149	16.16052
1 HLA I +0 HLA II	36	3.904555
3 HLA II	104	11.27983
2 HLA II	65	7.049892
1 HLA II	250	27.11497
fully matched	78	8.45987
Total	922	100

Table 6: Summary of HLA mismatch by HLA class I and II.

	B	S.E.	Wald	df	Sig.	Exp(B)	95% C.I.for EXP(B)	
							Lower	Upper
ALL v ANLL	0.427	0.143	8.92683	1	0.0028101	1.533921	1.158557	2.0309
Recipient age group <10y	-0.151	0.069	4.718277	1	0.0298436	0.859	0.748918	0.985262
8/8 HLA match	-0.303	0.145	4.324559	1	0.0375661	0.738402	0.55483	0.982711
Relapse	0.307	0.163	3.553663	1	0.0594142	1.360325	0.987856	1.873232
ABO major mismatch	0.134	0.079	2.859926	1	0.0908117	1.143999	0.978841	1.337022
TBI given	-0.346	0.215	2.595402	1	0.1071743	0.706824	0.463431	1.078048
Female to male transplant	-0.458	0.288	2.531509	1	0.1115935	0.632177	0.359336	1.112182
Donor age >30	-0.229	0.159	2.060951	1	0.1511158	1.257433	0.919734	1.719125
Recipient sex	0.24	0.189	1.605145	1	0.2051755	1.271931	0.876715	1.845307
CyA GVHD prophylaxis	0.09855	0.138	0.505388	1	0.477142	1.103564	0.841017	1.448073
High risk leukaemia	0.797	1.166	0.467833	1	0.4939857	2.220418	0.225799	21.83475
Non-Cy-TBI conditioning	0.0796	0.156	0.259843	1	0.6102281	1.082876	0.797305	1.47073
Donor age >40y	0.024	1.442	0.000283	1	0.9865867	1.024548	0.060624	17.315
Donor sex	-41.663	56841.8	5.37E-07	1	0.9994152	8.05E-19	0	.

Table 7: Multivariate analysis of risk factors for grade 2-4 acute GVHD in the finally chosen combined study cohort.

Gene Symbol	**status**
3.8-1	included
3.8-1.2	included
3.8-1.3	included
3.8-1.4	included
3.8-1.5	included
A2M	excluded - no marker
A2ML1	included
A4GALT	included
AATK	included
ABCA1	included
ABCB1	included
ABCC1	included
ABCC11	included
ABCC4	included
ABCF1	included
ABCG2	included
ABO	included
ACACA	included
ACE	included
ACE2	included
ACHE	included - new MS design
ACOT11	included
ACOT8	included
ACTA1	included
ACTB	included
ACTC1	included
ACTG1	included
ACTL7B	included
ACTN1	included
ACTN2	included
ACTN3	included
ADA	included
ADAM10	included
ADAM12	included
ADAM17	included
ADAM8	included
ADAMTS13	included
ADAT2	included
ADD1	included
ADIPOQ	excluded - no marker
ADK	included
ADM	included
ADORA1	included
ADORA2	included
ADORA3	included
AGER	included
AGPAT1	included
AGPAT4	included
AGPS	included
AGTR1	included
AGTR2	included
AGTRL1	included
AICDA	included
AIF1	included
AIFM1	included

AIM2	included
AIP	included
AIRE	included
AKAP12	included
AKAP13	included
AKAP7	included
AKT1	included
AKT2	included
AKT3	included
AKTIP	included - new MS design
ALAS2	included
ALCAM	included
ALK	included
ALKBH1	included
ALKBH2	included
ALKBH3	included
ALKBH4	included
ALKBH5	included
ALKBH6	included
ALKBH7	included
ALKBH8	included
ALOX12	included
ALOX12B	included
ALOX15	included
ALOX15B	included
ALOX5	included
ALOX5AP	included
ANGPT1	included
ANGPT2	included
ANGPTL1	included
ANK1	included
ANK2	included
ANK3	included
ANKDD1A	included
ANKRD6	included
ANP32B	included
ANPEP	included
ANXA1	included
ANXA2	included
ANXA5	included
APAF1	included
APBB1IP	included
APC	included
APEX1	included
API5	included
APLN	included
APOL6	included
APOM	included
APS	included
AQP1	included
AR	included
AREG	included
ARG1	included
ARHGDIA	included
ARHGDIB	included
ARID1B	included

ARL6IP5	included
ARRB1	included
ARRB2	included
ART1	included
ART4	included
ARTN	included
ARTS1	included
ASB1	included
ASCL1	included
ASPM	included
ATBF1	included
ATF1	included
ATF3	included
ATF4	included
ATF5	included
ATG5	included
ATM	included
ATP10A	included
ATP1B3	included
ATP6V1G2	included
ATXN1	included
AVEN	included
AXIN1	included
AXIN2	included
AZGP1	included
AZU1	included
B2M	included
B3GALNT1	included
B3GALT4	included
B3GAT1	included
B3GNT3	included
BAALC	included
BAD	included
BAG1	included
BAG2	included
BAG3	included
BAG4	included
BAG5	included
BAGE	included
BAGE2	included
BAGE3	included
BAGE4	included
BAGE5	included
BAI3	included
BAIAP2L1	included
BAK1	included
BANK1	included
BAT1	included
BAT2	included
BAT2, BAT2 GT, BAT2	included
BAT3	included
BAT4	included
BAT5	included
BAX	included
BAZ1A	included
BBC3	included

BCAM	included
BCAP31	included
BCAS2	included
BCKDHB	included
BCL10	included
BCL2	included
BCL2A1	included
BCL2L1	included
BCL2L10	included
BCL2L11	included
BCL2L12	included
BCL2L13	included
BCL2L14	included
BCL2L2	included
BCL3	included
BCR	included
BDKRB1	included
BDKRB2	included
BDNF	included
BFAR	excluded - no marker
BGN	included
BID	included
BIK	included
BIRC2	included
BIRC3	included
BIRC4	included
BIRC5	included
BIRC6	included
BIRC7	included
BIRC8	included
BLK	included
BLM	included
BLNK	included
BLR1	included
BLVRB	included
BMI-1	included
BMP2	included
BMP3	included
BMP4	included
BMP5	included
BMP6	included
BMP7	included
BMPR1A	included
BMPR1B	included
BMPR2	included
BMX	included
BNIP1	included
BNIP2	included
BNIP3	included
BNIP3L	included
BNIP3P	excluded - no marker
BNIPL	included
BOK	included
BPI	included
BRCA2	included
BRD2	included

BRD8	included
BRDG1	included
BRF1	included
BSG	included
BST1	included
BST2	included
BTAF	included
BTBD9	included
BTC	included
BTG1	included
BTG3	included
BTK	included
BTLA	included
BTN3A1	included
BTNL2	included
BTRC	included
BUB3	included
BXDC1	included
C10orf26	included
C19orf10	included
C1QA	included
C1QB	included
C1QBP	included
C1QG	included
C1QL1	included
C1QL2	included
C1QL3	included
C1QL4	included
C1QR	included
C1QTNF2	included
C1QTNF3	included
C1QTNF4	included
C1QTNF5	included
C1QTNF6	included
C1QTNF7	included
C1R	excluded - no marker
C1RL	included
C1S	excluded - no marker
C2	excluded - no marker
C2orf47	included
C3	included
C3AR1	included
C4A	excluded - no marker
C4B	excluded - no marker
C4BPA	included
C4BPB	included
C5	included
C5R1	included
C6	included
C6orf10	included
C6orf12	included
C6orf123	included
C6orf134	included
C6orf136	included
C6orf138	included
C6orf15	included

C6orf174,KIAA0408	included
C6orf18	included
C6orf204	included
C6orf205	included
C6orf21	included
C6orf25	included
C6orf27	included
C6orf47	included
C6orf48	included
C6orf65	included
C6orf91	included
C7	included
C8A	included
C8B	included
C8G	included
C9	included
CABIN1	included
CADM1	included
CADM2	included
CADM3	included
CADM4	included
CALR	included
CAMK2D	included
CAMK4	included
CAMP	excluded - no marker
CANX	included
CARD10	included
CARD11	included
CARD14	included
CARD6	included
CARD8	included
CARD9	excluded - no marker
CARM1	included
CASP1	included
CASP10	included
CASP12	included
CASP14	included
CASP2	included
CASP3	excluded - no marker
CASP4	included
CASP5	included
CASP7	included
CASP8	included
CASP8AP2	included
CASP9	included
CAT	included
CAV1	included
CBFA2T2	included
CBFB	included
CBL	excluded - no marker
CBLB	included
CCBP2	included
CCL1	included
CCL11	included
CCL13	included
CCL14	included

CCL15	included
CCL16	included
CCL17	included
CCL18	included
CCL19	included
CCL2	included
CCL20	included
CCL21	included
CCL22	included
CCL23	included
CCL24	included
CCL25	included
CCL26	included
CCL27	included
CCL28	included
CCL3	included
CCL3L1	excluded - no marker
CCL3L3	excluded - no marker
CCL4	included
CCL4L1	excluded - no marker
CCL4L2	excluded - no marker
CCL5	included
CCL7	included
CCL8	included
CCNA1	included
CCNA2	included
CCNB1	included
CCNB1IP1	included
CCNB2	included
CCNB3	included
CCNC	excluded - no marker
CCND1	included
CCND2	included
CCND3	included
CCNE1	included
CCNE2	included
CCNG1	included
CCNH	included
CCR1	included
CCR10	included
CCR2	included
CCR3	included
CCR4	included
CCR5	included
CCR6	included
CCR7	included
CCR8	included
CCR9	included
CCRL1	included
CCRL2	included
CCRN4L	included
CD109	included
CD139	excluded - unknown location
CD14	included
CD151	included
CD160	included

CD163	excluded - no marker
CD164	included
CD164L1	included
CD177	included
CD19	excluded - no marker
CD1A	included
CD1B	included
CD1C	included
CD1D	included
CD1E	included
CD2	included
CD200	included
CD200R1	included
CD200R2	included
CD207	included
CD209	included
CD22	included
CD24	included
CD244	included
CD245	excluded - unknown location
CD274	included
CD276	included
CD28	included
CD2AP	included
CD2BP2	included
CD300A	included
CD300C	included
CD300E	included
CD300LB	included
CD300LF	included
CD302	included
CD320	excluded - no marker
CD33	included
CD33L3	included
CD34	included
CD36	included
CD37	included
CD38	included
CD3D	included
CD3E	included
CD3EAP	included
CD3G	included
CD3Z	included
CD4	included
CD40LG	included
CD44	included
CD47	included
CD48	included
CD5	included
CD53	included
CD55	included
CD58	included
CD59	included
CD5L	included
CD6	excluded - no marker
CD63	included

CD65	excluded - unknown location
CD68	included
CD69	included
CD7	included
Cd72	included
CD74	included
CD79A	included
CD79B	included
CD80	included
CD81	included
CD82	included
CD83	included
CD84	included
CD86	included
CD8A	included
CD8B1	included
CD8BP	excluded - no marker
CD9	included
CD96	included
CD97	included
CD99	excluded - no marker
CD99L2	included
CDA	included
CDC2	included
CDC20	included
CDC25A	excluded - no marker
CDC25B	included
CDC37	included
CDC42	excluded - no marker
CDC42EP5	included
CDCP1	included
CDH1	included
CDH2	included
CDH5	included
CDK10	excluded - no marker
CDK2	included
CDK3	excluded - no marker
CDK4	included
CDK5	included
CDK6	included
CDK7	included
CDK8	included
CDK9	included
CDKAL1	included
CDKN1A	included
CDKN1B	excluded - no marker
CDKN1C	included
CDKN2A	included
CDKN2B	included
CDKN2C	included
CDKN2D	included
CDKN3	included
CDO1	included
CDSN	included
CDw12	excluded - unknown location
CDW52	included

CDW93	included
CDX2	included
CEACAM1	included
CEACAM3	included
CEACAM5	included
CEACAM6	included
CEACAM8	included
CEBPA	included
CEBPE	included
CEBPG	included
CENPF	included
CENPM	included
CERK	included
CES1	included
CFB	excluded - no marker
CFD	included
CFDP1	included
CFH	included
CFHR1	included
CFHR2	included
CFHR3	included
CFHR4	included
CFHR5	included
CFI	included
CFL1	included
CFL2	included
CFLAR	included
CFP	included
CGA	included
CGB	included
CHAF1B	included
CHERP	included
CHES1	included
CHI3L2	included
CHLI	included
CHMP1B	included
CHMP2A	included
CHMP2B	included
CHMP4A	included
CHMP4B	included
CHMP4C	included
CHMP5	included
CHMP6	included
CHMP7	included
CHRAC1	included
CHUK	included
CIDEA	excluded - no marker
CIITA	included
CIR	included
CISH	excluded - no marker
CITED2	included
CKLF	included
CKS1B	included
CKS2	included
CLASP1	included
CLASP2	included

CLC	included
CLCF1	included
CLDN23	included
CLDN3	included
CLEC12A	included
CLEC1A	included
CLEC1B	included
CLEC2B	included
CLEC3A	included
CLEC4a	included
CLEC4C	included
CLEC4D	included
CLEC4E	included
CLEC4M	included
CLEC5A	included
CLEC6A	excluded - no marker
CLEC7A	included
CLECSF10A	included
CLIC1	included
CLIP1	included
CLIP2	included
CLK1	included
CLU	included
CMKLR1	included
CMTM1	included
CMTM2	included
CMTM3	included
CMTM4	included
CMTM5	included
CMTM6	included
CMTM7	included
CMTM8	included
CNTN2	included
COL11A2	included
COL14A1	included
COL1A1	included
COL1A2	included
COL21A1	included
COL3A1	included
COL4A1	included
COL4A2	included
COL4A3	included
COL4A3BP	included
COL4A4	included
COL4A5	included
COL4A6	included
COL5A1	included
COL5A2	included
COL5A3	included
COL6A1	included
COL6A2	included
COL6A3	included
COLEC12	included
COP1	included
CORO1A	excluded - no marker
COX2	included

CPE	included
CPS1	included
CR1	included
CR1L	included
CR2	included
CRADD	included
CREB1	included
CREBBP	included
CREBL1	excluded - no marker
CREM	included
CRF1R	included
CRF2R	included
CRH	included
CRHR2	included
CRKL	included
CRLF1	included
CRLF2	excluded - no marker
CRLF3	included
CRP	included
CSDA	included
CSF1	included
CSF1R	included
CSF2	included
CSF2RA	excluded - no marker
CSF2RB	included
CSF3	included
CSF3R	included
CSH1	included
CSK	included
CSNK1A1	included
CSNK2B	included
CSPG2	included
CST1	included
CTDSP2	included
CTDSPL	included
CTF1	included
CTGF	included
CTLA4	included
CTNNB1	included
CTNS	included
CTPS	included
CTSA	included
CTSB	included
CTSD	included
CTSF	included
CTSG	included
CTSH	included
CTSK	included
CTSL1	included
CTSS	included
CTSZ	included
CUGBP2	included
CUL4A	included
CX3CL1	included
CX3CR1	included
CXCL1	included

CXCL10	included
CXCL11	included
CXCL12	included
CXCL13	included
CXCL14	included
CXCL16	included
CXCL2	included
CXCL3	included
CXCL5	included
CXCL6	included
CXCL9	included
CXCR3	included
CXCR4	included
CXCR6	included
CXCR7	included
CYBA	included
CYBB	included
CYCS	included
CYP11A1	included
CYP11B1	included
CYP11B2	included
CYP17A1	included
CYP19A1	included
CYP1A1	included
CYP1A2	included
CYP1B1	included
CYP20A1	included
CYP21A2	excluded - no marker
CYP26A1	included
CYP26B1	included
CYP26C1	included
CYP27A1	included
CYP27B1	included
CYP2A13	included
CYP2A6	included
CYP2A7	included
CYP2B	included
CYP2B6	included
CYP2C18	included
CYP2C19	included - new MS design
CYP2C8	included
CYP2C9	included - new MS design
CYP2D6	included
CYP2E1	included
CYP2F1	included
CYP2J2	included
CYP2R1	included
CYP2S1	included
CYP2U1	included
CYP2W1	included
CYP39A1	included
CYP3A11	included
CYP3A3	included
CYP3A43	included
CYP3A5	included
CYP3A7	included

CYP46A1	included
CYP4B1	included
CYP4F11	included
CYP4F12	included
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HECA	included

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LECT2	included
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LGALS3	included
LGALS3BP	included
LGALS4	included
LGALS5	excluded - unknown location
LGALS6	excluded - unknown location
LGALS7	included
LGALS8	included
LGALS9	included
LGMN	included
LGP2	included
LHB	included
LHCGR	included
LHFPL2	included
LIF	included
LIFR	included
LIG1	included
LIG4	included
LILRA1	included
LILRA2	included
LILRA3	included
LILRA4	included
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LILRA6	included
LILRB1	included
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LILRB3	included
LILRB4	included
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LILRP1	included
LILRP2	included
LIPA	included
LITAF	included
LMAN1	included
LOC401252	included
LOC441792	included
LOC643962	included
LOC645740	included
LOC646702	included
LOC728195	excluded - no marker
LPC2	included
LPO	excluded - no marker
LRDD	excluded - no marker
LRP1	excluded - no marker
LRP5	included
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LRRC16	included
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LST1	included
LTA	included
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LTB	included
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LTB4R2	included
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LTBR	included
LTC4S	included
LTF	included
LY64	included
LY6E	included
LY6G5B	included
LY6G5C	included
LY6G6C	included
LY6G6D	included
LY6G6E	included
LY75	included
LY86	included
LY9	included
LY96	included
LYG2	included
LYL1	included
LYN	included
LYPLA2P1	included
LYST	included
LYZ	excluded - no marker
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MADD	included
MAF	included
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MAML2	included
MAN1A1	included
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MAP2K2	included
MAP2K3	included
MAP2K4	included
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MAP2K6	included
MAP2K7	included
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MAP3K13	included
MAP3K14	included
MAP3K15	included
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MAP3K3	included
MAP3K4	included
MAP3K5	included
MAP3K6	excluded - no marker
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MAP3K7IP1	included
MAP3K7IP2	included
MAP3K8	included
MAP3K9	included
MAP4K1	included
MAP4K2	included

MAP4K3	included
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MAP4K5	included
MAP7	included
MAPK1	included
MAPK10	included
MAPK11	excluded - no marker
MAPK12	excluded - no marker
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MAPK8IP1	included
MAPK8IP2	included
MAPK8IP3	included
MAPK9	included
MAPKAPK2	included
MAPKAPK3	excluded - no marker
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MARCO	included
MASP1	included
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MBL2	included
MBP	included
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MC3R	included
MC4R	included
MC5R	included
MCAM	included
MCCD1	included
MCL1	included
MCM2	included
MCM6	included
MCP	included
MCRS1	included
MDC1	included
MDFIC	included
MDM2	included
MDM4	included
MEF2D	included
MEFV	included
MELK	included
MERTK	included
MET	included
MFI2	included
MGA	included
MGMT	included
MICA	included
MICB	included
MICC	included
MICD	included
MICE	included

MICF	included
MICG	included
MIF	included
MINK	included
MITF	included
MKLN1	included
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MME	included
MMP1	included
MMP10	included
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MMP17	excluded - no marker
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MMP2	included
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MMP23A	included
MMP23B	included
MMP24	included
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MMP26	included
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MMP28	included
MMP3	included
MMP7	included
MMP8	included
MMP9	included
MN1	included
MOAP1	included
MOG	included
MOXD1	included
MPG	included
MPL	included
MPO	included - new MS design
MPS1	included
MPZL1	included
MR1	included
MRC1	included
MRC1L1	included
MRC2	included
MRE11A	included
MRPL28	included
MRPS18B	included
MS4A1	included
MS4A3	included
MS4A5	included
MSH5	included
MSR1	included
MST1	included
MST1R	included
MT1A	included

MT1F	included
MT1G	included
MT1X	included
MT2A	included
MT3	included
MTHFR	included
MTMR11	included
MTRR	included
MUC1	included
MVP	included
MX1	included
MX2	included
MXD1	included
MYC	included
MYCL1	included
MYCN	included
MyD88	included - new MS design
MYH11	included
MYH2	included
MYH9	included
MYLK	included
MYO1F	included
MYO1G	included
MZF1	included
NAB2	included
NACA	included
NAIP	excluded - no marker
NAT2	included
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NCAPH	included
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NCF2	included
NCF3	included
NCKAP1L	included
NCOA3	included
NCOA7	included
NCOR1	included
NCOR2	included
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NCR2	included
NCR3	included
NDUFA2	included
NDUFS3	included
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NEU1	excluded - no marker
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NFATC2	included
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NFE2L1	included
NFIL3	included

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NFKBIA	included
NFKBIB	included
NFKBIE	included
NFKBIL1	included
NFKBIZ	included
NFX1	included
NFYA	included
NFYB	included
NFYC	included
NGFB	included
NGFR	included
NHLH1	included
NID1	included
NKAIN2	included
NKIRAS1	included
NKTR	included
NLRC3	included
NLRC4	included
NLRC5	included
NLRP1	included
NLRP10	included
NLRP11	included
NLRP12	included
NLRP13	included
NLRP14	included
NLRP2	included
NLRP2P	included
NLRP3	included
NLRP3P	included
NLRP4	included
NLRP5	included
NLRP6	included
NLRP7	included
NLRP8	included
NLRP9	included
NLRP9P	included
NLRX1	excluded - no marker
NME1	included
NMI	included
NOD1	included
NOD2	included
NOL3	included
NOS1	included
NOS2A	included
NOS3	included
NOSIP	included
NOTCH1	included
NOTCH2	included
NOTCH3	included
NOTCH4	included - new MS design
NOV	included
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NOX4	included

NOXA1	included - new MS design
NOXO1	included
NPM1	excluded - no marker
NPPA	included
NPPB	included
NPTN	included
NPY	included
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NR0B2	included
NR1D1	included
NR1D2	included
NR1H2	included
NR1H3	included
NR1H4	included
NR1I2	included
NR1I3	included
NR2C1	included
NR2C2	included
NR2D1	included
NR2E1	included
NR2E3	included
NR2F1	included
NR2F2	included
NR2F6	included
NR3C1	included
NR3C2	included
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NR4A2	included
NR4A3	included
NR5A1	included
NR5A2	included
NR6A1	included
NRAS	included
NRF1	included
NRG2	included
NRG3	included
NRG4	included
NRM	included
NRP1	included
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NT5E	included
NUMA1	included
NUSAP1	included
NXF1	included
OAS1	included
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OFCC1	included
OLIG2	included
OLR1	included
OPMR1	included
OPRK1	included
OPRL1	included

ORM1	included
ORM2	included
OSCAR	included
OSM	included
P2RX1	included
P2RX2	included
P2RX3	included
P2RX4	included
P2RX5	included
P2RX6	included
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P2RY11	included
P2RY13	included
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P2RY5	included
P2RY6	included
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P5-05	included
P5-07	included
P5-09	included
P5-11	included
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PADI4	included
PAFAH1B1	included
PAFAH1B2	excluded - no marker
PAFAH1B3	included
PAFAH2	included
PAG1	included
PAK1	included
PAK2	included
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PARK2	included
PARP1	included
PARVG	included
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PBEF1	included
PBX2	included
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PCDHB5	included
PCMT1	included
PCOLN3	excluded - no marker
PDCD1	included
PDCD10	included
PDCD1LG2	included
PDCD2	included
PDCD5	included
PDCD6	included
PDCD6IP	included
PDCD7	included
PDE10A	included
PDE4A	included
PDE4B	included

PDE4C	included
PDE4D	included
PDGFA	excluded - no marker
PDGFB	included
PDGFRA	included
PDGFRB	included
PDIA3	included - new MS design
PDK1	included
PDK2	included
PDRG1	included
PDXK	included
PEA15	excluded - no marker
PECAM1	included
PELI1	included
PELI2	included
PELI3	included
PEX6	included
PF4	included
PF4V1	included
PFDN6	included
PFN1	included
PGDS	included
PGLYRP1	included
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PGR	included
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PHACTR2	included
PHLDA2	excluded - no marker
PI3	included
PI4K2B	included
PIAS4	included
PIGF	included
PIK3C2A	included
PIK3C2B	included
PIK3C2G	included
PIK3C3	included
PIK3CA	included
PIK3CB	included
PIK3CD	included
PIK3CG	included
PIK3R1	included
PIK3R2	included
PIK3R3	included
PIK3R4	included
PIK3R5	included
PIK4CA	excluded - no marker
PIK4CB	included
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PILRA	included
PIM1	included
PIN1	included
PINX1	included
PKD1	included
PKD2	included

PKD3	included
PKHD1	included
PLA1A	included
PLA2G10	excluded - no marker
PLA2G2D	included
PLA2G6	included
PLA2G7	included
PLA2R1	included
PLAA	included
PLAU	included
PLAUR	included
PLCB2	included
PLCB3	included
PLCG1	included
PLCL2	included
PLEC1	excluded - no marker
PLEKHB1	included
PLEKHH2	included
PLK1	included
PLK3	included
PLK4	included
PLXNA1	included
PLXNB1	included
PLXNC1	included
PLXND1	included
PMS2L3	included
POLA2	included
POLD3	included
POLDIP3	included
POLE3	included
POMC	included
POP1	included
POT1	included
POU2AF1	included
POU2F3	included
POU4F1	included
POU5F1	included
PPAP2B	included
PPARA	included
PPARD	included
PPARG	included
PPBP	included
PPIA	included
PPIAL	included
PPIAL4	included
PPIB	included
PPIC	included
PPID	included
PPIE	included
PPIF	included
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PPIH	included
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PPIL5	included
PPIL6	included
PPIP9	included
PPP1R10	included
PPP1R11	included
PPP1R16A	included
PPP1R16B	excluded - no marker
PPP1R2P1	included
PPP2R4	included
PPP3CA	included
PPP3CB	included
PPP3CC	included
PPP3R1	included
PPP3R2	included
PPT2	included
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PRDM1	included
PRDX4	included
PRDX6	included
PRF1	included
PRG1	included
PRG2	included
PRG4	included
PRKAA2	included
PRKACA	included
PRKACB	included
PRKACG	included
PRKCA	included
PRKCB1	included
PRKCD	included
PRKCG	included
PRKCH	included
PRKCI	included
PRKCQ	included
PRKCZ	included
PRKD1	included
PRKDC	included
PRKRIR	included
PRL	included
PRLR	included
PRM3	included
PRMT1	included
PRMT2	included
PRMT3	included
PRMT5	included
PRMT6	included
PRMT7	included
PRMT8	included
PRNP	included
PROC	included
PROCR	included
PROM1	included
Protein S	included
PRPF40A	included
PRR3	included
PRRT1	included

PRSS16	included
PRTN3	included
PSCD1	included
PSCDBP	included
PSG1	included
PSMB1	included
PSMB10	included
PSMB5	included
PSMB6	included
PSMB7	included
PSMB8	included
PSMB9	included
PSMC6	included
PSME1	included
PSME2	included
PSME3	included
PSMF1	included
PSORS1C1	included
PSORS1C2	included
PSTPIP1	included
PTAFR	included
PTCH1	included
PTDSR	included
PTDSS1	included
PTEN	included
PTGDR	included
PTGDS	included
PTGER1	included
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PTGER4	included
PTGES	included
PTGES2	included
PTGFR	included
PTGFRN	included
PTGIR	excluded - no marker
PTGIS	included
PTGS1	included
PTGS2	included
PTH	included
PTHLH	included
PTHR1	included
PTK 2B	included
PTK2	included
PTK7	included
PTP4A1	included
PTP4A2	included
PTP4A3	included
PTPMT1	included
PTPN1	included
PTPN11	included
PTPN12	included
PTPN13	included
PTPN14	included
PTPN18	included
PTPN2	included

PTPN20A	excluded - no marker
PTPN20B	excluded - no marker
PTPN20C	included
PTPN21	included
PTPN22	included
PTPN23	included
PTPN3	included
PTPN4	included
PTPN5	included
PTPN6	included
PTPN7	included
PTPN9	included
PTPRA	included
PTPRB	included
PTPRC	included
PTPRCAP	included
PTPRD	included
PTPRE	included
PTPRF	included
PTPRG	included
PTPRH	included
PTPRJ	included
PTPRK	included
PTPRM	included
PTPRN	included
PTPRN2	included
PTPRO	included
PTPRQ	included
PTPRR	included
PTPRS	included
PTPRT	included
PTPRU	included
PTPRV	included
PTPRZ1	included
PTX3	included
PVR	included
PVRL1	included
PVRL2	included
PVRL3	included
PXDN	included
PXMP3	included
PYCARD	excluded - no marker
PYDC1	excluded - no marker
QSCN6	included
RAB19	included
RAB3D	included
RAC1	included
RAC2	included
RAC3	excluded - no marker
RAD23A	included
RAD50	included
RAD51	included - new MS design
RAD9A	included
RAD9B	included
RAE1	included
RAET1E	included

RAF1	excluded - no marker
RAG1	included
RAG2	included
RAGE	included
RALBP1	included
RAN	included
RANBP2	included
RANP1	included
RAP1A	included
RAPGEF1	included
RARA	included
RARB	included
RARG	included
RARRES2	included
RARRES3	included
RASA1	included
RASGRP1	included
RASGRP2	included
RASGRP3	included
RASSF5	included
RAX	included
RBPSUH	included
RDBP	excluded - no marker
RDX	included
REL	included
RELA	included
RELB	included
RELN	included
RFC1	included
RFX1	included
RFX2	included
RFX3	included
RFX4	included
RFX5	included
RFXANK	included
RFXAP	included
RFXDC1	included
RGL2	included
RGS13	included
RHAG	included
RHBDL2	included
RHCE	included
RHD	included
RHOA	included
RHOC	included
RHOD	included
RHOH	included
RING1	included
RIPK1	included
RIPK2	included
RIPK3	included
RNASE6	included
RNASE7	included
RNASEH2A	included
RND2	excluded - no marker
RNF39	included

RNF4	included
RNF5	included
RNF7	included
RNMT	included
ROCK1	included
ROCK2	included
RORA	included
RORB	included
RORC	included
RPA3	included
RPL23AP1	included
RPL32P1	included
RPL7AP7	included
RPLP1	included
RPP21	included
RPS18	included
RPS4X	included
RPS4Y1	included - new MS design
RPS6KA2	included
RRM1	included
RSAD2	included
RUNX1	included
RUNX1T1	included
RUNX2	included
RUNX3	included
RXRA	excluded - no marker
RXRB	included
RXRG	included
S100A11	included
S100A12	included
S100A4	included
S100A6	included
S100A8	included
S100A9	included
SAA1	included
SAA2	included
SAA3P	included
SAMHD1	included
SAP18	included
SARM1	included
SATB1	excluded - no marker
SCAP1	included
SCARA3	included
SCARA5	included
SCARB1	included
SCARB2	included
SCARF1	included
SCARF2	included
SCGB3A1	included
SCL11A1	included
SCMH1	included
SCML2	included
SCYE1	included
SDC1	included
SDC2	included
SDC3	included

SDC4	included
SDCBP	included
SDF2	excluded - no marker
SDF2L1	included
SEC61A1	included
SEC61A2	included
SEC61B	included
SECTM1	included
SELE	included
SELL	included
SELP	included
SELPLG	included
SEMA3E	included
SEMA4D	included
SEMA7A	included
SEMG1	included
SEPHS2	included
SEPT2	included
SERPINA2	included
SERPINB2	included
SERPINB8	included
SERPINB9	included
SERPINC1	included
SERPINE1	included
SERPING1	included
SET	included
SFRS2IP	included
SFTBA1B	excluded - no marker
SFTPA1	included
SFTPB	included
SFTPD	included
SGK	included
SH2D1A	included
SH2D1B	included
SH2D2A	included
SH3KBP1	included
SHB	included
SHH	included
SHMT1	excluded - no marker
SHMT2	included - new MS design
SIGIRR	included - new MS design
SIGLEC1	included
SIGLEC10	included
SIGLEC5	included
SIGLEC6	included
SIGLEC7	included
SIGLEC8	included
SIGLEC9	included
SILV	included
SIM1	included
SIPA1	included
SIRPA	included
SIRPB1	included
SIRPB2	included
SIT1	included
SIVA	included

SKAP1	included
SKIV2L	excluded - no marker
SKP2	included
SLAMF1	included
SLAMF6	included
SLAMF7	included
SLAMF8	included
SLAMF9	included
SLC14A1	included
SLC19A1	included - new MS design
SLC1A5	included
SLC22A1	included
SLC22A4	included
SLC22A5	included
SLC25A19	included
SLC39A7	included
SLC3A2	included
SLC40A1	included
SLC44A1	included
SLC44A4	excluded - no marker
SLC4A1	included
SLC6A4	included
SLC7A5	included
SLC9A1	included
SLC9A2	included
SLC9A3	included
SLC9A4	included
SLC9A5	included
SLC9A6	included
SLC9A7	included
SLC9A8	included
SLC9A9	included
SLPI	included
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SMAD7	included
SMARCA1	included
SMARCA2	included
SMARCA4	included
SMARCA5	included
SMARCAL1	included
SMC3	included
SMG6	included
SMO	included
SNFT	included
SNRP70	included
SNRPN	included
SNX9	included
SOBP	included
SOCS1	included
SOCS2	included
SOCS3	included
SOCS4	included
SOCS5	included
SOCS6	included
SOCS6/CBLN2	included

SOCS7	excluded - no marker
SOD1	included - new MS design
SOD2	included
SOD3	included
SORL1	included
SOS1	included
SOX13	included
SP1	included
SP110	included
SP3	included
SPEN	included
SPHK1	included
SPHK2	included
SPI1	included
SPN	included
SPP1	included
SQSTM1	included
SRC	included
SREBF1	included
SRPK1	included
SRPK2	included
SRPK3	excluded - no marker
SST	included
SSTR1	included
SSTR2	included
ST3GAL5	included
ST6GAL1	included
ST8SIA6	included
STAB1	included
STAT1	included
STAT2	included
STAT3	included
STAT4	included
STAT5A	included
STAT5B	included
STAT6	included
STIL	included
STK17A	included
STK17B	included
STK19	excluded - no marker
STK3	included
STK38	included
STK4	included
STT3B	included
STX11	included
STXBP5	included
STYX	included
SULT1C2	included
SUMO1	excluded - no marker
SUV39H1	included
SVEP1/MUSK	included
SYK	included
SYN3/LARGE	included
SYNE1	included
SYT7	included
SYTL1	excluded - no marker

Tac1	included
TACC1	included
TACSTD1	included
TAF13	included
TAF9	included
TAL1	included
TAL2	included
TA-NFKBH	included
TANK	included
TAP1	included
TAP2	included
TAPBP	included
TBK1	excluded - no marker
TBL1X	included
TBL1XR1	included
TBL1Y	included
TBP	included
TBX21	included
TBXAR2	included
TBXAS1	included
TCAM2	included
TCD@	included
TCF12	included
TCF19	included
TCF3	included
TCF4	included
TCF7	excluded - no marker
TCF8	included
TCIRG1	included
TCN2	included
TEC	included
TEK	included
TEP1	included
TERC	included
TERT	included
TFAP2C	included
TFB1M	included
TFDP2	included
TFF1	excluded - no marker
TFF2	excluded - no marker
TFF3	included
TFRC	included
TGFA	included
TGFB1	included - new MS design
TGFB2	included
TGFB3	included
TGFBR1	included
TGFBR2	included
TGFBR3	included
TGIF1	included
TGM3	included
THBD	included
THBS1	included
THOC1	included
THPO	included
THRA	included

THRB	included
THY1	included
TIAF1	included
TICAM1	included
TIMELESS	included
TIMP1	included
TIMP2	included
TIMP3	included
TIMP4	included
TIRAP	included
TIRG1	included
TLE3	included
TLN1	included
TLR1	included
TLR10	included - new MS design
TLR11	excluded - unknown location
TLR12	excluded - unknown location
TLR13	excluded - unknown location
TLR2	included
TLR3	included
TLR4	included
TLR5	included
TLR6	included
TLR7	included
TLR8	included
TLR9	included
TM7SF4	included
TMC8	included
TMEM142A	excluded - no marker
TMEM158	included
TMEM37	included
TMPO	included
TMPRSS11D	included
TMSB4X	included
TMSB4Y	included
TNC	included
TNF	included
TNFa	included
TNFAIP3	included
TNFb	included
TNFd	included
TNFRSF10A	included - new MS design
TNFRSF10B	included
TNFRSF10C	included - new MS design
TNFRSF10D	included - new MS design
TNFRSF11A	included
TNFRSF11B	included
TNFRSF12A	included
TNFRSF13B	included
TNFRSF13C	included
TNFRSF14	included - new MS design
TNFRSF17	included - new MS design
TNFRSF18	included - new MS design
TNFRSF19	included
TNFRSF19L	included
TNFRSF1A	included

TNFRSF1B	included
TNFRSF21	included
TNFRSF25	included
TNFRSF4	excluded - no marker
TNFRSF5	included
TNFRSF6	included
TNFRSF6B	included
TNFRSF7	included
TNFRSF8	included
TNFRSF9	included
TNFSF10	included
TNFSF11	included
TNFSF12	included
TNFSF12-13	included
TNFSF13	included
TNFSF13B	included
TNFSF14	included
TNFSF15	included
TNFSF18	included
TNFSF4	included
TNFSF6	included
TNFSF7	included
TNFSF8	included
TNFSF9	included
TNN	included
TNR	included
TNXB	excluded - no marker
TOLLIP	excluded - no marker
TOP2A	included
TOR3A	included
TP35	included
TP73L	included
TPMT	included
TPT1	included
TRA@	included
TRADD	included
TRAF1	included
TRAF2	included
TRAF3	included
TRAF3IP1	included
TRAF4	excluded - no marker
TRAF5	included
TRAF6	included
TRAF7	included
TRAM1	included
TRAM2	included
TRAT1	included
TRB@	included
TREM1	included
TREM2	included
TREML1	included
TREML2	included
TREML3	included
TREML4	included
TRERF1	included
TRG@	included

TRH	included
TRHR	included
TRIM10	included
TRIM15	included
TRIM22	included
TRIM25	included
TRIM26	included
TRIM31	included
TRIM39	included
TRIM40	included
TRIM59	included
TRPM2	included
TRPV1	included
TRPV2	included
TSC22D3	included
TSHB	included
TSHR	included
TSLP	included
TSPAN7	included
TSPYL2	included
TTRAP	included
TTYH1	included
TUBA1	included
TUBA1A	included
TUBB	included
TWIST1	included
TXK	included
TXN	included
TXNDC	included
TXNRD1	included
TYK2	included
TYMS	included
TYR	included
TYROBP	included
UBB	excluded - no marker
UBC	included
UBD	included
UBE2D1	included
UBE2L6	included
UBE2N	included
UBE2V1	included
UCN	included
UGCG	included
UGT1A1	included
UGT1A9	included
UGT2B17	included
UGT2B28	included
UGT2B7	included
ULBP1	included
ULBP2	included
ULBP3	included
UNC5CL	included
UNC84B	included
UNC93B1	included
UNG	included
Unknown	included

USF1	included
USF2	included
USP18	excluded - no marker
USP9Y	included
UTRN	included
UTY	included
UVRAG	included
VARS	included
VARSL	included
VASP	included
VAV1	included
VAV2	included
VAV3	included
VCAM1	included
VDR	included
VEGFA	included
VEGFB	included
VEGFC	included
VIM	included
VIP	included
VISA	included
VNN1	included
VPREB1	included
VPS24	included
VPS52	included
VRK2	included
VTCN1	included
VTN	included
VWF	included
WAS	included
WASF1	included
WASF3	included
WDR46	included
WFDC12	included
WIPF1	included
WNT1	included
WNT3	included
WNT4	included
WNT5A	included
WRNIP1	included
WT1	excluded - no marker
WTAP	included
XBP1	included
XCL1	included
XCL2	included
XCR1	included
XDH	included
XG	included
XK	included
XPA	included
XPC	included
XRCC1	included
XRCC3	included
XRCC5	included
YES1	included
YWHA2	included

YWHAQ	included
YY1	included
ZAP70	included
ZBTB12	excluded - no marker
ZBTB22	included
ZBTB32	included
ZBTB7	excluded - no marker
ZFAND3	included
ZFP36	included
ZNF192	included
ZNF193	included
ZNF3	included
ZNF451	included
ZNRD1	included

Gene Symbol	**Aliases**	**Gene location (genecard)**	**Chromosome**
TNFRSF18	GITR	Chromosome 1:1,128,751-1,131,952	1
DVL1	DSH	Chromosome 1:1,260,521-1,274,623	1
MMP23B		Chromosome 1:1,557,337-1,623,109	1
PRKCZ	PKCξ	Chromosome 1:1,971,769-2,106,694	1
DFFA		Chromosome 1:10,439,166-10,455,200	1
VCAM1	CD106	Chromosome 1:100,957,885-100,977,189	1
EDG1	sphingosine-1-phosphate	Chromosome 1:101,475,032-101,479,662	1
PRMT6	PRMT6	Chromosome 1:107,400,824-107,403,439	1
VAV3		Chromosome 1:107,915,305-108,309,108	1
VAV3		Chromosome 1:107,915,305-108,309,108	1
VAV3		Chromosome 1:107,915,305-108,309,108	1
VAV3		Chromosome 1:107,915,305-108,309,108	1
TAF13	POLII	Chromosome 1:109,406,644-109,420,147	1
GNAI3	G protein alpha i3	Chromosome 1:109,892,824-109,938,498	1
GNAI3	G protein alpha i3	Chromosome 1:109,892,824-109,938,498	1
MASP2	MAp19	Chromosome 1:11,009,167-11,029,877	1
MASP2	MAp19	Chromosome 1:11,009,167-11,029,877	1
FRAP1	mTOR	Chromosome 1:11,089,179-11,245,176	1
FRAP1	mTOR	Chromosome 1:11,089,179-11,245,176	1
FRAP1	mTOR	Chromosome 1:11,089,179-11,245,176	1
MTHFR		Chromosome 1:11,768,367-11,788,702	1
NPPA	ANP	Chromosome 1:11,828,353-11,830,989	1
CSF1	M-CSF	Chromosome 1:110,254,778-110,275,144	1
CD53		Chromosome 1:111,215,344-111,244,081	1
CD53		Chromosome 1:111,215,344-111,244,081	1
CHI3L2	Chi3l3	Chromosome 1:111,571,804-111,587,585	1
ADORA3	Adenosin receptor 3	Chromosome 1:111,827,493-111,908,107	1
ADORA3	Adenosin receptor 3	Chromosome 1:111,827,493-111,908,107	1
RAP1A	Rap-1	Chromosome 1:111,886,363-112,060,836	1
RHOC	RhoC	Chromosome 1:113,045,251-113,051,579	1
PTPN22		Chromosome 1:114,092,981-114,215,904	1
PTPN22		Chromosome 1:114,092,981-114,215,904	1
BCAS2		Chromosome 1:114,911,701-114,925,788	1
NRAS	Ras	Chromosome 1:115,048,613-115,102,147	1
TSHB	TSHB	Chromosome 1:115,373,938-115,378,464	1
NGFB	NGFB	Chromosome 1:115,630,060-115,682,380	1
CD58	LFA-3	Chromosome 1:116,858,680-116,915,184	1
IGSF3		Chromosome 1:116,918,554-117,011,898	1
CD2	LFA-2	Chromosome 1:117,098,530-117,113,374	1
PTGFRN	CD315, prostaglandin rec	Chromosome 1:117,254,202-117,334,503	1
PTGFRN	CD315, prostaglandin rec	Chromosome 1:117,254,202-117,334,503	1
VTCN1		Chromosome 1:117,487,732-117,555,079	1
VTCN1		Chromosome 1:117,487,732-117,555,079	1
HSD3B1	3 beta hydroxysteroid deh	Chromosome 1:119,851,356-119,859,200)	1
TNFRSF8	CD30	Chromosome 1:12,046,021-12,126,851	1
TNFRSF1B	CD120b	Chromosome 1:12,149,647-12,191,872	1
NOTCH2		Chromosome 1:120,255,699-120,413,799	1
FCGR1B		Chromosome 1:120,728,502-120,737,460	1
FCGR1B		Chromosome 1:120,728,502-120,737,460	1
ITGA10		Chromosome 1:144,236,248-144,255,225	1
CD160		Chromosome 1:144,407,155-144,426,971	1
PPIAL4		Chromosome 1:146,418,535-146,422,374	1
FCGR1A	CD64	Chromosome 1:146,567,361-146,577,147	1
MTMR11	CRA	Chromosome 1:148,167,168-148,175,396	1
MCL1		Chromosome 1:148,813,658-148,818,760	1

CTSS	Cathepsin S	Chromosome 1:148,969,175-149,005,057	1
CTSK	cathepsin K	Chromosome 1:149,035,311-149,047,436	1
CTSK	cathepsin K	Chromosome 1:149,035,311-149,047,436	1
BNIPL		Chromosome 1:149,275,670-149,286,700	1
PIK4CB		Chromosome 1:149,531,037-149,566,815	1
ELA2A		Chromosome 1:15,655,811-15,690,482	1
ELA2B		Chromosome 1:15,655,811-15,690,482	1
RORC	RORg, NR1F3	Chromosome 1:150,039,364-150,070,972	1
S100A11	S100a11	Chromosome 1:150,271,606-150,276,135	1
PGLYRP3	PGRP-Ia	Chromosome 1:151,536,962-151,549,818	1
S100A12	S100A12	Chromosome 1:151,612,808-151,614,749	1
S100A6	S100a6	Chromosome 1:151,773,699-151,775,344	1
S100A4	S100a4	Chromosome 1:151,782,713-151,789,236	1
ILF2		Chromosome 1:151,900,905-151,910,148	1
ILF2		Chromosome 1:151,900,905-151,910,148	1
MPS1		Chromosome 1:152,229,853-152,231,250	1
MPS1		Chromosome 1:152,229,853-152,231,250	1
IL6R	CD126	Chromosome 1:152,644,293-152,708,550	1
IL6R	CD126	Chromosome 1:152,644,293-152,708,550	1
CKS1B		Chromosome 1:153,213,753-153,218,348	1
EFNA1	Ephrin A1	Chromosome 1:153,366,560-153,374,010	1
MUC1	MUC1	Chromosome 1:153,424,924-153,429,330	1
MEF2D		Chromosome 1:154,700,143-154,737,244	1
SH2D2A	RIBP	Chromosome 1:155,042,659-155,053,270	1
SH2D2A	RIBP	Chromosome 1:155,042,659-155,053,270	1
FCRL5	CD307	Chromosome 1:155,749,791-155,788,934	1
FCRL4		Chromosome 1:155,810,163-155,834,494	1
FCRL2		Chromosome 1:155,982,145-156,013,546	1
FCRL2		Chromosome 1:155,982,145-156,013,546	1
CD1D		Chromosome 1:156,416,361-156,421,310	1
CD1C		Chromosome 1:156,526,200-156,530,044	1
IFI16	Ifi204	Chromosome 1:157,236,382-157,291,569	1
IFI16	Ifi204	Chromosome 1:157,236,382-157,291,569	1
DARC	CD234, Duffy blood group	Chromosome 1:157,408,023-157,442,914	1
FCER1A		Chromosome 1:157,526,128-157,544,638	1
CRP		Chromosome 1:157,948,703-157,951,003	1
DUSP23		Chromosome 1:158,017,346-158,018,957	1
IGSF9		Chromosome 1:158,163,453-158,182,010	1
IGSF8	CD316	Chromosome 1:158,327,754-158,335,103	1
NHLH1	HEN1	Chromosome 1:158,603,481-158,609,262	1
SLAMF6	NTBA	Chromosome 1:158,721,444-158,759,676	1
CD48		Chromosome 1:158,915,160-158,948,265	1
LY9	CD229	Chromosome 1:159,032,552-159,064,669	1
JAM1	CD321, JAM-A, F11R	Chromosome 1:159,231,625-159,275,404	1
JAM1	CD321, JAM-A, F11R	Chromosome 1:159,231,625-159,275,404	1
FCER1G		Chromosome 1:159,451,693-159,457,113	1
NR1I3	NR1I3	Chromosome 1:159,466,079-159,474,590	1
FCGR2A	CD32	Chromosome 1:159,741,844-159,755,984	1
FCGR3B	CD16b	Chromosome 1:159,859,610-159,867,620	1
SPEN	SHARP	Chromosome 1:16,046,946-16,139,542	1
SH2D1B	EAT2b	Chromosome 1:160,631,680-160,648,552	1
RXRG	NR2B3	Chromosome 1:163,636,778-163,681,057	1
CD3Z	CD247, CD3 zeta chain	Chromosome 1:165,666,501-165,754,471	1
CD3Z	CD247, CD3 zeta chain	Chromosome 1:165,666,501-165,754,471	1
MPZL1	concanavalin A receptor	Chromosome 1:165,957,832-166,026,684	1
XCL2		Chromosome 1:166,776,626-166,779,859	1

XCL1		Chromosome 1:166,812,335-166,817,939	1
F5	Factor V	Chromosome 1:167,750,028-167,822,450	1
SELP	CD62P	Chromosome 1:167,824,661-167,866,031	1
SELP	CD62P	Chromosome 1:167,824,661-167,866,031	1
SELL	L-Selectin, CD62L	Chromosome 1:167,926,432-167,947,463	1
PADI4		Chromosome 1:17,507,277-17,563,086	1
TNFSF6	CD178, FASL	Chromosome 1:170,894,777-170,902,637	1
TNFSF6	CD178, FASL	Chromosome 1:170,894,777-170,902,637	1
TNFSF18	GITRL	Chromosome 1:171,275,723-171,286,679	1
TNFSF18	GITRL	Chromosome 1:171,275,723-171,286,679	1
TNFSF4	CD252, OX40L	Chromosome 1:171,419,493-171,443,094	1
TNFSF4	CD252, OX40L	Chromosome 1:171,419,493-171,443,094	1
PRDX6		Chromosome 1:171,713,028-171,724,569	1
SERPINC1	Antithrombin	Chromosome 1:172,139,562-172,153,139	1
TNN	tenascin	Chromosome 1:173,303,617-173,383,825	1
TNR	tenascin	Chromosome 1:173,558,558-173,979,529	1
TNR	tenascin	Chromosome 1:173,558,558-173,979,529	1
TNR	tenascin	Chromosome 1:173,558,558-173,979,529	1
TNR	tenascin	Chromosome 1:173,558,558-173,979,529	1
TNR	tenascin	Chromosome 1:173,558,558-173,979,529	1
TNR	tenascin	Chromosome 1:173,558,558-173,979,529	1
ANGPTL1	Angioarrestin	Chromosome 1:177,085,293-177,106,838	1
TOR3A	ADIR	Chromosome 1:177,317,735-177,333,653	1
TOR3A	ADIR	Chromosome 1:177,317,735-177,333,653	1
QSCN6		Chromosome 1:178,390,591-178,439,788	1
QSCN6		Chromosome 1:178,390,591-178,439,788	1
MR1	MR1=HLALS	Chromosome 1:179,269,762-179,292,312	1
IGSF21		Chromosome 1:18,306,827-18,577,563	1
IGSF21		Chromosome 1:18,306,827-18,577,563	1
IGSF21		Chromosome 1:18,306,827-18,577,563	1
IGSF21		Chromosome 1:18,306,827-18,577,563	1
DHX9		Chromosome 1:181,075,127-181,123,510	1
DHX9		Chromosome 1:181,075,127-181,123,510	1
LAMC2		Chromosome 1:181,422,022-181,480,662	1
LAMC2		Chromosome 1:181,422,022-181,480,662	1
NCF2	neutrophil cytosolic factor	Chromosome 1:181,791,320-181,826,634	1
PRG4	MSF	Chromosome 1:184,532,034-184,550,317	1
PTGES2		Chromosome 1:184,907,546-184,916,179	1
RGS13		Chromosome 1:190,871,905-190,896,059	1
RGS13		Chromosome 1:190,871,905-190,896,059	1
CFH		Chromosome 1:194,887,631-194,983,257	1
CFH		Chromosome 1:194,887,631-194,983,257	1
CFHR4		Chromosome 1:195,010,571-195,154,386	1
CFHR2		Chromosome 1:195,179,520-195,194,979	1
PTPRC	CD45	Chromosome 1:196,874,424-196,993,035	1
NR5A2	LRH-1	Chromosome 1:198,263,353-198,413,175	1
DDX59		Chromosome 1:198,859,647-198,905,749	1
DDX59		Chromosome 1:198,859,647-198,905,749	1
TNFRSF14	CD270, LIGHTR, HVEM	Chromosome 1:2,479,150-2,486,613	1
TNFRSF14	CD270, LIGHTR, HVEM	Chromosome 1:2,479,150-2,486,613	1
PLA2G2D	Phospholipase	Chromosome 1:20,311,019-20,318,637	1
PLA2G2D	Phospholipase	Chromosome 1:20,311,019-20,318,637	1
PLA2G2D	Phospholipase	Chromosome 1:20,311,019-20,318,637	1
CDA	CDD	Chromosome 1:20,788,028-20,817,988	1
CDA		Chromosome 1:20,788,028-20,817,988	1
ELF3	ERT	Chromosome 1:200,243,696-200,252,939	1

PTPN7		Chromosome 1:200,382,764-200,397,332	1
PTPRV		Chromosome 1:200,403,802-200,425,104	1
ADORA1	Adenosin receptor 1	Chromosome 1:201,326,405-201,403,156	1
ADORA1	Adenosin receptor 1	Chromosome 1:201,326,405-201,403,156	1
ADORA1	Adenosin receptor 1	Chromosome 1:201,326,405-201,403,156	1
FMOD	Fibromodulin	Chromosome 1:201,576,375-201,587,240	1
LAX1		Chromosome 1:202,000,957-202,012,123	1
SOX13	SOX13 (SRY box 13)	Chromosome 1:202,308,866-202,363,494	1
SOX13	SOX13 (SRY box 13)	Chromosome 1:202,308,866-202,363,494	1
PIK3C2B		Chromosome 1:202,658,379-202,726,175	1
MDM4		Chromosome 1:202,752,134-202,793,871	1
CNTN2		Chromosome 1:203,278,963-203,313,761	1
CNTN2		Chromosome 1:203,278,963-203,313,761	1
ELK4		Chromosome 1:203,833,330-203,868,623	1
IKBKE	IKKepsilon, IKKi	Chromosome 1:204,710,414-204,736,846	1
DYRK3		Chromosome 1:204,875,504-204,924,381	1
MAPKAPK2		Chromosome 1:204,924,912-204,974,251	1
IL10	Interleukin 10	Chromosome 1:205,007,570-205,012,462	1
IL19		Chromosome 1:205,038,838-205,082,949	1
IL20		Chromosome 1:205,105,322-205,109,191	1
IL24		Chromosome 1:205,137,411-205,144,107	1
C4BPB		Chromosome 1:205,328,810-205,339,961	1
C4BPA		Chromosome 1:205,344,230-205,384,940	1
CD55	CD55, DAF	Chromosome 1:205,561,476-205,600,934	1
CR2	CD21	Chromosome 1:205,694,198-205,729,863	1
CR1		Chromosome 1:205,736,096-205,881,733	1
CR1		Chromosome 1:205,736,096-205,881,733	1
CR1		Chromosome 1:205,736,096-205,881,733	1
MCP	CD46	Chromosome 1:205,992,025-206,035,481	1
CD34		Chromosome 1:206,116,942-206,151,370	1
CD34		Chromosome 1:206,116,942-206,151,370	1
CD34		Chromosome 1:206,116,942-206,151,370	1
LAMB3		Chromosome 1:207,854,838-207,892,443	1
LAMB3		Chromosome 1:207,854,838-207,892,443	1
LAMB3		Chromosome 1:207,854,838-207,892,443	1
IRF6		Chromosome 1:208,025,659-208,046,102	1
TRAF5		Chromosome 1:209,566,580-209,614,911	1
TRAF5		Chromosome 1:209,566,580-209,614,911	1
ATF3	ATF3	Chromosome 1:210,805,374-210,860,742	1
ATF3	ATF3	Chromosome 1:210,805,374-210,860,742	1
PTPN14		Chromosome 1:212,597,474-212,791,265	1
PTPN14		Chromosome 1:212,597,474-212,791,265	1
CENPF	Centromere protein F	Chromosome 1:212,843,155-212,904,537	1
ESRRG	NR3B3	Chromosome 1:214,743,211-215,377,720	1
ESRRG	NR3B3	Chromosome 1:214,743,211-215,377,720	1
ESRRG	NR3B3	Chromosome 1:214,743,211-215,377,720	1
ESRRG	NR3B3	Chromosome 1:214,743,211-215,377,720	1
ESRRG	NR3B3	Chromosome 1:214,743,211-215,377,720	1
ESRRG	NR3B3	Chromosome 1:214,743,211-215,377,720	1
ESRRG	NR3B3	Chromosome 1:214,743,211-215,377,720	1
TGFB2		Chromosome 1:216,586,200-216,684,584	1
HLX1	Hlx	Chromosome 1:219,119,366-219,125,022	1
HLX1	Hlx	Chromosome 1:219,119,366-219,125,022	1
DUSP10	MKP-5	Chromosome 1:219,941,389-219,982,141	1
DUSP10	MKP-5	Chromosome 1:219,941,389-219,982,141	1
DUSP10	MKP-5	Chromosome 1:219,941,389-219,982,141	1

HSPG2	Perlecan	Chromosome 1:22,021,324-22,136,377	1
WNT4		Chromosome 1:22,318,177-22,342,197	1
C1QA		Chromosome 1:22,835,705-22,838,762	1
C1QA		Chromosome 1:22,835,705-22,838,762	1
C1QA		Chromosome 1:22,835,705-22,838,762	1
EPHB2		Chromosome 1:22,910,045-23,114,405	1
TLR5	CD285	Chromosome 1:221,350,270-221,383,247	1
EPHX1		Chromosome 1:224,064,459-224,099,884	1
EPHX1		Chromosome 1:224,064,459-224,099,884	1
PARP1		Chromosome 1:224,615,015-224,662,414	1
PARP1		Chromosome 1:224,615,015-224,662,414	1
ITPKB		Chromosome 1:224,886,014-224,993,647	1
ITPKB		Chromosome 1:224,886,014-224,993,647	1
HIST3H2A	Histone 3	Chromosome 1:226,711,303-226,712,197	1
ACTA1	F-actin	Chromosome 1:227,633,615-227,636,468	1
ACTA1	F-actin	Chromosome 1:227,633,615-227,636,468	1
LYST		Chromosome 1:233,890,964-234,113,563	1
LYST		Chromosome 1:233,890,964-234,113,563	1
LYST		Chromosome 1:233,890,964-234,113,563	1
LYST		Chromosome 1:233,890,964-234,113,563	1
NID1	entactin	Chromosome 1:234,205,753-234,303,706	1
NID1	entactin	Chromosome 1:234,205,753-234,303,706	1
EDARADD		Chromosome 1:234,624,303-234,714,649	1
EDARADD		Chromosome 1:234,624,303-234,714,649	1
EDARADD		Chromosome 1:234,624,303-234,714,649	1
ACTN2	alpha actinin 2	Chromosome 1:234,916,422-234,994,554	1
IL22RA1		Chromosome 1:24,318,848-24,342,198	1
IL22RA1		Chromosome 1:24,318,848-24,342,198	1
IL22RA1		Chromosome 1:24,318,848-24,342,198	1
EXO1		Chromosome 1:240,078,105-240,119,864	1
AKT3	PKB	Chromosome 1:241,718,158-242,080,053	1
AKT3	PKB	Chromosome 1:241,718,158-242,080,053	1
AKT3	PKB	Chromosome 1:241,718,158-242,080,053	1
AKT3	PKB	Chromosome 1:241,718,158-242,080,053	1
AKT3	PKB	Chromosome 1:241,718,158-242,080,053	1
NLRP3	NALP3, CIAS1, PYPAF1,	Chromosome 1:245,647,974-245,679,033	1
NLRP3	NALP3, CIAS1, PYPAF1,	Chromosome 1:245,647,974-245,679,033	1
RUNX3		Chromosome 1:25,098,596-25,164,062	1
RUNX3		Chromosome 1:25,098,596-25,164,062	1
RHD	RhD antigen, CD240D	Chromosome 1:25,471,568-25,529,523	1
RHCE	CD240CE	Chromosome 1:25,561,327-25,629,270	1
PAFAH2	PAF, platelet activating fa	Chromosome 1:26,158,845-26,197,235	1
PAFAH2	PAF, platelet activating fa	Chromosome 1:26,158,845-26,197,235	1
CDW52	CD52, CAMPATH	Chromosome 1:26,516,998-26,519,601	1
GPATCH3	NR0B2	Chromosome 1:27,089,567-27,099,549	1
NR0B2	NR0B2	Chromosome 1:27,110,566-27,113,047	1
SLC9A1	NHE-1	Chromosome 1:27,297,893-27,366,059	1
SLC9A1	NHE-1	Chromosome 1:27,297,893-27,366,059	1
FGR		Chromosome 1:27,811,162-27,834,375	1
FGR		Chromosome 1:27,811,162-27,834,375	1
PTAFR		Chromosome 1:28,346,264-28,392,971	1
PTAFR		Chromosome 1:28,346,264-28,392,971	1
PTPRU		Chromosome 1:29,435,611-29,525,899	1
PTPRU		Chromosome 1:29,435,611-29,525,899	1
DFFB		Chromosome 1:3,763,705-3,791,853	1
SDC3	Syndecan	Chromosome 1:31,114,901-31,166,301	1

SDC3	Syndecan	Chromosome 1:31,114,901-31,166,301	1
FABP3	FABP3	Chromosome 1:31,610,687-31,618,510	1
FABP3	FABP3	Chromosome 1:31,610,687-31,618,510	1
PTP4A2		Chromosome 1:32,144,609-32,176,578	1
PTP4A2		Chromosome 1:32,144,609-32,176,578	1
KHDRBS1		Chromosome 1:32,252,017-32,299,037	1
LCK		Chromosome 1:32,489,480-32,524,353	1
LCK		Chromosome 1:32,489,480-32,524,353	1
HDAC1		Chromosome 1:32,530,274-32,571,823	1
CSF3R	CD114	Chromosome 1:36,704,231-36,721,466	1
CSF3R	CD114	Chromosome 1:36,704,231-36,721,466	1
GNL2	Ngp	Chromosome 1:37,805,004-37,834,109	1
PPIE		Chromosome 1:39,977,117-40,002,173	1
PPIE		Chromosome 1:39,977,117-40,002,173	1
MYCL1	l-myc	Chromosome 1:40,133,685-40,140,274	1
NFYC		Chromosome 1:40,929,829-41,009,864	1
NFYC		Chromosome 1:40,929,829-41,009,864	1
CTPS	CTP synthase	Chromosome 1:41,217,951-41,250,815	1
SCMH1	Scmh1	Chromosome 1:41,265,461-41,480,375	1
SCMH1	Scmh1	Chromosome 1:41,265,461-41,480,375	1
FOXJ3		Chromosome 1:42,414,797-42,574,135	1
FOXJ3		Chromosome 1:42,414,797-42,574,135	1
PPIH		Chromosome 1:42,896,635-42,915,016	1
ERMAP		Chromosome 1:43,055,363-43,083,247	1
ERMAP		Chromosome 1:43,055,363-43,083,247	1
MPL	CD110, F36VMpl, thromb	Chromosome 1:43,576,062-43,592,722	1
CDC20		Chromosome 1:43,597,213-43,601,461	1
PTPRF		Chromosome 1:43,769,134-43,861,924	1
PTPRF		Chromosome 1:43,769,134-43,861,924	1
ARTN	ARTN	Chromosome 1:44,171,579-44,175,499	1
PLK3		Chromosome 1:45,038,623-45,049,479	1
PIK3R3		Chromosome 1:46,278,399-46,371,054	1
CYP4B1		Chromosome 1:47,037,305-47,057,672	1
CYP4B1		Chromosome 1:47,037,305-47,057,672	1
CYP4X1		Chromosome 1:47,261,827-47,289,010	1
TAL1	SCL=TAL1	Chromosome 1:47,454,550-47,469,974	1
TAL1	SCL=TAL1	Chromosome 1:47,454,550-47,469,974	1
FOXE3		Chromosome 1:47,654,331-47,656,311	1
FOXD2		Chromosome 1:47,674,276-47,678,950	1
FAF1		Chromosome 1:50,677,738-51,198,524	1
FAF1		Chromosome 1:50,677,738-51,198,524	1
FAF1		Chromosome 1:50,677,738-51,198,524	1
FAF1		Chromosome 1:50,677,738-51,198,524	1
FAF1		Chromosome 1:50,677,738-51,198,524	1
FAF1		Chromosome 1:50,677,738-51,198,524	1
PPAP2B		Chromosome 1:56,732,527-56,817,845	1
PPAP2B		Chromosome 1:56,732,527-56,817,845	1
PPAP2B		Chromosome 1:56,732,527-56,817,845	1
PRKAA2	AMPK	Chromosome 1:56,883,583-56,953,596	1
C8A		Chromosome 1:57,093,065-57,156,482	1
JUN	AP-1	Chromosome 1:59,019,048-59,022,587	1
TNFRSF25	TRAMP	Chromosome 1:6,443,798-6,502,708	1
TNFRSF25	TRAMP	Chromosome 1:6,443,798-6,502,708	1
CYP2J2		Chromosome 1:60,131,568-60,165,050	1
FOXD3		Chromosome 1:63,561,300-63,563,385	1
JAK1		Chromosome 1:65,071,500-65,204,775	1

JAK1		Chromosome 1:65,071,500-65,204,775	1
JAK1		Chromosome 1:65,071,500-65,204,775	1
LEPR	CD295, leptin receptor	Chromosome 1:65,658,858-65,879,830	1
LEPR	CD295, leptin receptor	Chromosome 1:65,658,858-65,879,830	1
LEPR	CD295, leptin receptor	Chromosome 1:65,658,858-65,879,830	1
PDE4B	Phosphodiesterases	Chromosome 1:66,030,781-66,612,850	1
PDE4B	Phosphodiesterases	Chromosome 1:66,030,781-66,612,850	1
PDE4B	Phosphodiesterases	Chromosome 1:66,030,781-66,612,850	1
PDE4B	Phosphodiesterases	Chromosome 1:66,030,781-66,612,850	1
PDE4B	Phosphodiesterases	Chromosome 1:66,030,781-66,612,850	1
IL23R		Chromosome 1:67,404,671-67,498,250	1
IL23R		Chromosome 1:67,404,671-67,498,250	1
IL12RB2		Chromosome 1:67,545,635-67,635,171	1
TNFRSF9	CDw137, 4-1BB	Chromosome 1:7,902,494-7,923,513	1
TNFRSF9	CDw137, 4-1BB	Chromosome 1:7,902,494-7,923,513	1
PTGER3	EP3	Chromosome 1:71,090,624-71,286,079	1
PTGER3	EP3	Chromosome 1:71,090,624-71,286,079	1
PTGER3	EP3	Chromosome 1:71,090,624-71,286,079	1
PTGER3	EP3	Chromosome 1:71,090,624-71,286,079	1
PTGFR		Chromosome 1:78,542,156-78,778,974	1
PTGFR		Chromosome 1:78,542,156-78,778,974	1
PTGFR		Chromosome 1:78,542,156-78,778,974	1
IFI44		Chromosome 1:78,888,104-78,902,351	1
IFI44		Chromosome 1:78,888,104-78,902,351	1
EGFTM7		Chromosome 1:79,128,037-79,279,105	1
EGFTM7		Chromosome 1:79,128,037-79,279,105	1
PRKACB		Chromosome 1:84,316,329-84,476,769	1
PRKACB		Chromosome 1:84,316,329-84,476,769	1
BCL10		Chromosome 1:85,504,519-85,516,359	1
BCL10		Chromosome 1:85,504,519-85,516,359	1
DDAH1		Chromosome 1:85,556,756-85,703,415	1
DDAH1		Chromosome 1:85,556,756-85,703,415	1
GTF2B	TFIIB	Chromosome 1:89,091,203-89,129,889	1
GBP3		Chromosome 1:89,244,948-89,261,132	1
GBP2		Chromosome 1:89,344,403-89,414,311	1
GBP5		Chromosome 1:89,498,853-89,511,119	1
PIK3CD		Chromosome 1:9,634,390-9,711,564	1
TGFBR3	Betaglycan	Chromosome 1:91,918,488-92,144,147	1
TGFBR3	Betaglycan	Chromosome 1:91,918,488-92,144,147	1
TGFBR3	Betaglycan	Chromosome 1:91,918,488-92,144,147	1
ISG15	G1P2, ISRE, UCRP	Chromosome 1:938,666-939,783	1
GCLM		Chromosome 1:94,123,349-94,147,600	1
F3	CD142, coag factor 3, tiss	Chromosome 1:94,767,369-94,779,944	1
CHUK	IKK1	Chromosome 10:101,899,841-101,979,366	10
CHUK	IKK1	Chromosome 10:101,899,841-101,979,366	10
BTRC	Beta-TRCP	Chromosome 10:103,103,810-103,307,068	10
BTRC	Beta-TRCP	Chromosome 10:103,103,810-103,307,068	10
BTRC	Beta-TRCP	Chromosome 10:103,103,810-103,307,068	10
FGF8	FGF8	Chromosome 10:103,519,877-103,525,817	10
NFKB2	p100, p52	Chromosome 10:104,144,320-104,152,271	10
C10orf26	OPAL1	Chromosome 10:104,525,996-104,566,011	10
CYP17A1	17 alpha hydroxylase	Chromosome 10:104,580,278-104,587,280	10
CUGBP2		Chromosome 10:11,087,290-11,418,680	10
CUGBP2		Chromosome 10:11,087,290-11,418,680	10
CUGBP2		Chromosome 10:11,087,290-11,418,680	10
CUGBP2		Chromosome 10:11,087,290-11,418,680	10

CUGBP2		Chromosome 10:11,087,290-11,418,680	10
CUGBP2		Chromosome 10:11,087,290-11,418,680	10
DUSP5	VH3	Chromosome 10:112,247,586-112,261,292	10
SMC3	BAM11	Chromosome 10:112,317,439-112,354,384	10
SMC3	BAM11	Chromosome 10:112,317,439-112,354,384	10
CASP7		Chromosome 10:115,428,925-115,480,654	10
SEC61A2		Chromosome 10:12,211,642-12,251,966	10
SEC61A2		Chromosome 10:12,211,642-12,251,966	10
BAG3		Chromosome 10:121,400,872-121,427,321	10
BAG3		Chromosome 10:121,400,872-121,427,321	10
FGFR2	KGF/FGF receptor, CD33	Chromosome 10:122,473,377-123,347,962	10
FGFR2	KGF/FGF receptor, CD33	Chromosome 10:122,473,377-123,347,962	10
FGFR2	KGF/FGF receptor, CD33	Chromosome 10:122,473,377-123,347,962	10
FGFR2	KGF/FGF receptor, CD33	Chromosome 10:122,473,377-123,347,962	10
FGFR2	KGF/FGF receptor, CD33	Chromosome 10:122,473,377-123,347,962	10
FGFR2	KGF/FGF receptor, CD33	Chromosome 10:122,473,377-123,347,962	10
FGFR2	KGF/FGF receptor, CD33	Chromosome 10:122,473,377-123,347,962	10
FGFR2	KGF/FGF receptor, CD33	Chromosome 10:122,473,377-123,347,962	10
FGFR2	KGF/FGF receptor, CD33	Chromosome 10:122,473,377-123,347,962	10
FGFR2	KGF/FGF receptor, CD33	Chromosome 10:122,473,377-123,347,962	10
FGFR2	KGF/FGF receptor, CD33	Chromosome 10:122,473,377-123,347,962	10
FGFR2	KGF/FGF receptor, CD33	Chromosome 10:122,473,377-123,347,962	10
FGFR2	KGF/FGF receptor, CD33	Chromosome 10:122,473,377-123,347,962	10
DMBT1	gp340	Chromosome 10:124,310,171-124,393,242	10
DMBT1	gp340	Chromosome 10:124,310,171-124,393,242	10
BUB3		Chromosome 10:124,903,783-124,914,876	10
BUB3		Chromosome 10:124,903,783-124,914,876	10
MMP21		Chromosome 10:127,445,012-127,454,380	10
DHX32		Chromosome 10:127,514,896-127,575,017	10
ADAM12	metalloproteinase desine	Chromosome 10:127,690,940-128,067,055	10
ADAM12	metalloproteinase desine	Chromosome 10:127,690,940-128,067,055	10
ADAM12	metalloproteinase desine	Chromosome 10:127,690,940-128,067,055	10
ADAM12	metalloproteinase desine	Chromosome 10:127,690,940-128,067,055	10
FOXI2		Chromosome 10:129,425,504-129,429,440	10
PTPRE		Chromosome 10:129,595,315-129,774,155	10
PTPRE		Chromosome 10:129,595,315-129,774,155	10
MGMT		Chromosome 10:131,155,456-131,455,358	10
MGMT		Chromosome 10:131,155,456-131,455,358	10
MGMT		Chromosome 10:131,155,456-131,455,358	10
BNIP3		Chromosome 10:133,631,181-133,645,450	10
ADAM8	CD156a	Chromosome 10:134,925,898-134,940,362	10
CYP2E1		Chromosome 10:135,190,857-135,224,714	10
DCLRE1C		Chromosome 10:14,979,364-15,036,437	10
DCLRE1C		Chromosome 10:14,979,364-15,036,437	10
ITGA8		Chromosome 10:15,595,954-15,802,130	10
ITGA8		Chromosome 10:15,595,954-15,802,130	10
ITGA8		Chromosome 10:15,595,954-15,802,130	10
ITGA8		Chromosome 10:15,595,954-15,802,130	10
C1QL3		Chromosome 10:16,595,748-16,604,010	10
C1QL3		Chromosome 10:16,595,748-16,604,010	10
VIM	Vimentin	Chromosome 10:17,311,283-17,319,598	10
MRC1L1	Mannose receptor	Chromosome 10:17,891,368-17,993,184	10
MRC1	CD206, Mannose recepto	Chromosome 10:18,138,358-18,240,097	10
BMI-1	BMI-1	Chromosome 10:22,650,146-22,660,194	10
APBB1IP	RIAM, PEL1	Chromosome 10:26,767,138-26,896,738	10
APBB1IP	RIAM, PEL1	Chromosome 10:26,767,138-26,896,738	10

APBB1IP	RIAM, PEL1	Chromosome 10:26,767,138-26,896,738	10
MAP3K8	TPL2	Chromosome 10:30,762,872-30,790,768	10
MAP3K8	TPL2	Chromosome 10:30,762,872-30,790,768	10
TCF8		Chromosome 10:31,647,430-31,858,748	10
TCF8		Chromosome 10:31,647,430-31,858,748	10
TCF8		Chromosome 10:31,647,430-31,858,748	10
TCF8		Chromosome 10:31,647,430-31,858,748	10
TCF8		Chromosome 10:31,647,430-31,858,748	10
TCF8		Chromosome 10:31,647,430-31,858,748	10
ITGB1	CD29	Chromosome 10:33,229,326-33,287,204	10
ITGB1	CD29	Chromosome 10:33,229,326-33,287,204	10
NRP1	CD304, BDCA4, Neuropil	Chromosome 10:33,506,426-33,665,196	10
NRP1	CD304, BDCA4, Neuropil	Chromosome 10:33,506,426-33,665,196	10
CREM	ICER	Chromosome 10:35,455,807-35,541,892	10
CREM	ICER	Chromosome 10:35,455,807-35,541,892	10
CREM	ICER	Chromosome 10:35,455,807-35,541,892	10
CXCL12	SDF1	Chromosome 10:44,185,611-44,200,548	10
ALOX5	5-LO	Chromosome 10:45,189,635-45,261,571	10
ALOX5	5-LO	Chromosome 10:45,189,635-45,261,571	10
PTPN20C		Chromosome 10:48,926,216-49,033,022	10
MAPK8	JNK	Chromosome 10:49,184,739-49,317,409	10
MAPK8	JNK	Chromosome 10:49,184,739-49,317,409	10
MBL2		Chromosome 10:54,195,146-54,201,466	10
UBE2D1	UBCH5	Chromosome 10:59,764,745-59,800,515	10
UBE2D1	UBCH5	Chromosome 10:59,764,745-59,800,515	10
IL15RA		Chromosome 10:6,034,340-6,060,156	10
IL2RA		Chromosome 10:6,092,658-6,144,294	10
PRKCQ	PKCλ	Chromosome 10:6,509,111-6,662,269	10
PRKCQ	PKCλ	Chromosome 10:6,509,111-6,662,269	10
PRKCQ	PKCλ	Chromosome 10:6,509,111-6,662,269	10
ANK3		Chromosome 10:61,458,165-61,819,494	10
ANK3		Chromosome 10:61,458,165-61,819,494	10
ANK3		Chromosome 10:61,458,165-61,819,494	10
ANK3		Chromosome 10:61,458,165-61,819,494	10
ANK3		Chromosome 10:61,458,165-61,819,494	10
CDC2	CDK1	Chromosome 10:62,205,690-62,224,616	10
EGR2		Chromosome 10:64,241,762-64,246,133	10
EGR2		Chromosome 10:64,241,762-64,246,133	10
DDX50		Chromosome 10:70,331,040-70,376,609	10
PRG1	serglycin	Chromosome 10:70,517,834-70,534,573	10
PRF1	Perforin	Chromosome 10:72,027,110-72,032,521	10
PPP3CB	calcineurin	Chromosome 10:74,866,192-74,925,765	10
PPP3CB	calcineurin	Chromosome 10:74,866,192-74,925,765	10
PLAU	Plasminogen activator	Chromosome 10:75,340,896-75,347,261	10
ADK	adenosine kinase	Chromosome 10:75,580,971-76,139,067	10
ADK	adenosine kinase	Chromosome 10:75,580,971-76,139,067	10
ADK	adenosine kinase	Chromosome 10:75,580,971-76,139,067	10
ADK	adenosine kinase	Chromosome 10:75,580,971-76,139,067	10
ADK	adenosine kinase	Chromosome 10:75,580,971-76,139,067	10
ADK	adenosine kinase	Chromosome 10:75,580,971-76,139,067	10
DUSP13		Chromosome 10:76,524,196-76,538,976	10
DLG5		Chromosome 10:79,220,557-79,356,384	10
DLG5		Chromosome 10:79,220,557-79,356,384	10
GATA3		Chromosome 10:8,136,662-8,157,170	10
GATA3		Chromosome 10:8,136,662-8,157,170	10
PPIF		Chromosome 10:80,777,226-80,785,096	10

PPIF		Chromosome 10:80,777,226-80,785,096	10
SFTPD	SP-D	Chromosome 10:81,687,476-81,698,841	10
NRG3	NRG3	Chromosome 10:83,624,786-84,736,913	10
NRG3	NRG3	Chromosome 10:83,624,786-84,736,913	10
NRG3	NRG3	Chromosome 10:83,624,786-84,736,913	10
NRG3	NRG3	Chromosome 10:83,624,786-84,736,913	10
NRG3	NRG3	Chromosome 10:83,624,786-84,736,913	10
NRG3	NRG3	Chromosome 10:83,624,786-84,736,913	10
NRG3	NRG3	Chromosome 10:83,624,786-84,736,913	10
NRG3	NRG3	Chromosome 10:83,624,786-84,736,913	10
NRG3	NRG3	Chromosome 10:83,624,786-84,736,913	10
NRG3	NRG3	Chromosome 10:83,624,786-84,736,913	10
NRG3	NRG3	Chromosome 10:83,624,786-84,736,913	10
NRG3	NRG3	Chromosome 10:83,624,786-84,736,913	10
NRG3	NRG3	Chromosome 10:83,624,786-84,736,913	10
NRG3	NRG3	Chromosome 10:83,624,786-84,736,913	10
BMPR1A	CD292	Chromosome 10:88,506,376-88,674,925	10
PTEN		Chromosome 10:89,612,850-89,721,667	10
PTEN		Chromosome 10:89,612,850-89,721,667	10
TNFRSF6	FAS, CD95	Chromosome 10:90,739,206-90,765,522	10
LIPA		Chromosome 10:90,963,306-91,164,294	10
LIPA		Chromosome 10:90,963,306-91,164,294	10
LIPA		Chromosome 10:90,963,306-91,164,294	10
CYP26C1		Chromosome 10:94,811,011-94,818,444	10
CYP2C18		Chromosome 10:96,433,368-96,485,937	10
CYP2C19		Chromosome 10:96,512,371-96,603,007	10
CYP2C19		Chromosome 10:96,512,371-96,603,007	10
CYP2C9		Chromosome 10:96,688,418-96,739,137	10
CYP2C8		Chromosome 10:96,786,519-96,819,244	10
ENTPD1	CD39	Chromosome 10:97,461,526-97,619,442	10
ENTPD1	CD39	Chromosome 10:97,461,526-97,619,442	10
ENTPD1	CD39	Chromosome 10:97,461,526-97,619,442	10
BLNK		Chromosome 10:97,941,445-98,021,316	10
DNTT		Chromosome 10:98,054,075-98,088,311	10
DNTT		Chromosome 10:98,054,075-98,088,311	10
CTSD	cathepsin D	Chromosome 11:1,730,558-1,741,798	11
CTSD	cathepsin D	Chromosome 11:1,730,558-1,741,798	11
LSP1		Chromosome 11:1,830,776-1,870,069	11
ADM		Chromosome 11:10,283,172-10,285,499	11
PGR	NR3C3	Chromosome 11:100,414,313-100,506,465	11
PGR	NR3C3	Chromosome 11:100,414,313-100,506,465	11
BIRC3		Chromosome 11:101,693,404-101,713,675	11
MMP7		Chromosome 11:101,896,449-101,906,688	11
MMP20		Chromosome 11:101,952,776-102,001,273	11
MMP27		Chromosome 11:102,067,625-102,081,678	11
MMP10		Chromosome 11:102,146,444-102,156,569	11
MMP3		Chromosome 11:102,211,738-102,219,552	11
MMP13		Chromosome 11:102,318,934-102,331,672	11
MMP13		Chromosome 11:102,318,934-102,331,672	11
CASP12	Caspase 12	Chromosome 11:104,261,876-104,274,607	11
CASP4		Chromosome 11:104,318,804-104,345,373	11
CASP5		Chromosome 11:104,370,180-104,384,909	11
ICEBERG		Chromosome 11:104,513,879-104,515,663	11
ICEBERG		Chromosome 11:104,513,879-104,515,663	11
ALKBH8		Chromosome 11:106,878,664-106,941,637	11
ALKBH8		Chromosome 11:106,878,664-106,941,637	11

ATM	Ataxia teleangiectasia mu	Chromosome 11:107,598,769-107,745,036	11
ATM	Ataxia teleangiectasia mu	Chromosome 11:107,598,769-107,745,036	11
ATM	Ataxia teleangiectasia mu	Chromosome 11:107,598,769-107,745,036	11
ATM	Ataxia teleangiectasia mu	Chromosome 11:107,598,769-107,745,036	11
DDX10		Chromosome 11:108,041,014-108,316,866	11
DDX10		Chromosome 11:108,041,014-108,316,866	11
DDX10		Chromosome 11:108,041,014-108,316,866	11
RDX		Chromosome 11:109,605,376-109,672,647	11
RDX		Chromosome 11:109,605,376-109,672,647	11
POU2AF1		Chromosome 11:110,728,190-110,755,627	11
POU2AF1		Chromosome 11:110,728,190-110,755,627	11
IL18		Chromosome 11:111,519,186-111,540,050	11
IL18		Chromosome 11:111,519,186-111,540,050	11
NCAM1	CD56	Chromosome 11:112,337,368-112,653,781	11
NCAM1	CD56	Chromosome 11:112,337,368-112,653,781	11
NCAM1	CD56	Chromosome 11:112,337,368-112,653,781	11
CADM1		Chromosome 11:114,550,227-114,880,325	11
CADM1		Chromosome 11:114,550,227-114,880,325	11
CADM1		Chromosome 11:114,550,227-114,880,325	11
CADM1		Chromosome 11:114,550,227-114,880,325	11
CADM1		Chromosome 11:114,550,227-114,880,325	11
CADM1		Chromosome 11:114,550,227-114,880,325	11
IL10RA	CDw210a, IL10R1	Chromosome 11:117,362,319-117,377,404	11
IL10RA	CDw210a, IL10R1	Chromosome 11:117,362,319-117,377,404	11
CD3E	CD3	Chromosome 11:117,680,662-117,692,100	11
CD3D	CD3	Chromosome 11:117,710,475-117,718,669	11
DDX6		Chromosome 11:118,125,623-118,167,082	11
DDX6		Chromosome 11:118,125,623-118,167,082	11
BLR1	CD185, CXCR5	Chromosome 11:118,259,777-118,272,181	11
BLR1	CD185, CXCR5	Chromosome 11:118,259,777-118,272,181	11
MCAM	CD146	Chromosome 11:118,684,444-118,693,050	11
PVRL1	CD111	Chromosome 11:119,014,018-119,104,645	11
PVRL1	CD111	Chromosome 11:119,014,018-119,104,645	11
POU2F3		Chromosome 11:119,616,256-119,695,863	11
POU2F3		Chromosome 11:119,616,256-119,695,863	11
POU2F3		Chromosome 11:119,616,256-119,695,863	11
SORL1		Chromosome 11:120,828,130-121,005,621	11
SORL1		Chromosome 11:120,828,130-121,005,621	11
DDX25		Chromosome 11:125,279,550-125,298,215	11
DDX25		Chromosome 11:125,279,550-125,298,215	11
TIRAP	Mal	Chromosome 11:125,658,192-125,672,683	11
TIRAP	Mal	Chromosome 11:125,658,192-125,672,683	11
PTH		Chromosome 11:13,470,177-13,474,143	11
IGSF9B		Chromosome 11:133,290,395-133,327,321	11
IGSF9B		Chromosome 11:133,290,395-133,327,321	11
IGSF9B		Chromosome 11:133,290,395-133,327,321	11
JAM3	CD323	Chromosome 11:133,444,030-133,526,861	11
JAM3	CD323	Chromosome 11:133,444,030-133,526,861	11
B3GAT1	CD57	Chromosome 11:133,753,608-133,787,022	11
CYP2R1		Chromosome 11:14,856,131-14,870,327	11
PIK3C2A		Chromosome 11:17,067,861-17,147,864	11
PIK3C2A		Chromosome 11:17,067,861-17,147,864	11
SAA3P	Saa3	Chromosome 11:18,090,596-18,094,695	11
SAA2		Chromosome 11:18,223,365-18,226,758	11
SAA2		Chromosome 11:18,223,365-18,226,758	11
GTF2H1		Chromosome 11:18,300,719-18,345,153	11

IGSF22		Chromosome 11:18,682,435-18,704,353	11
PTPN5		Chromosome 11:18,706,051-18,769,965	11
IGF2	IGF2	Chromosome 11:2,106,918-2,125,616	11
CD81	TAPA1	Chromosome 11:2,355,096-2,375,225	11
CD81	TAPA1	Chromosome 11:2,355,096-2,375,225	11
CDKN1C		Chromosome 11:2,861,019-2,863,577	11
PRMT3	PRMT3	Chromosome 11:20,365,679-20,487,404	11
PRMT3	PRMT3	Chromosome 11:20,365,679-20,487,404	11
GAS2	GAS2	Chromosome 11:22,646,230-22,791,123	11
GAS2	GAS2	Chromosome 11:22,646,230-22,791,123	11
GAS2	GAS2	Chromosome 11:22,646,230-22,791,123	11
NLRP6	NALP6, PYPAF5, PAN3	Chromosome 11:268,570-275,304	11
NLRP6	NALP6, PYPAF5, PAN3	Chromosome 11:268,570-275,304	11
BDNF	BDNF	Chromosome 11:27,633,016-27,699,872	11
BDNF	BDNF	Chromosome 11:27,633,016-27,699,872	11
ART1	CHAT1, ADP ribosyl trans	Chromosome 11:3,622,937-3,642,222	11
CD59	protectin, MIRL	Chromosome 11:33,681,132-33,714,600	11
CD59	protectin, MIRL	Chromosome 11:33,681,132-33,714,600	11
CAT	Catalase	Chromosome 11:34,417,054-34,450,183	11
CD44		Chromosome 11:35,116,993-35,210,525	11
CD44		Chromosome 11:35,116,993-35,210,525	11
CD44		Chromosome 11:35,116,993-35,210,525	11
TRAF6		Chromosome 11:36,467,299-36,488,398	11
RAG1		Chromosome 11:36,546,139-36,557,877	11
SIGIRR		Chromosome 11:395,716-407,397	11
SIGIRR		Chromosome 11:395,716-407,397	11
MMP26		Chromosome 11:4,745,076-4,970,235	11
MMP26		Chromosome 11:4,745,076-4,970,235	11
MMP26		Chromosome 11:4,745,076-4,970,235	11
MMP26		Chromosome 11:4,745,076-4,970,235	11
API5		Chromosome 11:43,290,109-43,322,655	11
ALKBH3		Chromosome 11:43,858,971-43,898,392	11
CD82	CD82, KAI1	Chromosome 11:44,543,717-44,597,915	11
CD82	CD82, KAI1	Chromosome 11:44,543,717-44,597,915	11
MAPK8IP1		Chromosome 11:45,863,778-45,884,592	11
MAPK8IP1		Chromosome 11:45,863,778-45,884,592	11
F2	Alpha-Thrombin, prothrom	Chromosome 11:46,697,331-46,717,631	11
F2	Alpha-Thrombin, prothrom	Chromosome 11:46,697,331-46,717,631	11
NR1H3	NR1H3	Chromosome 11:47,227,083-47,246,972	11
NR1H3	NR1H3	Chromosome 11:47,227,083-47,246,972	11
NDUFS3	NADH dehydrogenase	Chromosome 11:47,543,464-47,562,690	11
NDUFS3	NADH dehydrogenase	Chromosome 11:47,543,464-47,562,690	11
C1QTNF4		Chromosome 11:47,567,792-47,580,516	11
PTPRJ	CD148	Chromosome 11:47,958,689-48,146,246	11
PTPRJ	CD148	Chromosome 11:47,958,689-48,146,246	11
HBD	Hbb-b1	Chromosome 11:5,203,270-5,212,454	11
HBD	Hbb-b1	Chromosome 11:5,203,270-5,212,454	11
TRIM22		Chromosome 11:5,667,495-5,688,669	11
TRIM22		Chromosome 11:5,667,495-5,688,669	11
TRIM22		Chromosome 11:5,667,495-5,688,669	11
AGTRL1	apelin receptor	Chromosome 11:56,757,630-56,761,489	11
P2RX3	P2X3	Chromosome 11:56,862,525-56,894,125	11
PRG2		Chromosome 11:56,910,832-56,914,706	11
UBE2L6	Ubch8	Chromosome 11:57,075,705-57,092,333	11
SERPING1		Chromosome 11:57,121,603-57,138,902	11
SERPING1		Chromosome 11:57,121,603-57,138,902	11

MS4A3		Chromosome 11:59,580,677-59,595,164	11
MS4A5		Chromosome 11:59,953,638-59,971,841	11
ILK	Integrin linked kinase	Chromosome 11:6,581,540-6,588,677	11
ILK	Integrin linked kinase	Chromosome 11:6,581,540-6,588,677	11
ILK	Integrin linked kinase	Chromosome 11:6,581,540-6,588,677	11
GPR44	CRTH2	Chromosome 11:60,374,983-60,380,020	11
CD5	Leu1	Chromosome 11:60,626,543-60,651,900	11
SYT7	SytVII	Chromosome 11:61,039,361-61,104,874	11
SYT7	SytVII	Chromosome 11:61,039,361-61,104,874	11
FEN1	ok	Chromosome 11:61,316,726-61,321,286	11
NXF1	TAP	Chromosome 11:62,316,219-62,329,529	11
SLC3A2	CD98	Chromosome 11:62,380,094-62,412,929	11
LGALS12	galectin12	Chromosome 11:63,030,132-63,040,815	11
VEGFB		Chromosome 11:63,758,646-63,762,835	11
FKBP2	Calcineurin	Chromosome 11:63,764,989-63,768,262	11
ESRRA	NR3B1	Chromosome 11:63,829,616-63,840,786	11
RASGRP2	CalDAG-GEFI	Chromosome 11:64,250,959-64,269,504	11
GPHA2	GPHA2	Chromosome 11:64,458,519-64,459,936	11
GPHA2	GPHA2	Chromosome 11:64,458,519-64,459,936	11
POLA2		Chromosome 11:64,786,006-64,821,664	11
LTBP3		Chromosome 11:65,062,850-65,082,275	11
LTBP3		Chromosome 11:65,062,850-65,082,275	11
RELA	p65	Chromosome 11:65,177,649-65,186,959	11
CFL1	cofilin	Chromosome 11:65,378,858-65,383,462	11
CFL1	cofilin	Chromosome 11:65,378,858-65,383,462	11
CD164L1	CD248, endosialin, TEM1	Chromosome 11:65,838,534-65,841,091	11
PELI3	Pellino3	Chromosome 11:65,990,974-66,001,382	11
ACTN3	alpha actinin 3	Chromosome 11:66,070,967-66,087,373	11
CTSF	Cathepsin F	Chromosome 11:66,087,511-66,092,623	11
RHOD	RHOD	Chromosome 11:66,580,897-66,596,060	11
RHOD	RHOD	Chromosome 11:66,580,897-66,596,060	11
CLCF1	cardiotrophin-like cytokine	Chromosome 11:66,888,215-66,897,782	11
CLCF1	cardiotrophin-like cytokine	Chromosome 11:66,888,215-66,897,782	11
AIP		Chromosome 11:67,007,097-67,015,150	11
GSTP1		Chromosome 11:67,107,862-67,110,701	11
UNC93B1		Chromosome 11:67,515,151-67,528,169	11
TCIRG1	V-ATPase	Chromosome 11:67,563,059-67,574,942	11
LRP5		Chromosome 11:67,836,674-67,973,317	11
LRP5		Chromosome 11:67,836,674-67,973,317	11
LRP5		Chromosome 11:67,836,674-67,973,317	11
LRP5		Chromosome 11:67,836,674-67,973,317	11
LRP5		Chromosome 11:67,836,674-67,973,317	11
CCND1	cyclinD1	Chromosome 11:69,165,054-69,178,423	11
FGF4	FGF4	Chromosome 11:69,296,978-69,299,352	11
FADD	MC159	Chromosome 11:69,726,917-69,731,144	11
NLRP14	NALP14, LRR, NOD5, GC	Chromosome 11:7,016,373-7,049,333	11
NLRP14	NALP14, LRR, NOD5, GC	Chromosome 11:7,016,373-7,049,333	11
NLRP10	NALP10, PYNOD, PAN5,	Chromosome 11:7,937,547-7,941,780	11
NLRP10	NALP10, PYNOD, PAN5,	Chromosome 11:7,937,547-7,941,780	11
DFB108B		Chromosome 11:71,221,894-71,226,256	11
IL18BP		Chromosome 11:71,387,587-71,394,409	11
P2RY2	P2Y2	Chromosome 11:72,606,992-72,625,045	11
P2RY2	P2Y2	Chromosome 11:72,606,992-72,625,045	11
P2RY2	P2Y2	Chromosome 11:72,606,992-72,625,045	11
TNFRSF19L		Chromosome 11:72,765,053-72,786,167	11
PLEKHB1		Chromosome 11:73,023,592-73,051,512	11

POLD3		Chromosome 11:73,981,277-74,031,413	11
ARRB1	Beta arrestin 1	Chromosome 11:74,654,130-74,740,521	11
ARRB1	Beta arrestin 1	Chromosome 11:74,654,130-74,740,521	11
UVRAG		Chromosome 11:75,203,923-75,531,342	11
UVRAG		Chromosome 11:75,203,923-75,531,342	11
UVRAG		Chromosome 11:75,203,923-75,531,342	11
UVRAG		Chromosome 11:75,203,923-75,531,342	11
PRKRIR	PKR	Chromosome 11:75,738,652-75,769,528	11
PRKRIR	PKR	Chromosome 11:75,738,652-75,769,528	11
PAK1	PAK	Chromosome 11:76,710,708-76,862,581	11
PAK1	PAK	Chromosome 11:76,710,708-76,862,581	11
GAB2		Chromosome 11:77,603,990-77,806,414	11
GAB2		Chromosome 11:77,603,990-77,806,414	11
GAB2		Chromosome 11:77,603,990-77,806,414	11
CD151		Chromosome 11:822,952-828,835	11
FZD4	CD344, FZ4	Chromosome 11:86,334,369-86,344,081	11
FZD4	CD344, FZ4	Chromosome 11:86,334,369-86,344,081	11
TYR		Chromosome 11:88,550,268-88,668,474	11
TYR		Chromosome 11:88,550,268-88,668,474	11
TYR		Chromosome 11:88,550,268-88,668,474	11
NOX4		Chromosome 11:88,699,160-88,864,301	11
MRE11A		Chromosome 11:93,790,114-93,866,688	11
MRE11A		Chromosome 11:93,790,114-93,866,688	11
CLEC12A	MICL	Chromosome 12:10,015,281-10,029,461	12
CLEC12A	MICL	Chromosome 12:10,015,281-10,029,461	12
CLEC1A		Chromosome 12:10,113,421-10,142,872	12
OLR1	SCARE1, LOX1, LDL rec	Chromosome 12:10,202,167-10,216,004	12
OLR1	SCARE1, LOX1, LDL rec	Chromosome 12:10,202,167-10,216,004	12
KLRD1	CD94/NKG2A	Chromosome 12:10,351,684-10,359,983	12
KLRC3		Chromosome 12:10,456,181-10,464,461	12
KLRA1	Ly49	Chromosome 12:10,633,039-10,643,431	12
CSDA		Chromosome 12:10,742,955-10,767,171	12
IGF1	IGF1	Chromosome 12:101,313,806-101,398,471	12
IGF1	IGF1	Chromosome 12:101,313,806-101,398,471	12
ASCL1	MASH1	Chromosome 12:101,875,594-101,878,421	12
ASCL1	MASH1	Chromosome 12:101,875,594-101,878,421	12
FEEL-2	FEEL-2	Chromosome 12:102,505,181-102,684,635	12
FEEL-2	FEEL-2	Chromosome 12:102,505,181-102,684,635	12
FEEL-2	FEEL-2	Chromosome 12:102,505,181-102,684,635	12
FEEL-2	FEEL-2	Chromosome 12:102,505,181-102,684,635	12
FEEL-2	FEEL-2	Chromosome 12:102,505,181-102,684,635	12
HSP90B1	gp96 phox	Chromosome 12:102,848,290-102,865,833	12
NFYB		Chromosome 12:103,034,988-103,056,170	12
NFYB		Chromosome 12:103,034,988-103,056,170	12
TXNRD1	TrxR alpha	Chromosome 12:103,204,857-103,268,192	12
RFX4	RFX4	Chromosome 12:105,501,163-105,680,711	12
RFX4	RFX4	Chromosome 12:105,501,163-105,680,711	12
RFX4	RFX4	Chromosome 12:105,501,163-105,680,711	12
CMKLR1	ChemR23	Chromosome 12:107,208,800-107,257,218	12
SELPLG	CD162, PSGL1, CLA, 6-s	Chromosome 12:107,539,800-107,551,799	12
ALKBH2		Chromosome 12:108,010,379-108,015,660	12
ALKBH2		Chromosome 12:108,010,379-108,015,660	12
FOXN4		Chromosome 12:108,200,167-108,231,408	12
FOXN4		Chromosome 12:108,200,167-108,231,408	12
RAD9B		Chromosome 12:109,424,388-109,454,274	12
RAD9B		Chromosome 12:109,424,388-109,454,274	12

ETV6		Chromosome 12:11,694,055-11,939,603	12
ETV6		Chromosome 12:11,694,055-11,939,603	12
ETV6		Chromosome 12:11,694,055-11,939,603	12
ETV6		Chromosome 12:11,694,055-11,939,603	12
PTPN11	SHP2	Chromosome 12:111,340,919-111,432,100	12
PTPN11	SHP2	Chromosome 12:111,340,919-111,432,100	12
OAS1		Chromosome 12:111,829,122-111,854,374	12
DTX1	DELTEX	Chromosome 12:111,980,045-112,020,216	12
DTX1	DELTEX	Chromosome 12:111,980,045-112,020,216	12
HRK	harakiri	Chromosome 12:115,783,410-115,803,615	12
HRK	harakiri	Chromosome 12:115,783,410-115,803,615	12
NOS1	NO synthase	Chromosome 12:116,135,362-116,283,965	12
NOS1	NO synthase	Chromosome 12:116,135,362-116,283,965	12
NOS1	NO synthase	Chromosome 12:116,135,362-116,283,965	12
HSP B8		Chromosome 12:118,100,978-118,116,934	12
HSP B8		Chromosome 12:118,100,978-118,116,934	12
OASL		Chromosome 12:119,942,478-119,961,164	12
OASL		Chromosome 12:119,942,478-119,961,164	12
BCL2L14		Chromosome 12:12,115,145-12,255,214	12
BCL2L14		Chromosome 12:12,115,145-12,255,214	12
LRP6		Chromosome 12:12,164,953-12,311,013	12
DUSP16		Chromosome 12:12,520,098-12,606,584	12
DUSP16		Chromosome 12:12,520,098-12,606,584	12
DUSP16		Chromosome 12:12,520,098-12,606,584	12
DDX47		Chromosome 12:12,770,130-12,874,182	12
P2RX7	P2X7, P2Z	Chromosome 12:120,055,061-120,108,259	12
P2RX7	P2X7, P2Z	Chromosome 12:120,055,061-120,108,259	12
IL31		Chromosome 12:121,222,530-121,224,699	12
CLIP1	RSN	Chromosome 12:121,321,934-121,473,069	12
CLIP1	RSN	Chromosome 12:121,321,934-121,473,069	12
GPR109B	HM74	Chromosome 12:121,765,256-121,767,297	12
DDX55		Chromosome 12:122,652,625-122,671,435	12
GTF2H3	TFIIH, TFIIK	Chromosome 12:122,684,333-122,711,573	12
NCOR2	SMRT	Chromosome 12:123,374,914-123,568,793	12
NCOR2	SMRT	Chromosome 12:123,374,914-123,568,793	12
NCOR2	SMRT	Chromosome 12:123,374,914-123,568,793	12
NCOR2	SMRT	Chromosome 12:123,374,914-123,568,793	12
NCOR2	SMRT	Chromosome 12:123,374,914-123,568,793	12
SCARB1	SR-BI	Chromosome 12:123,828,129-123,914,346	12
SCARB1		Chromosome 12:123,828,129-123,914,346	12
DHX37		Chromosome 12:123,997,325-124,039,620	12
NLRP9P	NOD25	Chromosome 12:128,063,805-128,067,640	12
FZD10	CD350	Chromosome 12:129,212,957-129,216,238	12
FZD10	CD350	Chromosome 12:129,212,957-129,216,238	12
RAN		Chromosome 12:129,922,521-129,927,316	12
P2RX2	P2X2	Chromosome 12:131,705,476-131,709,045	12
ART4	CD297	Chromosome 12:14,873,512-14,887,680	12
ART4	CD297	Chromosome 12:14,873,512-14,887,680	12
ARHGDIB	Rho GD2	Chromosome 12:14,986,217-15,005,870	12
ARHGDIB	Rho GD2	Chromosome 12:14,986,217-15,005,870	12
PTPRO	PTPROt	Chromosome 12:15,366,754-15,641,602	12
PTPRO	PTPROt	Chromosome 12:15,366,754-15,641,602	12
PTPRO	PTPROt	Chromosome 12:15,366,754-15,641,602	12
PTPRO	PTPROt	Chromosome 12:15,366,754-15,641,602	12
PIK3C2G		Chromosome 12:18,305,741-18,692,617	12
PIK3C2G		Chromosome 12:18,305,741-18,692,617	12

PIK3C2G		Chromosome 12:18,305,741-18,692,617	12
PIK3C2G		Chromosome 12:18,305,741-18,692,617	12
PIK3C2G		Chromosome 12:18,305,741-18,692,617	12
FKBP4	Calcineurin	Chromosome 12:2,774,414-2,783,385	12
FKBP4	Calcineurin	Chromosome 12:2,774,414-2,783,385	12
KRAS		Chromosome 12:25,249,447-25,295,121	12
KRAS		Chromosome 12:25,249,447-25,295,121	12
ITPR2		Chromosome 12:26,377,193-26,877,398	12
ITPR2		Chromosome 12:26,377,193-26,877,398	12
ITPR2		Chromosome 12:26,377,193-26,877,398	12
ITPR2		Chromosome 12:26,377,193-26,877,398	12
ITPR2		Chromosome 12:26,377,193-26,877,398	12
ITPR2		Chromosome 12:26,377,193-26,877,398	12
ITPR2		Chromosome 12:26,377,193-26,877,398	12
ITPR2		Chromosome 12:26,377,193-26,877,398	12
PTHLH	PTHrP	Chromosome 12:28,002,284-28,016,183	12
PTHLH	PTHrP	Chromosome 12:28,002,284-28,016,183	12
PTHLH	PTHrP	Chromosome 12:28,002,284-28,016,183	12
ERGIC2		Chromosome 12:29,381,556-29,425,410	12
ERGIC2		Chromosome 12:29,381,556-29,425,410	12
PRMT8	PRMT8	Chromosome 12:3,470,686-3,573,400	12
PRMT8	PRMT8	Chromosome 12:3,470,686-3,573,400	12
PRMT8	PRMT8	Chromosome 12:3,470,686-3,573,400	12
DDX11		Chromosome 12:31,118,061-31,148,992	12
DDX11		Chromosome 12:31,118,061-31,148,992	12
CCND2		Chromosome 12:4,253,199-4,284,777	12
FGF6	FGF6	Chromosome 12:4,413,569-4,425,041	12
DYRK4		Chromosome 12:4,569,505-4,593,302	12
DYRK4		Chromosome 12:4,569,505-4,593,302	12
IRAK4		Chromosome 12:42,439,047-42,468,166	12
IRAK4		Chromosome 12:42,439,047-42,468,166	12
SFRS2IP	Caspase 11	Chromosome 12:44,601,459-44,670,615	12
SFRS2IP	Caspase 11	Chromosome 12:44,601,459-44,670,615	12
HDAC7A		Chromosome 12:46,462,772-46,499,924	12
HDAC7A		Chromosome 12:46,462,772-46,499,924	12
DDX23		Chromosome 12:47,509,806-47,532,224	12
DDX23		Chromosome 12:47,509,806-47,532,224	12
WNT1		Chromosome 12:47,658,503-47,662,746	12
DHH	desert Hh	Chromosome 12:47,769,471-47,774,869	12
TUBA1A		Chromosome 12:47,864,847-47,869,153	12
C1QL4		Chromosome 12:48,012,467-48,017,238	12
MCRS1	Mcrs1	Chromosome 12:48,238,352-48,248,178	12
ATF1		Chromosome 12:49,444,128-49,500,328	12
ATF1		Chromosome 12:49,444,128-49,500,328	12
ATF1		Chromosome 12:49,444,128-49,500,328	12
VWF	vWf	Chromosome 12:5,928,301-6,104,097	12
VWF	vWf	Chromosome 12:5,928,301-6,104,097	12
VWF	vWf	Chromosome 12:5,928,301-6,104,097	12
VWF	vWf	Chromosome 12:5,928,301-6,104,097	12
VWF	vWf	Chromosome 12:5,928,301-6,104,097	12
ELA1		Chromosome 12:50,008,494-50,026,730	12
KRT6A	Keratin 6	Chromosome 12:51,167,231-51,173,289	12
KRT8	CARD2	Chromosome 12:51,577,238-51,585,127	12
KRT8	CARD2	Chromosome 12:51,577,238-51,585,127	12
ITGB7	LPAM (integrin alpha4/be	Chromosome 12:51,871,374-51,887,267	12
RARG	RARgamma, NR1B3	Chromosome 12:51,890,621-51,912,253	12

SP1		Chromosome 12:52,060,246-52,096,497	12
SP1		Chromosome 12:52,060,246-52,096,497	12
HOXC11	HOX cluster	Chromosome 12:52,653,177-52,656,470	12
NFE2	NF-E2 p45	Chromosome 12:52,972,162-52,981,058	12
NFE2	NF-E2 p45	Chromosome 12:52,972,162-52,981,058	12
ITGA5	CD49e	Chromosome 12:53,075,312-53,099,317	12
DCD	dermicidin	Chromosome 12:53,324,642-53,328,416	12
DCD	dermicidin	Chromosome 12:53,324,642-53,328,416	12
ITGA7		Chromosome 12:54,364,619-54,387,949	12
ITGA7		Chromosome 12:54,364,619-54,387,949	12
DGK alpha		Chromosome 12:54,611,213-54,634,074	12
SILV	SIL	Chromosome 12:54,634,156-54,646,765	12
IL23A		Chromosome 12:55,018,926-55,020,461	12
NACA	NAC	Chromosome 12:55,392,484-55,407,248	12
NACA	NAC	Chromosome 12:55,392,484-55,407,248	12
NAB2		Chromosome 12:55,769,157-55,775,526	12
SHMT2	serine hydroxymethyltrans	Chromosome 12:55,909,819-55,914,981	12
SHMT2	serine hydroxymethyltrans	Chromosome 12:55,909,819-55,914,981	12
INHBC	inhibin	Chromosome 12:56,114,810-56,130,876	12
INHBE	inhibin	Chromosome 12:56,135,363-56,138,058	12
CDK4		Chromosome 12:56,428,270-56,432,431	12
CTDSP2	NIF2	Chromosome 12:56,499,977-56,527,014	12
CD9	MRP1	Chromosome 12:6,179,134-6,217,688	12
TNFRSF1A	CD120a	Chromosome 12:6,308,184-6,321,522	12
TNFRSF1A	CD120a	Chromosome 12:6,308,184-6,321,522	12
LTBR	LTbetaR	Chromosome 12:6,363,595-6,370,994	12
GAPDH	GAPD	Chromosome 12:6,513,872-6,517,797	12
GAPDH	GAPD	Chromosome 12:6,513,872-6,517,797	12
CD4	OKT4, Leu3a	Chromosome 12:6,768,912-6,800,237	12
GNB3	G-protein beta	Chromosome 12:6,819,636-6,826,819	12
IRAK3	IRAK M	Chromosome 12:64,869,270-64,928,684	12
IRAK3	IRAK M	Chromosome 12:64,869,270-64,928,684	12
DYRK2		Chromosome 12:66,329,021-66,340,410	12
DYRK2		Chromosome 12:66,329,021-66,340,410	12
IFNG		Chromosome 12:66,834,816-66,839,790	12
IFNG		Chromosome 12:66,834,816-66,839,790	12
IFNG		Chromosome 12:66,834,816-66,839,790	12
IFNG	Interferon gamma	Chromosome 12:66,834,816-66,839,790	12
IL22		Chromosome 12:66,928,292-66,933,651	12
MDM2		Chromosome 12:67,488,247-67,520,481	12
MDM2		Chromosome 12:67,488,247-67,520,481	12
PTPRB		Chromosome 12:69,201,231-69,317,469	12
PTPRB		Chromosome 12:69,201,231-69,317,469	12
PTPRR		Chromosome 12:69,318,129-69,600,853	12
PTPRR		Chromosome 12:69,318,129-69,600,853	12
C1RL		Chromosome 12:7,138,291-7,153,069	12
CLEC4C	BDCA2	Chromosome 12:7,773,278-7,793,336	12
CLEC4C	BDCA2	Chromosome 12:7,773,278-7,793,336	12
PAWR	PRKC1	Chromosome 12:78,509,876-78,608,921	12
PTPRQ		Chromosome 12:79,318,597-79,598,099	12
PTPRQ		Chromosome 12:79,318,597-79,598,099	12
PTPRQ		Chromosome 12:79,318,597-79,598,099	12
FOXJ2		Chromosome 12:8,076,626-8,099,385	12
FOXJ2		Chromosome 12:8,076,626-8,099,385	12
CLEC4a	DCIR	Chromosome 12:8,167,493-8,182,470	12
CLEC4D		Chromosome 12:8,557,403-8,566,229	12

A2ML1	alpha 2 microglobulin-like	Chromosome 12:8,866,484-8,920,646	12
KITLG	Stem cell factor=SCF	Chromosome 12:87,410,697-87,498,369	12
KITLG	Stem cell factor=SCF	Chromosome 12:87,410,697-87,498,369	12
DUSP6		Chromosome 12:88,265,968-88,270,427	12
DUSP6		Chromosome 12:88,265,968-88,270,427	12
KLRG1		Chromosome 12:9,033,484-9,054,610	12
DDX12		Chromosome 12:9,460,894-9,492,092	12
DDX12		Chromosome 12:9,460,894-9,492,092	12
DDX12		Chromosome 12:9,460,894-9,492,092	12
KLRB1	CD161	Chromosome 12:9,638,415-9,651,764	12
KLRF1		Chromosome 12:9,871,344-9,888,871	12
DCN	Decorin	Chromosome 12:90,063,166-90,100,937	12
DCN	Decorin	Chromosome 12:90,063,166-90,100,937	12
BTG1		Chromosome 12:91,061,030-91,063,751	12
EEA1		Chromosome 12:91,693,257-91,847,138	12
EEA1		Chromosome 12:91,693,257-91,847,138	12
UBE2N	UBC13	Chromosome 12:92,326,219-92,360,157	12
SOCS2		Chromosome 12:92,487,729-92,494,109	12
SOCS2		Chromosome 12:92,487,729-92,494,109	12
CRADD	CED-3, RAIDD	Chromosome 12:92,595,282-92,768,663	12
CRADD	CED-3, RAIDD	Chromosome 12:92,595,282-92,768,663	12
CRADD	CED-3, RAIDD	Chromosome 12:92,595,282-92,768,663	12
CRADD	CED-3, RAIDD	Chromosome 12:92,595,282-92,768,663	12
PLXNC1	CD232, Plexin C1	Chromosome 12:93,066,630-93,223,356	12
PLXNC1	CD232, Plexin C1	Chromosome 12:93,066,630-93,223,356	12
PLXNC1	CD232, Plexin C1	Chromosome 12:93,066,630-93,223,356	12
NR2C1	NR2C1	Chromosome 12:93,939,802-93,991,487	12
LTA4H		Chromosome 12:94,918,742-94,953,496	12
LTA4H		Chromosome 12:94,918,742-94,953,496	12
TMPO	thymopoietin	Chromosome 12:97,433,527-97,468,250	12
TMPO	thymopoietin	Chromosome 12:97,433,527-97,468,250	12
APAF1	CED-4	Chromosome 12:97,563,209-97,653,342	12
APAF1	CED-4	Chromosome 12:97,563,209-97,653,342	12
APAF1	CED-4	Chromosome 12:97,563,209-97,653,342	12
NR1H4	NR1H4	Chromosome 12:99,391,810-99,481,774	12
NR1H4	NR1H4	Chromosome 12:99,391,810-99,481,774	12
NR1H4	NR1H4	Chromosome 12:99,391,810-99,481,774	12
NR1H4	NR1H4	Chromosome 12:99,391,810-99,481,774	12
ITGBL1		Chromosome 13:100,902,857-101,169,146	13
ITGBL1		Chromosome 13:100,902,857-101,169,146	13
ITGBL1		Chromosome 13:100,902,857-101,169,146	13
ITGBL1		Chromosome 13:100,902,857-101,169,146	13
FGF14	FGF14	Chromosome 13:101,169,308-101,852,156	13
FGF14	FGF14	Chromosome 13:101,169,308-101,852,156	13
FGF14	FGF14	Chromosome 13:101,169,308-101,852,156	13
FGF14	FGF14	Chromosome 13:101,169,308-101,852,156	13
FGF14	FGF14	Chromosome 13:101,169,308-101,852,156	13
FGF14	FGF14	Chromosome 13:101,169,308-101,852,156	13
FGF14	FGF14	Chromosome 13:101,169,308-101,852,156	13
ERCC5		Chromosome 13:102,295,195-102,326,346	13
LIG4		Chromosome 13:107,657,791-107,668,717	13
TNFSF13B	CD257, BAFF, BLYS	Chromosome 13:107,719,978-107,758,826	13
COL4A1		Chromosome 13:109,599,311-109,757,505	13
COL4A1		Chromosome 13:109,599,311-109,757,505	13
COL4A2		Chromosome 13:109,757,632-109,963,375	13
LAMP1	CD107a	Chromosome 13:112,999,557-113,025,746	13

IL17D		Chromosome 13:20,175,479-20,195,237	13
SAP18		Chromosome 13:20,612,650-20,621,221	13
SAP18		Chromosome 13:20,612,650-20,621,221	13
FGF9	FGF9	Chromosome 13:21,143,170-21,176,637	13
FGF9	FGF9	Chromosome 13:21,143,170-21,176,637	13
TNFRSF19		Chromosome 13:23,042,723-23,148,232	13
TNFRSF19		Chromosome 13:23,042,723-23,148,232	13
TNFRSF19		Chromosome 13:23,042,723-23,148,232	13
CDK8		Chromosome 13:25,726,276-25,877,375	13
CDK8		Chromosome 13:25,726,276-25,877,375	13
CDK8		Chromosome 13:25,726,276-25,877,375	13
WASF3	Wiskott Aldrich	Chromosome 13:26,029,840-26,161,085	13
GTF3A		Chromosome 13:26,896,681-26,907,823	13
GTF3A		Chromosome 13:26,896,681-26,907,823	13
CDX2		Chromosome 13:27,434,273-27,441,317	13
FLT3	CD135	Chromosome 13:27,475,411-27,572,729	13
FLT3	CD135	Chromosome 13:27,475,411-27,572,729	13
FLT1	CD308, VEGFR1	Chromosome 13:27,773,790-27,967,232	13
FLT1	CD308, VEGFR1	Chromosome 13:27,773,790-27,967,232	13
FLT1	CD308, VEGFR1	Chromosome 13:27,773,790-27,967,232	13
HMGB1		Chromosome 13:29,930,884-30,089,729	13
HMGB1		Chromosome 13:29,930,884-30,089,729	13
HMGB1		Chromosome 13:29,930,884-30,089,729	13
HMGB1		Chromosome 13:29,930,884-30,089,729	13
ALOX5AP		Chromosome 13:30,207,645-30,236,556	13
BRCA2		Chromosome 13:31,787,617-31,871,809	13
CCNA1		Chromosome 13:35,904,495-35,915,008	13
RFXAP		Chromosome 13:36,291,339-36,301,740	13
FOXO1A		Chromosome 13:40,027,801-40,138,734	13
FOXO1A		Chromosome 13:40,027,801-40,138,734	13
TNFSF11	CD254, TRANCE, OPGL,	Chromosome 13:42,034,872-42,080,148	13
TNFSF11	CD254, TRANCE, OPGL,	Chromosome 13:42,034,872-42,080,148	13
GTF2F2		Chromosome 13:44,592,650-44,756,237	13
GTF2F2		Chromosome 13:44,592,650-44,756,237	13
GTF2F2		Chromosome 13:44,592,650-44,756,237	13
TPT1		Chromosome 13:44,809,008-44,813,505	13
HTR2A	5-HT2A	Chromosome 13:46,305,514-46,368,179	13
HTR2A	5-HT2A	Chromosome 13:46,305,514-46,368,179	13
P2RY5		Chromosome 13:47,883,170-47,887,947	13
P2RY5		Chromosome 13:47,883,170-47,887,947	13
CYSLTR2		Chromosome 13:48,178,692-48,181,499	13
LECT1	chondromodulin 1	Chromosome 13:52,175,400-52,211,948	13
ABCC4	ABCC4, MRP4	Chromosome 13:94,470,084-94,751,688	13
ABCC4	ABCC4, MRP4	Chromosome 13:94,470,084-94,751,688	13
ABCC4	ABCC4, MRP4	Chromosome 13:94,470,084-94,751,688	13
ABCC4	ABCC4, MRP4	Chromosome 13:94,470,084-94,751,688	13
EBI2		Chromosome 13:98,744,790-98,757,708	13
EBI2		Chromosome 13:98,744,790-98,757,708	13
HSP90AA1	HSP90	Chromosome 14:101,617,139-101,675,776	14
RAGE		Chromosome 14:101,762,375-101,841,284	14
TRAF3		Chromosome 14:102,313,569-102,442,381	14
TRAF3		Chromosome 14:102,313,569-102,442,381	14
BAG5		Chromosome 14:103,092,642-103,098,907	14
XRCC3		Chromosome 14:103,233,707-103,251,549	14
SIVA		Chromosome 14:104,290,529-104,297,036	14
GPR132	G2A	Chromosome 14:104,586,782-104,602,799	14

IGHD1-20		Chromosome 14:105,428,094-105,428,110	14
IGHD1-20		Chromosome 14:105,428,094-105,428,110	14
CCNB1IP1		Chromosome 14:19,849,367-19,871,297	14
CCNB1IP1		Chromosome 14:19,849,367-19,871,297	14
RNASE6		Chromosome 14:20,319,050-20,320,464	14
RNASE7	ribonuclease	Chromosome 14:20,580,251-20,582,226	14
TRA@	TCR	Chromosome 14:21,159,897-22,090,915	14
TRA@	TCR	Chromosome 14:21,159,897-22,090,915	14
TRA@	TCR	Chromosome 14:21,159,897-22,090,915	14
TRA@	TCR	Chromosome 14:21,159,897-22,090,915	14
TRA@	TCR	Chromosome 14:21,159,897-22,090,915	14
TRA@	TCR	Chromosome 14:21,159,897-22,090,915	14
TRA@	TCR	Chromosome 14:21,159,897-22,090,915	14
TRA@	TCR	Chromosome 14:21,159,897-22,090,915	14
TRA@	TCR	Chromosome 14:21,159,897-22,090,915	14
MMP14		Chromosome 14:22,375,633-22,386,643	14
MMP14		Chromosome 14:22,375,633-22,386,643	14
PRMT5	PRMT5	Chromosome 14:22,459,573-22,468,501	14
CEBPE		Chromosome 14:22,656,355-22,658,665	14
BCL2L2		Chromosome 14:22,845,866-22,850,798	14
IL25	IL17E	Chromosome 14:22,911,858-22,915,452	14
PSME1		Chromosome 14:23,661,207-23,678,016	14
CHMP4A	CHMP4A	Chromosome 14:23,748,627-23,755,020	14
NFATC4		Chromosome 14:23,907,094-23,918,650	14
CTSG	carthepsin G	Chromosome 14:24,112,564-24,115,306	14
GZMB	Granzyme B	Chromosome 14:24,170,000-24,173,313	14
GZMB	Granzyme B	Chromosome 14:24,170,000-24,173,313	14
FOXG1C		Chromosome 14:28,304,801-28,308,621	14
FOXG1C		Chromosome 14:28,304,801-28,308,621	14
PRKD1		Chromosome 14:29,115,436-29,466,651	14
PRKD1		Chromosome 14:29,115,436-29,466,651	14
PRKD1		Chromosome 14:29,115,436-29,466,651	14
PRKD1		Chromosome 14:29,115,436-29,466,651	14
PRKD1		Chromosome 14:29,115,436-29,466,651	14
CFL2		Chromosome 14:34,249,398-34,253,649	14
CFL2		Chromosome 14:34,249,398-34,253,649	14
NFKBIA	IkB alpha	Chromosome 14:34,940,468-34,943,703	14
NFKBIA	IkB alpha	Chromosome 14:34,940,468-34,943,703	14
FOXA1		Chromosome 14:37,128,940-37,134,240	14
FOXA1		Chromosome 14:37,128,940-37,134,240	14
SSTR1	sst1 receptor	Chromosome 14:37,746,955-37,752,019	14
SSTR1	sst1 receptor	Chromosome 14:37,746,955-37,752,019	14
FKBP3	Calcineurin	Chromosome 14:44,654,859-44,674,272	14
PPIL5		Chromosome 14:49,135,165-49,151,140	14
MAP4K5		Chromosome 14:49,954,993-50,069,126	14
MAP4K5		Chromosome 14:49,954,993-50,069,126	14
TXNDC		Chromosome 14:50,776,686-50,792,512	14
PTGDR		Chromosome 14:51,804,181-51,813,192	14
PTGER2	EP2	Chromosome 14:51,850,863-51,865,074	14
PSMC6		Chromosome 14:52,243,668-52,264,466	14
BMP4	BMP4	Chromosome 14:53,486,207-53,493,362	14
BMP4	BMP4	Chromosome 14:53,486,207-53,493,362	14
CDKN3		Chromosome 14:53,933,423-53,956,682	14
SOCS4		Chromosome 14:54,563,594-54,585,960	14
PELI2	Pellino2	Chromosome 14:55,654,846-55,837,784	14
PELI2	Pellino2	Chromosome 14:55,654,846-55,837,784	14

PELI2	Pellino2	Chromosome 14:55,654,846-55,837,784	14
PELI2	Pellino2	Chromosome 14:55,654,846-55,837,784	14
PRKCH	PKCή	Chromosome 14:60,858,186-61,087,451	14
PRKCH	PKCή	Chromosome 14:60,858,186-61,087,451	14
PRKCH	PKCή	Chromosome 14:60,858,186-61,087,451	14
PRKCH	PKCή	Chromosome 14:60,858,186-61,087,451	14
GPHB5	GPHB5	Chromosome 14:62,849,395-62,854,316	14
GPHB5	GPHB5	Chromosome 14:62,849,395-62,854,316	14
ESR2	Estrogen receptor beta, N	Chromosome 14:63,621,388-63,875,070	14
ESR2	Estrogen receptor beta, N	Chromosome 14:63,621,388-63,875,070	14
ESR2	Estrogen receptor beta, N	Chromosome 14:63,621,388-63,875,070	14
GPX2		Chromosome 14:64,475,625-64,479,284	14
ACTN1	alpha actinin 1	Chromosome 14:68,410,793-68,515,747	14
ACTN1	alpha actinin 1	Chromosome 14:68,410,793-68,515,747	14
MAP3K9		Chromosome 14:70,264,605-70,345,641	14
MAP3K9		Chromosome 14:70,264,605-70,345,641	14
FOS	C-Fos	Chromosome 14:74,815,284-74,818,685	14
BTAF		Chromosome 14:75,058,537-75,083,086	14
BTAF		Chromosome 14:75,058,537-75,083,086	14
TGFB3		Chromosome 14:75,494,195-75,517,242	14
TGFB3		Chromosome 14:75,494,195-75,517,242	14
ESRRB	NR3B2	Chromosome 14:75,907,479-76,036,961	14
ESRRB	NR3B2	Chromosome 14:75,907,479-76,036,961	14
ESRRB	NR3B2	Chromosome 14:75,907,479-76,036,961	14
ALKBH1		Chromosome 14:77,208,502-77,244,109	14
ALKBH1		Chromosome 14:77,208,502-77,244,109	14
TSHR	thyroid stimulating hormo	Chromosome 14:80,491,528-80,682,399	14
TSHR	thyroid stimulating hormo	Chromosome 14:80,491,528-80,682,399	14
GTF2A1	TFIIA	Chromosome 14:80,716,147-80,757,328	14
GALC	Lactosylceramide	Chromosome 14:87,469,111-87,529,660	14
GALC	Lactosylceramide	Chromosome 14:87,469,111-87,529,660	14
PTPN21	PTPD1	Chromosome 14:88,003,867-88,090,876	14
PTPN21	PTPD1	Chromosome 14:88,003,867-88,090,876	14
CHES1	FOXN3	Chromosome 14:88,692,274-88,953,127	14
CHES1	FOXN3	Chromosome 14:88,692,274-88,953,127	14
CHES1	FOXN3	Chromosome 14:88,692,274-88,953,127	14
CHES1	FOXN3	Chromosome 14:88,692,274-88,953,127	14
GPR68	OGR1, I-2	Chromosome 14:90,768,629-90,789,977	14
GPR68	OGR1, I-2	Chromosome 14:90,768,629-90,789,977	14
LGMN	AEP	Chromosome 14:92,239,907-92,284,765	14
LGMN	AEP	Chromosome 14:92,239,907-92,284,765	14
MOAP1		Chromosome 14:92,718,294-92,721,002	14
DDX24		Chromosome 14:93,587,019-93,617,311	14
DDX24		Chromosome 14:93,587,019-93,617,311	14
SERPINA2	Serpin a3g	Chromosome 14:93,900,404-93,914,178	14
SERPINA2	Serpin a3g	Chromosome 14:93,900,404-93,914,178	14
BDKRB2	Bradykinin receptor	Chromosome 14:95,740,950-95,780,542	14
BDKRB2	Bradykinin receptor	Chromosome 14:95,740,950-95,780,542	14
CYP46A1		Chromosome 14:99,220,407-99,263,391	14
CYP46A1		Chromosome 14:99,220,407-99,263,391	14
YY1		Chromosome 14:99,774,855-99,814,557	14
YY1		Chromosome 14:99,774,855-99,814,557	14
SNRPN		Chromosome 15:22,619,887-23,215,702	15
SNRPN		Chromosome 15:22,619,887-23,215,702	15
SNRPN		Chromosome 15:22,619,887-23,215,702	15
SNRPN		Chromosome 15:22,619,887-23,215,702	15

SNRPN		Chromosome 15:22,619,887-23,215,702	15
AVEN		Chromosome 15:31,945,720-32,118,595	15
AVEN		Chromosome 15:31,945,720-32,118,595	15
AVEN		Chromosome 15:31,945,720-32,118,595	15
ACTC1	F-actin	Chromosome 15:32,869,723-32,875,181	15
ACTC1	F-actin	Chromosome 15:32,869,723-32,875,181	15
RASGRP1	rasGRP	Chromosome 15:36,567,590-36,644,224	15
THBS1	thrombospondin	Chromosome 15:37,660,572-37,676,960	15
THBS1	thrombospondin	Chromosome 15:37,660,572-37,676,960	15
PLCB2	phospholipase beta 2	Chromosome 15:38,366,448-38,387,330	15
RAD51		Chromosome 15:38,774,661-38,811,646	15
DLL4	Delta4	Chromosome 15:39,008,839-39,018,529	15
DLL4	Delta4	Chromosome 15:39,008,839-39,018,529	15
NUSAP1		Chromosome 15:39,412,361-39,460,538	15
MGA		Chromosome 15:39,739,902-39,849,433	15
MGA		Chromosome 15:39,739,902-39,849,433	15
HISPPD2A	IPS1	Chromosome 15:41,612,949-41,769,525	15
HISPPD2A	IPS1	Chromosome 15:41,612,949-41,769,525	15
PDIA3	ERp57	Chromosome 15:41,825,882-41,852,096	15
B2M	Beta-2 microglobulin	Chromosome 15:42,790,977-42,797,649	15
B2M	Beta-2 microglobulin	Chromosome 15:42,790,977-42,797,649	15
FGF7	KGF	Chromosome 15:47,502,751-47,566,815	15
FGF7	KGF	Chromosome 15:47,502,751-47,566,815	15
HDC		Chromosome 15:48,321,436-48,345,218	15
CYP19A1		Chromosome 15:49,288,961-49,418,086	15
CYP19A1		Chromosome 15:49,288,961-49,418,086	15
MAPK6		Chromosome 15:50,098,739-50,145,754	15
BCL2L10		Chromosome 15:50,189,114-50,192,264	15
TCF12	HEB/SCBP	Chromosome 15:54,998,125-55,368,008	15
TCF12	HEB/SCBP	Chromosome 15:54,998,125-55,368,008	15
TCF12	HEB/SCBP	Chromosome 15:54,998,125-55,368,008	15
TCF12	HEB/SCBP	Chromosome 15:54,998,125-55,368,008	15
TCF12	HEB/SCBP	Chromosome 15:54,998,125-55,368,008	15
ADAM10	CDw156c	Chromosome 15:56,675,802-56,829,469	15
ADAM10	CDw156c	Chromosome 15:56,675,802-56,829,469	15
CCNB2	cyclin B2	Chromosome 15:57,184,612-57,204,536	15
GTF2A2		Chromosome 15:57,718,358-57,736,991	15
FOXB1		Chromosome 15:58,084,427-58,085,434	15
FOXB1		Chromosome 15:58,084,427-58,085,434	15
ANXA2	Annexin-2	Chromosome 15:58,426,642-58,477,477	15
RORA	RORa, NR1F1	Chromosome 15:58,576,755-59,308,794	15
RORA	RORa, NR1F1	Chromosome 15:58,576,755-59,308,794	15
RORA	RORa, NR1F1	Chromosome 15:58,576,755-59,308,794	15
RORA	RORa, NR1F1	Chromosome 15:58,576,755-59,308,794	15
RORA	RORa, NR1F1	Chromosome 15:58,576,755-59,308,794	15
RORA	RORa, NR1F1	Chromosome 15:58,576,755-59,308,794	15
RORA	RORa, NR1F1	Chromosome 15:58,576,755-59,308,794	15
DAPK2		Chromosome 15:61,986,288-62,125,574	15
DAPK2		Chromosome 15:61,986,288-62,125,574	15
DAPK2		Chromosome 15:61,986,288-62,125,574	15
PPIB		Chromosome 15:62,235,067-62,242,407	15
ANKDD1A		Chromosome 15:62,995,046-63,038,086	15
ANKDD1A		Chromosome 15:62,995,046-63,038,086	15
PDCD7		Chromosome 15:63,196,770-63,213,227	15
MAP2K1	MEK1	Chromosome 15:64,466,674-64,570,936	15
MAP2K1	MEK1	Chromosome 15:64,466,674-64,570,936	15

MAP2K1	MEK1	Chromosome 15:64,466,674-64,570,936	15
SMAD3		Chromosome 15:65,145,249-65,274,587	15
SMAD3		Chromosome 15:65,145,249-65,274,587	15
MAP2K5		Chromosome 15:65,622,075-65,886,506	15
MAP2K5		Chromosome 15:65,622,075-65,886,506	15
MAP2K5		Chromosome 15:65,622,075-65,886,506	15
ITGA11		Chromosome 15:66,381,096-66,511,546	15
ITGA11		Chromosome 15:66,381,096-66,511,546	15
ITGA11		Chromosome 15:66,381,096-66,511,546	15
RPLP1	P1	Chromosome 15:67,532,177-67,534,939	15
TLE3		Chromosome 15:68,127,597-68,177,310	15
TLE3		Chromosome 15:68,127,597-68,177,310	15
NR2E3	NR2E3	Chromosome 15:69,889,948-69,897,654	15
NR2E3	NR2E3	Chromosome 15:69,889,948-69,897,654	15
HEXA	Hexasaminidase	Chromosome 15:70,364,122-70,455,868	15
NPTN	SDFR1	Chromosome 15:71,639,410-71,712,806	15
CD276	B7-H3	Chromosome 15:71,763,675-71,793,912	15
CYP11A1		Chromosome 15:72,417,157-72,447,134	15
CYP11A1		Chromosome 15:72,417,157-72,447,134	15
CYP1A1		Chromosome 15:72,798,943-72,804,930	15
CYP1A1		Chromosome 15:72,798,943-72,804,930	15
PTPN9		Chromosome 15:73,546,515-73,658,680	15
NRG4	NRG4	Chromosome 15:74,020,333-74,091,842	15
NRG4	NRG4	Chromosome 15:74,020,333-74,091,842	15
PSTPIP1		Chromosome 15:75,074,609-75,116,727	15
PSTPIP1		Chromosome 15:75,074,609-75,116,727	15
CTSH	Cathepsin H	Chromosome 15:77,001,162-77,024,475	15
CTSH	Cathepsin H	Chromosome 15:77,001,162-77,024,475	15
BCL2A1	Bfl-1, BCL2-A1, BCL2a1b	Chromosome 15:78,040,290-78,050,698	15
IL16		Chromosome 15:79,262,148-79,392,157	15
IL16		Chromosome 15:79,262,148-79,392,157	15
IL16		Chromosome 15:79,262,148-79,392,157	15
AKAP13	HA-3	Chromosome 15:83,578,821-84,093,590	15
AKAP13	HA-3	Chromosome 15:83,578,821-84,093,590	15
AKAP13	HA-3	Chromosome 15:83,578,821-84,093,590	15
AKAP13	HA-3	Chromosome 15:83,578,821-84,093,590	15
AKAP13	HA-3	Chromosome 15:83,578,821-84,093,590	15
AKAP13	HA-3	Chromosome 15:83,578,821-84,093,590	15
ISG20		Chromosome 15:86,983,039-87,000,684	15
ISG20		Chromosome 15:86,983,039-87,000,684	15
ANPEP	CD13	Chromosome 15:88,129,130-88,159,072	15
ANPEP	CD13	Chromosome 15:88,129,130-88,159,072	15
BLM	Bloom syndrome	Chromosome 15:89,061,606-89,159,688	15
BLM	Bloom syndrome	Chromosome 15:89,061,606-89,159,688	15
BLM	Bloom syndrome	Chromosome 15:89,061,606-89,159,688	15
FURIN		Chromosome 15:89,212,889-89,227,691	15
NR2F2	NR2F2	Chromosome 15:94,674,950-94,683,048	15
NR2F2	NR2F2	Chromosome 15:94,674,950-94,683,048	15
IGF1R	CD221	Chromosome 15:97,010,288-97,319,034	15
IGF1R	CD221	Chromosome 15:97,010,288-97,319,034	15
IGF1R	CD221	Chromosome 15:97,010,288-97,319,034	15
IGF1R	CD221	Chromosome 15:97,010,288-97,319,034	15
MAPK8IP3		Chromosome 16:1,696,222-1,760,319	16
NOXO1		Chromosome 16:1,968,919-1,971,441	16
CIITA	MHC2TA=CIITA, C2ta	Chromosome 16:10,867,648-10,926,341	16
CIITA	MHC2TA=CIITA, C2ta	Chromosome 16:10,867,648-10,926,341	16

SOCS1		Chromosome 16:11,255,775-11,257,540	16
SOCS1		Chromosome 16:11,255,775-11,257,540	16
LITAF	lipopolysaccharide induce	Chromosome 16:11,549,357-11,588,823	16
LITAF	lipopolysaccharide induce	Chromosome 16:11,549,357-11,588,823	16
TNFRSF17	CD269, BCMA	Chromosome 16:11,966,465-11,969,426	16
TNFRSF17	CD269, BCMA	Chromosome 16:11,966,465-11,969,426	16
MYH11		Chromosome 16:15,704,493-15,858,388	16
MYH11		Chromosome 16:15,704,493-15,858,388	16
MYH11		Chromosome 16:15,704,493-15,858,388	16
ABCC1	MRP	Chromosome 16:15,950,935-16,143,774	16
HBA2		Chromosome 16:162,875-163,708	16
TRAF7		Chromosome 16:2,145,800-2,168,131	16
IGSF6		Chromosome 16:21,559,426-21,571,473	16
IGSF6		Chromosome 16:21,559,426-21,571,473	16
PLK1	Plk1	Chromosome 16:23,597,692-23,609,189	16
PLK1	Plk1	Chromosome 16:23,597,692-23,609,189	16
PRKCB1	PKC beta	Chromosome 16:23,754,823-24,139,358	16
PRKCB1	PKC beta	Chromosome 16:23,754,823-24,139,358	16
PRKCB1	PKC beta	Chromosome 16:23,754,823-24,139,358	16
PRKCB1	PKC beta	Chromosome 16:23,754,823-24,139,358	16
PRKCB1	PKC beta	Chromosome 16:23,754,823-24,139,358	16
PRKCB1	PKC beta	Chromosome 16:23,754,823-24,139,358	16
IL4R	CD124	Chromosome 16:27,232,752-27,283,600	16
IL4R	CD124	Chromosome 16:27,232,752-27,283,600	16
GTF3C1		Chromosome 16:27,379,436-27,468,775	16
AXIN1		Chromosome 16:277,441-342,465	16
IL27		Chromosome 16:28,418,184-28,425,656	16
IL27		Chromosome 16:28,418,184-28,425,656	16
SPN	CD43	Chromosome 16:29,581,801-29,589,688	16
MVP	lung resistance protein	Chromosome 16:29,731,591-29,766,842	16
TNFRSF12A	CD266, TWEAKR	Chromosome 16:3,010,343-3,012,385	16
TNFRSF12A	CD266, TWEAKR	Chromosome 16:3,010,343-3,012,385	16
MEFV	Pyrin	Chromosome 16:3,232,029-3,246,628	16
MEFV	Pyrin	Chromosome 16:3,232,029-3,246,628	16
NLRC3	NOD3	Chromosome 16:3,531,826-3,567,290	16
NLRC3	NOD3	Chromosome 16:3,531,826-3,567,290	16
DNASE1		Chromosome 16:3,630,847-3,654,064	16
CREBBP	CBP	Chromosome 16:3,716,568-3,870,723	16
CREBBP	CBP	Chromosome 16:3,716,568-3,870,723	16
CREBBP	CBP	Chromosome 16:3,716,568-3,870,723	16
SEPHS2	SPS2	Chromosome 16:30,362,453-30,364,725	16
ITGAL	LFA1, CD11a	Chromosome 16:30,391,551-30,442,007	16
CTF1	CTF1	Chromosome 16:30,815,429-30,822,382	16
ITGAM	Mac-1, CD11B	Chromosome 16:31,178,789-31,251,714	16
ITGAM	Mac-1, CD11B	Chromosome 16:31,178,789-31,251,714	16
ITGAX	CD11c, CR4	Chromosome 16:31,274,010-31,301,819	16
HMOX2		Chromosome 16:4,466,426-4,500,349	16
ITFG1	CDA08, TIP	Chromosome 16:45,746,798-46,052,519	16
ITFG1	CDA08, TIP	Chromosome 16:45,746,798-46,052,519	16
ITFG1	CDA08, TIP	Chromosome 16:45,746,798-46,052,519	16
ABCC11	MRP8	Chromosome 16:46,758,323-46,838,806	16
ABCC11	MRP8	Chromosome 16:46,758,323-46,838,806	16
NOD2	BLAU, CARD15, CD, PS	Chromosome 16:49,288,551-49,324,488	16
NOD2	BLAU, CARD15, CD, PS	Chromosome 16:49,288,551-49,324,488	16
AKTIP	FTS	Chromosome 16:52,082,693-52,094,671	16
AKTIP	FTS	Chromosome 16:52,082,693-52,094,671	16

MMP2		Chromosome 16:54,070,589-54,098,104	16
MMP2		Chromosome 16:54,070,589-54,098,104	16
CES1	Carboxylesterase 3	Chromosome 16:54,394,264-54,424,576	16
MT3		Chromosome 16:55,180,768-55,182,501	16
MT3		Chromosome 16:55,180,768-55,182,501	16
NLRC5	NOD27	Chromosome 16:55,581,018-55,673,941	16
NLRC5	NOD27	Chromosome 16:55,581,018-55,673,941	16
NLRC5	NOD27	Chromosome 16:55,581,018-55,673,941	16
CCL22		Chromosome 16:55,950,219-55,957,602	16
CCL17		Chromosome 16:55,996,180-56,007,475	16
MMP15		Chromosome 16:56,616,783-56,638,306	16
MMP15		Chromosome 16:56,616,783-56,638,306	16
CDH5	CD144, VE-cadherin	Chromosome 16:64,958,064-64,996,190	16
CDH5	CD144, VE-cadherin	Chromosome 16:64,958,064-64,996,190	16
CKLF		Chromosome 16:65,143,967-65,170,463	16
CBFB		Chromosome 16:65,620,551-65,692,462	16
CBFB		Chromosome 16:65,620,551-65,692,462	16
TRADD		Chromosome 16:65,745,605-65,751,306	16
NOL3	MYC	Chromosome 16:65,765,371-65,767,127	16
PSMB10	proteasome subunit	Chromosome 16:66,525,908-66,528,254	16
PSMB10	proteasome subunit	Chromosome 16:66,525,908-66,528,254	16
NFATC3		Chromosome 16:66,676,845-66,818,338	16
PRMT7	PRMT7	Chromosome 16:66,902,446-66,948,663	16
MPG		Chromosome 16:67,018-75,845	16
CDH1	CD324, E-cadherin	Chromosome 16:67,328,696-67,426,945	16
NFAT5		Chromosome 16:68,156,498-68,296,054	16
NFAT5		Chromosome 16:68,156,498-68,296,054	16
DDX19B		Chromosome 16:68,890,573-68,925,232	16
DHX38		Chromosome 16:70,685,116-70,704,312	16
DHX38		Chromosome 16:70,685,116-70,704,312	16
ATBF1		Chromosome 16:71,378,456-71,639,775	16
ATBF1		Chromosome 16:71,378,456-71,639,775	16
ATBF1		Chromosome 16:71,378,456-71,639,775	16
ATBF1		Chromosome 16:71,378,456-71,639,775	16
ATBF1		Chromosome 16:71,378,456-71,639,775	16
ATBF1		Chromosome 16:71,378,456-71,639,775	16
CFDP1		Chromosome 16:73,885,109-74,024,888	16
CFDP1		Chromosome 16:73,885,109-74,024,888	16
CFDP1		Chromosome 16:73,885,109-74,024,888	16
CLEC3A		Chromosome 16:76,613,992-76,623,499	16
MAF	cMaf	Chromosome 16:78,185,732-78,192,112	16
MAF	cMaf	Chromosome 16:78,185,732-78,192,112	16
GINS2		Chromosome 16:84,268,781-84,280,089	16
IRF8	ICSBP	Chromosome 16:84,490,275-84,513,713	16
IRF8	ICSBP	Chromosome 16:84,490,275-84,513,713	16
FOXF1		Chromosome 16:85,101,659-85,105,548	16
FOXF1		Chromosome 16:85,101,659-85,105,548	16
SLC7A5		Chromosome 16:86,421,130-86,460,615	16
SLC7A5		Chromosome 16:86,421,130-86,460,615	16
IL17C		Chromosome 16:87,232,502-87,234,383	16
MC1R	MC1	Chromosome 16:88,512,527-88,529,713	16
SCARF1		Chromosome 17:1,483,902-1,495,792	17
SCARF1		Chromosome 17:1,483,902-1,495,792	17
SMG6		Chromosome 17:1,909,888-2,220,160	17
SMG6		Chromosome 17:1,909,888-2,220,160	17
SMG6		Chromosome 17:1,909,888-2,220,160	17

SMG6		Chromosome 17:1,909,888-2,220,160	17
MYH2	myosin heavy chain 2a	Chromosome 17:10,365,192-10,393,704	17
MYH2	myosin heavy chain 2a	Chromosome 17:10,365,192-10,393,704	17
MAP2K4	MKK4	Chromosome 17:11,864,860-11,987,865	17
IL6STP		Chromosome 17:15,616,046-15,629,130	17
IL6STP		Chromosome 17:15,616,046-15,629,130	17
NCOR1	NCoR	Chromosome 17:15,875,983-16,059,570	17
NCOR1	NCoR	Chromosome 17:15,875,983-16,059,570	17
TRPV2		Chromosome 17:16,259,613-16,281,042	17
TNFRSF13B	CD267, TAC1	Chromosome 17:16,783,123-16,816,127	17
SREBF1	SREBP1a,b,c	Chromosome 17:17,655,794-17,681,050	17
DRG2	DRG2	Chromosome 17:17,932,008-17,952,017	17
DRG2	DRG2	Chromosome 17:17,932,008-17,952,017	17
ALKBH5		Chromosome 17:18,028,014-18,053,993	17
FOXO3B		Chromosome 17:18,516,347-18,516,964	17
MAPK7		Chromosome 17:19,221,659-19,227,445	17
PAFAH1B1	PAF, platelet activating fa	Chromosome 17:2,443,686-2,535,638	17
PAFAH1B1	PAF, platelet activating fa	Chromosome 17:2,443,686-2,535,638	17
PAFAH1B1	PAF, platelet activating fa	Chromosome 17:2,443,686-2,535,638	17
MAP2K3		Chromosome 17:21,128,581-21,159,118	17
LGALS9	Galectin 9	Chromosome 17:22,980,951-23,000,711	17
NOS2A	NO synthase, iNOS	Chromosome 17:23,107,919-23,151,682	17
NOS2A	NO synthase, iNOS	Chromosome 17:23,107,919-23,151,682	17
VTN		Chromosome 17:23,718,425-23,721,844	17
FOXN1		Chromosome 17:23,875,086-23,889,302	17
TIAF1	TGF antiapoptotic factor	Chromosome 17:24,424,663-24,531,556	17
TIAF1	TGF antiapoptotic factor	Chromosome 17:24,424,663-24,531,556	17
TIAF1	TGF antiapoptotic factor	Chromosome 17:24,424,663-24,531,556	17
TIAF1	TGF antiapoptotic factor	Chromosome 17:24,424,663-24,531,556	17
SLC6A4	5-HTT	Chromosome 17:25,549,032-25,586,831	17
SLC6A4	5-HTT	Chromosome 17:25,549,032-25,586,831	17
CRLF3		Chromosome 17:26,133,828-26,175,826	17
CRLF3		Chromosome 17:26,133,828-26,175,826	17
CCL2	MCP1	Chromosome 17:29,606,409-29,608,335	17
CCL13	MCP4	Chromosome 17:29,707,584-29,709,742	17
CCL1		Chromosome 17:29,711,512-29,714,365	17
TRPV1	VR1	Chromosome 17:3,415,491-3,459,454	17
TRPV1	VR1	Chromosome 17:3,415,491-3,459,454	17
CTNS		Chromosome 17:3,486,522-3,511,585	17
ITGAE	HML-1, CD103	Chromosome 17:3,564,671-3,660,578	17
P2RX1	P2X1	Chromosome 17:3,746,634-3,766,709	17
MMP28		Chromosome 17:31,116,989-31,146,753	17
CCL5	RANTES	Chromosome 17:31,222,611-31,231,490	17
LOC441792	NO synthase	Chromosome 17:31,811,186-31,816,297	17
ACACA	BCL2A1-ACC1	Chromosome 17:32,516,040-32,841,015	17
ACACA	BCL2A1-ACC1	Chromosome 17:32,516,040-32,841,015	17
ACACA	BCL2A1-ACC1	Chromosome 17:32,516,040-32,841,015	17
DUSP14		Chromosome 17:32,924,064-32,947,709	17
DDX52		Chromosome 17:33,046,526-33,077,600	17
ERBB2	CD340	Chromosome 17:35,097,919-35,138,441	17
ERBB2	CD340	Chromosome 17:35,097,919-35,138,441	17
CSF3		Chromosome 17:35,425,214-35,427,592	17
THRA	NR1A1	Chromosome 17:35,472,589-35,503,646	17
NR1D1	NR1D1	Chromosome 17:35,502,567-35,510,499	17
NR1D1	NR1D1	Chromosome 17:35,502,567-35,510,499	17
RARA	NR1B1	Chromosome 17:35,718,972-35,767,420	17

TOP2A		Chromosome 17:35,798,321-35,827,695	17
CCR7	CD197	Chromosome 17:35,963,547-35,975,250	17
CCR7	CD197	Chromosome 17:35,963,547-35,975,250	17
KRT34	HA-4	Chromosome 17:36,787,447-36,792,181	17
KRT35	HA-5	Chromosome 17:36,886,467-36,891,194	17
KRT35	HA-5	Chromosome 17:36,886,467-36,891,194	17
FKBP10		Chromosome 17:37,222,727-37,232,995	17
FKBP10		Chromosome 17:37,222,727-37,232,995	17
LGP2		Chromosome 17:37,506,952-37,518,277	17
LGP2		Chromosome 17:37,506,952-37,518,277	17
STAT5B		Chromosome 17:37,604,721-37,681,950	17
STAT5B		Chromosome 17:37,604,721-37,681,950	17
STAT5B		Chromosome 17:37,604,721-37,681,950	17
CCR10		Chromosome 17:38,084,961-38,087,371	17
PSME3		Chromosome 17:38,238,949-38,249,303	17
DHX8		Chromosome 17:38,916,860-38,957,206	17
DHX8		Chromosome 17:38,916,860-38,957,206	17
DHX8		Chromosome 17:38,916,860-38,957,206	17
DUSP3		Chromosome 17:39,199,015-39,211,872	17
DUSP3		Chromosome 17:39,199,015-39,211,872	17
DUSP3		Chromosome 17:39,199,015-39,211,872	17
HDAC5		Chromosome 17:39,509,647-39,556,540	17
HDAC5		Chromosome 17:39,509,647-39,556,540	17
SLC4A1	CD233	Chromosome 17:39,682,566-39,700,993	17
ITGA2B	CD41, HPA1	Chromosome 17:39,805,076-39,822,399	17
ALOX15		Chromosome 17:4,480,963-4,491,709	17
ARRB2	Beta arrestin 2	Chromosome 17:4,560,533-4,571,544	17
PSMB6		Chromosome 17:4,646,397-4,648,756	17
MINK		Chromosome 17:4,683,351-4,742,135	17
GP1BA	HPA5a,b, CD42b	Chromosome 17:4,776,372-4,779,067	17
PFN1	Profilin	Chromosome 17:4,789,692-4,793,067	17
C1QL1		Chromosome 17:40,392,587-40,401,170	17
C1QL1		Chromosome 17:40,392,587-40,401,170	17
MAP3K14	NIK	Chromosome 17:40,696,278-40,750,148	17
MAP3K14	NIK	Chromosome 17:40,696,278-40,750,148	17
MAP3K14	NIK	Chromosome 17:40,696,278-40,750,148	17
CRF1R	CRHR1	Chromosome 17:41,217,449-41,268,973	17
CRF1R	CRHR1	Chromosome 17:41,217,449-41,268,973	17
CRF1R	CRHR1	Chromosome 17:41,217,449-41,268,973	17
WNT3		Chromosome 17:42,196,855-42,251,081	17
WNT3		Chromosome 17:42,196,855-42,251,081	17
WNT3		Chromosome 17:42,196,855-42,251,081	17
ITGB3	CD60, HPA2, Mac-2, GPI	Chromosome 17:42,686,207-42,745,076	17
ITGB3	CD60, HPA2, Mac-2, GPI	Chromosome 17:42,686,207-42,745,076	17
ITGB3	CD60, HPA2, Mac-2, GPI	Chromosome 17:42,686,207-42,745,076	17
TBX21	T-bet	Chromosome 17:43,165,609-43,178,484	17
TBX21	T-bet	Chromosome 17:43,165,609-43,178,484	17
TBX21	T-bet	Chromosome 17:43,165,609-43,178,484	17
NFE2L1		Chromosome 17:43,480,720-43,493,841	17
SKAP1	SKAP55	Chromosome 17:43,565,804-43,862,551	17
SKAP1	SKAP55	Chromosome 17:43,565,804-43,862,551	17
SKAP1	SKAP55	Chromosome 17:43,565,804-43,862,551	17
HOXB4	HOX cluster	Chromosome 17:44,007,868-44,010,742	17
NGFR	CD271	Chromosome 17:44,927,654-44,947,360	17
DLX3	Delta-like 2	Chromosome 17:45,422,368-45,427,587	17
COL1A1	collagen alpha 1	Chromosome 17:45,616,456-45,633,992	17

COL1A1	collagen alpha 1	Chromosome 17:45,616,456-45,633,992	17
NME1	NM23H1	Chromosome 17:46,585,919-46,604,103	17
C1QBP		Chromosome 17:5,276,823-5,283,195	17
DHX33		Chromosome 17:5,284,956-5,312,905	17
NLRP1	NALP1, CARD7, DEFCA	Chromosome 17:5,343,472-5,428,553	17
HLF	Hlf	Chromosome 17:50,697,370-50,755,886	17
HLF	Hlf	Chromosome 17:50,697,370-50,755,886	17
TRIM25	ZNF147	Chromosome 17:52,320,269-52,346,408	17
TRIM25	ZNF147	Chromosome 17:52,320,269-52,346,408	17
EPX	eosinophil peroxidase	Chromosome 17:53,625,088-53,636,783	17
MPO		Chromosome 17:53,702,201-53,713,295	17
MPO		Chromosome 17:53,702,201-53,713,295	17
DHX40		Chromosome 17:54,997,668-55,040,484	17
DHX40		Chromosome 17:54,997,668-55,040,484	17
MRC2	Endo180, CD280, manno	Chromosome 17:58,058,494-58,124,629	17
MRC2	Endo180, CD280, manno	Chromosome 17:58,058,494-58,124,629	17
MRC2	Endo180, CD280, manno	Chromosome 17:58,058,494-58,124,629	17
ACE	CD143	Chromosome 17:58,908,166-58,952,935	17
DDX42		Chromosome 17:59,205,299-59,250,409	17
GH1	GH1	Chromosome 17:59,348,294-59,349,930	17
PECAM1	CD31	Chromosome 17:59,754,142-59,817,723	17
DDX5		Chromosome 17:59,926,200-59,932,872	17
ALOX12		Chromosome 17:6,840,108-6,856,220	17
CLECSF10A	CD301, MGL1, CLEC10A	Chromosome 17:6,918,580-6,924,324	17
GNA13		Chromosome 17:60,437,295-60,483,216	17
GNA13		Chromosome 17:60,437,295-60,483,216	17
AXIN2		Chromosome 17:60,955,143-60,988,227	17
AXIN2		Chromosome 17:60,955,143-60,988,227	17
PRKCA	PKC alpha	Chromosome 17:61,729,388-62,237,324	17
PRKCA	PKC alpha	Chromosome 17:61,729,388-62,237,324	17
PRKCA	PKC alpha	Chromosome 17:61,729,388-62,237,324	17
PRKCA	PKC alpha	Chromosome 17:61,729,388-62,237,324	17
PRKCA	PKC alpha	Chromosome 17:61,729,388-62,237,324	17
PRKCA	PKC alpha	Chromosome 17:61,729,388-62,237,324	17
PRKCA	PKC alpha	Chromosome 17:61,729,388-62,237,324	17
MAP2K6		Chromosome 17:64,922,433-65,051,067	17
MAP2K6		Chromosome 17:64,922,433-65,051,067	17
SSTR2	sst2 receptor	Chromosome 17:68,672,755-68,679,689	17
SSTR2	sst2 receptor	Chromosome 17:68,672,755-68,679,689	17
SSTR2	sst2 receptor	Chromosome 17:68,672,755-68,679,689	17
CD300A	IGSF12, MAIR1, IRC1, IR	Chromosome 17:69,974,117-69,992,528	17
CD300A	IGSF12, MAIR1, IRC1, IR	Chromosome 17:69,974,117-69,992,528	17
GPS2		Chromosome 17:7,156,702-7,173,362	17
FGF11	FGF11	Chromosome 17:7,283,413-7,288,980	17
TNFRSF13C	CD268, BAFFR	Chromosome 17:7,392,932-7,405,649	17
TNFSF12-13		Chromosome 17:7,393,099-7,405,649	17
ALOX15B		Chromosome 17:7,883,083-7,893,177	17
CD300C	CMRF35A1-6, -H, LIR	Chromosome 17:70,048,842-70,053,877	17
ENSG00000204	MAIR2, CD300d	Chromosome 17:70,087,099-70,100,017	17
CD300LF	IREM1	Chromosome 17:70,202,047-70,220,712	17
SLC25A19	Mup1	Chromosome 17:70,780,669-70,797,109	17
SLC25A19	Mup1	Chromosome 17:70,780,669-70,797,109	17
ITGB4	CD104	Chromosome 17:71,229,111-71,265,494	17
FOXJ1		Chromosome 17:71,644,009-71,648,966	17
FOXJ1		Chromosome 17:71,644,009-71,648,966	17
SPHK1	sphingosine kinase	Chromosome 17:71,892,297-71,895,536	17

SPHK1	sphingosine kinase	Chromosome 17:71,892,297-71,895,536	17
PTDSR		Chromosome 17:72,220,514-72,234,158	17
BIRC5	SURVIVIN	Chromosome 17:73,721,872-73,733,311	17
BIRC5	SURVIVIN	Chromosome 17:73,721,872-73,733,311	17
SOCS3		Chromosome 17:73,864,454-73,867,753	17
SOCS3		Chromosome 17:73,864,454-73,867,753	17
PSCD1	Cytohesin-1	Chromosome 17:74,181,727-74,289,971	17
PSCD1	Cytohesin-1	Chromosome 17:74,181,727-74,289,971	17
TIMP2		Chromosome 17:74,360,654-74,433,067	17
EIF4A3		Chromosome 17:75,723,612-75,735,533	17
EIF4A3		Chromosome 17:75,723,612-75,735,533	17
CHMP6	CHMP6	Chromosome 17:76,580,274-76,588,528	17
AATK		Chromosome 17:76,705,160-76,754,467	17
ACTG1	F-actin	Chromosome 17:77,091,594-77,094,422	17
ARHGDIA	Rho GD1	Chromosome 17:77,418,886-77,422,527	17
CD7	gp40, gp41	Chromosome 17:77,866,035-77,868,769	17
SECTM1		Chromosome 17:77,872,189-77,884,930	17
FOXK2	ILF1	Chromosome 17:78,070,883-78,153,743	17
FOXK2	ILF1	Chromosome 17:78,070,883-78,153,743	17
PIK3R5		Chromosome 17:8,722,953-8,756,559	17
PIK3R5		Chromosome 17:8,722,953-8,756,559	17
PIK3R5		Chromosome 17:8,722,953-8,756,559	17
GNAL	G protein alpha	Chromosome 18:11,679,263-11,871,922	18
GNAL	G protein alpha	Chromosome 18:11,679,263-11,871,922	18
GNAL	G protein alpha	Chromosome 18:11,679,263-11,871,922	18
GNAL	G protein alpha	Chromosome 18:11,679,263-11,871,922	18
GNAL	G protein alpha	Chromosome 18:11,679,263-11,871,922	18
PTPN2		Chromosome 18:12,775,480-12,874,334	18
PTPN2		Chromosome 18:12,775,480-12,874,334	18
RNMT		Chromosome 18:13,716,680-13,754,554	18
RNMT		Chromosome 18:13,716,680-13,754,554	18
MC5R	melanocortin receptor 5	Chromosome 18:13,815,543-13,816,861	18
ROCK1		Chromosome 18:16,787,533-16,944,869	18
ROCK1		Chromosome 18:16,787,533-16,944,869	18
GATA6		Chromosome 18:18,003,414-18,036,225	18
LAMA3		Chromosome 18:19,523,560-19,789,028	18
LAMA3		Chromosome 18:19,523,560-19,789,028	18
LAMA3		Chromosome 18:19,523,560-19,789,028	18
HRH4		Chromosome 18:20,294,591-20,313,919	18
HRH4		Chromosome 18:20,294,591-20,313,919	18
THOC1		Chromosome 18:204,522-258,049	18
CDH2	CD325, N-cadherin	Chromosome 18:23,784,933-24,011,189	18
CDH2	CD325, N-cadherin	Chromosome 18:23,784,933-24,011,189	18
CDH2	CD325, N-cadherin	Chromosome 18:23,784,933-24,011,189	18
CDH2	CD325, N-cadherin	Chromosome 18:23,784,933-24,011,189	18
CDH2	CD325, N-cadherin	Chromosome 18:23,784,933-24,011,189	18
TGIF1		Chromosome 18:3,402,072-3,448,409	18
TGIF1		Chromosome 18:3,402,072-3,448,409	18
TGIF1		Chromosome 18:3,402,072-3,448,409	18
COLEC12	SRCL-1, SCARA4	Chromosome 18:309,356-490,685	18
COLEC12	SRCL-1, SCARA4	Chromosome 18:309,356-490,685	18
PIK3C3		Chromosome 18:37,789,197-37,915,446	18
PIK3C3		Chromosome 18:37,789,197-37,915,446	18
PIK3C3		Chromosome 18:37,789,197-37,915,446	18
SLC14A1	Kidd antigen	Chromosome 18:41,558,155-41,585,297	18
SLC14A1	Kidd antigen	Chromosome 18:41,558,155-41,585,297	18

CD33L3		Chromosome 18:41,659,543-41,678,045	18
SMAD7		Chromosome 18:44,700,221-44,731,079	18
SMAD7		Chromosome 18:44,700,221-44,731,079	18
MAPK4		Chromosome 18:46,340,482-46,512,194	18
MAPK4		Chromosome 18:46,340,482-46,512,194	18
MAPK4		Chromosome 18:46,340,482-46,512,194	18
TCF4	ITF2	Chromosome 18:51,045,967-51,406,858	18
TCF4	ITF2	Chromosome 18:51,045,967-51,406,858	18
TCF4	ITF2	Chromosome 18:51,045,967-51,406,858	18
TCF4	ITF2	Chromosome 18:51,045,967-51,406,858	18
MALT1		Chromosome 18:54,489,598-54,568,350	18
MALT1		Chromosome 18:54,489,598-54,568,350	18
RAX		Chromosome 18:55,085,251-55,091,605	18
RAX		Chromosome 18:55,085,251-55,091,605	18
LMAN1	MBL1	Chromosome 18:55,148,088-55,177,463	18
MC4R	melanocortin receptor 4	Chromosome 18:56,189,564-56,190,562	18
MC4R	melanocortin receptor 4	Chromosome 18:56,189,564-56,190,562	18
TNFRSF11A	CD265, OPG, RANK	Chromosome 18:58,143,500-58,205,872	18
TNFRSF11A	CD265, OPG, RANK	Chromosome 18:58,143,500-58,205,872	18
BCL2		Chromosome 18:58,941,559-59,137,593	18
BCL2		Chromosome 18:58,941,559-59,137,593	18
BCL2		Chromosome 18:58,941,559-59,137,593	18
SERPINB2		Chromosome 18:59,705,922-59,722,100	18
HMSD		Chromosome 18:59,767,574-59,779,093	18
LAMA1	laminin	Chromosome 18:6,931,885-7,107,813	18
LAMA1	laminin	Chromosome 18:6,931,885-7,107,813	18
LAMA1	laminin	Chromosome 18:6,931,885-7,107,813	18
TYMS	Thymidylate synthase, TS	Chromosome 18:647,619-663,492	18
DNAM1	CD226	Chromosome 18:65,681,172-65,775,140	18
DNAM1	CD226	Chromosome 18:65,681,172-65,775,140	18
DNAM1	CD226	Chromosome 18:65,681,172-65,775,140	18
SOCS6		Chromosome 18:66,107,243-66,145,329	18
SOCS6		Chromosome 18:66,107,243-66,145,329	18
PTPRM		Chromosome 18:7,557,817-8,396,854	18
PTPRM		Chromosome 18:7,557,817-8,396,854	18
PTPRM		Chromosome 18:7,557,817-8,396,854	18
PTPRM		Chromosome 18:7,557,817-8,396,854	18
PTPRM		Chromosome 18:7,557,817-8,396,854	18
PTPRM		Chromosome 18:7,557,817-8,396,854	18
PTPRM		Chromosome 18:7,557,817-8,396,854	18
PTPRM		Chromosome 18:7,557,817-8,396,854	18
PTPRM		Chromosome 18:7,557,817-8,396,854	18
YES1		Chromosome 18:711,592-802,547	18
YES1		Chromosome 18:711,592-802,547	18
MBP		Chromosome 18:72,819,777-72,973,762	18
MBP		Chromosome 18:72,819,777-72,973,762	18
NFATC1		Chromosome 18:75,256,760-75,390,311	18
NFATC1		Chromosome 18:75,256,760-75,390,311	18
RALBP1	RIP1	Chromosome 18:9,465,007-9,528,106	18
HMHA1	HA-1	Chromosome 19:1,018,174-1,037,627	19
TCF3	E12	Chromosome 19:1,560,293-1,603,328	19
TCF3	E12	Chromosome 19:1,560,293-1,603,328	19
TCF3	E12	Chromosome 19:1,560,293-1,603,328	19
P2RY11	P2Y11	Chromosome 19:10,083,197-10,087,065	19
P2RY11	P2Y11	Chromosome 19:10,083,197-10,087,065	19
ICAM4	CD242	Chromosome 19:10,258,650-10,260,198	19

TYK2		Chromosome 19:10,322,205-10,352,211	19
KEAP1		Chromosome 19:10,457,796-10,475,243	19
DNM2	Dynamin2	Chromosome 19:10,673,106-10,803,579	19
CARM1	PRMT4	Chromosome 19:10,843,253-10,894,448	19
SMARCA4	SWI/SNF	Chromosome 19:10,932,606-11,033,953	19
LDLR	LDL receptor	Chromosome 19:11,061,132-11,105,490	19
RAB3D	Rab3d	Chromosome 19:11,296,093-11,311,321	19
EPOR		Chromosome 19:11,348,883-11,356,019	19
ECSIT		Chromosome 19:11,477,744-11,500,972	19
JUNB		Chromosome 19:12,763,286-12,765,129	19
CALR	Calreticulin	Chromosome 19:12,910,423-12,916,303	19
RAD23A	CARD1	Chromosome 19:12,917,654-12,925,455	19
RFX1	RFX1	Chromosome 19:13,933,352-13,978,097	19
RFX1	RFX1	Chromosome 19:13,933,352-13,978,097	19
PRKACA	PKA alpha	Chromosome 19:14,063,500-14,089,559	19
CD97		Chromosome 19:14,353,213-14,380,535	19
PTGER1	EP1	Chromosome 19:14,444,278-14,447,174	19
EMR3	CD313	Chromosome 19:14,570,918-14,646,810	19
EMR2	CD312	Chromosome 19:14,704,205-14,750,353	19
CASP14		Chromosome 19:15,024,015-15,027,900	19
CASP14		Chromosome 19:15,024,015-15,027,900	19
NOTCH3		Chromosome 19:15,131,444-15,172,792	19
PGLYRP2	PGRP-L	Chromosome 19:15,440,463-15,451,312	19
CYP4F8		Chromosome 19:15,587,421-15,601,445	19
CYP4F3		Chromosome 19:15,612,707-15,634,634	19
CYP4F2		Chromosome 19:15,849,834-15,869,885	19
CYP4F11		Chromosome 19:15,884,181-15,906,326	19
HSH2D		Chromosome 19:16,105,838-16,130,381	19
HSH2D		Chromosome 19:16,105,838-16,130,381	19
HSH2D		Chromosome 19:16,105,838-16,130,381	19
KLF2	KLF2	Chromosome 19:16,296,648-16,299,345	19
CHERP	calcium homooestasis reg	Chromosome 19:16,489,705-16,514,248	19
NR2F6	NR2F6	Chromosome 19:17,203,694-17,217,151	19
NR2F6	NR2F6	Chromosome 19:17,203,694-17,217,151	19
BST2	CD317	Chromosome 19:17,374,755-17,377,457	19
BST2	CD317	Chromosome 19:17,374,755-17,377,457	19
B3GNT3		Chromosome 19:17,766,658-17,785,385	19
B3GNT3		Chromosome 19:17,766,658-17,785,385	19
JAK3		Chromosome 19:17,788,322-17,819,800	19
IL12RB1	CD212	Chromosome 19:18,031,371-18,058,702	19
PIK3R2		Chromosome 19:18,125,016-18,142,343	19
GDF15	CA19-9, MIC1	Chromosome 19:18,357,968-18,360,987	19
GDF15	CA19-9, MIC1	Chromosome 19:18,357,968-18,360,987	19
FKBP8	Calcineurin	Chromosome 19:18,503,568-18,515,383	19
DDX49		Chromosome 19:18,891,494-18,900,436	19
RFXANK		Chromosome 19:19,164,008-19,173,678	19
GADD45B		Chromosome 19:2,427,135-2,429,257	19
GADD45B		Chromosome 19:2,427,135-2,429,257	19
TBXAR2	thromboxane A2 receptor	Chromosome 19:3,545,504-3,557,658	19
EEF2		Chromosome 19:3,927,054-3,936,461	19
PIAS4		Chromosome 19:3,958,748-3,990,383	19
CCNE1		Chromosome 19:34,994,741-35,007,059	19
CCNE1		Chromosome 19:34,994,741-35,007,059	19
PDCD5		Chromosome 19:37,763,944-37,770,171	19
CEBPA		Chromosome 19:38,482,776-38,485,160	19
CEBPA		Chromosome 19:38,482,776-38,485,160	19

CEBPA		Chromosome 19:38,482,776-38,485,160	19
MAP2K2	MEK3	Chromosome 19:4,041,319-4,075,126	19
EBI3	IL35	Chromosome 19:4,180,495-4,188,525	19
EBI3	IL35	Chromosome 19:4,180,495-4,188,525	19
C19orf10		Chromosome 19:4,608,557-4,621,415	19
C19orf10		Chromosome 19:4,608,557-4,621,415	19
TICAM1	TRIF	Chromosome 19:4,766,944-4,782,716	19
TICAM1	TRIF	Chromosome 19:4,766,944-4,782,716	19
USF2	USF2a,b	Chromosome 19:40,451,721-40,462,558	19
USF2	USF2a,b	Chromosome 19:40,451,721-40,462,558	19
ZBTB32	ROG	Chromosome 19:40,895,670-40,899,780	19
TA-NFKBH		Chromosome 19:41,070,983-41,085,025	19
TA-NFKBH		Chromosome 19:41,070,983-41,085,025	19
TA-NFKBH		Chromosome 19:41,070,983-41,085,025	19
ALKBH6		Chromosome 19:41,191,863-41,196,981	19
MAP4K1		Chromosome 19:43,770,121-43,800,471	19
MAP4K1		Chromosome 19:43,770,121-43,800,471	19
LGALS4	galectin 4	Chromosome 19:43,984,155-43,995,422	19
NFKBIB	IkB beta	Chromosome 19:44,082,455-44,091,374	19
NFKBIB	IkB beta	Chromosome 19:44,082,455-44,091,374	19
NFKBIB	IkB beta	Chromosome 19:44,082,455-44,091,374	19
IL28B		Chromosome 19:44,426,033-44,427,609	19
IL28A		Chromosome 19:44,450,997-44,452,572	19
ZFP36	TTP	Chromosome 19:44,589,293-44,591,885	19
LGALS13	galectin13	Chromosome 19:44,785,004-44,789,954	19
LGALS14		Chromosome 19:44,886,786-44,891,928	19
CLC	galectin 10	Chromosome 19:44,913,735-44,920,508	19
MADCAM1		Chromosome 19:447,490-456,342	19
MADCAM1		Chromosome 19:447,490-456,342	19
MAP3K10		Chromosome 19:45,389,491-45,413,314	19
MAP3K10		Chromosome 19:45,389,491-45,413,314	19
MAP3K10		Chromosome 19:45,389,491-45,413,314	19
BLVRB		Chromosome 19:45,645,541-45,663,516	19
BLVRB		Chromosome 19:45,645,541-45,663,516	19
CYP2A6		Chromosome 19:46,041,284-46,226,008	19
CYP2A7		Chromosome 19:46,041,286-46,226,008	19
CYP2A7		Chromosome 19:46,041,286-46,226,008	19
CYP2S1		Chromosome 19:46,390,955-46,405,284	19
TGFB1		Chromosome 19:46,528,254-46,551,656	19
TGFB1		Chromosome 19:46,528,254-46,551,656	19
CEACAM5	CD66e	Chromosome 19:46,904,377-46,925,686	19
CEACAM5	CD66e	Chromosome 19:46,904,377-46,925,686	19
CEACAM3	CD66d	Chromosome 19:46,992,381-47,007,431	19
CEACAM3	CD66d	Chromosome 19:46,992,381-47,007,431	19
DEDD2		Chromosome 19:47,394,592-47,416,115	19
DEDD2		Chromosome 19:47,394,592-47,416,115	19
KIR2DL5B		Chromosome 19:47,577,500-47,579,250	19
CEACAM1	CD66a	Chromosome 19:47,703,298-47,724,479	19
CEACAM8	CD66b	Chromosome 19:47,776,235-47,790,890	19
CEACAM8	CD66b	Chromosome 19:47,776,235-47,790,890	19
PSG1	CD66f	Chromosome 19:48,063,198-48,075,711	19
PSG1	CD66f	Chromosome 19:48,063,198-48,075,711	19
CD177	CD177, PRV1	Chromosome 19:48,549,651-48,559,368	19
CD177	CD177, PRV1	Chromosome 19:48,549,651-48,559,368	19
XRCC1		Chromosome 19:48,739,032-48,771,998	19
XRCC1		Chromosome 19:48,739,032-48,771,998	19

PLAUR	CD87	Chromosome 19:48,842,088-48,866,539	19
IRGC	IGTP, TGTP	Chromosome 19:48,912,078-48,916,013	19
IRGC	IGTP, TGTP	Chromosome 19:48,912,078-48,916,013	19
PVR	CD155	Chromosome 19:49,839,066-49,858,690	19
PVR	CD155	Chromosome 19:49,839,066-49,858,690	19
BCL3		Chromosome 19:49,943,820-49,955,140	19
BCL3		Chromosome 19:49,943,820-49,955,140	19
PTPRS		Chromosome 19:5,157,379-5,237,399	19
PTPRS		Chromosome 19:5,157,379-5,237,399	19
FUT3	CD174	Chromosome 19:5,793,902-5,802,482	19
FUT3	CD174	Chromosome 19:5,793,902-5,802,482	19
RFX2	RFX2	Chromosome 19:5,944,175-6,061,554	19
RFX2	RFX2	Chromosome 19:5,944,175-6,061,554	19
RELB		Chromosome 19:50,196,539-50,233,292	19
ERCC2	XPD	Chromosome 19:50,546,686-50,565,669	19
ERCC2	XPD	Chromosome 19:50,546,686-50,565,669	19
ERCC1		Chromosome 19:50,604,712-50,619,017	19
GPR4		Chromosome 19:50,784,865-50,797,294	19
FOXA3		Chromosome 19:51,059,358-51,068,895	19
FOXA3		Chromosome 19:51,059,358-51,068,895	19
FOXA3		Chromosome 19:51,059,358-51,068,895	19
PGLYRP1	PGRP-Ia	Chromosome 19:51,214,255-51,218,163	19
PKD2		Chromosome 19:51,869,413-51,911,597	19
KIR2DL4		Chromosome 19:52,356,000-52.367.000	19
BBC3	PUMA	Chromosome 19:52,415,921-52,427,863	19
C5R1	CD88	Chromosome 19:52,504,971-52,517,173	19
DHX34		Chromosome 19:52,544,386-52,577,795	19
LIG1		Chromosome 19:53,310,515-53,365,372	19
CARD8	TUCAN, CARDINAL	Chromosome 19:53,403,325-53,450,955	19
EMP3	Emp3	Chromosome 19:53,520,441-53,525,623	19
SPHK2	sphingosine kinase	Chromosome 19:53,814,360-53,825,474	19
FUT1	CD173	Chromosome 19:53,943,080-53,950,459	19
FGF21	FGF21	Chromosome 19:53,950,628-53,953,395	19
FGF21	FGF21	Chromosome 19:53,950,628-53,953,395	19
BAX		Chromosome 19:54,149,929-54,156,867	19
LHB	LHB	Chromosome 19:54,211,049-54,212,159	19
CGB	CGB	Chromosome 19:54,217,939-54,244,212	19
SNRP70		Chromosome 19:54,280,277-54,303,682	19
CD37		Chromosome 19:54,530,240-54,535,675	19
CD37		Chromosome 19:54,530,240-54,535,675	19
CD37		Chromosome 19:54,530,240-54,535,675	19
FCGRT	FCRn	Chromosome 19:54,708,304-54,721,402	19
FCGRT	FCRn	Chromosome 19:54,708,304-54,721,402	19
NOSIP	NO synthase	Chromosome 19:54,750,780-54,775,626	19
IL4I1		Chromosome 19:55,084,723-55,124,598	19
NR1H2	LXRbeta	Chromosome 19:55,571,515-55,578,051	19
NR1H2	LXRbeta	Chromosome 19:55,571,515-55,578,051	19
SIGLEC9	CDw329	Chromosome 19:56,319,977-56,325,379	19
SIGLEC9	CDw329	Chromosome 19:56,319,977-56,325,379	19
SIGLEC10	CDw330	Chromosome 19:56,605,087-56,612,869	19
SIGLEC6	CDw327	Chromosome 19:56,714,795-56,726,922	19
SIGLEC5	CD170	Chromosome 19:56,806,996-56,831,696	19
FPR1		Chromosome 19:56,940,839-56,946,962	19
FPRL1	Annexin-1R, f-MLP	Chromosome 19:56,955,995-56,965,591	19
BIRC8		Chromosome 19:58,484,666-58,486,687	19
BIRC8		Chromosome 19:58,484,666-58,486,687	19

NLRP12	NALP12, RNO2, PYPAF7	Chromosome 19:58,988,650-59,019,409	19
NLRP12	NALP12, RNO2, PYPAF7	Chromosome 19:58,988,650-59,019,409	19
PRKCG	PKC gamma, Cgamma	Chromosome 19:59,077,279-59,102,713	19
PRKCG	PKC gamma, Cgamma	Chromosome 19:59,077,279-59,102,713	19
OSCAR		Chromosome 19:59,289,745-59,297,806	19
OSCAR		Chromosome 19:59,289,745-59,297,806	19
LILRB3	CD85a, PIRB (mouse)	Chromosome 19:59,412,549-59,418,709	19
LILRA3		Chromosome 19:59,491,666-59,496,077	19
LAIR1	CD305	Chromosome 19:59,557,047-59,568,533	19
TTYH1		Chromosome 19:59,618,417-59,639,882	19
KIR3DX1	KIR3DL0	Chromosome 19:59,738,595-59,748,862	19
LILRP2	ILT10	Chromosome 19:59,911,791-59,916,501	19
GTF2F1	TFIIF	Chromosome 19:6,235,811-6,344,184	19
ALKBH7		Chromosome 19:6,323,444-6,326,040	19
TNFSF9	4-1BBL	Chromosome 19:6,482,037-6,486,933	19
TNFSF7	CD70	Chromosome 19:6,536,850-6,542,163	19
C3	C3bBb, C3bBb3b	Chromosome 19:6,628,878-6,671,660	19
C3	C3bBb, C3bBb3b	Chromosome 19:6,628,878-6,671,660	19
VAV1		Chromosome 19:6,723,722-6,808,371	19
EMR1	CD311	Chromosome 19:6,838,577-6,891,464	19
EMR1	CD311	Chromosome 19:6,838,577-6,891,464	19
FCAR	CD89	Chromosome 19:60,077,361-60,095,055	19
NLRP2	NALP2, LRR,PYPAF2, N	Chromosome 19:60,168,465-60,204,318	19
PTPRH		Chromosome 19:60,384,428-60,412,654	19
NLRP9	NALP9, NOD6	Chromosome 19:60,911,610-60,941,580	19
NLRP9	NALP9, NOD6	Chromosome 19:60,911,610-60,941,580	19
NLRP13	NALP13, NOD14	Chromosome 19:61,099,123-61,135,489	19
CHMP2A	CHMP2A	Chromosome 19:63,754,745-63,758,298	19
INSR	CD220, Insulin receptor	Chromosome 19:7,067,049-7,245,045	19
INSR	CD220, Insulin receptor	Chromosome 19:7,067,049-7,245,045	19
INSR	CD220, Insulin receptor	Chromosome 19:7,067,049-7,245,045	19
FCER2	CD23	Chromosome 19:7,659,662-7,673,032	19
FCER2	CD23	Chromosome 19:7,659,662-7,673,032	19
CLEC4M	CD299, DC-SIGN-R, L-SI	Chromosome 19:7,734,081-7,740,491	19
MAP2K7		Chromosome 19:7,874,728-7,885,363	19
AZU1	HBP, CAP37	Chromosome 19:776,097-783,017	19
CCL25		Chromosome 19:8,023,934-8,033,547	19
MYO1F	IF	Chromosome 19:8,491,689-8,548,330	19
CFD		Chromosome 19:810,665-814,624	19
PIN1		Chromosome 19:9,806,999-9,821,358	19
COL5A3		Chromosome 19:9,931,237-9,982,147	19
PXDN		Chromosome 2:1,614,666-1,727,298	2
KLF11	TIEG	Chromosome 2:10,101,133-10,112,414	2
MAP4K4		Chromosome 2:101,680,920-101,877,584	2
IL1R2	CD121b	Chromosome 2:101,974,738-102,011,317	2
IL1R1	CD121a	Chromosome 2:102,125,678-102,162,766	2
IL1RL2		Chromosome 2:102,169,865-102,222,243	2
IL1RL1	ST2	Chromosome 2:102,294,394-102,334,929	2
IL18R1	CDw218a	Chromosome 2:102,345,529-102,381,650	2
IL18RAP	CDw218b	Chromosome 2:102,401,686-102,435,457	2
SLC9A2	NHE-2	Chromosome 2:102,602,598-102,694,241	2
SULT1C2		Chromosome 2:108,360,853-108,370,702	2
SULT1C2		Chromosome 2:108,360,853-108,370,702	2
RANBP2		Chromosome 2:108,702,369-108,767,683	2
EDAR		Chromosome 2:108,877,361-108,972,260	2
ROCK2	ROCKalpha	Chromosome 2:11,239,229-11,402,162	2

ROCK2	ROCKalpha	Chromosome 2:11,239,229-11,402,162	2
ROCK2	ROCKalpha	Chromosome 2:11,239,229-11,402,162	2
BCL2L11	Bim, BIM	Chromosome 2:111,597,781-111,641,058	2
BCL2L11	Bim, BIM	Chromosome 2:111,597,781-111,641,058	2
MERTK	Mer Receptor Tyrosine ki	Chromosome 2:112,372,662-112,503,416	2
MERTK	Mer Receptor Tyrosine ki	Chromosome 2:112,372,662-112,503,416	2
IL1A		Chromosome 2:113,247,963-113,259,442	2
IL1B		Chromosome 2:113,303,808-113,310,827	2
IL1B		Chromosome 2:113,303,808-113,310,827	2
IL1B		Chromosome 2:113,303,808-113,310,827	2
IL1F7		Chromosome 2:113,387,017-113,392,930	2
IL1F7		Chromosome 2:113,387,017-113,392,930	2
IL1F7		Chromosome 2:113,387,017-113,392,930	2
IL1F9		Chromosome 2:113,452,077-113,459,698	2
IL1RN	CD25, IL1RA	Chromosome 2:113,591,941-113,608,064	2
IL1RN	CD25, IL1RA	Chromosome 2:113,591,941-113,608,064	2
DDX18		Chromosome 2:118,288,725-118,306,425	2
MARCO	SCARA2	Chromosome 2:119,416,215-119,468,706	2
MARCO	SCARA2	Chromosome 2:119,416,215-119,468,706	2
C1QL2		Chromosome 2:119,630,289-119,632,941	2
C1QL2		Chromosome 2:119,630,289-119,632,941	2
TMEM37		Chromosome 2:119,905,950-119,911,486	2
TMEM37		Chromosome 2:119,905,950-119,911,486	2
PTPN4		Chromosome 2:120,233,677-120,451,507	2
PTPN4		Chromosome 2:120,233,677-120,451,507	2
PTPN4		Chromosome 2:120,233,677-120,451,507	2
INHBB	Inhibin B	Chromosome 2:120,819,469-120,825,444	2
INHBB	Inhibin B	Chromosome 2:120,819,469-120,825,444	2
GLI2	Gli2	Chromosome 2:121,266,327-121,466,321	2
GLI2	Gli2	Chromosome 2:121,266,327-121,466,321	2
GLI2	Gli2	Chromosome 2:121,266,327-121,466,321	2
GLI2	Gli2	Chromosome 2:121,266,327-121,466,321	2
CLASP1	clAP1	Chromosome 2:121,811,825-122,123,522	2
CLASP1	clAP1	Chromosome 2:121,811,825-122,123,522	2
CLASP1	clAP1	Chromosome 2:121,811,825-122,123,522	2
CLASP1	clAP1	Chromosome 2:121,811,825-122,123,522	2
CLASP1	clAP1	Chromosome 2:121,811,825-122,123,522	2
GYPC	CD236c, CD236d, CD236	Chromosome 2:127,130,154-127,170,716	2
GYPC	CD236c, CD236d, CD236	Chromosome 2:127,130,154-127,170,716	2
GYPC	CD236c, CD236d, CD236	Chromosome 2:127,130,154-127,170,716	2
MAP3K2		Chromosome 2:127,778,609-127,817,240	2
MAP3K2		Chromosome 2:127,778,609-127,817,240	2
PROC	activated protein C	Chromosome 2:127,892,486-127,903,288	2
PROC	activated protein C	Chromosome 2:127,892,486-127,903,288	2
PTPN18		Chromosome 2:130,830,088-130,848,614	2
PTPN18		Chromosome 2:130,830,088-130,848,614	2
MCM6		Chromosome 2:136,313,666-136,350,481	2
MCM6		Chromosome 2:136,313,666-136,350,481	2
CXCR4	CD184	Chromosome 2:136,705,639-136,709,450	2
CXCR4	CD184	Chromosome 2:136,705,639-136,709,450	2
HNMT	HMT	Chromosome 2:138,438,278-138,490,404	2
HNMT	HMT	Chromosome 2:138,438,278-138,490,404	2
DDX1		Chromosome 2:15,648,753-15,688,676	2
DDX1		Chromosome 2:15,648,753-15,688,676	2
MYCN	n-myc	Chromosome 2:15,998,134-16,004,580	2
MYCN	n-myc	Chromosome 2:15,998,134-16,004,580	2

NMI		Chromosome 2:151,835,231-151,854,620	2
NMI		Chromosome 2:151,835,231-151,854,620	2
PRPF40A	FNBP3	Chromosome 2:153,216,334-153,283,014	2
PRPF40A	FNBP3	Chromosome 2:153,216,334-153,283,014	2
NR4A2	NR4A2, NURR1	Chromosome 2:156,889,194-156,897,474	2
PSCDBP	CYTIP	Chromosome 2:157,979,377-158,008,850	2
PSCDBP	CYTIP	Chromosome 2:157,979,377-158,008,850	2
MARCH7_	Axotrophin	Chromosome 2:160,277,256-160,333,330	2
MARCH7_	Axotrophin	Chromosome 2:160,277,256-160,333,330	2
MARCH7_	Axotrophin	Chromosome 2:160,277,256-160,333,330	2
LY75	CD205, DEC-205	Chromosome 2:160,368,118-160,469,493	2
PLA2R1	phospholipase A3	Chromosome 2:160,505,506-160,627,367	2
ITGB6		Chromosome 2:160,664,438-160,765,009	2
TANK	NFKB activator	Chromosome 2:161,701,712-161,800,928	2
TANK	NFKB activator	Chromosome 2:161,701,712-161,800,928	2
DPP4	CD26	Chromosome 2:162,557,001-162,639,298	2
DPP4	CD26	Chromosome 2:162,557,001-162,639,298	2
IFIH1	MDA5, Ifit1	Chromosome 2:162,831,835-162,883,285	2
PPIG		Chromosome 2:170,149,096-170,202,500	2
PPIG		Chromosome 2:170,149,096-170,202,500	2
HAT1		Chromosome 2:172,487,204-172,556,846	2
HAT1		Chromosome 2:172,487,204-172,556,846	2
ITGA6	CD49f	Chromosome 2:173,000,616-173,079,256	2
PDK1		Chromosome 2:173,129,025-173,172,108	2
SP3	chondromodulin transcrip	Chromosome 2:174,481,504-174,538,676	2
SP3	chondromodulin transcrip	Chromosome 2:174,481,504-174,538,676	2
CIR		Chromosome 2:174,921,124-174,968,689	2
CIR		Chromosome 2:174,921,124-174,968,689	2
WIPF1	WASPIP	Chromosome 2:175,132,548-175,255,873	2
WIPF1	WASPIP	Chromosome 2:175,132,548-175,255,873	2
HOXD10	HOX cluster	Chromosome 2:176,689,738-176,692,916	2
HOXD10	HOX cluster	Chromosome 2:176,689,738-176,692,916	2
AGPS	ADAP, alkylglycerone pho	Chromosome 2:177,965,731-178,112,411	2
AGPS	ADAP, alkylglycerone pho	Chromosome 2:177,965,731-178,112,411	2
AGPS	ADAP, alkylglycerone pho	Chromosome 2:177,965,731-178,112,411	2
ITGA4	VLA4, CD49d	Chromosome 2:182,029,864-182,110,719	2
ITGA4	VLA4, CD49d	Chromosome 2:182,029,864-182,110,719	2
FRZB	sFRP3	Chromosome 2:183,406,982-183,439,743	2
DUSP19		Chromosome 2:183,651,732-183,673,616	2
DUSP19		Chromosome 2:183,651,732-183,673,616	2
ITGAV	CD51	Chromosome 2:187,163,045-187,253,873	2
ITGAV	CD51	Chromosome 2:187,163,045-187,253,873	2
ITGAV	CD51	Chromosome 2:187,163,045-187,253,873	2
COL3A1		Chromosome 2:189,547,344-189,585,717	2
COL3A1		Chromosome 2:189,547,344-189,585,717	2
COL3A1		Chromosome 2:189,547,344-189,585,717	2
SLC40A1	ferroportin	Chromosome 2:190,133,561-190,153,858	2
SLC40A1	ferroportin	Chromosome 2:190,133,561-190,153,858	2
STAT1		Chromosome 2:191,542,121-191,587,181	2
STAT1		Chromosome 2:191,542,121-191,587,181	2
STAT4		Chromosome 2:191,602,551-191,724,539	2
GTF3C3		Chromosome 2:197,336,917-197,372,670	2
GTF3C3		Chromosome 2:197,336,917-197,372,670	2
HSPD1	HSP65	Chromosome 2:198,059,553-198,073,243	2
SDC1	Syndecan, CD138	Chromosome 2:20,264,039-20,288,675	2
PPIL3		Chromosome 2:201,443,924-201,462,244	2

PPIL3		Chromosome 2:201,443,924-201,462,244	2
CASP10		Chromosome 2:201,756,100-201,802,372	2
CFLAR	cFLIP, vFLIP	Chromosome 2:201,806,396-201,854,521	2
BMPR2		Chromosome 2:202,949,916-203,140,719	2
BMPR2		Chromosome 2:202,949,916-203,140,719	2
CYP20A1		Chromosome 2:203,811,658-203,878,579	2
CYP20A1		Chromosome 2:203,811,658-203,878,579	2
CD28		Chromosome 2:204,279,443-204,310,801	2
CD28		Chromosome 2:204,279,443-204,310,801	2
CTLA4	CD152	Chromosome 2:204,440,754-204,446,928	2
CTLA4	CD152	Chromosome 2:204,440,754-204,446,928	2
CTLA4	CD152	Chromosome 2:204,440,754-204,446,928	2
KLF7		Chromosome 2:207,653,323-207,738,859	2
KLF7		Chromosome 2:207,653,323-207,738,859	2
KLF7		Chromosome 2:207,653,323-207,738,859	2
CREB1		Chromosome 2:208,102,931-208,171,818	2
CPS1		Chromosome 2:211,050,678-211,252,076	2
CPS1		Chromosome 2:211,050,678-211,252,076	2
CPS1		Chromosome 2:211,050,678-211,252,076	2
CPS1		Chromosome 2:211,050,678-211,252,076	2
FN1	fibronectin	Chromosome 2:215,933,409-216,009,041	2
FN1	fibronectin	Chromosome 2:215,933,409-216,009,041	2
XRCC5		Chromosome 2:216,680,435-216,779,248	2
XRCC5		Chromosome 2:216,680,435-216,779,248	2
XRCC5		Chromosome 2:216,680,435-216,779,248	2
SMARCAL1		Chromosome 2:216,985,441-217,056,021	2
SMARCAL1		Chromosome 2:216,985,441-217,056,021	2
SMARCAL1		Chromosome 2:216,985,441-217,056,021	2
IGFBP2		Chromosome 2:217,206,372-217,237,404	2
IGFBP2		Chromosome 2:217,206,372-217,237,404	2
IL8RB	CD128b, CXCR2	Chromosome 2:218,698,991-218,710,220	2
SCL11A1	NRAMP1	Chromosome 2:218,955,161-218,968,994	2
SCL11A1	NRAMP1	Chromosome 2:218,955,161-218,968,994	2
CYP27A1		Chromosome 2:219,354,745-219,388,259	2
CYP27A1		Chromosome 2:219,354,745-219,388,259	2
CYP27A1		Chromosome 2:219,354,745-219,388,259	2
IHH	indian Hh	Chromosome 2:219,628,173-219,633,433	2
IHH	indian Hh	Chromosome 2:219,628,173-219,633,433	2
IHH	indian Hh	Chromosome 2:219,628,173-219,633,433	2
TUBA1		Chromosome 2:219,822,677-219,826,882	2
INHA	Inhibin A	Chromosome 2:220,145,161-220,148,679	2
COL4A4		Chromosome 2:227,578,168-227,737,519	2
COL4A4		Chromosome 2:227,578,168-227,737,519	2
COL4A3		Chromosome 2:227,737,525-227,887,751	2
HRB	HIV binding protein	Chromosome 2:228,045,286-228,130,548	2
CCL20		Chromosome 2:228,386,814-228,390,494	2
CCL20		Chromosome 2:228,386,814-228,390,494	2
SP110		Chromosome 2:230,741,896-230,792,932	2
SP110		Chromosome 2:230,741,896-230,792,932	2
SP110		Chromosome 2:230,741,896-230,792,932	2
HTR2B	5-HT2B	Chromosome 2:231,681,199-231,698,068	2
HTR2B	5-HT2B	Chromosome 2:231,681,199-231,698,068	2
INPP5D	SHIP1	Chromosome 2:233,633,433-233,781,288	2
INPP5D	SHIP1	Chromosome 2:233,633,433-233,781,288	2
UGT1A1	UGT1	Chromosome 2:234,191,030-234,346,695	2
UGT1A1	UGT1	Chromosome 2:234,191,030-234,346,695	2

UGT1A1	UGT1	Chromosome 2:234,191,030-234,346,695	2
UGT1A1	UGT1	Chromosome 2:234,191,030-234,346,695	2
CXCR7	CMKOR1	Chromosome 2:237,143,182-237,155,730	2
CXCR7	CMKOR1	Chromosome 2:237,143,182-237,155,730	2
COL6A3		Chromosome 2:237,897,401-237,987,559	2
COL6A3		Chromosome 2:237,897,401-237,987,559	2
TRAF3IP1		Chromosome 2:238,893,821-238,972,536	2
TRAF3IP1		Chromosome 2:238,893,821-238,972,536	2
TRAF3IP1		Chromosome 2:238,893,821-238,972,536	2
ASB1		Chromosome 2:239,000,365-239,025,630	2
ASB1		Chromosome 2:239,000,365-239,025,630	2
HDAC4		Chromosome 2:239,635,319-239,987,580	2
HDAC4		Chromosome 2:239,635,319-239,987,580	2
HDAC4		Chromosome 2:239,635,319-239,987,580	2
HDAC4		Chromosome 2:239,635,319-239,987,580	2
FKBP1B	Calcineurin	Chromosome 2:24,126,075-24,140,055	2
FKBP1B	Calcineurin	Chromosome 2:24,126,075-24,140,055	2
DUSP28		Chromosome 2:241,148,144-241,152,104	2
DUSP28		Chromosome 2:241,148,144-241,152,104	2
SEPT2		Chromosome 2:241,903,396-241,942,115	2
SEPT2		Chromosome 2:241,903,396-241,942,115	2
BOK		Chromosome 2:242,146,865-242,162,226	2
PDCD1	CD279, PD1	Chromosome 2:242,440,711-242,449,731	2
POMC	POMC	Chromosome 2:25,237,226-25,245,063	2
POMC	POMC	Chromosome 2:25,237,226-25,245,063	2
UCN	urocortin	Chromosome 2:27,383,769-27,384,634	2
ALK	CD246	Chromosome 2:29,269,144-29,997,936	2
ALK	CD246	Chromosome 2:29,269,144-29,997,936	2
ALK	CD246	Chromosome 2:29,269,144-29,997,936	2
ALK	CD246	Chromosome 2:29,269,144-29,997,936	2
ALK	CD246	Chromosome 2:29,269,144-29,997,936	2
ALK	CD246	Chromosome 2:29,269,144-29,997,936	2
XDH	Xanthine oxidoreductase	Chromosome 2:31,410,691-31,491,117	2
XDH	Xanthine oxidoreductase	Chromosome 2:31,410,691-31,491,117	2
XDH	Xanthine oxidoreductase	Chromosome 2:31,410,691-31,491,117	2
XDH	Xanthine oxidoreductase	Chromosome 2:31,410,691-31,491,117	2
NLRC4	CARD12, IPAF, CLAN	Chromosome 2:32,303,022-32,344,427	2
NLRC4	CARD12, IPAF, CLAN	Chromosome 2:32,303,022-32,344,427	2
BIRC6		Chromosome 2:32,435,234-32,697,470	2
BIRC6		Chromosome 2:32,435,234-32,697,470	2
LTBP1		Chromosome 2:33,025,896-33,478,080	2
LTBP1		Chromosome 2:33,025,896-33,478,080	2
LTBP1		Chromosome 2:33,025,896-33,478,080	2
LTBP1		Chromosome 2:33,025,896-33,478,080	2
LTBP1		Chromosome 2:33,025,896-33,478,080	2
LTBP1		Chromosome 2:33,025,896-33,478,080	2
LTBP1		Chromosome 2:33,025,896-33,478,080	2
LTBP1		Chromosome 2:33,025,896-33,478,080	2
LTBP1		Chromosome 2:33,025,896-33,478,080	2
RASGRP3		Chromosome 2:33,514,920-33,643,162	2
PKD3		Chromosome 2:37,331,149-37,398,541	2
PKD3		Chromosome 2:37,331,149-37,398,541	2
PKD3		Chromosome 2:37,331,149-37,398,541	2
CYP1B1	Cytochromes	Chromosome 2:38,148,154-38,156,796	2
CYP1B1	Cytochromes	Chromosome 2:38,148,154-38,156,796	2
DHX57		Chromosome 2:38,878,375-38,956,525	2

DHX57		Chromosome 2:38,878,375-38,956,525	2
DHX57		Chromosome 2:38,878,375-38,956,525	2
SOS1		Chromosome 2:39,066,469-39,201,067	2
SOS1		Chromosome 2:39,066,469-39,201,067	2
MAP4K3		Chromosome 2:39,329,911-39,517,946	2
MAP4K3		Chromosome 2:39,329,911-39,517,946	2
MAP4K3		Chromosome 2:39,329,911-39,517,946	2
PLEKHH2	MAX1	Chromosome 2:43,717,916-43,848,630	2
PRKCD	PKC epsilon	Chromosome 2:45,732,547-46,268,633	2
PRKCD	PKC epsilon	Chromosome 2:45,732,547-46,268,633	2
PRKCD	PKC epsilon	Chromosome 2:45,732,547-46,268,633	2
PRKCD	PKC epsilon	Chromosome 2:45,732,547-46,268,633	2
PRKCD	PKC epsilon	Chromosome 2:45,732,547-46,268,633	2
PIGF		Chromosome 2:46,661,580-46,697,708	2
PIGF		Chromosome 2:46,661,580-46,697,708	2
SOCS5		Chromosome 2:46,779,595-46,843,431	2
FOXN2		Chromosome 2:48,395,374-48,459,938	2
FOXN2		Chromosome 2:48,395,374-48,459,938	2
LHCGR	LH-R	Chromosome 2:48,767,471-48,836,321	2
FSHR	follitropin receptor	Chromosome 2:49,043,156-49,235,134	2
FSHR	follitropin receptor	Chromosome 2:49,043,156-49,235,134	2
FSHR	follitropin receptor	Chromosome 2:49,043,156-49,235,134	2
FSHR	follitropin receptor	Chromosome 2:49,043,156-49,235,134	2
VRK2		Chromosome 2:58,127,224-58,240,510	2
VRK2		Chromosome 2:58,127,224-58,240,510	2
RSAD2	CIG5	Chromosome 2:6,935,247-6,955,821	2
RSAD2	CIG5	Chromosome 2:6,935,247-6,955,821	2
RSAD2	CIG5	Chromosome 2:6,935,247-6,955,821	2
REL	cREL	Chromosome 2:60,962,254-61,003,682	2
PELI1	Pellino1	Chromosome 2:64,173,499-64,225,062	2
PELI1	Pellino1	Chromosome 2:64,173,499-64,225,062	2
PPP3R1		Chromosome 2:68,203,572-68,341,866	2
PPP3R1		Chromosome 2:68,203,572-68,341,866	2
PPP3R1		Chromosome 2:68,203,572-68,341,866	2
MXD1	MAD	Chromosome 2:69,995,707-70,023,581	2
MXD1	MAD	Chromosome 2:69,995,707-70,023,581	2
MXD1	MAD	Chromosome 2:69,995,707-70,023,581	2
TGFA	TGF alpha	Chromosome 2:70,527,924-70,634,438	2
TGFA	TGF alpha	Chromosome 2:70,527,924-70,634,438	2
TGFA	TGF alpha	Chromosome 2:70,527,924-70,634,438	2
CD207	CD207, langerin	Chromosome 2:70,910,855-70,916,461	2
CYP26B1		Chromosome 2:72,209,875-72,228,471	2
DUSP11		Chromosome 2:73,842,837-73,860,756	2
DQX1		Chromosome 2:74,598,766-74,606,826	2
DQX1		Chromosome 2:74,598,766-74,606,826	2
DOK1		Chromosome 2:74,634,795-74,638,181	2
SFTPB	SP-B	Chromosome 2:85,737,951-85,748,823	2
SFTPB	SP-B	Chromosome 2:85,737,951-85,748,823	2
ST3GAL5	Lactosylceramide	Chromosome 2:85,919,782-85,969,648	2
ST3GAL5	Lactosylceramide	Chromosome 2:85,919,782-85,969,648	2
JMJD1A	H3K9me	Chromosome 2:86,521,954-86,573,350	2
JMJD1A	H3K9me	Chromosome 2:86,521,954-86,573,350	2
JMJD1A	H3K9me	Chromosome 2:86,521,954-86,573,350	2
CD8A		Chromosome 2:86,865,239-86,871,638	2
CD8B1	CD8B1	Chromosome 2:86,895,971-86,942,549	2
IGKV1-12		Chromosome 2:89,120,836-89,121,310	2

IGKV1-12		Chromosome 2:89,120,836-89,121,310	2
ITGB1BP1		Chromosome 2:9,463,264-9,481,127	2
YWHAQ		Chromosome 2:9,641,552-9,688,629	2
DUSP2	PAC-1	Chromosome 2:96,172,638-96,174,906	2
NCAPH	BRRN1	Chromosome 2:96,365,211-96,405,001	2
ZAP70		Chromosome 2:97,696,461-97,722,755	2
ZAP70		Chromosome 2:97,696,461-97,722,755	2
LYG2	lysozyme like	Chromosome 2:99,225,141-99,238,002	2
LYG2	lysozyme like	Chromosome 2:99,225,141-99,238,002	2
PSMF1		Chromosome 20:1,041,939-1,097,022	20
PSMF1		Chromosome 20:1,041,939-1,097,022	20
FKBP1A	Calcineurin	Chromosome 20:1,297,622-1,321,806	20
SIRPB2	CD172g	Chromosome 20:1,399,386-1,420,233	20
SIRPB1	CD172b	Chromosome 20:1,491,568-1,548,655	20
SIRPB1	CD172b	Chromosome 20:1,491,568-1,548,655	20
SIRPA	SIRPalpha1	Chromosome 20:1,822,813-1,868,543	20
SIRPA	SIRPalpha1	Chromosome 20:1,822,813-1,868,543	20
JAG1	CD339, Jagged-1	Chromosome 20:10,566,334-10,602,636	20
JAG1	CD339, Jagged-1	Chromosome 20:10,566,334-10,602,636	20
DFB128		Chromosome 20:116,527-118,264	20
DFB129		Chromosome 20:155,899-158,527	20
TGM3		Chromosome 20:2,224,647-2,269,725	20
TGM3		Chromosome 20:2,224,647-2,269,725	20
PTPRA		Chromosome 20:2,769,366-2,967,320	20
PTPRA		Chromosome 20:2,769,366-2,967,320	20
PTPRA		Chromosome 20:2,769,366-2,967,320	20
FOXA2		Chromosome 20:22,509,643-22,514,102	20
THBD	CD141, thrombomodulin	Chromosome 20:22,974,270-22,978,301	20
THBD	CD141, thrombomodulin	Chromosome 20:22,974,270-22,978,301	20
C1QR	CD93	Chromosome 20:23,007,995-23,014,977	20
CST1	SN	Chromosome 20:23,676,190-23,679,574	20
CST1	SN	Chromosome 20:23,676,190-23,679,574	20
DFB115		Chromosome 20:29,309,128-29,311,096	20
DFB122		Chromosome 20:29,466,712-29,480,644	20
HM13	H13	Chromosome 20:29,565,892-29,621,031	20
BCL2L1	BCL-XL, Bcl-x (L)	Chromosome 20:29,715,916-29,774,366	20
DUSP15		Chromosome 20:29,899,102-29,922,211	20
PDRG1	p53	Chromosome 20:29,996,419-30,003,556	20
SIGLEC1	CD169	Chromosome 20:3,615,617-3,635,775	20
SIGLEC1	CD169	Chromosome 20:3,615,617-3,635,775	20
SIGLEC1	CD169	Chromosome 20:3,615,617-3,635,775	20
CDC25B		Chromosome 20:3,724,386-3,734,762	20
HCK		Chromosome 20:30,103,715-30,153,320	20
HCK		Chromosome 20:30,103,715-30,153,320	20
CBFA2T2		Chromosome 20:31,541,589-31,701,503	20
CBFA2T2		Chromosome 20:31,541,589-31,701,503	20
CBFA2T2		Chromosome 20:31,541,589-31,701,503	20
CHMP4B	CHMP4B	Chromosome 20:31,862,780-31,905,831	20
ITCH		Chromosome 20:32,414,702-32,562,859	20
ITCH		Chromosome 20:32,414,702-32,562,859	20
PROCR	EPCR, CD201	Chromosome 20:33,212,131-33,228,828	20
PROCR	EPCR, CD201	Chromosome 20:33,212,131-33,228,828	20
PROCR	EPCR, CD201	Chromosome 20:33,212,131-33,228,828	20
MMP24		Chromosome 20:33,278,095-33,328,218	20
SAMHD1	Mg11	Chromosome 20:34,953,761-35,013,590	20
SRC		Chromosome 20:35,406,502-35,467,239	20

SRC		Chromosome 20:35,406,502-35,467,239	20
BPI		Chromosome 20:36,365,991-36,399,321	20
LBP		Chromosome 20:36,408,299-36,439,067	20
PPP1R16B		Chromosome 20:36,867,762-36,985,081	20
PPP1R16B		Chromosome 20:36,867,762-36,985,081	20
DHX35		Chromosome 20:37,024,409-37,101,778	20
PLCG1		Chromosome 20:39,199,291-39,237,775	20
PRNP	CD230	Chromosome 20:4,614,996-4,630,236	20
PRNP	CD230	Chromosome 20:4,614,996-4,630,236	20
PTPRT		Chromosome 20:40,134,806-41,252,024	20
PTPRT		Chromosome 20:40,134,806-41,252,024	20
PTPRT		Chromosome 20:40,134,806-41,252,024	20
PTPRT		Chromosome 20:40,134,806-41,252,024	20
PTPRT		Chromosome 20:40,134,806-41,252,024	20
PTPRT		Chromosome 20:40,134,806-41,252,024	20
PTPRT		Chromosome 20:40,134,806-41,252,024	20
PTPRT		Chromosome 20:40,134,806-41,252,024	20
PTPRT		Chromosome 20:40,134,806-41,252,024	20
PTPRT		Chromosome 20:40,134,806-41,252,024	20
PTPRT		Chromosome 20:40,134,806-41,252,024	20
PTPRT		Chromosome 20:40,134,806-41,252,024	20
PPIAL		Chromosome 20:41,292,801-41,293,515	20
HNF4A	HNF4 alpha 1,2,3,4, NR2	Chromosome 20:42,417,855-42,493,444	20
HNF4A	HNF4 alpha 1,2,3,4, NR2	Chromosome 20:42,417,855-42,493,444	20
ADA	adenosine deaminase	Chromosome 20:42,681,577-42,713,797	20
ADA	adenosine deaminase	Chromosome 20:42,681,577-42,713,797	20
STK4	MST1/STK4	Chromosome 20:43,028,529-43,142,014	20
STK4	MST1/STK4	Chromosome 20:43,028,529-43,142,014	20
STK4	MST1/STK4	Chromosome 20:43,028,529-43,142,014	20
WFDC12		Chromosome 20:43,185,480-43,186,520	20
SEMG1		Chromosome 20:43,269,052-43,271,827	20
SDC4	Syndecan	Chromosome 20:43,387,342-43,410,478	20
SDC4	Syndecan	Chromosome 20:43,387,342-43,410,478	20
ACOT8		Chromosome 20:43,903,768-43,919,442	20
CTSA	Cathepsin A	Chromosome 20:43,952,190-43,960,866	20
MMP9		Chromosome 20:44,070,954-44,078,607	20
MMP9		Chromosome 20:44,070,954-44,078,607	20
TNFRSF5	CD40, 41	Chromosome 20:44,180,313-44,366,257	20
TNFRSF5	CD40, 41	Chromosome 20:44,180,313-44,366,257	20
TNFRSF5	CD40, 41	Chromosome 20:44,180,313-44,366,257	20
PTGIS		Chromosome 20:47,553,818-47,618,114	20
PTGIS		Chromosome 20:47,553,818-47,618,114	20
PTGIS		Chromosome 20:47,553,818-47,618,114	20
SLC9A8	NHE-8	Chromosome 20:47,862,657-47,942,179	20
SLC9A8	NHE-8	Chromosome 20:47,862,657-47,942,179	20
UBE2V1	UEV1A	Chromosome 20:48,131,068-48,203,678	20
UBE2V1	UEV1A	Chromosome 20:48,131,068-48,203,678	20
PTPN1		Chromosome 20:48,560,294-48,634,706	20
PTPN1		Chromosome 20:48,560,294-48,634,706	20
PTPN1		Chromosome 20:48,560,294-48,634,706	20
NFATC2		Chromosome 20:49,441,083-49,592,665	20
NFATC2		Chromosome 20:49,441,083-49,592,665	20
NFATC2		Chromosome 20:49,441,083-49,592,665	20
MC3R	melanocortin receptor 3	Chromosome 20:54,257,195-54,258,278	20
MC3R	melanocortin receptor 3	Chromosome 20:54,257,195-54,258,278	20
TFAP2C		Chromosome 20:54,637,765-54,647,746	20

BMP7	BMP7	Chromosome 20:55,177,211-55,275,091	20
BMP7	BMP7	Chromosome 20:55,177,211-55,275,091	20
BMP7	BMP7	Chromosome 20:55,177,211-55,275,091	20
RAE1		Chromosome 20:55,359,535-55,387,618	20
CTSZ	Cathepsin Z	Chromosome 20:56,990,597-57,015,697	20
CTSZ	Cathepsin Z	Chromosome 20:56,990,597-57,015,697	20
EDN3	endothelin 3	Chromosome 20:57,308,877-57,334,442	20
EDN3	endothelin 3	Chromosome 20:57,308,877-57,334,442	20
BMP2	BMP2	Chromosome 20:6,696,311-6,708,927	20
BMP2	BMP2	Chromosome 20:6,696,311-6,708,927	20
HRH3		Chromosome 20:60,223,421-60,228,718	20
LAMA5		Chromosome 20:60,317,510-60,375,763	20
GATA5		Chromosome 20:60,471,948-60,484,421	20
DIDO1	DATF1, Dio1	Chromosome 20:60,979,535-61,039,743	20
BIRC7	LIVIN	Chromosome 20:61,337,680-61,342,299	20
EEF1A2	EF-1 alpha	Chromosome 20:61,589,810-61,600,949	20
TNFRSF6B	DcR3	Chromosome 20:61,759,607-61,800,495	20
TNFRSF6B	DcR3	Chromosome 20:61,759,607-61,800,495	20
OPRL1	ORL1	Chromosome 20:62,181,932-62,215,047	20
BAGE4		Chromosome 21:10,042,713-10,120,798	21
BAGE4		Chromosome 21:10,042,713-10,120,798	21
BTG3		Chromosome 21:17,887,842-17,907,136	21
BTG3		Chromosome 21:17,887,842-17,907,136	21
JAM2	CD322	Chromosome 21:25,933,460-26,009,106	21
JAM2	CD322	Chromosome 21:25,933,460-26,009,106	21
GRIK1		Chromosome 21:29,831,125-30,234,153	21
GRIK1		Chromosome 21:29,831,125-30,234,153	21
GRIK1		Chromosome 21:29,831,125-30,234,153	21
GRIK1		Chromosome 21:29,831,125-30,234,153	21
GRIK1		Chromosome 21:29,831,125-30,234,153	21
GRIK1		Chromosome 21:29,831,125-30,234,153	21
SOD1	Superoxide dismutase, IP	Chromosome 21:31,953,806-31,963,115	21
SOD1	Superoxide dismutase, IP	Chromosome 21:31,953,806-31,963,115	21
OLIG2	RACK17	Chromosome 21:33,320,023-33,323,374	21
IFNAR2		Chromosome 21:33,524,076-33,559,839	21
IFNAR2		Chromosome 21:33,524,076-33,559,839	21
IFNAR1		Chromosome 21:33,619,079-33,654,038	21
IFNGR2		Chromosome 21:33,697,072-33,731,698	21
RUNX1	RUNX	Chromosome 21:35,081,968-35,343,511	21
RUNX1	RUNX	Chromosome 21:35,081,968-35,343,511	21
RUNX1	RUNX	Chromosome 21:35,081,968-35,343,511	21
RUNX1	RUNX	Chromosome 21:35,081,968-35,343,511	21
RUNX1	RUNX	Chromosome 21:35,081,968-35,343,511	21
RUNX1	RUNX	Chromosome 21:35,081,968-35,343,511	21
CHAF1B		Chromosome 21:36,679,559-36,710,995	21
CHAF1B		Chromosome 21:36,679,559-36,710,995	21
DYRK1A		Chromosome 21:37,661,729-37,809,347	21
DYRK1A		Chromosome 21:37,661,729-37,809,347	21
DYRK1A		Chromosome 21:37,661,729-37,809,347	21
ERG		Chromosome 21:38,675,671-38,955,488	21
ERG		Chromosome 21:38,675,671-38,955,488	21
ERG		Chromosome 21:38,675,671-38,955,488	21
ERG		Chromosome 21:38,675,671-38,955,488	21
IGSF5		Chromosome 21:40,039,204-40,095,893	21
IGSF5		Chromosome 21:40,039,204-40,095,893	21
DSCAM		Chromosome 21:40,306,213-41,140,909	21

DSCAM		Chromosome 21:40,306,213-41,140,909	21
DSCAM		Chromosome 21:40,306,213-41,140,909	21
DSCAM		Chromosome 21:40,306,213-41,140,909	21
DSCAM		Chromosome 21:40,306,213-41,140,909	21
DSCAM		Chromosome 21:40,306,213-41,140,909	21
DSCAM		Chromosome 21:40,306,213-41,140,909	21
DSCAM		Chromosome 21:40,306,213-41,140,909	21
DSCAM		Chromosome 21:40,306,213-41,140,909	21
DSCAM		Chromosome 21:40,306,213-41,140,909	21
MX2		Chromosome 21:41,655,820-41,702,739	21
MX2		Chromosome 21:41,655,820-41,702,739	21
MX1		Chromosome 21:41,720,024-41,753,008	21
TFF3	Tff3	Chromosome 21:42,599,751-42,608,775	21
PDXK		Chromosome 21:43,963,406-44,006,608	21
PDXK		Chromosome 21:43,963,406-44,006,608	21
PDXK		Chromosome 21:43,963,406-44,006,608	21
ICOSLG	CD275	Chromosome 21:44,467,313-44,485,262	21
AIRE		Chromosome 21:44,530,191-44,542,530	21
ITGB2	CD18, Mac-1, CR3	Chromosome 21:45,130,296-45,173,181	21
SLC19A1	RFC	Chromosome 21:45,737,914-45,786,779	21
COL6A1		Chromosome 21:46,226,091-46,249,391	21
COL6A1		Chromosome 21:46,226,091-46,249,391	21
COL6A2		Chromosome 21:46,342,470-46,377,190	21
PRMT2	PRMT2	Chromosome 21:46,879,507-46,909,291	21
IL17RA	CDw217, IL17R	Chromosome 22:15,945,849-15,971,405	22
BCL2L13		Chromosome 22:16,501,485-16,593,383	22
BID		Chromosome 22:16,591,460-16,631,812	22
BID		Chromosome 22:16,591,460-16,631,812	22
GGT2		Chromosome 22:17,141,172-17,159,474	22
DGCR2		Chromosome 22:17,403,798-17,489,962	22
DGCR2		Chromosome 22:17,403,798-17,489,962	22
GP1BB	CD42c, HPA3	Chromosome 22:18,091,066-18,092,297	22
GP1BB	CD42c, HPA3	Chromosome 22:18,091,066-18,092,297	22
SCARF2		Chromosome 22:19,108,875-19,122,146	22
CRKL	crkl	Chromosome 22:19,601,714-19,638,034	22
CRKL	crkl	Chromosome 22:19,601,714-19,638,034	22
P2RX6	P2X6	Chromosome 22:19,699,449-19,713,119	22
SDF2L1	stromal cell derived factor	Chromosome 22:20,326,542-20,328,588	22
MAPK1	p42 MAPK, Erk	Chromosome 22:20,443,946-20,551,970	22
VPREB1	CD179a	Chromosome 22:20,929,200-20,929,926	22
PRAME		Chromosome 22:21,220,123-21,231,768	22
BCR	B cell receptor	Chromosome 22:21,852,552-21,990,224	22
BCR	B cell receptor	Chromosome 22:21,852,552-21,990,224	22
IGLL1	Ig kappa light chain, CD1	Chromosome 22:22,245,312-22,252,495	22
IGLL1	Ig kappa light chain, CD1	Chromosome 22:22,245,312-22,252,495	22
MIF		Chromosome 22:22,369,647-22,567,417	22
MIF		Chromosome 22:22,369,647-22,567,417	22
GSST1		Chromosome 22:22,706,141-22,714,271	22
CABIN1		Chromosome 22:22,737,765-22,904,596	22
CABIN1		Chromosome 22:22,737,765-22,904,596	22
ADORA2	Adenosin receptor 2	Chromosome 22:23,153,537-23,168,325	22
GGT1	CD224	Chromosome 22:23,309,718-23,354,972	22
MN1		Chromosome 22:26,474,265-26,527,486	22
MN1		Chromosome 22:26,474,265-26,527,486	22
XBP1	XBP1	Chromosome 22:27,520,548-27,526,560	22
LIF		Chromosome 22:28,966,441-28,972,748	22

LIF		Chromosome 22:28,966,441-28,972,748	22
TCN2	transcobalamin 2	Chromosome 22:29,333,161-29,353,047	22
DUSP18		Chromosome 22:29,388,039-29,393,872	22
DRG1	DRG1	Chromosome 22:30,125,539-30,160,438	22
DRG1	DRG1	Chromosome 22:30,125,539-30,160,438	22
TIMP3		Chromosome 22:31,526,802-31,589,028	22
TIMP3		Chromosome 22:31,526,802-31,589,028	22
HMOX1	Heme oxygenease 1	Chromosome 22:34,107,057-34,120,194	22
APOL6		Chromosome 22:34,374,370-34,394,402	22
APOL6		Chromosome 22:34,374,370-34,394,402	22
MYH9		Chromosome 22:35,007,272-35,113,958	22
CACNG2		Chromosome 22:35,290,050-35,428,849	22
NCF3	neutrophil cytosolic factor	Chromosome 22:35,586,976-35,604,005	22
NCF3	neutrophil cytosolic factor	Chromosome 22:35,586,976-35,604,005	22
IL2RB	CD122	Chromosome 22:35,851,824-35,875,908	22
C1QTNF6		Chromosome 22:35,906,152-35,914,276	22
C1QTNF6		Chromosome 22:35,906,152-35,914,276	22
RAC2	Rac2	Chromosome 22:35,951,238-35,970,251	22
CARD10	CARD10	Chromosome 22:36,216,346-36,245,193	22
CARD10	CARD10	Chromosome 22:36,216,346-36,245,193	22
PLA2G6	Phospholipase	Chromosome 22:36,837,448-36,907,763	22
PLA2G6	Phospholipase	Chromosome 22:36,837,448-36,907,763	22
DDX17		Chromosome 22:37,209,389-37,232,262	22
DDX17		Chromosome 22:37,209,389-37,232,262	22
UNC84B		Chromosome 22:37,460,681-37,481,928	22
UNC84B		Chromosome 22:37,460,681-37,481,928	22
PDGFB		Chromosome 22:37,949,310-37,971,006	22
MAP3K7IP1	TAB1	Chromosome 22:38,125,692-38,163,078	22
ATF4		Chromosome 22:38,246,515-38,248,637	22
GRAP2	Gads	Chromosome 22:38,627,032-38,698,204	22
GRAP2	Gads	Chromosome 22:38,627,032-38,698,204	22
EP300		Chromosome 22:39,817,736-39,906,024	22
CENPM	PANE1	Chromosome 22:40,664,687-40,673,094	22
CENPM	PANE1	Chromosome 22:40,664,687-40,673,094	22
CYP2D6		Chromosome 22:40,852,445-40,856,827	22
TCF20		Chromosome 22:40,885,963-40,941,389	22
NFAM1		Chromosome 22:41,108,917-41,158,340	22
NFAM1		Chromosome 22:41,108,917-41,158,340	22
POLDIP3	S6K1	Chromosome 22:41,309,671-41,340,906	22
A4GALT	CD77, Lactosylceramide	Chromosome 22:41,418,071-41,446,820	22
BIK		Chromosome 22:41,836,701-41,855,662	22
BIK		Chromosome 22:41,836,701-41,855,662	22
PPARA	PPARalpha, NR1C1	Chromosome 22:44,925,163-45,018,317	22
DIP	DIP	Chromosome 22:45,394,963-45,454,352	22
DIP	DIP	Chromosome 22:45,394,963-45,454,352	22
CERK	ceramide kinase	Chromosome 22:45,458,971-45,512,816	22
ECGF1		Chromosome 22:49,311,047-49,315,321	22
MAPK8IP2		Chromosome 22:49,385,997-49,396,843	22
SHANK3		Chromosome 22:49,459,936-49,518,507	22
IRAK2		Chromosome 3:10,181,563-10,260,427	3
NFKBIZ		Chromosome 3:103,029,547-103,062,556	3
NFKBIZ		Chromosome 3:103,029,547-103,062,556	3
ALCAM	CD166	Chromosome 3:106,568,403-106,778,434	3
ALCAM	CD166	Chromosome 3:106,568,403-106,778,434	3
ALCAM	CD166	Chromosome 3:106,568,403-106,778,434	3
CBLB		Chromosome 3:106,859,799-107,070,577	3

CBLB		Chromosome 3:106,859,799-107,070,577	3
CBLB		Chromosome 3:106,859,799-107,070,577	3
CD47	IAP	Chromosome 3:109,244,631-109,292,625	3
CD47	IAP	Chromosome 3:109,244,631-109,292,625	3
CD47	IAP	Chromosome 3:109,244,631-109,292,625	3
HRH1		Chromosome 3:11,269,400-11,279,415	3
HRH1		Chromosome 3:11,269,400-11,279,415	3
TRAT1	TRIM	Chromosome 3:110,024,321-110,056,542	3
PVRL3	CDw113	Chromosome 3:112,273,555-112,395,063	3
PVRL3	CDw113	Chromosome 3:112,273,555-112,395,063	3
CD96		Chromosome 3:112,743,546-112,853,906	3
CD96		Chromosome 3:112,743,546-112,853,906	3
CD96		Chromosome 3:112,743,546-112,853,906	3
CD200		Chromosome 3:113,522,943-113,564,349	3
CD200		Chromosome 3:113,522,943-113,564,349	3
BTLA	CD272=BTLA	Chromosome 3:113,667,463-113,701,066	3
CD200R2		Chromosome 3:114,017,246-114,047,487	3
CD200R2		Chromosome 3:114,017,246-114,047,487	3
CD200R1		Chromosome 3:114,122,746-114,176,650	3
TIMP4		Chromosome 3:12,169,568-12,175,851	3
TIMP4		Chromosome 3:12,169,568-12,175,851	3
TIMP4		Chromosome 3:12,169,568-12,175,851	3
PPARG	PPARgamma, NR1C3	Chromosome 3:12,304,359-12,450,843	3
PPARG	PPARgamma, NR1C3	Chromosome 3:12,304,359-12,450,843	3
PPARG	PPARgamma, NR1C3	Chromosome 3:12,304,359-12,450,843	3
IGSF11		Chromosome 3:120,102,167-120,347,588	3
IGSF11		Chromosome 3:120,102,167-120,347,588	3
IGSF11		Chromosome 3:120,102,167-120,347,588	3
CD80	B7-1	Chromosome 3:120,725,832-120,761,139	3
CD80	B7-1	Chromosome 3:120,725,832-120,761,139	3
PLA1A	Phospholipase	Chromosome 3:120,792,984-120,831,342	3
NR1I2	NR1I2	Chromosome 3:120,982,021-121,020,022	3
GSK3B		Chromosome 3:121,028,233-121,295,954	3
GTF2E1	TFIIE	Chromosome 3:121,937,926-121,984,605	3
CD86	B7-2	Chromosome 3:123,256,911-123,322,673	3
CD86	B7-2	Chromosome 3:123,256,911-123,322,673	3
CD86	B7-2	Chromosome 3:123,256,911-123,322,673	3
MYLK	myosin light chain kinase	Chromosome 3:124,813,833-125,085,839	3
MYLK	myosin light chain kinase	Chromosome 3:124,813,833-125,085,839	3
ITGB5		Chromosome 3:125,964,485-126,088,842	3
ITGB5		Chromosome 3:125,964,485-126,088,842	3
ITGB5		Chromosome 3:125,964,485-126,088,842	3
PLXNA1	Plexin-A1	Chromosome 3:128,190,192-128,238,922	3
PLXNA1	Plexin-A1	Chromosome 3:128,190,192-128,238,922	3
MCM2		Chromosome 3:128,799,943-128,823,969	3
MCM2		Chromosome 3:128,799,943-128,823,969	3
SEC61A1		Chromosome 3:129,253,902-129,273,216	3
SEC61A1		Chromosome 3:129,253,902-129,273,216	3
GATA2		Chromosome 3:129,680,960-129,694,718	3
GP9	CD42a	Chromosome 3:130,262,300-130,263,941	3
PLXND1	Plexin-D1	Chromosome 3:130,756,708-130,808,351	3
PLXND1	Plexin-D1	Chromosome 3:130,756,708-130,808,351	3
TRH	TRH	Chromosome 3:131,176,253-131,179,470	3
TRH	TRH	Chromosome 3:131,176,253-131,179,470	3
TRH	TRH	Chromosome 3:131,176,253-131,179,470	3
PIK3R4		Chromosome 3:131,880,468-131,948,340)	3

PIK3R4		Chromosome 3:131,880,468-131,948,340)	3
CCRL1		Chromosome 3:133,798,784-133,804,072	3
EPHB1		Chromosome 3:135,996,950-136,461,999	3
EPHB1		Chromosome 3:135,996,950-136,461,999	3
EPHB1		Chromosome 3:135,996,950-136,461,999	3
EPHB1		Chromosome 3:135,996,950-136,461,999	3
EPHB1		Chromosome 3:135,996,950-136,461,999	3
EPHB1		Chromosome 3:135,996,950-136,461,999	3
EPHB1		Chromosome 3:135,996,950-136,461,999	3
IL20RB		Chromosome 3:138,159,397-138,212,610	3
IL20RB		Chromosome 3:138,159,397-138,212,610	3
PIK3CB		Chromosome 3:139,856,921-139,960,875	3
PIK3CB		Chromosome 3:139,856,921-139,960,875	3
XPC		Chromosome 3:14,161,648-14,195,143	3
NR2C2	NR2C2	Chromosome 3:14,964,240-15,065,784	3
NR2C2	NR2C2	Chromosome 3:14,964,240-15,065,784	3
FOXL2		Chromosome 3:140,145,756-140,148,491	3
FOXL2		Chromosome 3:140,145,756-140,148,491	3
RNF7		Chromosome 3:142,939,741-142,947,933	3
RNF7		Chromosome 3:142,939,741-142,947,933	3
ATP1B3	CD298	Chromosome 3:143,078,160-143,128,072	3
SLC9A9	NHE-9	Chromosome 3:144,466,754-145,049,979	3
SLC9A9	NHE-9	Chromosome 3:144,466,754-145,049,979	3
SLC9A9	NHE-9	Chromosome 3:144,466,754-145,049,979	3
SLC9A9	NHE-9	Chromosome 3:144,466,754-145,049,979	3
SLC9A9	NHE-9	Chromosome 3:144,466,754-145,049,979	3
SLC9A9	NHE-9	Chromosome 3:144,466,754-145,049,979	3
SLC9A9	NHE-9	Chromosome 3:144,466,754-145,049,979	3
SLC9A9	NHE-9	Chromosome 3:144,466,754-145,049,979	3
SLC9A9	NHE-9	Chromosome 3:144,466,754-145,049,979	3
AGTR1	Angiotensin receptor	Chromosome 3:149,898,355-149,943,478	3
AGTR1	Angiotensin receptor	Chromosome 3:149,898,355-149,943,478	3
AGTR1	Angiotensin receptor	Chromosome 3:149,898,355-149,943,478	3
HLTF		Chromosome 3:150,230,604-150,287,007	3
HLTF		Chromosome 3:150,230,604-150,287,007	3
HPS3	Hermansky-Pudlak syndr	Chromosome 3:150,330,061-150,373,995	3
P2RY14	P2Y14	Chromosome 3:152,412,595-152,478,847	3
P2RY14	P2Y14	Chromosome 3:152,412,595-152,478,847	3
IGSF10		Chromosome 3:152,637,167-152,659,187	3
P2RY1	P2Y1	Chromosome 3:154,035,426-154,038,535	3
P2RY1	P2Y1	Chromosome 3:154,035,426-154,038,535	3
DHX36		Chromosome 3:155,476,152-155,524,971	3
DHX36		Chromosome 3:155,476,152-155,524,971	3
MME	CD10	Chromosome 3:156,280,153-156,384,186	3
MME	CD10	Chromosome 3:156,280,153-156,384,186	3
PTX3		Chromosome 3:158,637,301-158,644,071	3
PLCL2		Chromosome 3:16,949,586-17,107,089	3
PLCL2		Chromosome 3:16,949,586-17,107,089	3
IL12A		Chromosome 3:161,189,323-161,196,500	3
IL12A		Chromosome 3:161,189,323-161,196,500	3
IL12A		Chromosome 3:161,189,323-161,196,500	3
TRIM59	MRF1	Chromosome 3:161,427,938-161,650,320	3
TRIM59	MRF1	Chromosome 3:161,427,938-161,650,320	3
TRIM59	MRF1	Chromosome 3:161,427,938-161,650,320	3
B3GALNT1		Chromosome 3:162,284,365-162,305,854	3
PDCD10		Chromosome 3:168,884,388-168,935,345	3

PDCD10		Chromosome 3:168,884,388-168,935,345	3
EVI1		Chromosome 3:170,285,244-170,347,054	3
EVI1		Chromosome 3:170,285,244-170,347,054	3
TERC		Chromosome 3:170,965,092-170,965,542	3
TERC		Chromosome 3:170,965,092-170,965,542	3
PRKCI	PKCθ	Chromosome 3:171,422,919-171,506,459	3
PRKCI	PKCθ	Chromosome 3:171,422,919-171,506,459	3
TNFSF10	CD253, TRAIL	Chromosome 3:173,706,158-173,723,963	3
TNFSF10	CD253, TRAIL	Chromosome 3:173,706,158-173,723,963	3
TBL1XR1	TBLR1	Chromosome 3:178,221,867-178,397,734	3
TBL1XR1	TBLR1	Chromosome 3:178,221,867-178,397,734	3
TBL1XR1	TBLR1	Chromosome 3:178,221,867-178,397,734	3
PIK3CA		Chromosome 3:180,349,005-180,435,194	3
PIK3CA		Chromosome 3:180,349,005-180,435,194	3
LAMP3	CD208, DC-LAMP	Chromosome 3:184,322,697-184,363,317	3
LAMP3	CD208, DC-LAMP	Chromosome 3:184,322,697-184,363,317	3
THPO	Thrombopoietin	Chromosome 3:185,572,467-185,578,626	3
THPO	Thrombopoietin	Chromosome 3:185,572,467-185,578,626	3
MAP3K13		Chromosome 3:186,563,664-186,683,322	3
KNG1	Bradykinin	Chromosome 3:187,917,814-187,944,437	3
KNG1	Bradykinin	Chromosome 3:187,917,814-187,944,437	3
ST6GAL1	CD75s	Chromosome 3:188,131,210-188,279,035	3
ST6GAL1	CD75s	Chromosome 3:188,131,210-188,279,035	3
ST6GAL1	CD75s	Chromosome 3:188,131,210-188,279,035	3
ST6GAL1	CD75s	Chromosome 3:188,131,210-188,279,035	3
MASP1	MASP3	Chromosome 3:188,418,632-188,492,446	3
IFRG28		Chromosome 3:188,568,862-188,572,066	3
IFRG28		Chromosome 3:188,568,862-188,572,066	3
SST	SST	Chromosome 3:188,869,388-188,870,895	3
SST	SST	Chromosome 3:188,869,388-188,870,895	3
SST	SST	Chromosome 3:188,869,388-188,870,895	3
TP73L	p63	Chromosome 3:190,831,910-191,097,759	3
TP73L	p63	Chromosome 3:190,831,910-191,097,759	3
TP73L	p63	Chromosome 3:190,831,910-191,097,759	3
IL1RAP		Chromosome 3:191,714,585-191,858,537	3
IL1RAP		Chromosome 3:191,714,585-191,858,537	3
IL1RAP		Chromosome 3:191,714,585-191,858,537	3
FGF12	FGF12	Chromosome 3:193,342,413-193,928,066	3
FGF12	FGF12	Chromosome 3:193,342,413-193,928,066	3
FGF12	FGF12	Chromosome 3:193,342,413-193,928,066	3
FGF12	FGF12	Chromosome 3:193,342,413-193,928,066	3
FGF12	FGF12	Chromosome 3:193,342,413-193,928,066	3
FGF12	FGF12	Chromosome 3:193,342,413-193,928,066	3
FGF12	FGF12	Chromosome 3:193,342,413-193,928,066	3
FGF12	FGF12	Chromosome 3:193,342,413-193,928,066	3
FGF12	FGF12	Chromosome 3:193,342,413-193,928,066	3
FGF12	FGF12	Chromosome 3:193,342,413-193,928,066	3
FGF12	FGF12	Chromosome 3:193,342,413-193,928,066	3
GP5	CD42d, HPA4	Chromosome 3:195,595,348-195,601,523	3
TFRC	transferrin receptor	Chromosome 3:197,260,553-197,293,343	3
PAK2		Chromosome 3:197,951,312-198,043,756	3
PAK2		Chromosome 3:197,951,312-198,043,756	3
MFI2	CD228	Chromosome 3:198,214,553-198,241,043	3
MFI2	CD228	Chromosome 3:198,214,553-198,241,043	3
CHLI		Chromosome 3:213,650-426,098	3
CHLI		Chromosome 3:213,650-426,098	3

CHLI		Chromosome 3:213,650-426,098	3
NKIRAS1		Chromosome 3:23,908,576-23,933,541	3
NR1D2		Chromosome 3:23,961,810-23,996,241	3
THRB	NR1A2	Chromosome 3:24,134,709-24,511,317	3
THRB	NR1A2	Chromosome 3:24,134,709-24,511,317	3
THRB	NR1A2	Chromosome 3:24,134,709-24,511,317	3
THRB	NR1A2	Chromosome 3:24,134,709-24,511,317	3
THRB	NR1A2	Chromosome 3:24,134,709-24,511,317	3
RARB	NR1B2	Chromosome 3:25,190,893-25,614,424	3
RARB	NR1B2	Chromosome 3:25,190,893-25,614,424	3
RARB	NR1B2	Chromosome 3:25,190,893-25,614,424	3
RARB	NR1B2	Chromosome 3:25,190,893-25,614,424	3
RARB	NR1B2	Chromosome 3:25,190,893-25,614,424	3
EOMES	eomesodermin	Chromosome 3:27,732,872-27,738,807	3
IL5RA	CD125	Chromosome 3:3,086,421-3,127,031	3
IL5RA	CD125	Chromosome 3:3,086,421-3,127,031	3
TGFBR2		Chromosome 3:30,622,998-30,710,638	3
TGFBR2		Chromosome 3:30,622,998-30,710,638	3
STT3B		Chromosome 3:31,549,495-31,652,560	3
CMTM8		Chromosome 3:32,255,175-32,386,817	3
CMTM8		Chromosome 3:32,255,175-32,386,817	3
CMTM8		Chromosome 3:32,255,175-32,386,817	3
CMTM7		Chromosome 3:32,408,167-32,471,337	3
CMTM7		Chromosome 3:32,408,167-32,471,337	3
CMTM6		Chromosome 3:32,497,808-32,519,869	3
CMTM6		Chromosome 3:32,497,808-32,519,869	3
CCR4	CD194	Chromosome 3:32,968,070-32,972,840	3
CLASP2	c1AP2	Chromosome 3:33,512,741-33,734,852	3
PDCD6IP		Chromosome 3:33,814,561-33,886,198	3
PDCD6IP		Chromosome 3:33,814,561-33,886,198	3
ITGA9		Chromosome 3:37,468,817-37,836,285	3
ITGA9		Chromosome 3:37,468,817-37,836,285	3
ITGA9		Chromosome 3:37,468,817-37,836,285	3
ITGA9		Chromosome 3:37,468,817-37,836,285	3
ITGA9		Chromosome 3:37,468,817-37,836,285	3
ITGA9		Chromosome 3:37,468,817-37,836,285	3
ITGA9		Chromosome 3:37,468,817-37,836,285	3
CTDSPL	NIF1	Chromosome 3:37,878,129-38,000,964	3
CTDSPL	NIF1	Chromosome 3:37,878,129-38,000,964	3
MyD88		Chromosome 3:38,155,009-38,159,517	3
MyD88		Chromosome 3:38,155,009-38,159,517	3
CX3CR1		Chromosome 3:39,279,989-39,298,190	3
CX3CR1		Chromosome 3:39,279,989-39,298,190	3
CX3CR1		Chromosome 3:39,279,989-39,298,190	3
CCR8	CD198	Chromosome 3:39,346,219-39,351,077	3
ITPR1		Chromosome 3:4,510,136-4,864,081	3
ITPR1		Chromosome 3:4,510,136-4,864,081	3
ITPR1		Chromosome 3:4,510,136-4,864,081	3
ITPR1		Chromosome 3:4,510,136-4,864,081	3
ITPR1		Chromosome 3:4,510,136-4,864,081	3
ITPR1		Chromosome 3:4,510,136-4,864,081	3
CTNNB1	beta-catenin	Chromosome 3:41,216,004-41,256,938	3
CTNNB1	beta-catenin	Chromosome 3:41,216,004-41,256,938	3
NKTR		Chromosome 3:42,617,151-42,665,237	3
CCBP2	D6	Chromosome 3:42,825,980-42,883,779	3
CYP8B1		Chromosome 3:42,888,688-42,892,637	3

CDCP1	CD318	Chromosome 3:45,098,773-45,162,918	3
CDCP1	CD318	Chromosome 3:45,098,773-45,162,918	3
CDCP1	CD318	Chromosome 3:45,098,773-45,162,918	3
TMEM158	RIS1	Chromosome 3:45,240,962-45,242,758	3
CCR9	CD198, 199	Chromosome 3:45,903,023-45,919,671	3
XCR1		Chromosome 3:46,037,295-46,043,983	3
CCR1	CD191	Chromosome 3:46,218,204-46,224,836	3
CCR3	CD193	Chromosome 3:46,227,186-46,283,166	3
CCRL2		Chromosome 3:46,423,725-46,426,018	3
LTF	Lactoferrin	Chromosome 3:46,452,500-46,481,657	3
PTHR1	PTHR1	Chromosome 3:46,894,240-46,926,585	3
PTHR1	PTHR1	Chromosome 3:46,894,240-46,926,585	3
PTPN23		Chromosome 3:47,397,528-47,429,935	3
DHX30		Chromosome 3:47,819,625-47,866,687	3
PLXNB1	Plexin-B	Chromosome 3:48,420,266-48,446,464	3
GPX1	GSH peroxidase, cGPx	Chromosome 3:49,369,613-49,370,795	3
RHOA	RHOA	Chromosome 3:49,371,582-49,424,530	3
DAG1	DAG	Chromosome 3:49,482,595-49,548,048	3
DAG1	DAG	Chromosome 3:49,482,595-49,548,048	3
MST1	MST1/STK4	Chromosome 3:49,696,391-49,701,099	3
MST1R	CDw136	Chromosome 3:49,899,439-49,916,074	3
MST1R	CDw136	Chromosome 3:49,899,439-49,916,074	3
MST1R	CDw136	Chromosome 3:49,899,439-49,916,074	3
DUSP7		Chromosome 3:52,059,799-52,065,329	3
DUSP7		Chromosome 3:52,059,799-52,065,329	3
TLR9	CD289	Chromosome 3:52,230,138-52,248,223	3
TLR9	CD289	Chromosome 3:52,230,138-52,248,223	3
STAB1	FEEL-1	Chromosome 3:52,504,396-52,533,551	3
STAB1	FEEL-1	Chromosome 3:52,504,396-52,533,551	3
PRKCD	PKC delta	Chromosome 3:53,170,263-53,201,773	3
IL17RB		Chromosome 3:53,855,612-53,874,867	3
IL17RB		Chromosome 3:53,855,612-53,874,867	3
WNT5A		Chromosome 3:55,474,783-55,496,371	3
ERC2		Chromosome 3:55,517,376-56,477,431	3
ERC2		Chromosome 3:55,517,376-56,477,431	3
ERC2		Chromosome 3:55,517,376-56,477,431	3
ERC2		Chromosome 3:55,517,376-56,477,431	3
ERC2		Chromosome 3:55,517,376-56,477,431	3
ERC2		Chromosome 3:55,517,376-56,477,431	3
ERC2		Chromosome 3:55,517,376-56,477,431	3
ERC2		Chromosome 3:55,517,376-56,477,431	3
ERC2		Chromosome 3:55,517,376-56,477,431	3
ERC2		Chromosome 3:55,517,376-56,477,431	3
IL17RD		Chromosome 3:57,103,316-57,179,374	3
IL17RD		Chromosome 3:57,103,316-57,179,374	3
IL17RD		Chromosome 3:57,103,316-57,179,374	3
PTPRG		Chromosome 3:61,522,285-62,255,613	3
PTPRG		Chromosome 3:61,522,285-62,255,613	3
PTPRG		Chromosome 3:61,522,285-62,255,613	3
PTPRG		Chromosome 3:61,522,285-62,255,613	3
PTPRG		Chromosome 3:61,522,285-62,255,613	3
PTPRG		Chromosome 3:61,522,285-62,255,613	3
PTPRG		Chromosome 3:61,522,285-62,255,613	3
PTPRG		Chromosome 3:61,522,285-62,255,613	3
ARL6IP5	JWA	Chromosome 3:69,216,780-69,237,929	3
MITF		Chromosome 3:69,871,323-70,100,177	3

MITF		Chromosome 3:69,871,323-70,100,177	3
MITF		Chromosome 3:69,871,323-70,100,177	3
MITF		Chromosome 3:69,871,323-70,100,177	3
FOXP1		Chromosome 3:71,087,426-71,715,830	3
FOXP1		Chromosome 3:71,087,426-71,715,830	3
FOXP1		Chromosome 3:71,087,426-71,715,830	3
FOXP1		Chromosome 3:71,087,426-71,715,830	3
FOXP1		Chromosome 3:71,087,426-71,715,830	3
FOXP1		Chromosome 3:71,087,426-71,715,830	3
FOXP1		Chromosome 3:71,087,426-71,715,830	3
FOXP1		Chromosome 3:71,087,426-71,715,830	3
FOXP1		Chromosome 3:71,087,426-71,715,830	3
FOXP1		Chromosome 3:71,087,426-71,715,830	3
FOXP1		Chromosome 3:71,087,426-71,715,830	3
CADM2		Chromosome 3:85,858,322-86,200,641	3
CADM2		Chromosome 3:85,858,322-86,200,641	3
CADM2		Chromosome 3:85,858,322-86,200,641	3
CADM2		Chromosome 3:85,858,322-86,200,641	3
CADM2		Chromosome 3:85,858,322-86,200,641	3
CHMP2B	CHMP2B	Chromosome 3:87,359,140-87,387,339	3
CHMP2B	CHMP2B	Chromosome 3:87,359,140-87,387,339	3
CHMP2B	CHMP2B	Chromosome 3:87,359,140-87,387,339	3
IL17RE		Chromosome 3:9,919,150-9,933,086	3
IL17RC		Chromosome 3:9,933,782-9,950,314	3
Protein S		Chromosome 3:95,074,647-95,175,412	3
FGFR3	CD333	Chromosome 4:1,764,832-1,780,396	4
H2AFZ		Chromosome 4:101,088,265-101,090,535	4
PPP3CA		Chromosome 4:102,163,610-102,487,376	4
PPP3CA		Chromosome 4:102,163,610-102,487,376	4
PPP3CA		Chromosome 4:102,163,610-102,487,376	4
PPP3CA		Chromosome 4:102,163,610-102,487,376	4
PPP3CA		Chromosome 4:102,163,610-102,487,376	4
PPP3CA		Chromosome 4:102,163,610-102,487,376	4
BANK1	B cell scaffold protein	Chromosome 4:102,930,919-103,214,918	4
BANK1	B cell scaffold protein	Chromosome 4:102,930,919-103,214,918	4
BANK1	B cell scaffold protein	Chromosome 4:102,930,919-103,214,918	4
NFKB1	p105, p50	Chromosome 4:103,641,518-103,757,507	4
NFKB1	p105, p50	Chromosome 4:103,641,518-103,757,507	4
SCYE1	SCYE1	Chromosome 4:107,456,302-107,489,097	4
SCYE1	SCYE1	Chromosome 4:107,456,302-107,489,097	4
CYP2U1		Chromosome 4:109,072,166-109,094,062	4
CYP2U1		Chromosome 4:109,072,166-109,094,062	4
HS3ST1		Chromosome 4:11,009,086-11,040,487	4
HS3ST1		Chromosome 4:11,009,086-11,040,487	4
CFI		Chromosome 4:110,881,301-110,942,590	4
EGF1		Chromosome 4:111,053,499-111,152,868	4
EGF1		Chromosome 4:111,053,499-111,152,868	4
EGF1		Chromosome 4:111,053,499-111,152,868	4
EGF1		Chromosome 4:111,053,499-111,152,868	4
ENPEP	CD249	Chromosome 4:111,616,697-111,702,872	4
ENPEP	CD249	Chromosome 4:111,616,697-111,702,872	4
ANK2		Chromosome 4:114,190,319-114,524,337	4
ANK2		Chromosome 4:114,190,319-114,524,337	4
ANK2		Chromosome 4:114,190,319-114,524,337	4
ANK2		Chromosome 4:114,190,319-114,524,337	4
CAMK2D	CaMKII	Chromosome 4:114,593,021-114,902,177	4

CAMK2D	CaMKII	Chromosome 4:114,593,021-114,902,177	4
CAMK2D	CaMKII	Chromosome 4:114,593,021-114,902,177	4
CAMK2D	CaMKII	Chromosome 4:114,593,021-114,902,177	4
CAMK2D	CaMKII	Chromosome 4:114,593,021-114,902,177	4
MAD2LI		Chromosome 4:121,200,029-121,207,411	4
MAD2LI		Chromosome 4:121,200,029-121,207,411	4
ANXA5		Chromosome 4:122,808,598-122,837,626	4
CCNA2		Chromosome 4:122,957,975-122,964,505	4
IL2		Chromosome 4:123,592,075-123,597,339	4
IL21		Chromosome 4:123,753,221-123,761,662	4
FGF2	FGF2	Chromosome 4:123,967,313-124,038,840	4
FGF2	FGF2	Chromosome 4:123,967,313-124,038,840	4
PLK4	Sak	Chromosome 4:129,021,551-129,039,377	4
C1QTNF7		Chromosome 4:14,950,658-15,056,887	4
C1QTNF7		Chromosome 4:14,950,658-15,056,887	4
CCRN4L		Chromosome 4:140,156,393-140,186,543	4
IL15		Chromosome 4:142,777,204-142,874,062	4
IL15		Chromosome 4:142,777,204-142,874,062	4
SMARCA5		Chromosome 4:144,654,066-144,694,017	4
SMARCA5		Chromosome 4:144,654,066-144,694,017	4
GYPB	MNSs antigen, CD235b	Chromosome 4:145,136,707-145,159,946	4
GYPA	MNSs antigen, CD235a	Chromosome 4:145,249,906-145,281,294	4
SMAD1		Chromosome 4:146,622,401-146,699,778	4
GTF2F2L		Chromosome 4:148,646,691-148,647,812	4
GTF2F2L		Chromosome 4:148,646,691-148,647,812	4
GTF2F2L		Chromosome 4:148,646,691-148,647,812	4
NR3C2	NR3C2	Chromosome 4:149,219,370-149,582,973	4
NR3C2	NR3C2	Chromosome 4:149,219,370-149,582,973	4
NR3C2	NR3C2	Chromosome 4:149,219,370-149,582,973	4
NR3C2	NR3C2	Chromosome 4:149,219,370-149,582,973	4
NR3C2	NR3C2	Chromosome 4:149,219,370-149,582,973	4
BST1	CD157	Chromosome 4:15,313,738-15,343,508	4
BST1	CD157	Chromosome 4:15,313,738-15,343,508	4
CD38		Chromosome 4:15,388,999-15,460,167	4
PROM1	CD133, SCA	Chromosome 4:15,578,955-15,686,664	4
PROM1	CD133, SCA	Chromosome 4:15,578,955-15,686,664	4
FBXW7		Chromosome 4:153,461,860-153,675,622	4
FBXW7		Chromosome 4:153,461,860-153,675,622	4
FBXW7		Chromosome 4:153,461,860-153,675,622	4
FBXW7		Chromosome 4:153,461,860-153,675,622	4
TLR2	CD282	Chromosome 4:154,824,891-154,846,693	4
TLR2	CD282	Chromosome 4:154,824,891-154,846,693	4
FGB	fibrinogen	Chromosome 4:155,703,596-155,711,688	4
NPY2R		Chromosome 4:156,349,231-156,357,678	4
PPID		Chromosome 4:159,849,729-159,864,002	4
PPID		Chromosome 4:159,849,729-159,864,002	4
CPE		Chromosome 4:166,519,538-166,638,926	4
CPE		Chromosome 4:166,519,538-166,638,926	4
HPGD		Chromosome 4:175,647,955-175,680,213	4
HPGD		Chromosome 4:175,647,955-175,680,213	4
HPGD		Chromosome 4:175,647,955-175,680,213	4
HPGD		Chromosome 4:175,647,955-175,680,213	4
VEGFC		Chromosome 4:177,841,685-177,950,889	4
IRF2		Chromosome 4:185,545,909-185,632,697	4
IRF2		Chromosome 4:185,545,909-185,632,697	4
IRF2		Chromosome 4:185,545,909-185,632,697	4

TLR3	CD283	Chromosome 4:187,227,303-187,243,246	4
CYP4V2		Chromosome 4:187,349,668-187,371,606	4
CYP4V2		Chromosome 4:187,349,668-187,371,606	4
RNF4		Chromosome 4:2,440,605-2,487,382	4
ADD1	alpha adducin	Chromosome 4:2,815,382-2,901,587	4
DHX15		Chromosome 4:24,138,185-24,195,282	4
DHX15		Chromosome 4:24,138,185-24,195,282	4
SOD3	IP01	Chromosome 4:24,405,153-24,411,562	4
SOD3	IP01	Chromosome 4:24,405,153-24,411,562	4
PI4K2B	PI4K2B	Chromosome 4:24,844,751-24,889,811	4
RBPSUH	RBP-Jk	Chromosome 4:25,930,430-26,045,851	4
RBPSUH	RBP-Jk	Chromosome 4:25,930,430-26,045,851	4
RBPSUH	RBP-Jk	Chromosome 4:25,930,430-26,045,851	4
RBPSUH	RBP-Jk	Chromosome 4:25,930,430-26,045,851	4
TLR10	CD290	Chromosome 4:38,450,255-38,460,984	4
TLR10	CD290	Chromosome 4:38,450,255-38,460,984	4
TLR6	CD286	Chromosome 4:38,504,618-38,507,555	4
RFC1	RFC	Chromosome 4:38,965,471-39,044,390	4
RFC1	RFC	Chromosome 4:38,965,471-39,044,390	4
RFC1	RFC	Chromosome 4:38,965,471-39,044,390	4
RHOH	RhoH	Chromosome 4:39,874,965-39,922,663	4
RHOH	RhoH	Chromosome 4:39,874,965-39,922,663	4
TXK	Txk, Rlk, thioredoxin	Chromosome 4:47,762,988-47,831,030	4
TXK	Txk, Rlk, thioredoxin	Chromosome 4:47,762,988-47,831,030	4
TXK	Txk, Rlk, thioredoxin	Chromosome 4:47,762,988-47,831,030	4
CYTL1	cytokine-like 1	Chromosome 4:5,067,214-5,072,100	4
CYTL1	cytokine-like 1	Chromosome 4:5,067,214-5,072,100	4
PDGFRA	CD140a	Chromosome 4:54,790,204-54,859,171	4
PDGFRA	CD140a	Chromosome 4:54,790,204-54,859,171	4
KIT	FLT3-ITD, CD117, c-KIT	Chromosome 4:55,218,842-55,301,638	4
KIT	FLT3-ITD, CD117, c-KIT	Chromosome 4:55,218,842-55,301,638	4
KIT	FLT3-ITD, CD117, c-KIT	Chromosome 4:55,218,842-55,301,638	4
KDR	CD309, VEGFR2	Chromosome 4:55,639,401-55,686,519	4
BRDG1		Chromosome 4:68,107,041-68,155,206	4
BRDG1		Chromosome 4:68,107,041-68,155,206	4
GNRHR	GNRH1-R	Chromosome 4:68,285,688-68,304,399	4
TMPRSS11D	HAT	Chromosome 4:68,369,189-68,432,311	4
TMPRSS11D	HAT	Chromosome 4:68,369,189-68,432,311	4
UGT2B17	UGT2	Chromosome 4:69,085,497-69,116,840	4
UGT2B7		Chromosome 4:69,996,782-70,013,293	4
UGT2B28		Chromosome 4:70,180,783-70,323,496	4
UGT2B28		Chromosome 4:70,180,783-70,323,496	4
HTN3	histatin 3	Chromosome 4:70,928,761-70,936,836	4
HTN3	histatin 3	Chromosome 4:70,928,761-70,936,836	4
IGJ		Chromosome 4:71,740,548-71,751,128	4
IL8	CXCL8	Chromosome 4:74,825,139-74,828,297	4
CXCL6		Chromosome 4:74,921,277-74,923,341	4
PF4	CXCL4	Chromosome 4:75,065,660-75,066,541	4
CXCL3		Chromosome 4:75,121,170-75,123,354	4
EREG	EREG	Chromosome 4:75,449,724-75,473,341	4
AREG	AREG	Chromosome 4:75,529,717-75,539,590	4
AREG	AREG	Chromosome 4:75,529,717-75,539,590	4
BTC	BTC betacellulin	Chromosome 4:75,889,001-75,938,853	4
BTC	BTC betacellulin	Chromosome 4:75,889,001-75,938,853	4
CXCL9	Mig	Chromosome 4:77,141,523-77,147,665	4
SCARB2		Chromosome 4:77,298,918-77,354,059	4

SCARB2		Chromosome 4:77,298,918-77,354,059	4
CXCL13		Chromosome 4:78,651,931-78,752,010	4
CXCL13		Chromosome 4:78,651,931-78,752,010	4
CXCL13		Chromosome 4:78,651,931-78,752,010	4
FGF5	FGF5	Chromosome 4:81,406,766-81,431,195	4
FGF5	FGF5	Chromosome 4:81,406,766-81,431,195	4
BMP3	BMP3	Chromosome 4:82,171,143-82,193,749	4
BMP3	BMP3	Chromosome 4:82,171,143-82,193,749	4
HPA		Chromosome 4:84,432,639-84,475,330	4
MAPK10		Chromosome 4:87,156,656-87,593,307	4
MAPK10		Chromosome 4:87,156,656-87,593,307	4
MAPK10		Chromosome 4:87,156,656-87,593,307	4
MAPK10		Chromosome 4:87,156,656-87,593,307	4
MAPK10		Chromosome 4:87,156,656-87,593,307	4
PTPN13		Chromosome 4:87,734,909-87,955,326	4
PTPN13		Chromosome 4:87,734,909-87,955,326	4
PTPN13		Chromosome 4:87,734,909-87,955,326	4
SPP1	Osteopontin, Eta1	Chromosome 4:89,115,826-89,123,592	4
SPP1	Osteopontin, Eta1	Chromosome 4:89,115,826-89,123,592	4
ABCG2	CD338, BCRP, MRX, MXI	Chromosome 4:89,230,440-89,299,035	4
HERC6	FLJ20637	Chromosome 4:89,518,915-89,583,272	4
HERC6	FLJ20637	Chromosome 4:89,518,915-89,583,272	4
HERC6	FLJ20637	Chromosome 4:89,518,915-89,583,272	4
DFB131		Chromosome 4:9,055,358-9,061,338	4
PGDS		Chromosome 4:95,438,730-95,483,050	4
BMPR1B	CD293	Chromosome 4:95,898,151-96,295,099	4
BMPR1B	CD293	Chromosome 4:95,898,151-96,295,099	4
BMPR1B	CD293	Chromosome 4:95,898,151-96,295,099	4
BMPR1B	CD293	Chromosome 4:95,898,151-96,295,099	4
BMPR1B	CD293	Chromosome 4:95,898,151-96,295,099	4
IBD5		Chromosome 5	5
IBD5		Chromosome 5	5
TERT		Chromosome 5:1,306,282-1,348,162	5
TERT		Chromosome 5:1,306,282-1,348,162	5
DAP		Chromosome 5:10,732,343-10,814,344	5
DAP		Chromosome 5:10,732,343-10,814,344	5
TSLP	Thymic stromal lymphopo	Chromosome 5:110,433,677-110,441,623	5
TSLP	Thymic stromal lymphopo	Chromosome 5:110,433,677-110,441,623	5
CAMK4	CaMKIV	Chromosome 5:110,587,968-110,858,483	5
CAMK4	CaMKIV	Chromosome 5:110,587,968-110,858,483	5
CAMK4	CaMKIV	Chromosome 5:110,587,968-110,858,483	5
CAMK4	CaMKIV	Chromosome 5:110,587,968-110,858,483	5
APC		Chromosome 5:112,101,483-112,209,835	5
APC		Chromosome 5:112,101,483-112,209,835	5
TCAM2	TIRP	Chromosome 5:114,942,247-114,989,610	5
TCAM2	TIRP	Chromosome 5:114,942,247-114,989,610	5
CDO1		Chromosome 5:115,168,329-115,180,304	5
PPIC		Chromosome 5:122,386,977-122,400,324	5
PPIC		Chromosome 5:122,386,977-122,400,324	5
IL3		Chromosome 5:131,424,121-131,426,796	5
SLC22A4	OCTN1	Chromosome 5:131,658,035-131,707,798	5
SLC22A4	OCTN1	Chromosome 5:131,658,035-131,707,798	5
SLC22A4	OCTN1	Chromosome 5:131,658,035-131,707,798	5
SLC22A5	OCTN2	Chromosome 5:131,733,343-131,759,205	5
IRF1		Chromosome 5:131,845,200-131,854,389	5
RAD50	rad50	Chromosome 5:131,920,529-132,007,651	5

LEAP2	liver expressed antimicrob	Chromosome 5:132,235,913-132,238,637	5
LEAP2	liver expressed antimicrob	Chromosome 5:132,235,913-132,238,637	5
HSPA4		Chromosome 5:132,415,561-132,468,608	5
DDX46		Chromosome 5:134,122,360-134,194,710	5
DDX46		Chromosome 5:134,122,360-134,194,710	5
CXCL14		Chromosome 5:134,934,274-134,942,868	5
IL9		Chromosome 5:135,255,834-135,259,415	5
IL9		Chromosome 5:135,255,834-135,259,415	5
IL9		Chromosome 5:135,255,834-135,259,415	5
BRD8	SMAP	Chromosome 5:137,503,358-137,542,257	5
BRD8	SMAP	Chromosome 5:137,503,358-137,542,257	5
BRD8	SMAP	Chromosome 5:137,503,358-137,542,257	5
EGR1		Chromosome 5:137,829,080-137,832,903	5
EGR1		Chromosome 5:137,829,080-137,832,903	5
NRG2	NRG2	Chromosome 5:139,207,444-139,403,063	5
NRG2	NRG2	Chromosome 5:139,207,444-139,403,063	5
NRG2	NRG2	Chromosome 5:139,207,444-139,403,063	5
HBEGF	HBEGF	Chromosome 5:139,692,612-139,706,359	5
HBEGF	HBEGF	Chromosome 5:139,692,612-139,706,359	5
CD14		Chromosome 5:139,991,501-139,993,439	5
NDUFA2	B8/HY	Chromosome 5:140,005,142-140,007,424	5
PCDHB5		Chromosome 5:140,494,984-140,497,888	5
PCDHB16		Chromosome 5:140,541,164-140,545,980	5
HDAC3		Chromosome 5:140,980,627-140,996,596	5
FGF1		Chromosome 5:141,951,927-142,046,134	5
FGF1		Chromosome 5:141,951,927-142,046,134	5
NR3C1	GR	Chromosome 5:142,637,689-142,795,270	5
NR3C1	GR	Chromosome 5:142,637,689-142,795,270	5
HMHB1	HB-1	Chromosome 5:143,171,919-143,180,477	5
HMHB1	HB-1	Chromosome 5:143,171,919-143,180,477	5
IL17B		Chromosome 5:148,734,023-148,739,031	5
IL17B		Chromosome 5:148,734,023-148,739,031	5
CSNK1A1	casein kinase 1	Chromosome 5:148,855,038-148,911,200	5
CSF1R	CD115	Chromosome 5:149,413,051-149,473,128	5
CSF1R	CD115	Chromosome 5:149,413,051-149,473,128	5
PDGFRB	CD140b	Chromosome 5:149,473,595-149,515,615	5
PDGFRB	CD140b	Chromosome 5:149,473,595-149,515,615	5
CD74	p41	Chromosome 5:149,761,393-149,772,685	5
IRGM	LRG47	Chromosome 5:150,207,879-150,260,488	5
GPX3		Chromosome 5:150,380,112-150,388,747	5
HAVCR2	TIM-3	Chromosome 5:156,445,421-156,468,716	5
ITK	Itk	Chromosome 5:156,540,432-156,614,687	5
ITK	Itk	Chromosome 5:156,540,432-156,614,687	5
EBF		Chromosome 5:158,058,006-158,459,347	5
EBF		Chromosome 5:158,058,006-158,459,347	5
EBF		Chromosome 5:158,058,006-158,459,347	5
EBF		Chromosome 5:158,058,006-158,459,347	5
EBF		Chromosome 5:158,058,006-158,459,347	5
EBF		Chromosome 5:158,058,006-158,459,347	5
IL12B		Chromosome 5:158,674,369-158,690,059	5
IL12B		Chromosome 5:158,674,369-158,690,059	5
IL12B		Chromosome 5:158,674,369-158,690,059	5
C1QTNF2		Chromosome 5:159,707,339-159,730,207	5
C1QTNF2		Chromosome 5:159,707,339-159,730,207	5
CCNG1		Chromosome 5:162,797,155-162,804,600	5
HMMR	CD168	Chromosome 5:162,820,241-162,851,525	5

DOCK2	dedicator of cytokinesis 2	Chromosome 5:168,996,871-169,442,959	5
DOCK2	dedicator of cytokinesis 2	Chromosome 5:168,996,871-169,442,959	5
DOCK2	dedicator of cytokinesis 2	Chromosome 5:168,996,871-169,442,959	5
DOCK2	dedicator of cytokinesis 2	Chromosome 5:168,996,871-169,442,959	5
DOCK2	dedicator of cytokinesis 2	Chromosome 5:168,996,871-169,442,959	5
DOCK2	dedicator of cytokinesis 2	Chromosome 5:168,996,871-169,442,959	5
DOCK2	dedicator of cytokinesis 2	Chromosome 5:168,996,871-169,442,959	5
DOCK2	dedicator of cytokinesis 2	Chromosome 5:168,996,871-169,442,959	5
FLJ46831	FOXI1	Chromosome 5:169,465,495-169,469,305	5
LCP2	SLP76	Chromosome 5:169,607,666-169,657,400	5
LPC2	SLP-76	Chromosome 5:169,607,666-169,657,400	5
DUSP1	MKP1	Chromosome 5:172,127,707-172,130,809	5
BNIP1		Chromosome 5:172,504,130-172,523,989	5
BNIP1		Chromosome 5:172,504,130-172,523,989	5
BNIP1		Chromosome 5:172,504,130-172,523,989	5
HRH2		Chromosome 5:175,017,637-175,045,847	5
HRH2		Chromosome 5:175,017,637-175,045,847	5
FGFR4	CD334	Chromosome 5:176,446,493-176,457,733	5
DDX41		Chromosome 5:176,871,184-176,876,573	5
DDX41		Chromosome 5:176,871,184-176,876,573	5
CANX		Chromosome 5:179,058,536-179,091,248	5
MAPK9		Chromosome 5:179,595,388-179,640,218	5
FLT4	CD310, VEGFR3	Chromosome 5:179,945,812-180,009,172	5
FLT4	CD310, VEGFR3	Chromosome 5:179,945,812-180,009,172	5
FLT4	CD310, VEGFR3	Chromosome 5:179,945,812-180,009,172	5
FOXO1B		Chromosome 5:180,458,383-180,460,484	5
FOXO1B		Chromosome 5:180,458,383-180,460,484	5
PDCD6		Chromosome 5:324,739-488,225	5
PDCD6		Chromosome 5:324,739-488,225	5
PDCD6		Chromosome 5:324,739-488,225	5
C1QTNF3		Chromosome 5:34,022,040-34,160,396	5
C1QTNF3		Chromosome 5:34,022,040-34,160,396	5
C1QTNF3		Chromosome 5:34,022,040-34,160,396	5
PRLR	PRLR	Chromosome 5:35,084,621-35,266,334	5
PRLR	PRLR	Chromosome 5:35,084,621-35,266,334	5
PRLR	PRLR	Chromosome 5:35,084,621-35,266,334	5
PRLR	PRLR	Chromosome 5:35,084,621-35,266,334	5
IL7R	CD127	Chromosome 5:35,892,748-35,915,462	5
IL7R	CD127	Chromosome 5:35,892,748-35,915,462	5
SKP2		Chromosome 5:36,187,946-36,219,904	5
SKP2		Chromosome 5:36,187,946-36,219,904	5
SKP2		Chromosome 5:36,187,946-36,219,904	5
LIFR	CD118	Chromosome 5:38,510,822-38,631,253	5
LIFR	CD118	Chromosome 5:38,510,822-38,631,253	5
LIFR	CD118	Chromosome 5:38,510,822-38,631,253	5
FYB	SLAP-130, ADAP	Chromosome 5:39,141,114-39,255,432	5
FYB	SLAP-130, ADAP	Chromosome 5:39,141,114-39,255,432	5
FYB	SLAP-130, ADAP	Chromosome 5:39,141,114-39,255,432	5
C9		Chromosome 5:39,320,061-39,400,412	5
PTGER4	EP4	Chromosome 5:40,715,789-40,729,594	5
PTGER4	EP4	Chromosome 5:40,715,789-40,729,594	5
CARD6		Chromosome 5:40,877,043-40,896,025	5
C7		Chromosome 5:40,945,356-41,018,798	5
C6		Chromosome 5:41,178,093-41,297,297	5
C6		Chromosome 5:41,178,093-41,297,297	5
GHR	growth hormone receptor	Chromosome 5:42,459,783-42,757,736	5

GHR	growth hormone receptor	Chromosome 5:42,459,783-42,757,736	5
GHR	growth hormone receptor	Chromosome 5:42,459,783-42,757,736	5
GHR	growth hormone receptor	Chromosome 5:42,459,783-42,757,736	5
CCL28		Chromosome 5:43,229,915-43,448,250	5
CCL28		Chromosome 5:43,229,915-43,448,250	5
CCL28		Chromosome 5:43,229,915-43,448,250	5
FGF10	FGF10	Chromosome 5:44,340,854-44,424,541	5
FGF10	FGF10	Chromosome 5:44,340,854-44,424,541	5
ITGA1	VLA1-3, CD49a	Chromosome 5:52,119,531-52,285,242	5
ITGA1	VLA1-3, CD49a	Chromosome 5:52,119,531-52,285,242	5
ITGA1	VLA1-3, CD49a	Chromosome 5:52,119,531-52,285,242	5
ITGA2	CD49b	Chromosome 5:52,321,014-52,423,947	5
ITGA2	CD49b	Chromosome 5:52,321,014-52,423,947	5
GZMK		Chromosome 5:54,355,838-54,366,155	5
GZMA	Granzyme A	Chromosome 5:54,434,230-54,441,837	5
DHX29		Chromosome 5:54,587,830-54,639,278	5
DDX4		Chromosome 5:55,069,609-55,148,362	5
DDX4		Chromosome 5:55,069,609-55,148,362	5
DDX4		Chromosome 5:55,069,609-55,148,362	5
IL31RA		Chromosome 5:55,183,091-55,248,922	5
IL6ST	CD130, gp130	Chromosome 5:55,266,680-55,326,529	5
MAP3K1	MEKK1	Chromosome 5:56,146,022-56,227,736	5
MAP3K1	MEKK1	Chromosome 5:56,146,022-56,227,736	5
PDE4D	Phosphodiesterases	Chromosome 5:58,302,468-59,320,301	5
PDE4D	Phosphodiesterases	Chromosome 5:58,302,468-59,320,301	5
PDE4D	Phosphodiesterases	Chromosome 5:58,302,468-59,320,301	5
PDE4D	Phosphodiesterases	Chromosome 5:58,302,468-59,320,301	5
PDE4D	Phosphodiesterases	Chromosome 5:58,302,468-59,320,301	5
PDE4D	Phosphodiesterases	Chromosome 5:58,302,468-59,320,301	5
PDE4D	Phosphodiesterases	Chromosome 5:58,302,468-59,320,301	5
PDE4D	Phosphodiesterases	Chromosome 5:58,302,468-59,320,301	5
PDE4D	Phosphodiesterases	Chromosome 5:58,302,468-59,320,301	5
PDE4D	Phosphodiesterases	Chromosome 5:58,302,468-59,320,301	5
PDE4D	Phosphodiesterases	Chromosome 5:58,302,468-59,320,301	5
PDE4D	Phosphodiesterases	Chromosome 5:58,302,468-59,320,301	5
PDE4D	Phosphodiesterases	Chromosome 5:58,302,468-59,320,301	5
PDE4D	Phosphodiesterases	Chromosome 5:58,302,468-59,320,301	5
LY64	CD180	Chromosome 5:66,513,872-66,528,368	5
LY64	CD180	Chromosome 5:66,513,872-66,528,368	5
LY64	CD180	Chromosome 5:66,513,872-66,528,368	5
PIK3R1		Chromosome 5:67,547,360-67,633,405	5
PIK3R1		Chromosome 5:67,547,360-67,633,405	5
CCNB1		Chromosome 5:68,498,593-68,509,828	5
CCNB1		Chromosome 5:68,498,593-68,509,828	5
CCNB1		Chromosome 5:68,498,593-68,509,828	5
TAF9	TAFII32	Chromosome 5:68,682,567-68,701,596	5
TAF9	TAFII32	Chromosome 5:68,682,567-68,701,596	5
MTRR		Chromosome 5:7,922,217-7,954,237	5
MTRR		Chromosome 5:7,922,217-7,954,237	5
FOXD1		Chromosome 5:72,777,839-72,780,108	5
FOXD1		Chromosome 5:72,777,839-72,780,108	5
ENC1		Chromosome 5:73,958,990-73,973,005	5
ENC1		Chromosome 5:73,958,990-73,973,005	5
ENC1		Chromosome 5:73,958,990-73,973,005	5
HMGCR	HMG-CoA reductase	Chromosome 5:74,668,790-74,693,685	5
HMGCR	HMG-CoA reductase	Chromosome 5:74,668,790-74,693,685	5

COL4A3BP		Chromosome 5:74,702,684-74,843,719	5
F2RL2	PAR3	Chromosome 5:75,947,063-75,954,996	5
F2RL2	PAR3	Chromosome 5:75,947,063-75,954,996	5
F2R	PAR1	Chromosome 5:76,047,542-76,067,054	5
F2RL1	PAR2	Chromosome 5:76,150,610-76,166,896	5
LHFPL2		Chromosome 5:77,816,794-77,841,979	5
LHFPL2		Chromosome 5:77,816,794-77,841,979	5
DHFR	ok	Chromosome 5:79,957,801-79,986,556)	5
DHFR	ok	Chromosome 5:79,957,801-79,986,556)	5
CSPG2	versican	Chromosome 5:82,803,339-82,912,737	5
CSPG2	versican	Chromosome 5:82,803,339-82,912,737	5
CSPG2	versican	Chromosome 5:82,803,339-82,912,737	5
RASA1		Chromosome 5:86,599,461-86,723,489	5
RASA1		Chromosome 5:86,599,461-86,723,489	5
RASA1		Chromosome 5:86,599,461-86,723,489	5
NR2F1	NR2F1	Chromosome 5:92,944,799-92,956,077	5
ARTS1	ERAP1	Chromosome 5:96,122,277-96,169,559	5
ARTS1	ERAP1	Chromosome 5:96,122,277-96,169,559	5
ARTS1	ERAP1	Chromosome 5:96,122,277-96,169,559	5
IBD3		Chromosome 6	6
IBD3		Chromosome 6	6
FOXQ1		Chromosome 6:1,257,675-1,259,983	6
FOXQ1		Chromosome 6:1,257,675-1,259,983	6
FOXF2		Chromosome 6:1,335,068-1,340,831	6
FOXC1		Chromosome 6:1,555,206-1,559,131	6
GMDS		Chromosome 6:1,569,040-2,190,845	6
GMDS		Chromosome 6:1,569,040-2,190,845	6
GMDS		Chromosome 6:1,569,040-2,190,845	6
GMDS		Chromosome 6:1,569,040-2,190,845	6
GCNT2		Chromosome 6:10,636,575-10,737,587	6
GCNT2		Chromosome 6:10,636,575-10,737,587	6
SIM1		Chromosome 6:100,939,606-101,019,494	6
SIM1		Chromosome 6:100,939,606-101,019,494	6
GRIK2		Chromosome 6:101,953,385-102,624,651	6
HACE1		Chromosome 6:105,282,661-105,414,867	6
HACE1		Chromosome 6:105,282,661-105,414,867	6
PRDM1	Blimp1	Chromosome 6:106,640,888-106,664,507	6
PRDM1	Blimp1	Chromosome 6:106,640,888-106,664,507	6
ATG5	Atg5	Chromosome 6:106,739,044-106,880,388	6
ATG5	Atg5	Chromosome 6:106,739,044-106,880,388	6
SOBP		Chromosome 6:107,918,010-108,089,195	6
SOBP		Chromosome 6:107,918,010-108,089,195	6
NR2D1	NR2D1	Chromosome 6:108,593,955-108,616,706	6
NR2D1	NR2D1	Chromosome 6:108,593,955-108,616,706	6
NR2D1	NR2D1	Chromosome 6:108,593,955-108,616,706	6
FOXO3A		Chromosome 6:108,987,719-109,108,661	6
FOXO3A		Chromosome 6:108,987,719-109,108,661	6
CD164		Chromosome 6:109,794,412-109,810,353	6
PPIL6		Chromosome 6:109,820,624-109,868,524	6
NEDD9	Cas-L, HEF1	Chromosome 6:11,291,517-11,490,535	6
NEDD9	Cas-L, HEF1	Chromosome 6:11,291,517-11,490,535	6
NEDD9	Cas-L, HEF1	Chromosome 6:11,291,517-11,490,535	6
NEDD9	Cas-L, HEF1	Chromosome 6:11,291,517-11,490,535	6
NEDD9	Cas-L, HEF1	Chromosome 6:11,291,517-11,490,535	6
WASF1	Wiskott Aldrich	Chromosome 6:110,527,715-110,607,900	6
WASF1	Wiskott Aldrich	Chromosome 6:110,527,715-110,607,900	6

BXDC1		Chromosome 6:111,409,984-111,453,487	6
FYN	FynT	Chromosome 6:112,088,228-112,301,348	6
FYN	FynT	Chromosome 6:112,088,228-112,301,348	6
FYN	FynT	Chromosome 6:112,088,228-112,301,348	6
FYN	FynT	Chromosome 6:112,088,228-112,301,348	6
LAMA4		Chromosome 6:112,536,654-112,682,605	6
LAMA4		Chromosome 6:112,536,654-112,682,605	6
LAMA4		Chromosome 6:112,536,654-112,682,605	6
HDAC2		Chromosome 6:114,368,571-114,399,029	6
HDAC2		Chromosome 6:114,368,571-114,399,029	6
FRK	FynT	Chromosome 6:116,369,386-116,488,614	6
FRK	FynT	Chromosome 6:116,369,386-116,488,614	6
RFXDC1	RFXDC1	Chromosome 6:117,305,068-117,360,008	6
C6orf204		Chromosome 6:118,892,932-119,137,924	6
C6orf204		Chromosome 6:118,892,932-119,137,924	6
C6orf204		Chromosome 6:118,892,932-119,137,924	6
C6orf204		Chromosome 6:118,892,932-119,137,924	6
MAN1A1		Chromosome 6:119,540,965-119,712,625	6
MAN1A1		Chromosome 6:119,540,965-119,712,625	6
EDN1		Chromosome 6:12,398,582-12,405,413	6
EDN1		Chromosome 6:12,398,582-12,405,413	6
PHACTR1		Chromosome 6:12,825,819-13,396,624	6
NKAIN2		Chromosome 6:124,166,768-125,188,502	6
NCOA7		Chromosome 6:126,144,000-126,293,950	6
C6orf174,KIAA0408		Chromosome 6:127,813,023-127,879,540	6
PTPRK		Chromosome 6:128,331,625-128,883,453	6
PTPRK		Chromosome 6:128,331,625-128,883,453	6
PTPRK		Chromosome 6:128,331,625-128,883,453	6
PTPRK		Chromosome 6:128,331,625-128,883,453	6
PTPRK		Chromosome 6:128,331,625-128,883,453	6
PTPRK		Chromosome 6:128,331,625-128,883,453	6
LAMA2		Chromosome 6:129,246,035-129,879,407	6
LAMA2		Chromosome 6:129,246,035-129,879,407	6
LAMA2		Chromosome 6:129,246,035-129,879,407	6
LAMA2		Chromosome 6:129,246,035-129,879,407	6
LAMA2		Chromosome 6:129,246,035-129,879,407	6
LAMA2		Chromosome 6:129,246,035-129,879,407	6
LAMA2		Chromosome 6:129,246,035-129,879,407	6
EPB41L2		Chromosome 6:131,202,180-131,426,017	6
EPB41L2		Chromosome 6:131,202,180-131,426,017	6
AKAP7		Chromosome 6:131,508,154-131,646,366	6
AKAP7		Chromosome 6:131,508,154-131,646,366	6
ARG1	Arginase 1	Chromosome 6:131,935,977-131,947,165	6
ARG1	Arginase 1	Chromosome 6:131,935,977-131,947,165	6
ARG1	Arginase 1	Chromosome 6:131,935,977-131,947,165	6
ENPP3	CD203c	Chromosome 6:132,000,135-132,110,243	6
ENPP3	CD203c	Chromosome 6:132,000,135-132,110,243	6
CTGF		Chromosome 6:132,310,199-132,314,206	6
CTGF		Chromosome 6:132,310,199-132,314,206	6
MOXD1		Chromosome 6:132,658,887-132,764,357	6
MOXD1		Chromosome 6:132,658,887-132,764,357	6
VNN1		Chromosome 6:133,044,422-133,076,881	6
VNN1		Chromosome 6:133,044,422-133,076,881	6
SGK		Chromosome 6:134,532,081-134,680,889	6
SGK		Chromosome 6:134,532,081-134,680,889	6
SGK		Chromosome 6:134,532,081-134,680,889	6

MAP7		Chromosome 6:136,705,565-136,913,485	6
MAP3K5		Chromosome 6:136,919,878-137,155,349	6
MAP3K5		Chromosome 6:136,919,878-137,155,349	6
MAP3K5		Chromosome 6:136,919,878-137,155,349	6
MAP3K5		Chromosome 6:136,919,878-137,155,349	6
IL20RA		Chromosome 6:137,362,801-137,407,991	6
IL20RA		Chromosome 6:137,362,801-137,407,991	6
IL22RA2		Chromosome 6:137,506,650-137,536,478	6
TNFAIP3		Chromosome 6:138,230,274-138,246,142)	6
TNFAIP3		Chromosome 6:138,230,274-138,246,142)	6
C6orf91		Chromosome 6:139,158,950-139,266,900	6
C6orf91		Chromosome 6:139,158,950-139,266,900	6
HECA		Chromosome 6:139,497,942-139,543,639	6
HECA		Chromosome 6:139,497,942-139,543,639	6
CITED2	p300	Chromosome 6:139,735,089-139,737,478	6
CD83		Chromosome 6:14,225,715-14,245,128	6
CD83		Chromosome 6:14,225,715-14,245,128	6
HIVEP2	Schnurri 2	Chromosome 6:143,114,297-143,308,031	6
HIVEP2	Schnurri 2	Chromosome 6:143,114,297-143,308,031	6
HIVEP2	Schnurri 2	Chromosome 6:143,114,297-143,308,031	6
HIVEP2	Schnurri 2	Chromosome 6:143,114,297-143,308,031	6
ADAT2		Chromosome 6:143,788,765-143,813,517	6
ADAT2		Chromosome 6:143,788,765-143,813,517	6
PHACTR2		Chromosome 6:143,971,010-144,194,014	6
PHACTR2		Chromosome 6:143,971,010-144,194,014	6
PHACTR2		Chromosome 6:143,971,010-144,194,014	6
STX11	Syntaxin 11	Chromosome 6:144,513,356-144,551,200	6
STX11	Syntaxin 11	Chromosome 6:144,513,356-144,551,200	6
STX11	Syntaxin 11	Chromosome 6:144,513,356-144,551,200	6
UTRN		Chromosome 6:144,654,566-145,215,863	6
STXBP5		Chromosome 6:147,566,565-147,748,588	6
STXBP5		Chromosome 6:147,566,565-147,748,588	6
STXBP5		Chromosome 6:147,566,565-147,748,588	6
FLJ43763		Chromosome 6:148,313-151,392	6
FLJ43763		Chromosome 6:148,313-151,392	6
MAP3K7IP2	TAB2	Chromosome 6:149,680,756-149,774,442	6
MAP3K7IP2	TAB2	Chromosome 6:149,680,756-149,774,442	6
MAP3K7IP2	TAB2	Chromosome 6:149,680,756-149,774,442	6
MAP3K7IP2	TAB2	Chromosome 6:149,680,756-149,774,442	6
MAP3K7IP2	TAB2	Chromosome 6:149,680,756-149,774,442	6
MAP3K7IP2	TAB2	Chromosome 6:149,680,756-149,774,442	6
PPIL4		Chromosome 6:149,867,324-149,908,864	6
PCMT1		Chromosome 6:150,112,273-150,174,249	6
RAET1E	ULBP4	Chromosome 6:150,251,294-150,253,863	6
ULBP2		Chromosome 6:150,304,829-150,312,064	6
AKAP12		Chromosome 6:151,603,202-151,719,602	6
AKAP12		Chromosome 6:151,603,202-151,719,602	6
ESR1	Estrogen receptor alpha,	Chromosome 6:152,170,379-152,466,099	6
ESR1	Estrogen receptor alpha,	Chromosome 6:152,170,379-152,466,099	6
ESR1	Estrogen receptor alpha,	Chromosome 6:152,170,379-152,466,099	6
ESR1	Estrogen receptor alpha,	Chromosome 6:152,170,379-152,466,099	6
SYNE1		Chromosome 6:152,484,515-153,000,227	6
SYNE1		Chromosome 6:152,484,515-153,000,227	6
SYNE1		Chromosome 6:152,484,515-153,000,227	6
SYNE1		Chromosome 6:152,484,515-153,000,227	6
VIP		Chromosome 6:153,113,626-153,122,593	6

OPMR1	MOR	Chromosome 6:154,402,136-154,609,693	6
TFB1M		Chromosome 6:155,620,488-155,686,932	6
TFB1M		Chromosome 6:155,620,488-155,686,932	6
NOX3		Chromosome 6:155,758,194-155,818,729	6
NOX3		Chromosome 6:155,758,194-155,818,729	6
NOX3		Chromosome 6:155,758,194-155,818,729	6
ARID1B		Chromosome 6:157,140,756-157,572,094	6
ARID1B		Chromosome 6:157,140,756-157,572,094	6
SNX9		Chromosome 6:158,164,282-158,286,097	6
SNX9		Chromosome 6:158,164,282-158,286,097	6
GTF2H5		Chromosome 6:158,509,372-158,535,008	6
GTF2H5		Chromosome 6:158,509,372-158,535,008	6
GTF2H5		Chromosome 6:158,509,372-158,535,008	6
ATXN1		Chromosome 6:16,407,322-16,869,700	6
SOD2	IP01	Chromosome 6:160,020,138-160,034,343	6
WTAP		Chromosome 6:160,066,607-160,097,341	6
IGF2R	CD222	Chromosome 6:160,310,121-160,447,573	6
IGF2R	CD222	Chromosome 6:160,310,121-160,447,573	6
IGF2R	CD222	Chromosome 6:160,310,121-160,447,573	6
SLC22A1		Chromosome 6:160,462,853-160,499,740	6
SLC22A1		Chromosome 6:160,462,853-160,499,740	6
SLC22A1		Chromosome 6:160,462,853-160,499,740	6
AGPAT4		Chromosome 6:161,471,047-161,615,097	6
AGPAT4		Chromosome 6:161,471,047-161,615,097	6
AGPAT4		Chromosome 6:161,471,047-161,615,097	6
PARK2		Chromosome 6:161,688,442-163,068,793	6
PACRG		Chromosome 6:163,068,154-163,656,514	6
PDE10A		Chromosome 6:165,660,766-165,995,578	6
RPS6KA2		Chromosome 6:166,742,844-167,195,761	6
CCR6	CD196	Chromosome 6:167,332,660-167,473,174	6
CCR6	CD196	Chromosome 6:167,332,660-167,473,174	6
CCR6	CD196	Chromosome 6:167,332,660-167,473,174	6
C6orf123		Chromosome 6:167,928,066-167,940,388	6
C6orf123		Chromosome 6:167,928,066-167,940,388	6
FAM120B		Chromosome 6:170,457,769-170,556,162	6
FAM120B		Chromosome 6:170,457,769-170,556,162	6
FAM120B		Chromosome 6:170,457,769-170,556,162	6
PSMB1		Chromosome 6:170,686,134-170,704,312	6
PSMB1		Chromosome 6:170,686,134-170,704,312	6
TPMT		Chromosome 6:18,236,521-18,263,353	6
WRNIP1		Chromosome 6:2,710,665-2,731,926	6
SERPINB9	PI-9	Chromosome 6:2,832,499-2,848,513	6
CDKAL1		Chromosome 6:20,642,667-21,340,614	6
PRL	Prolactin	Chromosome 6:22,395,459-22,405,709	6
PRL	Prolactin	Chromosome 6:22,395,459-22,405,709	6
HDGFL1		Chromosome 6:22,677,657-22,679,871	6
HDGFL1		Chromosome 6:22,677,657-22,679,871	6
DUSP22		Chromosome 6:237,053-296,355	6
DUSP22		Chromosome 6:237,053-296,355	6
TTRAP		Chromosome 6:24,758,184-24,775,240	6
TTRAP		Chromosome 6:24,758,184-24,775,240	6
LRRC16A		Chromosome 6:25,387,285-25,728,737	6
HFE		Chromosome 6:26,195,427-26,205,038	6
BTN3A1	CD277	Chromosome 6:26,510,460-26,523,445	6
BTN3A1	CD277	Chromosome 6:26,510,460-26,523,445	6
PRSS16	thymus serine protease	Chromosome 6:27,323,487-27,332,327	6

PRSS16	thymus serine protease	Chromosome 6:27,323,487-27,332,327	6
ZNF192		Chromosome 6:28,217,695-28,233,215	6
ZNF192		Chromosome 6:28,217,695-28,233,215	6
ZNF193		Chromosome 6:28,301,046-28,309,239	6
FAT10		Chromosome 6:29,631,368-29,778,041	6
UBD	Ubiquitin	Chromosome 6:29,631,368-29,778,041	6
MOG		Chromosome 6:29,732,755-29,748,128	6
HLA-F		Chromosome 6:29,798,531-29,803,052	6
HLA-F		Chromosome 6:29,799,096-29,803,052	6
HLA-F		Chromosome 6:29,799,096-29,803,052	6
HLA-F		Chromosome 6:29,799,096-29,803,052	6
HLA-F		Chromosome 6:29,799,096-29,803,052	6
RPL23AP1		Chromosome 6:29,802,425-29,802,895	6
HLA-A		Chromosome 6:29,902,723-30,021,633	6
RIPK1		Chromosome 6:3,009,212-3,060,420	6
HLA-A	M6S204	Chromosome 6:30,018,310-30,021,633	6
HLA-A	M6S213	Chromosome 6:30,018,310-30,021,633	6
HLA-A		Chromosome 6:30,018,310-30,021,633	6
HLA-A		Chromosome 6:30,018,310-30,021,633	6
HLA-A		Chromosome 6:30,018,310-30,021,633	6
HLA-A		Chromosome 6:30,018,310-30,021,633	6
HLA-A		Chromosome 6:30,018,310-30,021,633	6
HCG4P4		Chromosome 6:30,030,962-30,031,390	6
ETF1P1		Chromosome 6:30,107,469-30,109,633	6
TRIM40		Chromosome 6:30,212,487-30,224,491	6
TRIM10		Chromosome 6:30,227,701-30,236,690	6
RPP21		Chromosome 6:30,420,877-30,422,649	6
RANP1		Chromosome 6:30,561,651-30,562,700	6
HLA-E		Chromosome 6:30,565,250-30,569,077	6
HLA-E		Chromosome 6:30,565,250-30,569,077	6
GNL1		Chromosome 6:30,621,633-30,632,987	6
MDC1		Chromosome 6:30,775,563-30,793,645	6
hcg-2038200		Chromosome 6:30,888,622-30,906,415	6
GTF2H4		Chromosome 6:30,983,956-30,989,859	6
C6orf205		Chromosome 6:31,059,474-31,065,654	6
HLABC-CA		Chromosome 6:31,344,505-31,432,935	6
HLA-C	MICB-CA	Chromosome 6:31,344,505-31,432,935	6
HLA-C		Chromosome 6:31,344,505-31,432,935	6
HLA-C		Chromosome 6:31,344,505-31,432,935	6
HLA-C		Chromosome 6:31,344,505-31,432,935	6
HLA-B		Chromosome 6:31,429,628-31,432,914	6
HLA-B		Chromosome 6:31,429,628-31,432,914	6
HLA-B		Chromosome 6:31,429,628-31,432,914	6
MICA		Chromosome 6:31,475,540-31,491,069	6
HCP5		Chromosome 6:31,538,938-31,541,565	6
MCCD1	LOC401250	Chromosome 6:31,604,718-31,605,987	6
LTA	TNFb	Chromosome 6:31,648,042-31,650,080	6
LTA	TNFb	Chromosome 6:31,648,042-31,650,080	6
LTA	TNFb	Chromosome 6:31,648,042-31,650,080	6
LTA	TNFb	Chromosome 6:31,648,042-31,650,080	6
LTA	TNFb	Chromosome 6:31,648,042-31,650,080	6
LTA		Chromosome 6:31,648,072-31,650,077	6
TNF		Chromosome 6:31,651,329-31,654,091	6
AIF1		Chromosome 6:31,690,984-31,692,781	6
BAT2, BAT2 GT, BAT2CA		Chromosome 6:31,696,429-31,713,533	6
LY6G5C		Chromosome 6:31,752,440-31,759,796	6
HCG22		Chromosome 6:31129963-31135632	6

C2		Chromosome 6:32,003,473-32,021,428	6
C2		Chromosome 6:32,003,473-32,021,428	6
TNXB		Chromosome 6:32,084,175-32,185,131	6
FKBPL		Chromosome 6:32,204,462-32,206,045	6
NOTCH4		Chromosome 6:32,266,521-32,299,822	6
GPSM3		Chromosome 6:32,266,521-32,299,822	6
NOTCH4		Chromosome 6:32,270,598-32,299,822	6
C6orf10	TNFa/b	Chromosome 6:32,368,453-32,460,310	6
C6orf10		Chromosome 6:32,368,464-32,447,662	6
HLA-DRA		Chromosome 6:32,515,597-32,520,943	6
HLA-DRA	DRA_CA, HLA-DRB1	Chromosome 6:32,515,625-32,520,801	6
HLA-DRB1		Chromosome 6:32,654,524-32,665,603	6
HLA-DQA1		Chromosome 6:32,713,112-32,719,407	6
HLA-DPB1		Chromosome 6:32,735,222-32,754,296	6
HLA-DQB1	G5-11525, G51152, G511	Chromosome 6:32,735,222-32,754,296	6
HLA-DQB1		Chromosome 6:32,735,225-32,742,572	6
HLA-DQB2		Chromosome 6:32,831,445-32,839,446	6
HLA-DOB		Chromosome 6:32,888,518-32,892,803	6
TAP2		Chromosome 6:32,897,588-32,914,525	6
BRD2		Chromosome 6:33,044,415-33,057,075	6
HLA-DPB2		Chromosome 6:33,188,206-33,204,868	6
COL11A2		Chromosome 6:33,238,447-33,268,223	6
COL11A2	M2_4_25	Chromosome 6:33,238,447-33,268,223	6
COL11A2		Chromosome 6:33,238,447-33,268,223	6
SLC39A7		Chromosome 6:33,276,631-33,280,192	6
VPS52		Chromosome 6:33,326,027-33,347,640	6
TAPBP	Tapasin	Chromosome 6:33,375,449-33,390,142	6
BAK1		Chromosome 6:33,648,307-33,655,997	6
ITPR3		Chromosome 6:33,696,500-33,772,329	6
PACSIN1		Chromosome 6:34,541,883-34,610,984	6
PACSIN1		Chromosome 6:34,541,883-34,610,984	6
PPARD	PPARbeta, NR1C2	Chromosome 6:35,418,313-35,503,933	6
FKBP5	Calcineurin, Lymphoid eff	Chromosome 6:35,649,345-35,804,338	6
FKBP5	Calcineurin, Lymphoid eff	Chromosome 6:35,649,345-35,804,338	6
SRPK1	SFRS	Chromosome 6:35,908,789-35,996,942	6
SRPK1	SFRS	Chromosome 6:35,908,789-35,996,942	6
MAPK14	p38MAPK	Chromosome 6:36,103,551-36,186,513	6
MAPK13		Chromosome 6:36,129,769-36,215,820	6
MAPK13		Chromosome 6:36,129,769-36,215,820	6
STK38		Chromosome 6:36,569,647-36,623,234	6
STK38		Chromosome 6:36,569,647-36,623,234	6
CDKN1A		Chromosome 6:36,754,413-36,763,094	6
CDKN1A		Chromosome 6:36,754,413-36,763,094	6
PPIL1		Chromosome 6:36,930,581-36,950,778	6
PPIL1		Chromosome 6:36,930,581-36,950,778	6
PIM1	Pim-1	Chromosome 6:37,245,957-37,251,182	6
ZFAND3		Chromosome 6:37,895,285-38,230,375	6
ZFAND3		Chromosome 6:37,895,285-38,230,375	6
ZFAND3		Chromosome 6:37,895,285-38,230,375	6
BTBD9		Chromosome 6:38,250,711-38,673,848	6
BTBD9		Chromosome 6:38,250,711-38,673,848	6
DNAH8		Chromosome 6:38,792,313-39,106,545	6
DNAH8		Chromosome 6:38,792,313-39,106,545	6
DNAH8		Chromosome 6:38,792,313-39,106,545	6
DNAH8		Chromosome 6:38,792,313-39,106,545	6
DAAM2		Chromosome 6:39,868,120-39,980,622	6

DAAM2		Chromosome 6:39,868,120-39,980,622	6
UNC5CL		Chromosome 6:41,102,749-41,114,906	6
UNC5CL		Chromosome 6:41,102,749-41,114,906	6
TREML1	TLT1	Chromosome 6:41,224,979-41,230,048	6
TREML3		Chromosome 6:41,284,270-41,298,360	6
NCR2	CD336, NKp44	Chromosome 6:41,411,505-41,426,603	6
FOXP4		Chromosome 6:41,622,142-41,678,100	6
FOXP4		Chromosome 6:41,622,142-41,678,100	6
FOXP4		Chromosome 6:41,622,142-41,678,100	6
CCND3		Chromosome 6:42,010,649-42,124,404	6
CCND3		Chromosome 6:42,010,649-42,124,404	6
TRERF1		Chromosome 6:42,300,647-42,527,767	6
TRERF1		Chromosome 6:42,300,647-42,527,767	6
TRERF1		Chromosome 6:42,300,647-42,527,767	6
TRERF1		Chromosome 6:42,300,647-42,527,767	6
PEX6		Chromosome 6:43,039,586-43,054,936	6
PEX6		Chromosome 6:43,039,586-43,054,936	6
PTK7		Chromosome 6:43,152,007-43,237,435	6
VEGFA		Chromosome 6:43,845,924-43,862,202	6
VEGFA		Chromosome 6:43,845,924-43,862,202	6
HSP90AB1	HSP90	Chromosome 6:44,322,802-44,329,598	6
HSP90AB1	HSP90	Chromosome 6:44,322,802-44,329,598	6
NFKBIE		Chromosome 6:44,333,881-44,341,503	6
RUNX2		Chromosome 6:45,404,032-45,626,797	6
CYP39A1		Chromosome 6:46,625,404-46,728,482	6
CYP39A1		Chromosome 6:46,625,404-46,728,482	6
CYP39A1		Chromosome 6:46,625,404-46,728,482	6
PLA2G7	phospholipase A2	Chromosome 6:46,779,897-46,811,389	6
TNFRSF21		Chromosome 6:47,307,227-47,385,639	6
TNFRSF21		Chromosome 6:47,307,227-47,385,639	6
TNFRSF21		Chromosome 6:47,307,227-47,385,639	6
CD2AP		Chromosome 6:47,553,899-47,702,620	6
CD2AP		Chromosome 6:47,553,899-47,702,620	6
C6orf138		Chromosome 6:47,953,998-48,144,384	6
C6orf138		Chromosome 6:47,953,998-48,144,384	6
C6orf138		Chromosome 6:47,953,998-48,144,384	6
RHAG	CD241	Chromosome 6:49,680,830-49,712,511	6
RHAG	CD241	Chromosome 6:49,680,830-49,712,511	6
DFB114		Chromosome 6:50,035,964-50,039,777	6
DFB110		Chromosome 6:50,084,810-50,097,607	6
PKHD1		Chromosome 6:51,588,104-52,060,382	6
PKHD1		Chromosome 6:51,588,104-52,060,382	6
PKHD1		Chromosome 6:51,588,104-52,060,382	6
PKHD1		Chromosome 6:51,588,104-52,060,382	6
IL17A		Chromosome 6:52,159,144-52,163,395	6
IL17F		Chromosome 6:52,209,438-52,217,257	6
IL17F		Chromosome 6:52,209,438-52,217,257	6
EFHC1		Chromosome 6:52,392,953-52,468,540	6
TRAM2		Chromosome 6:52,470,159-52,549,821	6
GSTA1	Gluthation-S-transferase	Chromosome 6:52,764,183-52,776,616	6
GCLC		Chromosome 6:53,470,098-53,517,790	6
GCLC		Chromosome 6:53,470,098-53,517,790	6
GFRAL		Chromosome 6:55,300,226-55,375,250	6
GFRAL		Chromosome 6:55,300,226-55,375,250	6
BMP5	BMP5	Chromosome 6:55,726,402-55,848,334	6
BMP5	BMP5	Chromosome 6:55,726,402-55,848,334	6

BMP5	BMP5	Chromosome 6:55,726,402-55,848,334	6
BMP5	BMP5	Chromosome 6:55,726,402-55,848,334	6
COL21A1		Chromosome 6:56,029,347-56,366,851	6
COL21A1		Chromosome 6:56,029,347-56,366,851	6
COL21A1		Chromosome 6:56,029,347-56,366,851	6
C6orf65		Chromosome 6:56,927,732-57,000,099	6
ZNF451		Chromosome 6:57,019,470-57,143,057	6
BAG2		Chromosome 6:57,145,083-57,157,694	6
LY86	MD1	Chromosome 6:6,533,340-6,600,215	6
LY86	MD1	Chromosome 6:6,533,340-6,600,215	6
LY86	MD1	Chromosome 6:6,533,340-6,600,215	6
KHDRBS2		Chromosome 6:62,447,824-63,054,091	6
FKBP1AC		Chromosome 6:63,964,538-63,980,909	6
FKBP1AC		Chromosome 6:63,964,538-63,980,909	6
PTP4A1		Chromosome 6:64,339,879-64,351,448	6
EYS		Chromosome 6:66,095,895-66,473,839	6
BAI3		Chromosome 6:69,401,980-70,156,124	6
DSP		Chromosome 6:7,486,869-7,531,945	6
DSP		Chromosome 6:7,486,869-7,531,945	6
DSP		Chromosome 6:7,486,869-7,531,945	6
BMP6	BMP6	Chromosome 6:7,672,009-7,826,752	6
BMP6	BMP6	Chromosome 6:7,672,009-7,826,752	6
KCNQ5		Chromosome 6:73,388,241-73,965,295	6
DDX43		Chromosome 6:74,161,192-74,184,013	6
DDX43		Chromosome 6:74,161,192-74,184,013	6
EEF1A1	EF-1 alpha	Chromosome 6:74,282,194-74,288,344	6
EEF1A1	EF-1 alpha	Chromosome 6:74,282,194-74,288,344	6
CD109		Chromosome 6:74,462,548-74,591,509	6
CD109		Chromosome 6:74,462,548-74,591,509	6
CD109		Chromosome 6:74,462,548-74,591,509	6
HTR1B	5-HTR1B	Chromosome 6:78,228,641-78,229,900	6
HTR1B	5-HTR1B	Chromosome 6:78,228,641-78,229,900	6
IRAK1BP1		Chromosome 6:79,633,908-79,665,039	6
IRAK1BP1		Chromosome 6:79,633,908-79,665,039	6
HMGN3		Chromosome 6:79,967,681-80,001,174	6
HMGN3		Chromosome 6:79,967,681-80,001,174	6
BCKDHB		Chromosome 6:80,873,083-81,112,706	6
BCKDHB		Chromosome 6:80,873,083-81,112,706	6
BCKDHB		Chromosome 6:80,873,083-81,112,706	6
NT5E	CD73	Chromosome 6:86,216,528-86,262,215	6
NT5E	CD73	Chromosome 6:86,216,528-86,262,215	6
LOC643962		Chromosome 6:87,597,028-87,709,921	6
LOC643962		Chromosome 6:87,597,028-87,709,921	6
CGA	CGA	Chromosome 6:87,851,935-87,861,569	6
OFCC1		Chromosome 6:9,813,644-10,168,908	6
ANKRD6		Chromosome 6:90,199,616-90,400,123	6
ANKRD6		Chromosome 6:90,199,616-90,400,123	6
ANKRD6		Chromosome 6:90,199,616-90,400,123	6
CASP8AP2	FLASH	Chromosome 6:90,596,349-90,640,876	6
MAP3K7	TAK1	Chromosome 6:91,280,013-91,353,628	6
MAP3K7	TAK1	Chromosome 6:91,280,013-91,353,628	6
EPHA7		Chromosome 6:94,007,860-94,185,993	6
EPHA7		Chromosome 6:94,007,860-94,185,993	6
KLHL32		Chromosome 6:97,479,217-97,695,351	6
KLHL32		Chromosome 6:97,479,217-97,695,351	6
KLHL32		Chromosome 6:97,479,217-97,695,351	6

EPO		Chromosome 7:100,156,359-100,159,259	7
ACHE		Chromosome 7:100,325,551-100,331,651	7
ACHE		Chromosome 7:100,325,551-100,331,651	7
ACHE		Chromosome 7:100,325,551-100,331,651	7
SERPINE1	Plasminogen activator inh	Chromosome 7:100,557,172-100,569,026	7
SERPINE1	Plasminogen activator inh	Chromosome 7:100,557,172-100,569,026	7
APS	SH2 adaptor protein	Chromosome 7:101,715,172-101,748,898	7
ALKBH4		Chromosome 7:101,883,690-101,892,293	7
ALKBH4		Chromosome 7:101,883,690-101,892,293	7
RELN		Chromosome 7:102,899,473-103,417,199	7
RELN		Chromosome 7:102,899,473-103,417,199	7
RELN		Chromosome 7:102,899,473-103,417,199	7
RELN		Chromosome 7:102,899,473-103,417,199	7
RELN		Chromosome 7:102,899,473-103,417,199	7
RELN		Chromosome 7:102,899,473-103,417,199	7
SRPK2	SFRS	Chromosome 7:104,544,059-104,816,577	7
SRPK2	SFRS	Chromosome 7:104,544,059-104,816,577	7
SRPK2	SFRS	Chromosome 7:104,544,059-104,816,577	7
SRPK2	SFRS	Chromosome 7:104,544,059-104,816,577	7
SRPK2	SFRS	Chromosome 7:104,544,059-104,816,577	7
PBEF1	visfatin	Chromosome 7:105,677,892-105,712,603	7
PBEF1	visfatin	Chromosome 7:105,677,892-105,712,603	7
PBEF1	visfatin	Chromosome 7:105,677,892-105,712,603	7
PIK3CG		Chromosome 7:106,292,977-106,334,828	7
PIK3CG		Chromosome 7:106,292,977-106,334,828	7
LAMB1		Chromosome 7:107,351,499-107,431,040	7
LAMB1		Chromosome 7:107,351,499-107,431,040	7
LAMB4		Chromosome 7:107,451,232-107,558,036	7
IFRD1		Chromosome 7:111,850,462-111,903,483	7
IFRD1		Chromosome 7:111,850,462-111,903,483	7
FOXP2		Chromosome 7:113,842,288-114,117,391	7
FOXP2		Chromosome 7:113,842,288-114,117,391	7
FOXP2		Chromosome 7:113,842,288-114,117,391	7
FOXP2		Chromosome 7:113,842,288-114,117,391	7
CAV1	Caveolin-1	Chromosome 7:115,952,075-115,988,466	7
CAV1	Caveolin-1	Chromosome 7:115,952,075-115,988,466	7
CAV1	Caveolin-1	Chromosome 7:115,952,075-115,988,466	7
MET		Chromosome 7:116,099,695-116,225,676	7
MET		Chromosome 7:116,099,695-116,225,676	7
MET		Chromosome 7:116,099,695-116,225,676	7
PTPRZ1		Chromosome 7:121,300,395-121,489,326	7
PTPRZ1		Chromosome 7:121,300,395-121,489,326	7
PTPRZ1		Chromosome 7:121,300,395-121,489,326	7
PTPRZ1		Chromosome 7:121,300,395-121,489,326	7
POT1		Chromosome 7:124,250,549-124,357,110	7
POT1		Chromosome 7:124,250,549-124,357,110	7
POT1		Chromosome 7:124,250,549-124,357,110	7
LEP		Chromosome 7:127,668,567-127,684,917	7
LEP		Chromosome 7:127,668,567-127,684,917	7
IRF5		Chromosome 7:128,365,230-128,377,325	7
IRF5		Chromosome 7:128,365,230-128,377,325	7
SMO		Chromosome 7:128,615,949-128,640,622	7
SMO		Chromosome 7:128,615,949-128,640,622	7
NRF1	NRF1	Chromosome 7:129,038,791-129,184,158	7
NRF1	NRF1	Chromosome 7:129,038,791-129,184,158	7
NRF1	NRF1	Chromosome 7:129,038,791-129,184,158	7

ETV1		Chromosome 7:13,897,379-13,995,289	7
ETV1		Chromosome 7:13,897,379-13,995,289	7
ETV1		Chromosome 7:13,897,379-13,995,289	7
ETV1		Chromosome 7:13,897,379-13,995,289	7
MKLN1	Mkln1	Chromosome 7:130,663,175-130,831,931	7
MKLN1	Mkln1	Chromosome 7:130,663,175-130,831,931	7
MKLN1	Mkln1	Chromosome 7:130,663,175-130,831,931	7
MKLN1	Mkln1	Chromosome 7:130,663,175-130,831,931	7
KLRG2		Chromosome 7:138,786,805-138,818,998	7
TBXAS1		Chromosome 7:139,124,668-139,366,560	7
TBXAS1		Chromosome 7:139,124,668-139,366,560	7
TBXAS1		Chromosome 7:139,124,668-139,366,560	7
TBXAS1		Chromosome 7:139,124,668-139,366,560	7
TBXAS1		Chromosome 7:139,124,668-139,366,560	7
TBXAS1		Chromosome 7:139,124,668-139,366,560	7
RAB19	Rab19	Chromosome 7:139,753,916-139,772,419	7
CLEC5A	MDL1	Chromosome 7:141,273,626-141,293,252	7
CLEC5A	MDL1	Chromosome 7:141,273,626-141,293,252	7
TRB@	TCR	Chromosome 7:141,645,314-142,221,097	7
TRB@	TCR	Chromosome 7:141,645,314-142,221,097	7
TRB@	TCR	Chromosome 7:141,645,314-142,221,097	7
TRB@	TCR	Chromosome 7:141,645,314-142,221,097	7
TRB@	TCR	Chromosome 7:141,645,314-142,221,097	7
TRB@	TCR	Chromosome 7:141,645,314-142,221,097	7
TRB@	TCR	Chromosome 7:141,645,314-142,221,097	7
KEL	CD238	Chromosome 7:142,348,323-142,369,625	7
KEL	CD238	Chromosome 7:142,348,323-142,369,625	7
CASP2		Chromosome 7:142,695,524-142,714,907	7
EPHA1	Ephrin R	Chromosome 7:142,798,327-142,816,107	7
EZH2		Chromosome 7:148,135,408-148,212,347	7
EZH2		Chromosome 7:148,135,408-148,212,347	7
EZH2		Chromosome 7:148,135,408-148,212,347	7
RARRES2	chemerin	Chromosome 7:149,666,351-149,669,696	7
RARRES2	chemerin	Chromosome 7:149,666,351-149,669,696	7
NOS3	NO synthase	Chromosome 7:150,319,080-150,342,609	7
NOS3	NO synthase	Chromosome 7:150,319,080-150,342,609	7
CDK5		Chromosome 7:150,381,832-150,385,929	7
SHH	sonic Hh	Chromosome 7:155,288,319-155,297,728	7
SHH	sonic Hh	Chromosome 7:155,288,319-155,297,728	7
PTPRN2	PTPRP	Chromosome 7:157,024,516-158,073,179	7
PTPRN2	PTPRP	Chromosome 7:157,024,516-158,073,179	7
PTPRN2	PTPRP	Chromosome 7:157,024,516-158,073,179	7
PTPRN2	PTPRP	Chromosome 7:157,024,516-158,073,179	7
PTPRN2	PTPRP	Chromosome 7:157,024,516-158,073,179	7
PTPRN2	PTPRP	Chromosome 7:157,024,516-158,073,179	7
PTPRN2	PTPRP	Chromosome 7:157,024,516-158,073,179	7
HDAC9		Chromosome 7:18,501,894-19,003,518	7
HDAC9		Chromosome 7:18,501,894-19,003,518	7
HDAC9		Chromosome 7:18,501,894-19,003,518	7
HDAC9		Chromosome 7:18,501,894-19,003,518	7
HDAC9		Chromosome 7:18,501,894-19,003,518	7
HDAC9		Chromosome 7:18,501,894-19,003,518	7
HDAC9		Chromosome 7:18,501,894-19,003,518	7
HDAC9		Chromosome 7:18,501,894-19,003,518	7
HDAC9		Chromosome 7:18,501,894-19,003,518	7
HDAC9		Chromosome 7:18,501,894-19,003,518	7

TWIST1	Twist1	Chromosome 7:19,121,616-19,123,820	7
TWIST1	Twist1	Chromosome 7:19,121,616-19,123,820	7
CARD11	CARMA1	Chromosome 7:2,912,308-3,050,025	7
CARD11	CARMA1	Chromosome 7:2,912,308-3,050,025	7
ITGB8		Chromosome 7:20,337,250-20,421,907	7
ITGB8		Chromosome 7:20,337,250-20,421,907	7
ITGB8		Chromosome 7:20,337,250-20,421,907	7
IL6		Chromosome 7:22,732,028-22,738,141	7
IL6		Chromosome 7:22,732,028-22,738,141	7
GPNMB		Chromosome 7:23,252,841-23,281,254	7
NPY		Chromosome 7:24,290,332-24,298,002	7
NPY		Chromosome 7:24,290,332-24,298,002	7
CYCS		Chromosome 7:25,124,800-25,131,480	7
HOXA5	HOX cluster	Chromosome 7:27,147,521-27,149,812	7
HOXA5	HOX cluster	Chromosome 7:27,147,521-27,149,812	7
NOD1	CARD4	Chromosome 7:30,430,672-30,484,833	7
CRHR2		Chromosome 7:30,658,725-30,706,244	7
CRF2R	CRF2R	Chromosome 7:30,658,725-30,706,244	7
AQP1	Aquaporin 1	Chromosome 7:30,917,993-30,931,656	7
AQP1	Aquaporin 1	Chromosome 7:30,917,993-30,931,656	7
FKBP9		Chromosome 7:32,963,577-33,013,067	7
FKBP9		Chromosome 7:32,963,577-33,013,067	7
TRG@	TCR	Chromosome 7:38,246,150-38,374,181	7
TRG@	TCR	Chromosome 7:38,246,150-38,374,181	7
TRG@	TCR	Chromosome 7:38,246,150-38,374,181	7
TRG@	TCR	Chromosome 7:38,246,150-38,374,181	7
FOXK1		Chromosome 7:4,688,456-4,777,600	7
FOXK1		Chromosome 7:4,688,456-4,777,600	7
INHBA	Inhibin B, Activin A	Chromosome 7:41,695,126-41,709,231	7
INHBA	Inhibin B, Activin A	Chromosome 7:41,695,126-41,709,231	7
GLI3	Gli3	Chromosome 7:41,970,196-42,241,712	7
GLI3	Gli3	Chromosome 7:41,970,196-42,241,712	7
GLI3	Gli3	Chromosome 7:41,970,196-42,241,712	7
GLI3	Gli3	Chromosome 7:41,970,196-42,241,712	7
STK17A		Chromosome 7:43,589,251-43,632,247	7
STK17A		Chromosome 7:43,589,251-43,632,247	7
STK17A		Chromosome 7:43,589,251-43,632,247	7
GCK		Chromosome 7:44,150,395-44,195,563	7
GCK		Chromosome 7:44,150,395-44,195,563	7
DDX56		Chromosome 7:44,571,928-44,581,175	7
DDX56		Chromosome 7:44,571,928-44,581,175	7
PPIA		Chromosome 7:44,802,777-44,809,240	7
PPIA		Chromosome 7:44,802,777-44,809,240	7
MYO1G	HA-2	Chromosome 7:44,968,786-44,985,203	7
ACTB	F-actin	Chromosome 7:5,533,312-5,536,747	7
IKZF1	Ikaros	Chromosome 7:50,314,924-50,438,053	7
GRB10	Grb10/Grb1R	Chromosome 7:50,625,259-50,828,652	7
GRB10	Grb10/Grb1R	Chromosome 7:50,625,259-50,828,652	7
GRB10	Grb10/Grb1R	Chromosome 7:50,625,259-50,828,652	7
EGFR		Chromosome 7:55,054,219-55,242,525	7
FKBP9L		Chromosome 7:55,716,261-55,748,439	7
RAC1	Rac1	Chromosome 7:6,380,651-6,410,123	7
RAC1	Rac1	Chromosome 7:6,380,651-6,410,123	7
GUSB	glucuronidase beta - MPS	Chromosome 7:65,063,110-65,084,635	7
GUSB	glucuronidase beta - MPS	Chromosome 7:65,063,110-65,084,635	7
RPA3		Chromosome 7:7,643,100-7,724,763	7

RPA3		Chromosome 7:7,643,100-7,724,763	7
FZD9	CD349	Chromosome 7:72,486,045-72,488,386	7
CLDN3		Chromosome 7:72,821,263-72,822,536	7
LAT2	NTA, LAB, TFII-1, WBSC	Chromosome 7:73,262,023-73,282,100	7
LAT2	NTA, LAB, TFII-1, WBSC	Chromosome 7:73,262,023-73,282,100	7
CLIP2	CYLN2	Chromosome 7:73,341,741-73,458,201	7
CLIP2	CYLN2	Chromosome 7:73,341,741-73,458,201	7
GTF2IRD1	TFII-1	Chromosome 7:73,506,056-73,654,853	7
GTF2IRD1	TFII-1	Chromosome 7:73,506,056-73,654,853	7
GTF2I		Chromosome 7:73,709,966-73,812,958	7
NCF1	neutrophil cytosolic factor	Chromosome 7:73,826,245-73,841,595	7
GTF2IRD2		Chromosome 7:73,848,420-73,905,777	7
PMS2L3	PMS2L9	Chromosome 7:74,975,005-74,995,389	7
PMS2L3	PMS2L9	Chromosome 7:74,975,005-74,995,389	7
CCL26		Chromosome 7:75,236,778-75,257,150	7
CCL26		Chromosome 7:75,236,778-75,257,150	7
HSPB1	HSP27/28	Chromosome 7:75,769,859-75,771,548	7
FGL2		Chromosome 7:76,662,535-76,667,080	7
FGL2		Chromosome 7:76,662,535-76,667,080	7
PTPN12		Chromosome 7:77,004,351-77,107,324	7
PTPN12		Chromosome 7:77,004,351-77,107,324	7
GNAI1	Gi	Chromosome 7:79,602,076-79,686,661	7
GNAI1	Gi	Chromosome 7:79,602,076-79,686,661	7
CD36	SCARB3	Chromosome 7:80,069,459-80,144,262	7
CD36	SCARB3	Chromosome 7:80,069,459-80,144,262	7
HGF	hepatocyte growth factor	Chromosome 7:81,166,258-81,237,388	7
HGF	hepatocyte growth factor	Chromosome 7:81,166,258-81,237,388	7
SEMA3E		Chromosome 7:82,831,158-83,116,260	7
SEMA3E		Chromosome 7:82,831,158-83,116,260	7
SEMA3E		Chromosome 7:82,831,158-83,116,260	7
SEMA3E		Chromosome 7:82,831,158-83,116,260	7
SEMA3E		Chromosome 7:82,831,158-83,116,260	7
SEMA3E		Chromosome 7:82,831,158-83,116,260	7
SEMA3E		Chromosome 7:82,831,158-83,116,260	7
SEMA3E		Chromosome 7:82,831,158-83,116,260	7
ABCB1	CD243, MDR1	Chromosome 7:86,970,884-87,180,500	7
ABCB1	CD243, MDR1	Chromosome 7:86,970,884-87,180,500	7
ABCB1	CD243, MDR1	Chromosome 7:86,970,884-87,180,500	7
ABCB1	CD243, MDR1	Chromosome 7:86,970,884-87,180,500	7
CYP51A1		Chromosome 7:91,579,402-91,601,946	7
CYP51A1		Chromosome 7:91,579,402-91,601,946	7
CYP51A1		Chromosome 7:91,579,402-91,601,946	7
CDK6		Chromosome 7:92,072,171-92,301,148	7
CDK6		Chromosome 7:92,072,171-92,301,148	7
CDK6		Chromosome 7:92,072,171-92,301,148	7
COL1A2	collagen alpha 2	Chromosome 7:93,861,809-93,898,480	7
COL1A2	collagen alpha 2	Chromosome 7:93,861,809-93,898,480	7
COL1A2	collagen alpha 2	Chromosome 7:93,861,809-93,898,480	7
DSS1		Chromosome 7:96,156,015-96,177,139	7
DSS1		Chromosome 7:96,156,015-96,177,139	7
Tac1	Substance P	Chromosome 7:97,199,311-97,207,720	7
Tac1	Substance P	Chromosome 7:97,199,311-97,207,720	7
BAIAP2L1		Chromosome 7:97,760,007-97,868,316	7
BAIAP2L1		Chromosome 7:97,760,007-97,868,316	7
CYP2W1		Chromosome 7:989,361-995,802	7
CYP2W1		Chromosome 7:989,361-995,802	7

CYP3A3	CYP3A4	Chromosome 7:99,083,437-99,219,744	7
CYP3A3	CYP3A4	Chromosome 7:99,083,437-99,219,744	7
CYP3A43		Chromosome 7:99,263,572-99,302,109	7
ZNF3		Chromosome 7:99,499,406-99,517,299	7
PILB	PILRbeta	Chromosome 7:99,771,673-99,803,388	7
PILB	PILRbeta	Chromosome 7:99,771,673-99,803,388	7
DEFA1A3		Chromosome 8	8
DEFA1A3		Chromosome 8	8
PINX1		Chromosome 8:10,659,883-10,734,796	8
PINX1		Chromosome 8:10,659,883-10,734,796	8
PINX1		Chromosome 8:10,659,883-10,734,796	8
YWHA2		Chromosome 8:102,000,090-102,034,745	8
YWHA2		Chromosome 8:102,000,090-102,034,745	8
KLF10	TIEG1	Chromosome 8:103,730,188-103,737,128	8
KLF10	TIEG1	Chromosome 8:103,730,188-103,737,128	8
BAALC		Chromosome 8:104,222,097-104,311,709	8
BAALC		Chromosome 8:104,222,097-104,311,709	8
TM7SF4	DC-HIL	Chromosome 8:105,421,228-105,438,092	8
TM7SF4	DC-HIL	Chromosome 8:105,421,228-105,438,092	8
ANGPT1	Angiopoietin 1	Chromosome 8:108,330,886-108,579,459	8
ANGPT1	Angiopoietin 1	Chromosome 8:108,330,886-108,579,459	8
ANGPT1	Angiopoietin 1	Chromosome 8:108,330,886-108,579,459	8
ANGPT1	Angiopoietin 1	Chromosome 8:108,330,886-108,579,459	8
ANGPT1	Angiopoietin 1	Chromosome 8:108,330,886-108,579,459	8
BLK		Chromosome 8:11,388,919-11,459,522	8
BLK		Chromosome 8:11,388,919-11,459,522	8
BLK		Chromosome 8:11,388,919-11,459,522	8
GATA4		Chromosome 8:11,599,122-11,654,920	8
DFB137		Chromosome 8:11,868,871-11,869,517	8
TRHR	TRH-R	Chromosome 8:110,168,900-110,200,989	8
TRHR	TRH-R	Chromosome 8:110,168,900-110,200,989	8
DFB130		Chromosome 8:12,212,843-12,220,196	8
TNFRSF11B		Chromosome 8:120,004,977-120,033,492	8
TNFRSF11B		Chromosome 8:120,004,977-120,033,492	8
NOV	CCN3	Chromosome 8:120,497,882-120,505,776	8
NOV	CCN3	Chromosome 8:120,497,882-120,505,776	8
COL14A1	undulin	Chromosome 8:121,206,533-121,453,454	8
COL14A1	undulin	Chromosome 8:121,206,533-121,453,454	8
COL14A1	undulin	Chromosome 8:121,206,533-121,453,454	8
MYC	c-myc	Chromosome 8:128,817,498-128,822,856	8
MYC	c-myc	Chromosome 8:128,817,498-128,822,856	8
CHRAC1	nucleosome remodelling	Chromosome 8:141,590,586-141,596,434	8
CHRAC1	nucleosome remodelling	Chromosome 8:141,590,586-141,596,434	8
CHRAC1	nucleosome remodelling	Chromosome 8:141,590,586-141,596,434	8
PTK2	FAK	Chromosome 8:141,737,683-142,080,514	8
PTK2	FAK	Chromosome 8:141,737,683-142,080,514	8
PTK2	FAK	Chromosome 8:141,737,683-142,080,514	8
PTP4A3		Chromosome 8:142,501,189-142,510,802	8
CYP11B1	11 beta hydroxylase	Chromosome 8:143,950,775-143,958,238	8
LY6E	Ly6E/A	Chromosome 8:144,171,274-144,175,199	8
MAPK15		Chromosome 8:144,870,498-144,876,619	8
MSR1	CD204, SR-A, SCARA1	Chromosome 8:16,009,761-16,094,595	8
MSR1	CD204, SR-A, SCARA1	Chromosome 8:16,009,761-16,094,595	8
MSR1	CD204, SR-A, SCARA1	Chromosome 8:16,009,761-16,094,595	8
FGF20	FGF20	Chromosome 8:16,894,049-16,904,061	8
FGF20	FGF20	Chromosome 8:16,894,049-16,904,061	8

FGF20	FGF20	Chromosome 8:16,894,049-16,904,061	8
NAT2		Chromosome 8:18,293,035-18,303,003	8
NAT2		Chromosome 8:18,293,035-18,303,003	8
DOK2		Chromosome 8:21,822,330-21,827,151	8
DOK2		Chromosome 8:21,822,330-21,827,151	8
FGF17	FGF17	Chromosome 8:21,955,883-21,962,266	8
FGF17	FGF17	Chromosome 8:21,955,883-21,962,266	8
PPP3CC		Chromosome 8:22,354,541-22,454,583	8
PPP3CC		Chromosome 8:22,354,541-22,454,583	8
EGR3		Chromosome 8:22,601,117-22,606,760	8
EGR3		Chromosome 8:22,601,117-22,606,760	8
EGR3		Chromosome 8:22,601,117-22,606,760	8
TNFRSF10B	CD262, TRAILR2	Chromosome 8:22,933,591-22,982,637	8
TNFRSF10B	CD262, TRAILR2	Chromosome 8:22,933,591-22,982,637	8
TNFRSF10C	CD263, TRAILR3	Chromosome 8:23,016,377-23,030,895	8
TNFRSF10D	CD264, TRAILR4	Chromosome 8:23,049,046-23,077,488	8
TNFRSF10D	CD264, TRAILR4	Chromosome 8:23,049,046-23,077,488	8
TNFRSF10A	CD261, TRAILR1	Chromosome 8:23,104,009-23,138,584	8
TNFRSF10A	CD261, TRAILR1	Chromosome 8:23,104,009-23,138,584	8
CHMP7	CHMP7	Chromosome 8:23,157,114-23,175,452	8
GNRH1	GNRH1	Chromosome 8:25,332,693-25,338,087	8
EBF2		Chromosome 8:25,757,490-25,958,292	8
EBF2		Chromosome 8:25,757,490-25,958,292	8
EBF2		Chromosome 8:25,757,490-25,958,292	8
EBF2		Chromosome 8:25,757,490-25,958,292	8
BNIP3L		Chromosome 8:26,296,331-26,326,562	8
PTK 2B	PYK2	Chromosome 8:27,224,916-27,372,824	8
PTK 2B	PYK2	Chromosome 8:27,224,916-27,372,824	8
PTK 2B	PYK2	Chromosome 8:27,224,916-27,372,824	8
CLU		Chromosome 8:27,510,351-27,528,288	8
CLU		Chromosome 8:27,510,351-27,528,288	8
SCARA3	SCARA3	Chromosome 8:27,547,304-27,590,211	8
SCARA5		Chromosome 8:27,783,655-27,906,117	8
DUSP4		Chromosome 8:29,249,530-29,264,104	8
DUSP4		Chromosome 8:29,249,530-29,264,104	8
GTF2E2		Chromosome 8:30,555,422-30,635,274	8
GTF2E2		Chromosome 8:30,555,422-30,635,274	8
GTF2E2		Chromosome 8:30,555,422-30,635,274	8
DUSP26		Chromosome 8:33,568,393-33,577,043	8
DUSP26		Chromosome 8:33,568,393-33,577,043	8
BAG4		Chromosome 8:38,153,263-38,189,966	8
BAG4		Chromosome 8:38,153,263-38,189,966	8
FGFR1		Chromosome 8:38,389,406-38,445,296	8
FGFR1		Chromosome 8:38,389,406-38,445,296	8
FGFR1		Chromosome 8:38,389,406-38,445,296	8
TACC1		Chromosome 8:38,734,008-38,829,703	8
TACC1		Chromosome 8:38,734,008-38,829,703	8
INDO	IDO	Chromosome 8:39,890,485-39,905,120	8
INDO	IDO	Chromosome 8:39,890,485-39,905,120	8
ANK1		Chromosome 8:41,629,901-41,873,437	8
ANK1		Chromosome 8:41,629,901-41,873,437	8
ANK1		Chromosome 8:41,629,901-41,873,437	8
ANK1		Chromosome 8:41,629,901-41,873,437	8
IKBKB	IKK2	Chromosome 8:42,247,986-42,309,130	8
IKBKB	IKK2	Chromosome 8:42,247,986-42,309,130	8
PRKDC	DNA-PK	Chromosome 8:48,848,222-49,035,296	8

OPRK1	KOR	Chromosome 8:54,300,829-54,326,747	8
OPRK1	KOR	Chromosome 8:54,300,829-54,326,747	8
LYN	Lyn	Chromosome 8:56,954,926-57,086,493	8
LYN	Lyn	Chromosome 8:56,954,926-57,086,493	8
LYN	Lyn	Chromosome 8:56,954,926-57,086,493	8
CYP7A1		Chromosome 8:59,565,292-59,575,275	8
CYP7A1		Chromosome 8:59,565,292-59,575,275	8
NSMAF		Chromosome 8:59,658,617-59,734,940	8
ANGPT2	Angiopoietin-2	Chromosome 8:6,344,580-6,408,338	8
ANGPT2	Angiopoietin-2	Chromosome 8:6,344,580-6,408,338	8
CYP7B1		Chromosome 8:65,671,246-65,873,902	8
CYP7B1		Chromosome 8:65,671,246-65,873,902	8
CYP7B1		Chromosome 8:65,671,246-65,873,902	8
CRH		Chromosome 8:67,251,166-67,253,380	8
TRAM1		Chromosome 8:71,648,227-71,683,158	8
LY96	MD2	Chromosome 8:75,066,141-75,103,859	8
LY96	MD2	Chromosome 8:75,066,141-75,103,859	8
HNF4G	NR2A2	Chromosome 8:76,482,826-76,641,623	8
HNF4G	NR2A2	Chromosome 8:76,482,826-76,641,623	8
HNF4G	NR2A2	Chromosome 8:76,482,826-76,641,623	8
PXMP3		Chromosome 8:78,057,713-78,074,994	8
PXMP3		Chromosome 8:78,057,713-78,074,994	8
IL7		Chromosome 8:79,807,560-79,880,313	8
IL7		Chromosome 8:79,807,560-79,880,313	8
IL7		Chromosome 8:79,807,560-79,880,313	8
CLDN23		Chromosome 8:8,597,076-8,599,026	8
CLDN23		Chromosome 8:8,597,076-8,599,026	8
PAG1	PAG	Chromosome 8:82,042,600-82,186,858	8
PAG1	PAG	Chromosome 8:82,042,600-82,186,858	8
FABP5	FABP5	Chromosome 8:82,355,326-82,359,563	8
FABP5	FABP5	Chromosome 8:82,355,326-82,359,563	8
FABP4	FABP4	Chromosome 8:82,553,481-82,558,023	8
CHMP4C	CHMP4C	Chromosome 8:82,807,243-82,834,305	8
CHMP4C	CHMP4C	Chromosome 8:82,807,243-82,834,305	8
MMP16		Chromosome 8:89,118,576-89,408,892	8
MMP16		Chromosome 8:89,118,576-89,408,892	8
MMP16		Chromosome 8:89,118,576-89,408,892	8
MMP16		Chromosome 8:89,118,576-89,408,892	8
MMP16		Chromosome 8:89,118,576-89,408,892	8
RIPK2	CARD3, RIP2, RICK	Chromosome 8:90,839,110-90,872,433	8
RIPK2	CARD3, RIP2, RICK	Chromosome 8:90,839,110-90,872,433	8
NBS1	NBS1	Chromosome 8:91,014,740-91,066,075	8
RUNX1T1		Chromosome 8:93,040,328-93,176,619	8
RUNX1T1		Chromosome 8:93,040,328-93,176,619	8
RUNX1T1		Chromosome 8:93,040,328-93,176,619	8
GEM	GEM	Chromosome 8:95,330,657-95,343,733	8
GEM	GEM	Chromosome 8:95,330,657-95,343,733	8
CCNE2		Chromosome 8:95,961,628-95,976,660	8
CCNE2		Chromosome 8:95,961,628-95,976,660	8
PTDSS1		Chromosome 8:97,343,340-97,415,950	8
PTDSS1		Chromosome 8:97,343,340-97,415,950	8
PTDSS1		Chromosome 8:97,343,340-97,415,950	8
PTDSS1		Chromosome 8:97,343,340-97,415,950	8
SDC2	Syndecan	Chromosome 8:97,575,058-97,693,213	8
SDC2	Syndecan	Chromosome 8:97,575,058-97,693,213	8
SDC2	Syndecan	Chromosome 8:97,575,058-97,693,213	8

POP1		Chromosome 8:99,199,244-99,239,816	8
POP1		Chromosome 8:99,199,244-99,239,816	8
POP1		Chromosome 8:99,199,244-99,239,816	8
STK3		Chromosome 8:99,536,041-99,907,085	8
STK3		Chromosome 8:99,536,041-99,907,085	8
STK3		Chromosome 8:99,536,041-99,907,085	8
STK3		Chromosome 8:99,536,041-99,907,085	8
STK3		Chromosome 8:99,536,041-99,907,085	8
IL6RL1		Chromosome 9	9
IL6RL1		Chromosome 9	9
TGFBR1		Chromosome 9:100,907,233-100,956,406	9
TGFBR1		Chromosome 9:100,907,233-100,956,406	9
SEC61B		Chromosome 9:101,024,380-101,032,722	9
NR4A3		Chromosome 9:101,623,958-101,668,994	9
NR4A3		Chromosome 9:101,623,958-101,668,994	9
PPP3R2		Chromosome 9:103,393,718-103,397,104	9
PPP3R2		Chromosome 9:103,393,718-103,397,104	9
SLC44A1	CDW92	Chromosome 9:107,046,724-107,241,273	9
SLC44A1	CDW92	Chromosome 9:107,046,724-107,241,273	9
TAL2		Chromosome 9:107,464,599-107,465,214	9
ACTL7B		Chromosome 9:110,656,692-110,659,068	9
ACTL7B		Chromosome 9:110,656,692-110,659,068	9
PTPN3		Chromosome 9:111,177,800-111,300,407	9
PTPN3		Chromosome 9:111,177,800-111,300,407	9
TXN	Txk, Rlk, thioredoxin	Chromosome 9:112,045,912-112,058,741	9
TXN	Txk, Rlk, thioredoxin	Chromosome 9:112,045,912-112,058,741	9
SVEP1/MUSK		Chromosome 9:112,431,057-112,431,557	9
LTB4DH		Chromosome 9:113,364,678-113,401,917	9
LTB4DH		Chromosome 9:113,364,678-113,401,917	9
UGCG		Chromosome 9:113,698,867-113,737,470	9
UGCG		Chromosome 9:113,698,867-113,737,470	9
UGCG		Chromosome 9:113,698,867-113,737,470	9
FKBP15		Chromosome 9:114,967,620-115,024,010	9
FKBP15		Chromosome 9:114,967,620-115,024,010	9
POLE3		Chromosome 9:115,209,336-115,212,773	9
POLE3		Chromosome 9:115,209,336-115,212,773	9
ORM1	ORM3	Chromosome 9:116,125,157-116,128,578	9
ORM2		Chromosome 9:116,131,890-116,135,357	9
TNFSF15		Chromosome 9:116,591,421-116,608,229	9
TNFSF15		Chromosome 9:116,591,421-116,608,229	9
TNFSF8	CD153	Chromosome 9:116,704,945-116,732,591	9
TNC	tenascin	Chromosome 9:116,822,634-116,920,260	9
TNC	tenascin	Chromosome 9:116,822,634-116,920,260	9
TLR4	CD284	Chromosome 9:119,506,405-119,519,589	9
TLR4	CD284	Chromosome 9:119,506,405-119,519,589	9
TRAF1		Chromosome 9:122,704,492-122,730,868	9
TRAF1		Chromosome 9:122,704,492-122,730,868	9
C5		Chromosome 9:122,754,434-122,852,375	9
PTGS1	PG synthase	Chromosome 9:124,173,050-124,197,802	9
PTGS1	PG synthase	Chromosome 9:124,173,050-124,197,802	9
PSMB7		Chromosome 9:126,155,565-126,217,542	9
PSMB7		Chromosome 9:126,155,565-126,217,542	9
NR5A1		Chromosome 9:126,283,336-126,309,530	9
NR6A1	NR6A1	Chromosome 9:126,319,380-126,573,410	9
NR6A1	NR6A1	Chromosome 9:126,319,380-126,573,410	9
HSPA5	grp78	Chromosome 9:127,036,953-127,043,430	9

CDK9	pTEFb	Chromosome 9:129,587,898-129,592,887	9
CDK9	pTEFb	Chromosome 9:129,587,898-129,592,887	9
ENG	CD105, TGF beta recepto	Chromosome 9:129,617,112-129,656,856	9
LCN2	LCN2	Chromosome 9:129,951,171-129,956,333	9
SET		Chromosome 9:130,485,844-130,498,488	9
PPP2R4	PP2A	Chromosome 9:130,913,050-130,951,046	9
PTGES		Chromosome 9:131,540,433-131,555,165	9
PTGES		Chromosome 9:131,540,433-131,555,165	9
GPR107		Chromosome 9:131,855,526-131,942,264	9
GPR107		Chromosome 9:131,855,526-131,942,264	9
GPR107		Chromosome 9:131,855,526-131,942,264	9
LAMC3		Chromosome 9:132,874,325-132,958,267	9
LAMC3		Chromosome 9:132,874,325-132,958,267	9
RAPGEF1	C3G	Chromosome 9:133,441,978-133,605,282	9
RAPGEF1	C3G	Chromosome 9:133,441,978-133,605,282	9
DDX31		Chromosome 9:134,458,205-134,535,609	9
DDX31		Chromosome 9:134,458,205-134,535,609	9
GTF3C5		Chromosome 9:134,895,897-134,923,709	9
GTF3C5		Chromosome 9:134,895,897-134,923,709	9
ABO		Chromosome 9:135,120,384-135,140,451	9
ADAMTS13		Chromosome 9:135,276,941-135,314,329	9
ADAMTS13		Chromosome 9:135,276,941-135,314,329	9
VAV2		Chromosome 9:135,616,837-135,847,547	9
VAV2		Chromosome 9:135,616,837-135,847,547	9
VAV2		Chromosome 9:135,616,837-135,847,547	9
VAV2		Chromosome 9:135,616,837-135,847,547	9
VAV2		Chromosome 9:135,616,837-135,847,547	9
COL5A1		Chromosome 9:136,673,473-136,876,510	9
FCN1	ficolin	Chromosome 9:136,940,837-136,949,630	9
NOTCH1	Notch 1	Chromosome 9:138,508,717-138,560,135	9
TRAF2		Chromosome 9:138,900,786-138,940,888	9
NOXA1		Chromosome 9:139,437,668-139,448,679	9
NOXA1		Chromosome 9:139,437,668-139,448,679	9
LEDGF	p75	Chromosome 9:15,454,064-15,501,017	9
LEDGF	p75	Chromosome 9:15,454,064-15,501,017	9
SMARCA2	SWI/SNF	Chromosome 9:2,005,342-2,183,624	9
SMARCA2	SWI/SNF	Chromosome 9:2,005,342-2,183,624	9
SMARCA2	SWI/SNF	Chromosome 9:2,005,342-2,183,624	9
KIAA0020	HA-8, PEN, CD162R	Chromosome 9:2,794,152-2,834,095	9
KIAA0020	HA-8, PEN, CD162R	Chromosome 9:2,794,152-2,834,095	9
IFNB1	IRG47	Chromosome 9:21,067,104-21,067,962	9
IFNB1	IRG47	Chromosome 9:21,067,104-21,067,962	9
IFNW1		Chromosome 9:21,130,213-21,132,144	9
IFNA7		Chromosome 9:21,191,234-21,229,990	9
IFNA13		Chromosome 9:21,357,423-21,358,961	9
IFNE1		Chromosome 9:21,470,838-21,472,312	9
IFNE1		Chromosome 9:21,470,838-21,472,312	9
CDKN2A		Chromosome 9:21,957,751-21,984,490	9
CDKN2A		Chromosome 9:21,957,751-21,984,490	9
CDKN2B		Chromosome 9:21,992,902-21,999,312	9
PLAA	PLA activatinp protein	Chromosome 9:26,894,081-26,937,461	9
TEK	CD202b	Chromosome 9:27,099,236-27,220,173	9
TEK	CD202b	Chromosome 9:27,099,236-27,220,173	9
TEK	CD202b	Chromosome 9:27,099,236-27,220,173	9
IFNK		Chromosome 9:27,514,302-27,516,496	9
RFX3	RFX3	Chromosome 9:3,208,297-3,515,983	9

RFX3	RFX3	Chromosome 9:3,208,297-3,515,983	9
RFX3	RFX3	Chromosome 9:3,208,297-3,515,983	9
RFX3	RFX3	Chromosome 9:3,208,297-3,515,983	9
RFX3	RFX3	Chromosome 9:3,208,297-3,515,983	9
DDX58		Chromosome 9:32,445,300-32,516,322	9
DDX58		Chromosome 9:32,445,300-32,516,322	9
BAG1		Chromosome 9:33,242,469-33,254,744	9
CHMP5	CHMP5	Chromosome 9:33,254,167-33,271,525	9
IL11RA		Chromosome 9:34,636,635-34,651,884	9
IL11RA		Chromosome 9:34,636,635-34,651,884	9
Cd72		Chromosome 9:35,599,976-35,608,753	9
TLN1	Talin	Chromosome 9:35,687,334-35,722,369	9
TLN1	Talin	Chromosome 9:35,687,334-35,722,369	9
MELK	Melk	Chromosome 9:36,562,873-36,667,679	9
MELK	Melk	Chromosome 9:36,562,873-36,667,679	9
SHB		Chromosome 9:37,909,131-38,059,249	9
SHB		Chromosome 9:37,909,131-38,059,249	9
JAK2		Chromosome 9:4,975,245-5,118,183	9
JAK2		Chromosome 9:4,975,245-5,118,183	9
CD274	CD274, PD1 ligand 1, PD	Chromosome 9:5,440,525-5,460,547	9
CD274	CD274, PD1 ligand 1, PD	Chromosome 9:5,440,525-5,460,547	9
PDCD1LG2	CD273, PD1 ligand 2, PD	Chromosome 9:5,500,570-5,561,252	9
IL33		Chromosome 9:6,205,809-6,247,983	9
IL33		Chromosome 9:6,205,809-6,247,983	9
PRKACG		Chromosome 9:70,817,241-70,818,849	9
ANXA1	Annexin-1	Chromosome 9:74,956,493-74,975,129	9
ANXA1	Annexin-1	Chromosome 9:74,956,493-74,975,129	9
RORB	RORb, NR1F2	Chromosome 9:76,302,072-76,491,937	9
RORB	RORb, NR1F2	Chromosome 9:76,302,072-76,491,937	9
RORB	RORb, NR1F2	Chromosome 9:76,302,072-76,491,937	9
FOXB2		Chromosome 9:78,824,391-78,825,689	9
PTPRD		Chromosome 9:8,304,246-9,008,735	9
PTPRD		Chromosome 9:8,304,246-9,008,735	9
PTPRD		Chromosome 9:8,304,246-9,008,735	9
PTPRD		Chromosome 9:8,304,246-9,008,735	9
PTPRD		Chromosome 9:8,304,246-9,008,735	9
PTPRD		Chromosome 9:8,304,246-9,008,735	9
GAS1		Chromosome 9:88,749,098-88,751,924	9
DAPK1		Chromosome 9:89,301,963-89,513,369	9
DAPK1		Chromosome 9:89,301,963-89,513,369	9
DAPK1		Chromosome 9:89,301,963-89,513,369	9
DAPK1		Chromosome 9:89,301,963-89,513,369	9
CKS2		Chromosome 9:91,115,925-91,121,438	9
SEMA4D	CD100	Chromosome 9:91,181,972-91,302,708	9
SYK		Chromosome 9:92,603,890-92,700,652	9
SYK		Chromosome 9:92,603,890-92,700,652	9
NFIL3	nuclear factor interleukin	Chromosome 9:93,211,148-93,225,965	9
NFIL3	nuclear factor interleukin	Chromosome 9:93,211,148-93,225,965	9
PTCH1	Ptc	Chromosome 9:97,245,083-97,318,923	9
PTCH1	Ptc	Chromosome 9:97,245,083-97,318,923	9
PTCH1	Ptc	Chromosome 9:97,245,083-97,318,923	9
XPA		Chromosome 9:99,477,012-99,499,460	9
FOXE1		Chromosome 9:99,655,357-99,658,818	9
ANP32B	acidic nucelar phosphopr	Chromosome 9:99,785,462-99,818,046	9
BTK		Chromosome X:100,491,091-100,527,839	X
BTK		Chromosome X:100,491,091-100,527,839	X

IL1RAPL2		Chromosome X:103,697,652-104,898,478	X
IL1RAPL2		Chromosome X:103,697,652-104,898,478	X
IL1RAPL2		Chromosome X:103,697,652-104,898,478	X
IL1RAPL2		Chromosome X:103,697,652-104,898,478	X
IL1RAPL2		Chromosome X:103,697,652-104,898,478	X
IL1RAPL2		Chromosome X:103,697,652-104,898,478	X
IL1RAPL2		Chromosome X:103,697,652-104,898,478	X
IL1RAPL2		Chromosome X:103,697,652-104,898,478	X
IL1RAPL2		Chromosome X:103,697,652-104,898,478	X
IL1RAPL2		Chromosome X:103,697,652-104,898,478	X
IL1RAPL2		Chromosome X:103,697,652-104,898,478	X
IL1RAPL2		Chromosome X:103,697,652-104,898,478	X
IL1RAPL2		Chromosome X:103,697,652-104,898,478	X
GRAIL		Chromosome X:105,823,724-105,926,902	X
GRAIL		Chromosome X:105,823,724-105,926,902	X
GRAIL		Chromosome X:105,823,724-105,926,902	X
TSC22D3	DIP	Chromosome X:106,843,107-106,905,858	X
TSC22D3	DIP	Chromosome X:106,843,107-106,905,858	X
NLRP3P	NOD13	Chromosome X:107,103,687-107,105,431	X
COL4A6		Chromosome X:107,285,493-107,569,383	X
COL4A6		Chromosome X:107,285,493-107,569,383	X
COL4A6		Chromosome X:107,285,493-107,569,383	X
COL4A6		Chromosome X:107,285,493-107,569,383	X
COL4A5		Chromosome X:107,569,810-107,827,431	X
COL4A5		Chromosome X:107,569,810-107,827,431	X
PAK3		Chromosome X:110,226,244-110,350,816	X
IL13RA2	CD213a2	Chromosome X:114,144,794-114,159,792	X
AGTR2	Angiotensin receptor	Chromosome X:115,216,003-115,220,253	X
IL13RA1	CD213a1	Chromosome X:117,745,563-117,812,530	X
IL13RA1	CD213a1	Chromosome X:117,745,563-117,812,530	X
LAMP2	CD107b	Chromosome X:119,446,367-119,487,189	X
LAMP2	CD107b	Chromosome X:119,446,367-119,487,189	X
TLR7	CD287	Chromosome X:12,795,123-12,818,420	X
TLR8	CD288	Chromosome X:12,834,679-12,851,209	X
TMSB4X	thymosin beta 4	Chromosome X:12,903,148-12,905,267	X
BIRC4	XIAP	Chromosome X:122,821,558-122,875,510	X
BIRC4	XIAP	Chromosome X:122,821,558-122,875,510	X
SH2D1A	EAT2a, SAP	Chromosome X:123,307,875-123,334,686	X
SH2D1A	EAT2a, SAP	Chromosome X:123,307,875-123,334,686	X
SMARCA1	ISWI	Chromosome X:128,408,159-128,485,158	X
SMARCA1	ISWI	Chromosome X:128,408,159-128,485,158	X
SMARCA1	ISWI	Chromosome X:128,408,159-128,485,158	X
APLN	apelin	Chromosome X:128,607,006-128,616,595	X
APLN	apelin	Chromosome X:128,607,006-128,616,595	X
AIFM1	PDCD8	Chromosome X:129,091,018-129,127,489	X
AIFM1	PDCD8	Chromosome X:129,091,018-129,127,489	X
IGSF1		Chromosome X:130,235,161-130,361,358	X
IGSF1		Chromosome X:130,235,161-130,361,358	X
DDX26B		Chromosome X:134,482,215-134,544,100	X
SLC9A6	NHE-6	Chromosome X:134,895,264-134,957,089	X
SLC9A6	NHE-6	Chromosome X:134,895,264-134,957,089	X
CD40LG	CD40L, CD154, TNFSF5	Chromosome X:135,558,002-135,570,215	X
CD40LG	CD40L, CD154, TNFSF5	Chromosome X:135,558,002-135,570,215	X
FGF13	FGF13	Chromosome X:137,541,401-137,894,912	X
FGF13	FGF13	Chromosome X:137,541,401-137,894,912	X
FGF13	FGF13	Chromosome X:137,541,401-137,894,912	X

FGF13	FGF13	Chromosome X:137,541,401-137,894,912	X
FGF13	FGF13	Chromosome X:137,541,401-137,894,912	X
FGF13	FGF13	Chromosome X:137,541,401-137,894,912	X
CD99L2		Chromosome X:149,685,467-149,817,837	X
CD99L2		Chromosome X:149,685,467-149,817,837	X
FIGF	VEGFD	Chromosome X:15,273,639-15,312,498	X
FIGF	VEGFD	Chromosome X:15,273,639-15,312,498	X
FIGF	VEGFD	Chromosome X:15,273,639-15,312,498	X
BMX		Chromosome X:15,392,290-15,484,573	X
ACE2		Chromosome X:15,489,077-15,530,199	X
BGN		Chromosome X:152,413,591-152,428,206	X
BGN		Chromosome X:152,413,591-152,428,206	X
DUSP9		Chromosome X:152,561,182-152,569,975	X
L1CAM	CD171	Chromosome X:152,780,163-152,804,802	X
IRAK1	Pelle	Chromosome X:152,929,145-152,938,625	X
G6PD	G6PDH	Chromosome X:153,412,800-153,428,981	X
DKC1	dyskeratosis congenita	Chromosome X:153,644,229-153,659,158	X
SCML2		Chromosome X:18,167,355-18,282,768	X
SCML2		Chromosome X:18,167,355-18,282,768	X
MAP3K15		Chromosome X:19,288,095-19,443,363	X
MAP3K15		Chromosome X:19,288,095-19,443,363	X
MAP3K15		Chromosome X:19,288,095-19,443,363	X
SH3KBP1		Chromosome X:19,462,014-19,815,640	X
SH3KBP1		Chromosome X:19,462,014-19,815,640	X
SH3KBP1		Chromosome X:19,462,014-19,815,640	X
XG		Chromosome X:2,680,115-2,743,968	X
DDX53		Chromosome X:22,927,999-22,931,627	X
DDX53		Chromosome X:22,927,999-22,931,627	X
DDX53		Chromosome X:22,927,999-22,931,627	X
PRDX4		Chromosome X:23,592,300-23,614,437	X
IL1RAPL1		Chromosome X:28,515,437-29,884,761	X
IL1RAPL1		Chromosome X:28,515,437-29,884,761	X
IL1RAPL1		Chromosome X:28,515,437-29,884,761	X
IL1RAPL1		Chromosome X:28,515,437-29,884,761	X
IL1RAPL1		Chromosome X:28,515,437-29,884,761	X
IL1RAPL1		Chromosome X:28,515,437-29,884,761	X
IL1RAPL1		Chromosome X:28,515,437-29,884,761	X
IL1RAPL1		Chromosome X:28,515,437-29,884,761	X
IL1RAPL1		Chromosome X:28,515,437-29,884,761	X
IL1RAPL1		Chromosome X:28,515,437-29,884,761	X
IL1RAPL1		Chromosome X:28,515,437-29,884,761	X
NR0B1	NR0B1	Chromosome X:30,232,244-30,237,636	X
NR0B1	NR0B1	Chromosome X:30,232,244-30,237,636	X
NR0B1	NR0B1	Chromosome X:30,232,244-30,237,636	X
XK		Chromosome X:37,429,931-37,476,322	X
CYBB	NOX2	Chromosome X:37,524,208-37,557,658	X
TSPAN7	CD231	Chromosome X:38,305,553-38,433,118	X
TSPAN7	CD231	Chromosome X:38,305,553-38,433,118	X
DDX3X		Chromosome X:41,077,595-41,108,669	X
DDX3X		Chromosome X:41,077,595-41,108,669	X
DUSP21		Chromosome X:44,588,193-44,589,078	X
DUSP21		Chromosome X:44,588,193-44,589,078	X
SLC9A7	NHE-7	Chromosome X:46,349,697-46,503,434	X
SLC9A7	NHE-7	Chromosome X:46,349,697-46,503,434	X
SLC9A7	NHE-7	Chromosome X:46,349,697-46,503,434	X
TIMP1		Chromosome X:47,326,634-47,331,134	X

CFP	properdin, PFC	Chromosome X:47,368,557-47,374,648	X
WAS	Wiskott Aldrich, WASP	Chromosome X:48,427,112-48,434,762	X
SUV39H1	Suv39h1	Chromosome X:48,439,930-48,452,347	X
GATA1		Chromosome X:48,529,906-48,537,662	X
HDAC6		Chromosome X:48,545,170-48,568,336	X
FOXP3		Chromosome X:48,993,841-49,008,232	X
CCNB3		Chromosome X:49,856,156-50,111,653	X
CCNB3		Chromosome X:49,856,156-50,111,653	X
TSPYL2	CDA1	Chromosome X:53,128,274-53,134,447	X
TSPYL2	CDA1	Chromosome X:53,128,274-53,134,447	X
JARID1C	SMCY homolog	Chromosome X:53,238,059-53,271,329	X
JARID1C	SMCY homolog	Chromosome X:53,238,059-53,271,329	X
ALAS2	Alas2	Chromosome X:55,052,213-55,074,136	X
ALAS2	Alas2	Chromosome X:55,052,213-55,074,136	X
NLRP2P	NOD24	Chromosome X:57,719,936-57,723,438	X
AR	Androgen receptor, NR3C	Chromosome X:66,680,599-66,867,186	X
AR	Androgen receptor, NR3C	Chromosome X:66,680,599-66,867,186	X
EDA		Chromosome X:68,752,636-69,176,047	X
EDA		Chromosome X:68,752,636-69,176,047	X
EDA		Chromosome X:68,752,636-69,176,047	X
P2RY4	P2Y4	Chromosome X:69,394,741-69,396,379	X
P2RY4	P2Y4	Chromosome X:69,394,741-69,396,379	X
MLLT7	FOXO4	Chromosome X:70,232,772-70,240,110	X
IL2RG	CD132	Chromosome X:70,243,979-70,248,188	X
CXCR3	CD183	Chromosome X:70,752,491-70,755,092	X
CXCR3	CD183	Chromosome X:70,752,491-70,755,092	X
FLJ20105		Chromosome X:71,341,232-71,375,602	X
FLJ20105		Chromosome X:71,341,232-71,375,602	X
FLJ20105		Chromosome X:71,341,232-71,375,602	X
HDAC8		Chromosome X:71,466,091-71,709,623	X
HDAC8		Chromosome X:71,466,091-71,709,623	X
HDAC8		Chromosome X:71,466,091-71,709,623	X
FGF16	FGF16	Chromosome X:76,596,303-76,598,669	X
FGF16	FGF16	Chromosome X:76,596,303-76,598,669	X
CYSLTR1		Chromosome X:77,413,617-77,469,743	X
CYSLTR1		Chromosome X:77,413,617-77,469,743	X
TBL1X		Chromosome X:9,391,369-9,647,778	X
TBL1X		Chromosome X:9,391,369-9,647,778	X
TBL1X		Chromosome X:9,391,369-9,647,778	X
TBL1X		Chromosome X:9,391,369-9,647,778	X
DIAPH2		Chromosome X:95,826,365-96,746,652	X
DIAPH2		Chromosome X:95,826,365-96,746,652	X
DIAPH2		Chromosome X:95,826,365-96,746,652	X
DIAPH2		Chromosome X:95,826,365-96,746,652	X
DIAPH2		Chromosome X:95,826,365-96,746,652	X
DIAPH2		Chromosome X:95,826,365-96,746,652	X
DIAPH2		Chromosome X:95,826,365-96,746,652	X
DIAPH2		Chromosome X:95,826,365-96,746,652	X
DIAPH2		Chromosome X:95,826,365-96,746,652	X
DIAPH2		Chromosome X:95,826,365-96,746,652	X
DIAPH2		Chromosome X:95,826,365-96,746,652	X
NOX1		Chromosome X:99,984,969-100,015,990	X
NOX1		Chromosome X:99,984,969-100,015,990	X
USP9Y	A1/HY, DFFRY	Chromosome Y:13,322,554-13,482,162	Y
DDX3Y	DRB1*1501/HY, DBY, DQ	Chromosome Y:13,525,413-13,541,784	Y
DDX3Y	DRB1*1501/HY, DBY, DQ	Chromosome Y:13,525,413-13,541,784	Y

UTY	B60/HY	Chromosome Y:13,869,653-14,101,947	Y
UTY	B60/HY	Chromosome Y:13,869,653-14,101,947	Y
TMSB4Y	A33/HY	Chromosome Y:14,324,841-14,327,298	Y
CD24		Chromosome Y:19,611,898-19,614,093	Y
RPS4Y1	B52/HY	Chromosome Y:2,769,527-2,794,997	Y
RPS4Y1	B52/HY	Chromosome Y:2,769,527-2,794,997	Y
JARID1D	A2/HY, B7/HY, HLA-DQ5/	Chromosome Y:20,326,689-20,366,212	Y
TBL1Y		Chromosome Y:6,838,727-7,019,724	Y
TBL1Y		Chromosome Y:6,838,727-7,019,724	Y

Gene Start Position	Gene End Position	Internal marker name	Marker database name
1128751	1131952	TNFRSF18	new design
1,260,521	1,274,623	0119C03	D1S1394i
1,557,337	1,623,109	0109H08	D1S1252i
1,971,769	2,106,694	0114H07	D1S1708i
10,439,166	10,455,200	0113C07	D1S0305i
100,957,885	100,977,189	0113E08	D1S0467i
101,475,032	101,479,662	0108A11	D1S206
107,400,824	107,403,439	0119H04	D1S1192i
107,915,305	108,309,108	0111G07	D1S0718i
107,915,305	108,309,108	0108H03	D1S1026i
107,915,305	108,309,108	0117D07	D1S1469i
107,915,305	108,309,108	0104H04	D1S1607i
109,406,644	109,420,147	0101H03	G09558
109,892,824	109,938,498	0117B09	D1S0465i
109,892,824	109,938,498	0109E10	D1S1307i
11,009,167	11,029,877	0114H04	D1S0758i
11,009,167	11,029,877	0116B01	D1S1176i
11,089,179	11,245,176	0116C01	D1S0037i
11,089,179	11,245,176	0105B06	D1S0070i
11,089,179	11,245,176	0113B06	D1S0307i
11,768,367	11,788,702	0108B09	D1S0057i
11,828,353	11,830,989	0109E01	D1S2740
110,254,778	110,275,144	9902C03	D1S1016i
111,215,344	111,244,081	0117A09	D1S0464i
111,215,344	111,244,081	004C07	D1S2809
111,571,804	111,587,585	0114C11	D1S0836i
111,827,493	111,908,107	0117G08	D1S0458i
111,827,493	111,908,107	0102C07	D1S2789
111,886,363	112,060,836	0104A07	D1S2837
113,045,251	113,051,579	0108H10	D1S2756
114,092,981	114,215,904	0111B02	D1S0280i
114,092,981	114,215,904	0113E02	D1S0471i
114,911,701	114,925,788	0117C06	D1S1220i
115,048,613	115,102,147	0119C07	G12424
115,373,938	115,378,464	0102A02	D1S1693i
115,630,060	115,682,380	0110E08	D1S0034i
116,858,680	116,915,184	0112F09	D1S1147i
116,918,554	117,011,898	0113B12	D1S0455i
117,098,530	117,113,374	335G10	AL365325.4_109510
117,254,202	117,334,503	0106E06	D1S1532i
117,254,202	117,334,503	0109A03	D1S252
117,487,732	117,555,079	0111G04	D1S0475i
117,487,732	117,555,079	0115G02	D1S0644i
119,851,356	119,859,200	0112C03	D1S0895i
12,046,021	12,126,851	0116F09	D1S1559i
12,149,647	12,191,872	264A06	AL355998.4_40197
120,255,699	120,413,799	9902B01	D1S1785i
120728502	120737460	FCGR1B	new design
120728502	120737460	**FCGR1B2**	new design
144,236,248	144,255,225	T002F11	D1S2344
144,407,155	144,426,971	0102G04	D1S442
146,418,535	146,422,374	0110H02	D1S1378i
146,567,361	146,577,147	159F12	AL022240.8_87561
148,167,168	148,175,396	0113B01	D1S1407i
148,813,658	148,818,760	0119C12	D1S1299i

148,969,175	149,005,057	0101B10	D1S1006i
149,035,311	149,047,436	0111A05	D1S0479i
149,035,311	149,047,436	0119D06	D1S0483i
149,275,670	149,286,700	0113G07	D1S0513i
149,531,037	149,566,815	0118F04	D1S0139i
15,655,811	15,690,482	0104E01	D1S0157i
15,655,811	15,690,482	0118A12	D1S436
150,039,364	150,070,972	0108F12	D1S0489i
150,271,606	150,276,135	0119G12	D1S1490i
151,536,962	151,549,818	270A11	AL161636.7_109719
151,612,808	151,614,749	0119F05	D1S1558i
151,773,699	151,775,344	0111H06	D1S0685i
151,782,713	151,789,236	270G12	AL157404.7_111158
151,900,905	151,910,148	0110D05	D1S1454i
151,900,905	151,910,148	0101C02	Z67234
152,229,853	152,231,250	0116F05	D1S0498i
152,229,853	152,231,250	0109B03	D1S2858
152644293	152708550	IL6R1	new design
152644293	152708550	IL6R2	new design
153,213,753	153,218,348	336C06	AC027440.2_106016
153,366,560	153,374,010	0101F08	D1S1677i
153,424,924	153,429,330	0105D10	D1S0493i
154,700,143	154,737,244	690D09	DISD22_0000791
155,042,659	155,053,270	478G05	chr1.fa.O7frz.178252111
155,042,659	155,053,270	099D11	HUMUT2150
155,749,791	155,788,934	478C06	chr1.fa.O7frz.178941521
155,810,163	155,834,494	0119H03	D1S1317i
155,982,145	156,013,546	0115G06	D1S0009i
155,982,145	156,013,546	0116G01	D1S0030i
156,416,361	156,421,310	0108D08	D1S0898i
156,526,200	156,530,044	0117F06	D1S1291i
157,236,382	157,291,569	0112G02	D1S0886i
157,236,382	157,291,569	0105C04	Z67479
157,408,023	157,442,914	0106F05	D1S2635
157,526,128	157,544,638	0103A11	D1S1544i
157,948,703	157,951,003	0101E01	HUMUT1234
158,017,346	158,018,957	0102D01	D1S1636i
158,163,453	158,182,010	0119F10	D1S1617i
158,327,754	158,335,103	0105B03	D1S2707
158,603,481	158,609,262	0112D03	D1S0899i
158,721,444	158,759,676	0117E09	D1S0505i
158,915,160	158,948,265	0110H08	D1S0053i
159,032,552	159,064,669	0108D02	D1S0163i
159,231,625	159,275,404	336E06	AL354714.7_79226
159,231,625	159,275,404	0110F03	D1S1414i
159,451,693	159,457,113	0119H10	D1S1455i
159,466,079	159,474,590	0110G05	D1S1463i
159741844	159755984	FCGR2A	new design
159,859,610	159,867,620	0114F08	D1S0904i
16,046,946	16,139,542	0111C09	D1S0770i
160,631,680	160,648,552	0107H03	D1S0515i
163,636,778	163,681,057	0107C03	D1S2878
165,666,501	165,754,471	0109H06	D1S0005i
165,666,501	165,754,471	0115G11	D1S1554i
165,957,832	166,026,684	0109C03	D1S2750
166,776,626	166,779,859	0102H01	D1S0187i

166,812,335	166,817,939	0115C05	D1S0109i
167,750,028	167,822,450	0110A10	D1S0095i
167,824,661	167,866,031	0110D11	D1S0164i
167,824,661	167,866,031	0104F06	D1S0168i
167,926,432	167,947,463	0111B01	D1S0249i
17,507,277	17,563,086	0107H09	D1S1144i
170,894,777	170,902,637	0110G11	D1S0194i
170,894,777	170,902,637	0116D10	D1S0257i
171,275,723	171,286,679	0104C12	D1S0032i
171,275,723	171,286,679	0117C05	D1S0271i
171,419,493	171,443,094	0119F02	D1S0235i
171,419,493	171,443,094	0104G09	D1S1477i
171,713,028	171,724,569	0101F06	D1S1070i
172,139,562	172,153,139	479E02	chr1.fa.O7frz.196094961
173,303,617	173,383,825	0113E10	D1S0159i
173,558,558	173,979,529	160E02	AL021919.4_42117
173,558,558	173,979,529	0116G09	D1S0031i
173,558,558	173,979,529	0105F06	D1S0200i
173,558,558	173,979,529	0111G01	D1S0265i
173,558,558	173,979,529	0109H05	D1S1565
173,558,558	173,979,529	104D05	HUMUT417
177,085,293	177,106,838	0112G09	D1S1153i
177,317,735	177,333,653	0116G07	D1S0510i
177,317,735	177,333,653	0113F11	D1S0533i
178,390,591	178,439,788	0113F05	D1S0517i
178,390,591	178,439,788	0106C11	D1S2883
179,269,762	179,292,312	0115B10	D1S0542i
18,306,827	18,577,563	0116A06	D1S0315i
18,306,827	18,577,563	0112C12	D1S1227i
18,306,827	18,577,563	0102E10	D1S2826
18,306,827	18,577,563	0118E02	Z67335
181,075,127	181,123,510	0110H05	D1S1464i
181,075,127	181,123,510	0103B08	D1S2623
181,422,022	181,480,662	0113H02	D1S0682i
181,422,022	181,480,662	0112E12	D1S1236i
181,791,320	181,826,634	0110H06	D1S1488i
184,532,034	184,550,317	270C08	AC074116.5_2995
184,907,546	184,916,179	0113D07	D1S0134i
190,871,905	190,896,059	0101C07	D1S0261i
190,871,905	190,896,059	0112G08	D1S1098i
194,887,631	194,983,257	0116C10	D1S0102i
194,887,631	194,983,257	0118B06	D1S0250i
195,010,571	195,154,386	9902C05	D1S0537i
195,179,520	195,194,979	0104B03	D1S1417i
196,874,424	196,993,035	0101A08	Z67221
198,263,353	198,413,175	0107C11	D1S0540i
198,859,647	198,905,749	0115D11	D1S0687i
198,859,647	198,905,749	0110F07	D1S1514i
2479150	2486613	**TNF142**	new design
2479150	2486613	TNFRSF14	new design
20,311,019	20,318,637	0119B05	D1S1199i
20,311,019	20,318,637	0117C02	D1S1264i
20,311,019	20,318,637	0105A10	D1S2843
20,788,028	20,817,988	333C12	AL365439.2_120643
20,788,028	20,817,988	079D08	D1S1571
200,243,696	200,252,939	005G10	D1S2615

200,382,764	200,397,332	0109F03	D1S1727
200,403,802	200,425,104	0107D06	D1S0482i
201,326,405	201,403,156	0111F05	D1S0528i
201,326,405	201,403,156	0104D02	D1S0693i
201,326,405	201,403,156	0103D10	D1S2683
201,576,375	201,587,240	0108C09	D1S0543i
202,000,957	202,012,123	0113A12	HUMUT8081B
202,308,866	202,363,494	005D12	D1S2668
202,308,866	202,363,494	0118D09	D1S2717
202,658,379	202,726,175	9902D07	D1S1504i
202,752,134	202,793,871	0105G03	D1S0955i
203,278,963	203,313,761	337H04	AL359927.2_44777
203,278,963	203,313,761	0108D05	D1S1579i
203,833,330	203,868,623	0113F12	D1S0523i
204,710,414	204,736,846	0119B10	D1S1245i
204,875,504	204,924,381	0105F10	D1S1678i
204,924,912	204,974,251	0110H09	D1S0094i
205,007,570	205,012,462	IL10G	new design
205,038,838	205,082,949	0107C07	D1S2772
205,105,322	205,109,191	0111G05	D1S0548i
205,137,411	205,144,107	0106C01	D1S2735
205,328,810	205,339,961	006H01	D1S2727
205,344,230	205,384,940	0114A09	D1S1043i
205,561,476	205,600,934	0117G09	D1S0534i
205,694,198	205,729,863	0115A01	D1S1205i
205,736,096	205,881,733	9902G06	D1S1218i
205,736,096	205,881,733	0117H06	D1S1351i
205,736,096	205,881,733	0109A04	D1S2796
205,992,025	206,035,481	0105E03	D1S2685
206,116,942	206,151,370	0102C01	D1S0571i
206,116,942	206,151,370	0103G08	D1S2692
206,116,942	206,151,370	702B02	DID22N_0002526
207,854,838	207,892,443	0115F02	D1S0017i
207,854,838	207,892,443	0110F10	D1S0116i
207,854,838	207,892,443	0102F11	D1S471
208,025,659	208,046,102	0110C10	D1S0097i
209,566,580	209,614,911	0111A06	D1S0578i
209,566,580	209,614,911	0103A08	D1S2810
210,805,374	210,860,742	0115H07	D1S0456i
210,805,374	210,860,742	0113E12	D1S0556i
212,597,474	212,791,265	0103G05	D1S237
212,597,474	212,791,265	0119F01	D1S419
212,843,155	212,904,537	0117D12	D1S1134i
214,743,211	215,377,720	0111H04	D1S0478i
214,743,211	215,377,720	0112G04	D1S0944i
214,743,211	215,377,720	0101C08	D1S0967i
214,743,211	215,377,720	0112H06	D1S1047i
214,743,211	215,377,720	0112B07	D1S1053i
214,743,211	215,377,720	0109D04	D1S227
214,743,211	215,377,720	0118E09	Z66862
216,586,200	216,684,584	0103C08	D1S1390i
219,119,366	219,125,022	0113A01	D1S1593i
219,119,366	219,125,022	0105D06	D1S2641
219,941,389	219,982,141	0113F03	D1S0557i
219,941,389	219,982,141	0102C04	D1S2894
219,941,389	219,982,141	0113H10	HUMUT7354

22,021,324	22,136,377	0110E04	D1S1431i
22,318,177	22,342,197	0113F09	D1S0170i
22,835,705	22,838,762	333G05	AC025929.3_119355
22,835,705	22,838,762	0106C12	D1S0006i
22,835,705	22,838,762	0108H06	D1S1655i
22,910,045	23,114,405	0101B02	D1S2698
221,350,270	221,383,247	0110G01	D1S1361i
224,064,459	224,099,884	0101H06	D1S0569i
224,064,459	224,099,884	T001F03	D1S1230i
224,615,015	224,662,414	0107G03	D1S1644
224,615,015	224,662,414	0109C06	Z66645
224,886,014	224,993,647	0114C01	D1S0570i
224,886,014	224,993,647	0115B12	D1S1143i
226,711,303	226,712,197	0106G10	D1S1344i
227,633,615	227,636,468	0114D06	D1S1211i
227,633,615	227,636,468	0119D12	D1S1334i
233,890,964	234,113,563	336E08	AL390765.5_154842
233,890,964	234,113,563	0107H05	D1S0103i
233,890,964	234,113,563	0115H09	D1S0509i
233,890,964	234,113,563	0119A03	D1S235
234,205,753	234,303,706	0114H05	D1S0980i
234,205,753	234,303,706	0114D11	D1S1209i
234,624,303	234,714,649	0111H05	D1S0566i
234,624,303	234,714,649	9902H04	D1S1680
234,624,303	234,714,649	0109E04	D1S2850
234,916,422	234,994,554	0115H01	D1S1049i
24,318,848	24,342,198	0119E08	D1S1285i
24,318,848	24,342,198	0115F11	D1S1707i
24,318,848	24,342,198	0103C07	D1S1709i
240,078,105	240,119,864	0102F02	D1S0204i
241,718,158	242,080,053	0115F07	D1S0973i
241,718,158	242,080,053	0112E11	D1S1215i
241,718,158	242,080,053	0109C12	D1S1335i
241,718,158	242,080,053	0104E04	D1S1609
241,718,158	242,080,053	T002B01	D1S2811
245,647,974	245,679,033	0104B09	D1S0507i
245,647,974	245,679,033	0112F05	D1S0976i
25,098,596	25,164,062	0115D07	D1S0052i
25,098,596	25,164,062	0114E04	D1S0760i
25,471,568	25,529,523	0110B04	D1S1424i
25,561,327	25,629,270	0110C04	D1S1428i
26,158,845	26,197,235	0115H10	D1S0613i
26,158,845	26,197,235	0110F04	D1S1432i
26,516,998	26,519,601	0110A05	D1S1438i
27,089,567	27,099,549	0110E03	D1S1403i
27,110,566	27,113,047	002C08	D1S455
27,297,893	27,366,059	0101D08	D1S0325i
27,297,893	27,366,059	689G11	DISD22_0011961
27,811,162	27,834,375	0118E04	D1S0278i
27,811,162	27,834,375	002F08	D1S2639
28,346,264	28,392,971	0106D12	D1S1260i
28,346,264	28,392,971	0108C11	D1S1443i
29,435,611	29,525,899	0101D01	D1S0753i
29,435,611	29,525,899	0108C06	D1S1237i
3,763,705	3,791,853	0116H01	D1S0321i
31,114,901	31,166,301	0101D10	D1S513

31,114,901	31,166,301	095G12	HUMUT2521
31,610,687	31,618,510	0111H08	D1S0754i
31,610,687	31,618,510	0102B09	D1S1575i
32,144,609	32,176,578	0101G03	D1S0339i
32,144,609	32,176,578	0113B11	D1S0608i
32,252,017	32,299,037	0114F03	D1S0768i
32,489,480	32,524,353	0101H07	D1S0612i
32,489,480	32,524,353	0105E06	HUMUT7543
32,530,274	32,571,823	0218A07	D2S1413i
36,704,231	36,721,466	0210C02	D2S0082i
36,704,231	36,721,466	0218F01	D2S0144i
37,805,004	37,834,109	T002C12	D2S177
39,977,117	40,002,173	0210F02	D2S0106i
39,977,117	40,002,173	0203E12	D2S2238
40,133,685	40,140,274	0216G09	D2S0011i
40,929,829	41,009,864	0219H10	D2S1747i
40,929,829	41,009,864	0220B07	D2S1830i
41,217,951	41,250,815	091G10	HUMUT862
41,265,461	41,480,375	0203F12	D2S1229i
41,265,461	41,480,375	0213G06	D2S1251i
42,414,797	42,574,135	0216C06	D2S0976i
42,414,797	42,574,135	0205H06	D2S2306
42,896,635	42,915,016	338B07	AC013396.4_29951
43,055,363	43,083,247	0209F05	D2S1577i
43,055,363	43,083,247	0207F07	D2S1580i
43,576,062	43,592,722	0212B08	D2S0968i
43,597,213	43,601,461	0104F08	D1S0068i
43,769,134	43,861,924	0215D02	D2S0447i
43,769,134	43,861,924	0202C02	D2S2294
44,171,579	44,175,499	555F11	chr2.fa.O7frz.45953438
45,038,623	45,049,479	0204G12	D2S2174
46,278,399	46,371,054	0213H06	D2S1252i
47,037,305	47,057,672	0210D11	D2S0428i
47,037,305	47,057,672	716E12	DIJ28_10008354
47,261,827	47,289,010	0207C11	D2S1748i
47,454,550	47,469,974	0212C08	D2S0969i
47,454,550	47,469,974	0205A07	D2S1669i
47,654,331	47,656,311	0209H05	D2S1591i
47,674,276	47,678,950	0212G08	D2S0975i
50,677,738	51,198,524	170A08	AC007560.3_79097
50,677,738	51,198,524	0202C12	D2S0009i
50,677,738	51,198,524	0221B12	D2S0056i
50,677,738	51,198,524	0217F12	D2S0100i
50,677,738	51,198,524	0205G02	D2S0978i
50,677,738	51,198,524	0208A02	D2S2316
56,732,527	56,817,845	0206H06	D2S0079i
56,732,527	56,817,845	0219B03	D2S1406i
56,732,527	56,817,845	0213E11	D2S1414i
56,883,583	56,953,596	0207G01	D2S0021i
57,093,065	57,156,482	0221A09	D2S378
59,019,048	59,022,587	0210B02	D2S0081i
6,443,798	6,502,708	0102E07	D1S1391i
6,443,798	6,502,708	0105A07	D1S1448i
60,131,568	60,165,050	0116F10	D1S0367i
63,561,300	63,563,385	0104B01	HUMUT6372
65,071,500	65,204,775	334G11	AC025866.2_14272

65,071,500	65,204,775	266E11	AL354878.8_58838
65,071,500	65,204,775	0101G02	D1S0640i
65,658,858	65,879,830	0114C05	D1S0737i
65,658,858	65,879,830	0104B05	D1S1384i
65,658,858	65,879,830	T002E10	D1S2866
66,030,781	66,612,850	0116H10	D1S0390i
66,030,781	66,612,850	0114C04	D1S0713i
66,030,781	66,612,850	0105E05	D1S0716i
66,030,781	66,612,850	0102B02	D1S0721i
66,030,781	66,612,850	0105H11	D1S1484i
67,404,671	67,498,250	0116E06	D1S0407i
67,404,671	67,498,250	0106E05	D1S1158i
67,545,635	67,635,171	0107D10	D1S2806
7,902,494	7,923,513	0105G07	D1S0016i
7,902,494	7,923,513	0107A08	D1S0027i
71,090,624	71,286,079	159F03	AL031429.11_5207
71,090,624	71,286,079	0118D07	D1S0071i
71,090,624	71,286,079	0118A05	D1S0119i
71,090,624	71,286,079	0117G05	D1S0801i
78,542,156	78,778,974	0111F10	D1S0802i
78,542,156	78,778,974	0107G09	D1S0812i
78,542,156	78,778,974	T002H10	D1S2876
78,888,104	78,902,351	0113H01	D1S0408i
78,888,104	78,902,351	0116G11	D1S0412i
79,128,037	79,279,105	0111F11	D1S0818i
79,128,037	79,279,105	0116F02	D1S1196i
84,316,329	84,476,769	0111H11	D1S0824i
84,316,329	84,476,769	0117E02	D1S1301i
85,504,519	85,516,359	0114A07	D1S0428i
85,504,519	85,516,359	0111G10	D1S0803i
85,556,756	85,703,415	0117H04	D1S0035i
85,556,756	85,703,415	0103D05	D1S1676i
89,091,203	89,129,889	0108D07	D1S1380i
89,244,948	89,261,132	0116B12	D1S0421i
89,344,403	89,414,311	0109B07	D1S0391i
89,498,853	89,511,119	9902D01	D1S2004i
9,634,390	9,711,564	0104B07	D1S1626i
91,918,488	92,144,147	0119H02	D1S0406i
91,918,488	92,144,147	0112E10	D1S1185i
91,918,488	92,144,147	0106C07	D1S1314i
938,666	939,783	0105A06	D1S1425i
94,123,349	94,147,600	0105A03	D1S0252i
94,767,369	94,779,944	268F03	AL390314.6_23296
101,899,841	101,979,366	486G01	chr10.fa.O7frz.109393646
101,899,841	101,979,366	1010A07	D10S0301i
103,103,810	103,307,068	1006F10	D10S0600i
103,103,810	103,307,068	T001B11	D10S0605i
103,103,810	103,307,068	1010E04	HUMUT7406
103,519,877	103,525,817	1004D10	D10S0764i
104,144,320	104,152,271	1008D06	D10S0888i
104,525,996	104,566,011	1003B12	D10S1692
104,580,278	104,587,280	1002B10	D10S0155i
11,087,290	11,418,680	353D02	AC026887.4_12044
11,087,290	11,418,680	1002C02	D10S0127i
11,087,290	11,418,680	1008H04	D10S0169i
11,087,290	11,418,680	1011A02	D10S0698i

11,087,290	11,418,680	1007A03	D10S0709i
11,087,290	11,418,680	1001H05	D10S0715i
112,247,586	112,261,292	1009H06	D10S0682i
112,317,439	112,354,384	1009D11	D10S0516i
112,317,439	112,354,384	1005B04	G08785
115,428,925	115,480,654	1011F10	D10S0796i
12,211,642	12,251,966	1004F04	D10S0375i
12,211,642	12,251,966	1001B11	Z67393
121,400,872	121,427,321	212G07	AF134471.1_33637
121,400,872	121,427,321	1002F08	D10S0120i
122,473,377	123,347,962	320B08	AC009989.8_114829
122,473,377	123,347,962	591G08	chr10.fa.O7frz.132530934
122,473,377	123,347,962	578H05	chr10.fa.O7frz.133333262
122,473,377	123,347,962	1008F09	D10S0252i
122,473,377	123,347,962	1008B05	D10S0255i
122,473,377	123,347,962	1010A12	D10S0307i
122,473,377	123,347,962	1003D07	D10S0503i
122,473,377	123,347,962	1006D08	D10S0539i
122,473,377	123,347,962	1006H10	D10S0613i
122,473,377	123,347,962	1010D12	D10S0650i
122,473,377	123,347,962	1007D06	D10S0756i
122,473,377	123,347,962	1004E10	D10S0881i
122,473,377	123,347,962	1011E05	D10S0910i
124,310,171	124,393,242	1009F08	D10S0089i
124,310,171	124,393,242	1003A09	D10S0523i
124,903,783	124,914,876	1009E10	D10S0580i
124,903,783	124,914,876	1007G01	D10S0858i
127,445,012	127,454,380	1006B10	D10S0584i
127,514,896	127,575,017	1003E10	D10S0860i
127,690,940	128,067,055	1003F02	D10S0696i
127,690,940	128,067,055	1011C09	D10S0854i
127,690,940	128,067,055	1007G08	D10S0856i
127,690,940	128,067,055	1007B08	D10S0861i
129,425,504	129,429,440	T002F01	D10S217
129,595,315	129,774,155	1001D09	D10S0236i
129,595,315	129,774,155	1001F08	D10S0593i
131,155,456	131,455,358	1006H07	D10S0530i
131,155,456	131,455,358	1006A08	D10S0532i
131,155,456	131,455,358	1007C09	D10S0766i
133,631,181	133,645,450	1003E12	D10S0871i
134,925,898	134,940,362	1003E03	D10S0907i
135,190,857	135,224,714	1007F12	D10S0157i
14,979,364	15,036,437	1006H01	D10S0376i
14,979,364	15,036,437	1002G08	D10S0893i
15,595,954	15,802,130	1010D05	D10S0667i
15,595,954	15,802,130	1010G12	D10S0672i
15,595,954	15,802,130	1003A05	D10S0959i
15,595,954	15,802,130	1003D06	D10S1653
16,595,748	16,604,010	1002C12	D10S1477
16,595,748	16,604,010	1003H05	D10S674
17,311,283	17,319,598	1007A12	HUMUT463
17,891,368	17,993,184	1009E12	D10S0346i
18,138,358	18,240,097	1002A09	D10S0961i
22,650,146	22,660,194	1003A03	D10S0938i
26,767,138	26,896,738	1008G11	D10S0179i
26,767,138	26,896,738	1009C01	D10S0280i

26,767,138	26,896,738	1005H03	G10204
30,762,872	30,790,768	1006F09	D10S0570i
30,762,872	30,790,768	1011G06	D10S1674
31,647,430	31,858,748	212G02	AC005877.3_160520
31,647,430	31,858,748	212D08	AF225898.1_164426
31,647,430	31,858,748	146F11	AF225898.1_167611
31,647,430	31,858,748	1004G06	D10S0182i
31,647,430	31,858,748	1011D07	D10S208
31,647,430	31,858,748	1011F03	D10S565
33,229,326	33,287,204	318C04	AL133333.9_189168
33,229,326	33,287,204	1009C11	D10S0668i
33,506,426	33,665,196	1011D05	D10S0035i
33,506,426	33,665,196	1005E06	D10S0071i
35,455,807	35,541,892	1008G09	D10S0201i
35,455,807	35,541,892	1008A12	D10S0420i
35,455,807	35,541,892	1001B08	HUMUT5962
44,185,611	44,200,548	1003D03	D10S0927i
45,189,635	45,261,571	483G05	chr10.fa.O7frz.44957867
45,189,635	45,261,571	1008B11	D10S0203i
48,926,216	49,033,022	1004C01	D10S0911i
49,184,739	49,317,409	419G02	chr10.fa.O7frz.48816071
49,184,739	49,317,409	1008D07	D10S0556i
54,195,146	54,201,466	1005A12	D10S0330i
59,764,745	59,800,515	1002E01	D10S0909i
59,764,745	59,800,515	1005F03	Z67552
6,034,340	6,060,156	1006C09	D10S0559i
6,092,658	6,144,294	1009A11	D10S0177i
6,509,111	6,662,269	1010B12	D10S0063i
6,509,111	6,662,269	1011E11	D10S0096i
6,509,111	6,662,269	1002C04	D10S0951i
61,458,165	61,819,494	1006F04	D10S0460i
61,458,165	61,819,494	1006E08	D10S0549i
61,458,165	61,819,494	1001E08	D10S0892i
61,458,165	61,819,494	1007F01	D10S0919i
61,458,165	61,819,494	1002E12	D10S0971i
62,205,690	62,224,616	1006D11	D10S0627i
64,241,762	64,246,133	1007B11	D10S0087i
64,241,762	64,246,133	1006D01	D10S0351i
70,331,040	70,376,609	1002E02	D10S1678
70,517,834	70,534,573	578A01	chr10.fa.O7frz.73903894
72,027,110	72,032,521	1003G12	D10S537
74,866,192	74,925,765	1010D11	D10S0186i
74,866,192	74,925,765	1007E01	D10S0781i
75,340,896	75,347,261	603A10	chr10.fa.O7frz.79381928
75,580,971	76,139,067	1005C12	D10S0335i
75,580,971	76,139,067	1005G12	D10S0345i
75,580,971	76,139,067	1009D08	D10S0356i
75,580,971	76,139,067	1006G03	D10S0445i
75,580,971	76,139,067	1010C09	D10S0637i
75,580,971	76,139,067	1006G12	D10S0660i
76,524,196	76,538,976	1005B12	D10S0332i
79,220,557	79,356,384	1001B04	D10S0603i
79,220,557	79,356,384	1009C06	D10S0648i
8,136,662	8,157,170	1009C03	D10S0158i
8,136,662	8,157,170	9905E11	D10S0380i
80,777,226	80,785,096	1001B03	D10S0304i

80,777,226	80,785,096	1002D08	D10S201
81,687,476	81,698,841	9905F11	D10S0459i
83,624,786	84,736,913	1003F08	D10S0039i
83,624,786	84,736,913	1001F05	D10S0072i
83,624,786	84,736,913	1005B07	D10S0097i
83,624,786	84,736,913	1007B10	D10S0109i
83,624,786	84,736,913	1005D09	D10S0218i
83,624,786	84,736,913	1007H11	D10S0239i
83,624,786	84,736,913	1008C01	D10S0467i
83,624,786	84,736,913	1006F05	D10S0475i
83,624,786	84,736,913	1003C09	D10S0487i
83,624,786	84,736,913	1006E11	D10S0629i
83,624,786	84,736,913	1007E06	D10S0731i
83,624,786	84,736,913	1004E01	D10S0750i
83,624,786	84,736,913	1001E11	D10S0960i
83,624,786	84,736,913	1001E09	D10S1786
88,506,376	88,674,925	1008C12	D10S0585i
89,612,850	89,721,667	1001C07	D10S1765
89,612,850	89,721,667	1005D03	Z67254
90,739,206	90,765,522	1001F09	D10S1739
90,963,306	91,164,294	1008E02	D10S0221i
90,963,306	91,164,294	1006D06	D10S0485i
90,963,306	91,164,294	9906A02	D10S0771i
94,811,011	94,818,444	1010H09	D10S0671i
96,433,368	96,485,937	1005E04	HUMUT925
96512371	96603007	CYP2C191	new design
96512371	96603007	CYP2C192	new design
96688418	96739137	CYP2C9	new design
96,786,519	96,819,244	1006B06	D10S0481i
97,461,526	97,619,442	1003D10	D10S0154i
97,461,526	97,619,442	1001D06	D10S0899i
97,461,526	97,619,442	1011A08	D10S0953i
97,941,445	98,021,316	1005C10	D10S0254i
98,054,075	98,088,311	1001D03	D10S0939i
98,054,075	98,088,311	1002H01	D10S0946i
1,730,558	1,741,798	1108B01	D11S0457i
1,730,558	1,741,798	1111E09	D11S0827i
1,830,776	1,870,069	1101A06	D11S0967i
10,283,172	10,285,499	399D09	AC018539.4_114043
100,414,313	100,506,465	1106G10	D11S0557i
100,414,313	100,506,465	1104H02	D11S0935i
101,693,404	101,713,675	1109G04	D11S0870i
101,896,449	101,906,688	1110G10	HUMUT1283
101,952,776	102,001,273	1110B12	D11S4108
102,067,625	102,081,678	1105B12	D11S0258i
102,146,444	102,156,569	1105E12	D11S0269i
102,211,738	102,219,552	1104G07	Z66956
102,318,934	102,331,672	1109H10	D11S0391i
102,318,934	102,331,672	1102G06	D11S0599i
104,261,876	104,274,607	1106H10	D11S0558i
104,318,804	104,345,373	1105D02	D11S1886
104,370,180	104,384,909	1107A05	D11S0774i
104,513,879	104,515,663	1107F02	D11S0764i
104,513,879	104,515,663	1109B11	HUMUT2064
106,878,664	106,941,637	1102C11	D11S0559i
106,878,664	106,941,637	1103C02	D11S0944i

107,598,769	107,745,036	1108F07	D11S0615i
107,598,769	107,745,036	1109G09	D11S0619i
107,598,769	107,745,036	1111E02	D11S0622i
107,598,769	107,745,036	9906E05	D11S0848i
108,041,014	108,316,866	1109C07	D11S0404i
108,041,014	108,316,866	1102A06	D11S0409i
108,041,014	108,316,866	1104A09	D11S0952i
109,605,376	109,672,647	1103G06	D11S0285i
109,605,376	109,672,647	037E05	D11S927
110,728,190	110,755,627	1108A07	D11S0278i
110,728,190	110,755,627	1106C02	D11S0312i
111,519,186	111,540,050	1107B01	D11S0018i
111,519,186	111,540,050	1101D05	D11S0894i
112,337,368	112,653,781	1106B10	D11S0541i
112,337,368	112,653,781	1105G02	D11S3179
112,337,368	112,653,781	1105B03	Z67379
114,550,227	114,880,325	1108E09	D11S0537i
114,550,227	114,880,325	1109H05	D11S0542i
114,550,227	114,880,325	T001D11	D11S0568i
114,550,227	114,880,325	1110C08	D11S1885
114,550,227	114,880,325	684E12	DISD22_0006557
114,550,227	114,880,325	1102D05	Z67490
117,362,319	117,377,404	1104H05	D11S1356
117,362,319	117,377,404	111D09	U73649.1_16072
117,680,662	117,692,100	403B09	AC068591.2_86017
117,710,475	117,718,669	403A09	AP001582.3_115137
118,125,623	118,167,082	1108G11	D11S0300i
118,125,623	118,167,082	1110B06	D11S4104
118,259,777	118,272,181	704C08	DID22N_0040945
118,259,777	118,272,181	745B10	DIJ28_10013816
118,684,444	118,693,050	1109C12	D11S0315i
119,014,018	119,104,645	1101D10	D11S0560i
119,014,018	119,104,645	1107B04	D11S0857i
119,616,256	119,695,863	1108B06	D11S0563i
119,616,256	119,695,863	1111B03	D11S0632i
119,616,256	119,695,863	1103H02	Z67522
120,828,130	121,005,621	1107A01	D11S0765i
120,828,130	121,005,621	1107F05	D11S0778i
125,279,550	125,298,215	1106E03	D11S0341i
125,279,550	125,298,215	1108F01	D11S0427i
125,658,192	125,672,683	1106D11	D11S0573i
125,658,192	125,672,683	037H11	D11S934
13,470,177	13,474,143	1102A12	D11S926
133,290,395	133,327,321	1109A10	D11S0418i
133,290,395	133,327,321	1103E01	D11S968
133,290,395	133,327,321	1101H11	Z67178
133,444,030	133,526,861	1107C03	D11S0779i
133,444,030	133,526,861	1104G11	D11S4125
133,753,608	133,787,022	1104B12	D11S0676i
14,856,131	14,870,327	1111E01	D11S0104i
17,067,861	17,147,864	1111C04	D11S0661i
17,067,861	17,147,864	1103F07	D11S4160
18,090,596	18,094,695	1109E03	D11S0687i
18,223,365	18,226,758	1109G08	D11S0663i
18,223,365	18,226,758	1111G09	D11S0834i
18,300,719	18,345,153	1107F07	D11S0840i

18,682,435	18,704,353	1106D07	D11S0451i
18,706,051	18,769,965	740D01	DIJ28_10032405
2,106,918	2,125,616	1102D03	D11S0973i
2,355,096	2,375,225	1106A07	D11S0445i
2,355,096	2,375,225	1105B01	D11S1318
2,861,019	2,863,577	085D12	HUMUT6724B
20,365,679	20,487,404	1105C06	D11S0094i
20,365,679	20,487,404	1110B10	D11S4190
22,646,230	22,791,123	1107C08	D11S0353i
22,646,230	22,791,123	1106C04	D11S0356i
22,646,230	22,791,123	1101E12	D11S0363i
268,570	275,304	1108H05	D11S0006i
268,570	275,304	1101A04	D11S0978i
27,633,016	27,699,872	1111D01	D11S0077i
27,633,016	27,699,872	1110C05	D11S0144i
3,622,937	3,642,222	1104D09	D11S0838i
33,681,132	33,714,600	1107C12	D11S0166i
33,681,132	33,714,600	1111A02	D11S0460i
34,417,054	34,450,183	1111C07	D11S0739i
35,116,993	35,210,525	1105A04	D11S0012i
35,116,993	35,210,525	1105C04	D11S0020i
35,116,993	35,210,525	1105H07	D11S0139i
36,467,299	36,488,398	T003H08	D11S4083
36,546,139	36,557,877	1101E02	G10015
395716	407397	SIGIRR1	new design
395716	407397	SIGIRR2	new design
4,745,076	4,970,235	1105E06	D11S0102i
4,745,076	4,970,235	1108E08	D11S0105i
4,745,076	4,970,235	1108H06	D11S0582i
4,745,076	4,970,235	1103D12	D11S4181
43,290,109	43,322,655	1110C11	D11S0722i
43,858,971	43,898,392	591F11	chr11.fa.O7frz.46072222
44,543,717	44,597,915	1109F02	D11S0504i
44,543,717	44,597,915	1109A08	D11S0639i
45,863,778	45,884,592	1107D05	D11S0728i
45,863,778	45,884,592	1102G01	D11S0737i
46,697,331	46,717,631	1110C07	D11S0817i
46,697,331	46,717,631	1102B06	D11S0970i
47,227,083	47,246,972	1106D04	D11S0359i
47,227,083	47,246,972	1102B01	D11S0692i
47,543,464	47,562,690	400B11	AC067943.4_5205
47,543,464	47,562,690	1108A08	D11S0366i
47,567,792	47,580,516	1108F02	D11S0492i
47,958,689	48,146,246	1103F12	D11S1350
47,958,689	48,146,246	1101A10	D11S1784
5,203,270	5,212,454	1105A05	D11S0069i
5,203,270	5,212,454	1111C09	D11S0819i
5,667,495	5,688,669	487E06	chr11.fa.O7frz.5327809
5,667,495	5,688,669	1108A02	D11S0447i
5,667,495	5,688,669	1110D01	D11S0453i
56,757,630	56,761,489	1105A09	D11S0182i
56,862,525	56,894,125	1102A01	D11S0694i
56,910,832	56,914,706	1101E03	Z67514
57,075,705	57,092,333	T002G05	D11S0635i
57,121,603	57,138,902	1101E05	D11S0598i
57,121,603	57,138,902	1101B09	D11S1777

59,580,677	59,595,164	1108C05	D11S0872i
59,953,638	59,971,841	1104D05	D11S0690i
6,581,540	6,588,677	399A08	AC009796.4_61451
6,581,540	6,588,677	420H03	chr11.fa.O7frz.6316475
6,581,540	6,588,677	1109A02	D11S0577i
60,374,983	60,380,020	1111C12	D11S0927i
60,626,543	60,651,900	1109F05	D11S0506i
61,039,361	61,104,874	1102A08	D11S0075i
61,039,361	61,104,874	1110F06	D11S4076
61,316,726	61,321,286	1109H08	D11S0685i
62,316,219	62,329,529	1102G04	D11S0785i
62,380,094	62,412,929	1107F03	D11S0703i
63,030,132	63,040,815	1101E08	D11S0702i
63,758,646	63,762,835	1109G02	D11S0640i
63,764,989	63,768,262	1111D08	D11S0787i
63,829,616	63,840,786	1109E08	D11S0644i
64,250,959	64,269,504	1106F05	D11S0405i
64,458,519	64,459,936	563E04	chr11.fa.O7frz.68864733
64,458,519	64,459,936	682B03	DISO7_10017975
64,786,006	64,821,664	1108G05	D11S0645i
65,062,850	65,082,275	1101H05	D11S0388i
65,062,850	65,082,275	1102B05	HUMUT2269
65,177,649	65,186,959	1105A10	D11S0200i
65,378,858	65,383,462	401H03	AP001191.2_77147
65,378,858	65,383,462	1105D10	D11S0204i
65,838,534	65,841,091	1108G01	D11S0393i
65,990,974	66,001,382	1102F04	D11S0887i
66,070,967	66,087,373	1108B05	D11S0406i
66,087,511	66,092,623	1110F05	D11S0818i
66,580,897	66,596,060	1109D02	D11S0389i
66,580,897	66,596,060	1101G01	Z67088
66,888,215	66,897,782	1109H09	D11S0190i
66,888,215	66,897,782	1103A04	D11S0920i
67,007,097	67,015,150	1102A02	D11S1889
67,107,862	67,110,701	1103D10	D11S4155
67,515,151	67,528,169	1101C11	D11S0681i
67,563,059	67,574,942	1108G07	D11S0871i
67,836,674	67,973,317	1111G01	D11S0205i
67,836,674	67,973,317	1107B11	D11S0212i
67,836,674	67,973,317	1104A01	D11S1337
67,836,674	67,973,317	1110F11	D11S4178
67,836,674	67,973,317	1104C06	HUMUT5620
69,165,054	69,178,423	1111D06	D11S0717i
69,296,978	69,299,352	036B08	D11S4136
69,726,917	69,731,144	1105H03	HUMUT6360
7,016,373	7,049,333	1111D09	D11S0823i
7,016,373	7,049,333	1111F09	D11S0828i
7,937,547	7,941,780	1108C06	D11S0883i
7,937,547	7,941,780	726C10	DIJ28_10040944
71,221,894	71,226,256	1106D12	D11S0610i
71,387,587	71,394,409	1102E10	D11S0651i
72,606,992	72,625,045	1108F06	D11S0491i
72,606,992	72,625,045	1107A03	D11S0720i
72,606,992	72,625,045	1107G02	D11S0725i
72,765,053	72,786,167	1101D03	D11S0691i
73,023,592	73,051,512	1104C05	D11S916

73,981,277	74,031,413	1103A08	D11S0588i
74,654,130	74,740,521	1111D04	D11S0667i
74,654,130	74,740,521	1102E06	D11S0964i
75,203,923	75,531,342	1108B09	D11S0641i
75,203,923	75,531,342	1102D06	D11S0893i
75,203,923	75,531,342	1108F12	D11S0929i
75,203,923	75,531,342	1104A11	D11S1321
75,738,652	75,769,528	1104E06	D11S0174i
75,738,652	75,769,528	1109A07	D11S0515i
76,710,708	76,862,581	401D09	AP000486.4_115712
76,710,708	76,862,581	1103A07	D11S4186
77,603,990	77,806,414	1109G10	D11S0522i
77,603,990	77,806,414	1102F03	D11S0961i
77,603,990	77,806,414	1103B10	D11S937
822952	828835	CD151	new design
86,334,369	86,344,081	1109A06	D11S0221i
86,334,369	86,344,081	1111C11	D11S0903i
88,550,268	88,668,474	1108H03	D11S0254i
88,550,268	88,668,474	1101G07	D11S0260i
88,550,268	88,668,474	1106G09	D11S0529i
88,699,160	88,864,301	1105E10	D11S0223i
93,790,114	93,866,688	1101A11	D11S0226i
93,790,114	93,866,688	1106H09	D11S0532i
10,015,281	10,029,461	1205C11	D12S0288i
10,015,281	10,029,461	1203D03	D12S1674
10,113,421	10,142,872	1203F09	D12S1690
10,202,167	10,216,004	1211E02	D12S1696
10,202,167	10,216,004	1203C08	D12S77
10,351,684	10,359,983	1204B09	D12S0390i
10,456,181	10,464,461	1209H09	D12S0218i
10,633,039	10,643,431	1203F08	D12S0095i
10,742,955	10,767,171	1209C08	D12S0140i
101,313,806	101,398,471	1205C05	D12S0036i
101,313,806	101,398,471	1205F05	D12S0043i
101,875,594	101,878,421	1204A12	D12S0533i
101,875,594	101,878,421	9907E01	D12S0929i
102,505,181	102,684,635	357C05	AC063946.10_124699
102,505,181	102,684,635	9906B10	D12S0841i
102,505,181	102,684,635	1207B03	D12S0848i
102,505,181	102,684,635	9906H05	D12S360
102,505,181	102,684,635	1211B02	D12S865
102,848,290	102,865,833	099H02	HUMUT835B
103,034,988	103,056,170	565G02	chr12.fa.O7frz.111997282
103,034,988	103,056,170	1210G04	D12S338
103,204,857	103,268,192	1209H03	D12S0467i
105,501,163	105,680,711	1209B08	D12S0093i
105,501,163	105,680,711	1201C12	D12S0574i
105,501,163	105,680,711	1202G05	D12S330
107,208,800	107,257,218	1202A05	D12S1605
107,539,800	107,551,799	1204B04	D12S84
108,010,379	108,015,660	223A08	AC007637.9_40136
108,010,379	108,015,660	668F08	chr12.fa.O7frz.117355013
108,200,167	108,231,408	1210H01	D12S0004i
108,200,167	108,231,408	1210C05	D12S0070i
109,424,388	109,454,274	1204A03	D12S0030i
109,424,388	109,454,274	1210H05	D12S0174i

11,694,055	11,939,603	1204B01	D12S0024i
11,694,055	11,939,603	1205C09	D12S0172i
11,694,055	11,939,603	T003B10	D12S89
11,694,055	11,939,603	1202E01	D12S98
111,340,919	111,432,100	1207F10	D12S0747i
111,340,919	111,432,100	1208A06	HUMUT5428
111,829,122	111,854,374	040C04	D12S1340
111,980,045	112,020,216	1205G11	D12S0309i
111,980,045	112,020,216	1201F08	D12S0483i
115,783,410	115,803,615	1207E05	D12S0781i
115,783,410	115,803,615	1207D06	D12S0882i
116,135,362	116,283,965	1208H09	D12S0177i
116,135,362	116,283,965	9906H11	D12S0749i
116,135,362	116,283,965	9906A12	D12S0761i
118,100,978	118,116,934	1202A06	D12S0756i
118,100,978	118,116,934	658E07	DISO7_10003646
119,942,478	119,961,164	1211G05	D12S0076i
119,942,478	119,961,164	1201B03	D12S0573i
12,115,145	12,255,214	1209E11	D12S0050i
12,115,145	12,255,214	1205C10	D12S0217i
12,164,953	12,311,013	1204H10	D12S391
12,520,098	12,606,584	1208E12	D12S0041i
12,520,098	12,606,584	1203A07	D12S0983i
12,520,098	12,606,584	T003F09	D12S358
12,770,130	12,874,182	1204A02	D12S0120i
120,055,061	120,108,259	357F09	AC069209.16_27083
120,055,061	120,108,259	1209D12	D12S0011i
121,222,530	121,224,699	1206G02	D12S0378i
121,321,934	121,473,069	9906H08	D12S0382i
121,321,934	121,473,069	9906B09	D12S0550i
121,765,256	121,767,297	9906G09	D12S0767i
122,652,625	122,671,435	1210A09	D12S0307i
122,684,333	122,711,573	1210F12	D12S0606i
123,374,914	123,568,793	357B10	AC027706.2_46645
123,374,914	123,568,793	1209H07	D12S0808i
123,374,914	123,568,793	T001A02	D12S0811i
123,374,914	123,568,793	1201A12	D12S1611
123,374,914	123,568,793	040A07	D12S1612
123,828,129	123,914,346	1207B12	D12S0751i
123,828,129	123,914,346	1207E08	D12S0884i
123,997,325	124,039,620	1210C12	D12S0768i
128,063,805	128,067,640	1210D07	D12S0785i
129,212,957	129,216,238	1206C10	D12S0576i
129,212,957	129,216,238	1201G12	D12S0921i
129,922,521	129,927,316	1204D08	D12S0818i
131,705,476	131,709,045	1204D01	D12S357
14,873,512	14,887,680	1205A07	D12S0089i
14,873,512	14,887,680	1209F12	D12S0130i
14,986,217	15,005,870	1204C01	D12S0105i
14,986,217	15,005,870	1206H03	D12S0399i
15,366,754	15,641,602	1206B04	D12S0404i
15,366,754	15,641,602	1201E10	D12S0948i
15,366,754	15,641,602	1201E07	D12S0974i
15,366,754	15,641,602	1205E03	G08975
18,305,741	18,692,617	1206D03	D12S0392i
18,305,741	18,692,617	1204H11	D12S0629i

18,305,741	18,692,617	1207H10	D12S0849i
18,305,741	18,692,617	1207B08	D12S0855i
18,305,741	18,692,617	1210G07	D12S0859i
2,774,414	2,783,385	1205C08	D12S0129i
2,774,414	2,783,385	1201E09	D12S0132i
25,249,447	25,295,121	1204C10	D12S0103i
25,249,447	25,295,121	1203H11	D12S0922i
26,377,193	26,877,398	1205E12	D12S0325i
26,377,193	26,877,398	1206E01	D12S0354i
26,377,193	26,877,398	1204A10	D12S0523i
26,377,193	26,877,398	1207D04	D12S0648i
26,377,193	26,877,398	9906C11	D12S0658i
26,377,193	26,877,398	1202C05	D12S0667i
26,377,193	26,877,398	1207B05	D12S0671i
26,377,193	26,877,398	1207C10	D12S0679i
28,002,284	28,016,183	221B11	AC008011.11_31766
28,002,284	28,016,183	1203D06	D12S0923i
28,002,284	28,016,183	1211D01	HUMUT7594
29,381,556	29,425,410	1205E06	D12S0069i
29,381,556	29,425,410	1208B03	D12S0215i
3,470,686	3,573,400	1205C07	D12S0096i
3,470,686	3,573,400	1201D03	D12S1050
3,470,686	3,573,400	1201G01	D12S1062
31,118,061	31,148,992	1201C09	D12S0047i
31,118,061	31,148,992	1204C07	D12S0417i
4,253,199	4,284,777	1203A10	D12S1725
4,413,569	4,425,041	1205G09	D12S0185i
4,569,505	4,593,302	1205H07	D12S0117i
4,569,505	4,593,302	1201F07	D12S0191i
42,439,047	42,468,166	1206E10	D12S0580i
42,439,047	42,468,166	1205H01	D12S1663
44,601,459	44,670,615	1209B03	D12S0225i
44,601,459	44,670,615	1209E05	D12S0296i
46,462,772	46,499,924	1205H06	D12S0086i
46,462,772	46,499,924	1207E06	D12S0661i
47,509,806	47,532,224	1202B05	D12S0593i
47,509,806	47,532,224	1209H01	D12S0596i
47,658,503	47,662,746	9906C09	D12S0577i
47,769,471	47,774,869	1208B05	D12S0578i
47,864,847	47,869,153	432G04	chr12.fa.O7frz.51899683
48,012,467	48,017,238	1203G08	D12S1627
48,238,352	48,248,178	1206A01	D12S0333i
49,444,128	49,500,328	9906E06	D12S1135i
49,444,128	49,500,328	9906F06	D12S1137i
49,444,128	49,500,328	9906G07	D12S1214i
5,928,301	6,104,097	1210A05	D12S0009i
5,928,301	6,104,097	1205A10	D12S0199i
5,928,301	6,104,097	1203E01	D12S0939i
5,928,301	6,104,097	1203A02	D12S0966i
5,928,301	6,104,097	1201H05	D12S374
50,008,494	50,026,730	1202H07	D12S0865i
51,167,231	51,173,289	1210D01	G08922
51,577,238	51,585,127	1211E09	D12S0653i
51,577,238	51,585,127	9906C10	D12S0877i
51,871,374	51,887,267	1208F05	D12S0430i
51,890,621	51,912,253	1201B11	D12S0890i

52,060,246	52,096,497	1201F06	D12S0662i
52,060,246	52,096,497	1202B09	D12S1604
52,653,177	52,656,470	9906D06	D12S1131i
52,972,162	52,981,058	1207H01	D12S0426i
52,972,162	52,981,058	1206F10	D12S0589i
53,075,312	53,099,317	1209A02	D12S0248i
53,324,642	53,328,416	1208E08	D12S0431i
53,324,642	53,328,416	1201A03	D12S0609i
54,364,619	54,387,949	1201G05	D12S0801i
54,364,619	54,387,949	1201G02	D12S0950i
54,611,213	54,634,074	1202E02	D12S0802i
54,634,156	54,646,765	1203B02	D12S0585i
55,018,926	55,020,461	9906H09	D12S0797i
55,392,484	55,407,248	1206B06	D12S0449i
55,392,484	55,407,248	1206E11	D12S0605i
55,769,157	55,775,526	221D12	AF067572.1_2832
55909819	55914981	SHMT21	new design
55909819	55914981	SHMT22	new design
56,114,810	56,130,876	1203D11	D12S0982i
56,135,363	56,138,058	1206F06	D12S0455i
56,428,270	56,432,431	1206C11	D12S0601i
56,499,977	56,527,014	685G06	DISD22_0008338
6,179,134	6,217,688	1201F02	D12S0385i
6,308,184	6,321,522	1206B03	D12S0389i
6,308,184	6,321,522	1206D12	D12S0635i
6,363,595	6,370,994	1208A07	D12S0917i
6,513,872	6,517,797	1208B01	D12S0831i
6,513,872	6,517,797	1204A11	D12S0969i
6,768,912	6,800,237	1211C05	D12S0170i
6,819,636	6,826,819	1210B12	D12S0824i
64,869,270	64,928,684	322G08	AC025603.1_117614
64,869,270	64,928,684	1208F08	D12S0456i
66,329,021	66,340,410	1207A03	D12S0187i
66,329,021	66,340,410	1204A04	D12S335
66,834,816	66,839,790	224F06	AC007458.13_25451
66,834,816	66,839,790	1205C04	D12S0002i
66,834,816	66,839,790	1205D08	D12S0133i
66,834,816	66,839,790	IFNG	new design
66,928,292	66,933,651	1206D06	D12S0451i
67,488,247	67,520,481	1209F05	D12S0544i
67,488,247	67,520,481	1207G01	D12S0857i
69,201,231	69,317,469	1202G03	D12S1043
69,201,231	69,317,469	1203C06	D12S1722
69,318,129	69,600,853	1202B12	D12S0294i
69,318,129	69,600,853	1206H01	D12S0362i
7,138,291	7,153,069	1209G04	D12S0826i
7,773,278	7,793,336	1211E11	D12S0142i
7,773,278	7,793,336	1208A10	D12S0886i
78,509,876	78,608,921	1209H08	D12S0453i
79,318,597	79,598,099	1209C10	D12S0339i
79,318,597	79,598,099	1210F10	D12S0520i
79,318,597	79,598,099	1202D01	D12S0955i
8,076,626	8,099,385	1205E08	D12S0148i
8,076,626	8,099,385	069E07	D12S397
8,167,493	8,182,470	1207D08	D12S0842i
8,557,403	8,566,229	1206E12	D12S0636i

8,866,484	8,920,646	1210A07	D12S0638i
87,410,697	87,498,369	1210D08	D12S0267i
87,410,697	87,498,369	1209A03	D12S0907i
88,265,968	88,270,427	097F07	HUMUT2007B
88,265,968	88,270,427	1202F02	Z67021
9,033,484	9,054,610	T003E09	D12S1695
9,460,894	9,492,092	1211E10	D12S0023i
9,460,894	9,492,092	1210G05	D12S0158i
9,460,894	9,492,092	1210A06	D12S0195i
9,638,415	9,651,764	1204G07	HUMUT1833
9,871,344	9,888,871	1204E02	Z67367
90,063,166	90,100,937	1205F04	D12S0012i
90,063,166	90,100,937	1205F03	G09612
91,061,030	91,063,751	1201D11	D12S0261i
91,693,257	91,847,138	1211B11	D12S0820i
91,693,257	91,847,138	1207D10	D12S0847i
92,326,219	92,360,157	1209H05	D12S0484i
92,487,729	92,494,109	1211C10	D12S0116i
92,487,729	92,494,109	1209B11	D12S0810i
92,595,282	92,768,663	1204D10	D12S0064i
92,595,282	92,768,663	1209E12	D12S0127i
92,595,282	92,768,663	1206A09	D12S0529i
92,595,282	92,768,663	T003F10	D12S1346
93,066,630	93,223,356	453H02	chr12.fa.O7frz.100507297
93,066,630	93,223,356	1210G02	D12S0464i
93,066,630	93,223,356	1210C04	D12S327
93,939,802	93,991,487	565D01	chr12.fa.O7frz.101640988
94,918,742	94,953,496	1207F08	D12S0853i
94,918,742	94,953,496	1211F04	D12S309
97,433,527	97,468,250	1208G05	D12S0255i
97,433,527	97,468,250	1205B02	D12S1706
97,563,209	97,653,342	220B04	AC011248.8_84442
97,563,209	97,653,342	1203C05	D12S0074i
97,563,209	97,653,342	1208B09	D12S0258i
99,391,810	99,481,774	219F07	AC010200.7_102437
99,391,810	99,481,774	224A12	AC010200.7_92076
99,391,810	99,481,774	1205D06	D12S0063i
99,391,810	99,481,774	1208E02	D12S0068i
100,902,857	101,169,146	1304H06	D13S0112i
100,902,857	101,169,146	1303F09	D13S0608i
100,902,857	101,169,146	1305F12	D13S0611i
100,902,857	101,169,146	1303B08	D13S0614i
101,169,308	101,852,156	1302G09	D13S0657i
101,169,308	101,852,156	1301B09	D13S0665i
101,169,308	101,852,156	1301C04	D13S0672i
101,169,308	101,852,156	1308D04	D13S1266
101,169,308	101,852,156	1304G02	D13S1323
101,169,308	101,852,156	1302F04	D13S174
101,169,308	101,852,156	1301G02	G10095
102,295,195	102,326,346	1308A03	D13S0024i
107,657,791	107,668,717	1305B01	D13S0342i
107,719,978	107,758,826	1305H04	D13S0419i
109,599,311	109,757,505	1307E09	D13S0634i
109,599,311	109,757,505	1301B05	Z66602
109,757,632	109,963,375	1307E03	D13S0204i
112,999,557	113,025,746	1306A08	D13S0145i

20,175,479	20,195,237	1301B12	D13S0638i
20,612,650	20,621,221	1306B02	D13S0585i
20,612,650	20,621,221	1301F12	HUMUT6291
21,143,170	21,176,637	1304F05	D13S0077i
21,143,170	21,176,637	1307H07	D13S0129i
23,042,723	23,148,232	1303H10	D13S0522i
23,042,723	23,148,232	1302A04	D13S0692i
23,042,723	23,148,232	040E10	D13S292
25,726,276	25,877,375	1306F09	D13S0173i
25,726,276	25,877,375	1306G08	D13S0358i
25,726,276	25,877,375	1305F08	D13S0507i
26,029,840	26,161,085	1306B12	D13S0366i
26,896,681	26,907,823	1303D03	D13S0372i
26,896,681	26,907,823	1306B10	D13S0475i
27,434,273	27,441,317	1301B07	D13S0079i
27,475,411	27,572,729	1304C10	D13S0242i
27,475,411	27,572,729	1305F07	D13S0482i
27,773,790	27,967,232	1305A05	D13S0420i
27,773,790	27,967,232	1301G07	D13S0655i
27,773,790	27,967,232	1303H06	D13S1242
29,930,884	30,089,729	1306E09	D13S0095i
29,930,884	30,089,729	1306G03	D13S0126i
29,930,884	30,089,729	1303B09	D13S1246
29,930,884	30,089,729	1302A02	D13S289
30,207,645	30,236,556	1304C01	D13S1238
31,787,617	31,871,809	1306H07	D13S0458i
35,904,495	35,915,008	1305A09	D13S0518i
36,291,339	36,301,740	1302G03	D13S0368i
40,027,801	40,138,734	1304B06	D13S0090i
40,027,801	40,138,734	1301A08	D13S1233
42,034,872	42,080,148	1304E10	D13S0244i
42,034,872	42,080,148	041B03	D13S1297
44,592,650	44,756,237	565H08	chr13.fa.O7frz.44272759
44,592,650	44,756,237	1308B06	D13S0229i
44,592,650	44,756,237	1307B08	D13S0455i
44,809,008	44,813,505	1308H03	D13S1312
46,305,514	46,368,179	325E05	AL136958.7_37916
46,305,514	46,368,179	1307F09	D13S0134i
47,883,170	47,887,947	9907B02	D13S0042i
47,883,170	47,887,947	1304H10	D13S0260i
48,178,692	48,181,499	1304E01	D13S1307
52,175,400	52,211,948	1303A10	D13S0047i
94,470,084	94,751,688	1304A12	D13S0303i
94,470,084	94,751,688	1303H02	D13S0506i
94,470,084	94,751,688	1307D06	D13S0635i
94,470,084	94,751,688	1301F04	HUMUT7403
98,744,790	98,757,708	1301D09	D13S0582i
98,744,790	98,757,708	1308B03	D13S1271
101,617,139	101,675,776	1401H06	D14S0309i
101,762,375	101,841,284	1405H03	D14S0453i
102,313,569	102,442,381	1406B04	D14S0349i
102,313,569	102,442,381	1401F08	D14S272
103,092,642	103,098,907	1405C03	D14S0472i
103,233,707	103,251,549	1402C11	D14S0512i
104,290,529	104,297,036	1405F06	D14S0488i
104,586,782	104,602,799	1405H10	D14S0024i

105,428,094	105,428,110	147E07	AB019441.1_31065
105,428,094	105,428,110	1406F10	D14S0475i
19,849,367	19,871,297	1401G07	D14S0500i
19,849,367	19,871,297	732G03	DIJ28_10035246
20,319,050	20,320,464	1406B07	D14S0499i
20,580,251	20,582,226	1403F01	D14S1070
21,159,897	22,090,915	1404D01	D14S0121i
21,159,897	22,090,915	9907E08	D14S0463i
21,159,897	22,090,915	1405E05	D14S0467i
21,159,897	22,090,915	1405E03	D14S0514i
21,159,897	22,090,915	1402B07	D14S0532i
21,159,897	22,090,915	1402F02	D14S0552i
21,159,897	22,090,915	1401D04	D14S1003
21,159,897	22,090,915	1401F11	D14S283
21,159,897	22,090,915	1403B06	G10057
22,375,633	22,386,643	1405B01	D14S0528i
22,375,633	22,386,643	1407E05	HUMUT1079
22,459,573	22,468,501	1402H02	Z67550
22,656,355	22,658,665	1401G11	D14S990
22,845,866	22,850,798	1401B08	D14S0468i
22,911,858	22,915,452	9907F08	D14S0470i
23,661,207	23,678,016	1403B01	D14S64
23,748,627	23,755,020	1401H02	D14S0173i
23,907,094	23,918,650	1405G11	D14S0313i
24,112,564	24,115,306	1404D04	D14S0177i
24170000	24173313	GZMB1	new design
24170000	24173313	GZMB2	new design
28,304,801	28,308,621	1402A12	D14S1042
28,304,801	28,308,621	1401H05	Z66624
29,115,436	29,466,651	9907D08	D14S0440i
29,115,436	29,466,651	1401C02	D14S0448i
29,115,436	29,466,651	1401F12	D14S0451i
29,115,436	29,466,651	1401C08	D14S0516i
29,115,436	29,466,651	1407C01	D14S252
34,249,398	34,253,649	1406B06	D14S0213i
34,249,398	34,253,649	1402D02	HUMUT7222
34,940,468	34,943,703	1406G02	D14S0190i
34,940,468	34,943,703	1406D09	D14S0321i
37,128,940	37,134,240	1406D12	D14S0144i
37,128,940	37,134,240	1406B05	D14S0148i
37,746,955	37,752,019	1407A10	D14S0138i
37,746,955	37,752,019	1406C06	D14S0329i
44,654,859	44,674,272	1405B12	D14S0136i
49,135,165	49,151,140	1402F09	Z67256
49,954,993	50,069,126	1407B06	D14S0158i
49,954,993	50,069,126	1407C06	D14S0162i
50,776,686	50,792,512	9907G08	D14S0490i
51,804,181	51,813,192	1406E10	D14S0323i
51,850,863	51,865,074	1406F08	D14S0160i
52,243,668	52,264,466	1404A11	D14S0331i
53,486,207	53,493,362	1404A06	D14S0217i
53,486,207	53,493,362	1401G05	Z67708
53,933,423	53,956,682	1405G10	D14S0230i
54,563,594	54,585,960	1401C10	D14S0548i
55,654,846	55,837,784	1401C01	D14S0112i
55,654,846	55,837,784	1407E10	D14S0342i

55,654,846	55,837,784	1403A03	D14S1056
55,654,846	55,837,784	1403D02	D14S1064
60,858,186	61,087,451	1404C03	D14S0154i
60,858,186	61,087,451	1404E03	D14S0159i
60,858,186	61,087,451	1404E11	D14S0339i
60,858,186	61,087,451	1405E04	D14S0375i
62,849,395	62,854,316	1404G07	D14S0262i
62,849,395	62,854,316	T003B12	D14S1012
63,621,388	63,875,070	1406F12	D14S0503i
63,621,388	63,875,070	1406A03	D14S0506i
63,621,388	63,875,070	T003C12	D14S63
64,475,625	64,479,284	1407E07	D14S0257i
68,410,793	68,515,747	1406E09	D14S0360i
68,410,793	68,515,747	1403B05	Z66914
70,264,605	70,345,641	1407E09	D14S0263i
70,264,605	70,345,641	1407F02	D14S1002
74,815,284	74,818,685	043D07	D14S76
75,058,537	75,083,086	1402F08	D14S0014i
75,058,537	75,083,086	1405C11	D14S0082i
75,494,195	75,517,242	1403B09	D14S0033i
75,494,195	75,517,242	1407G05	D14S0050i
75,907,479	76,036,961	1406E06	D14S0356i
75,907,479	76,036,961	1407C11	D14S0376i
75,907,479	76,036,961	1401A09	D14S0515i
77,208,502	77,244,109	1405E06	D14S594
77,208,502	77,244,109	1403C07	HUMUT1235
80,491,528	80,682,399	1403F10	D14S0071i
80,491,528	80,682,399	1407G07	D14S0275i
80,716,147	80,757,328	1403A09	D14S0031i
87,469,111	87,529,660	1407D03	D14S0045i
87,469,111	87,529,660	1404H09	D14S0301i
88,003,867	88,090,876	1402H11	D14S0272i
88,003,867	88,090,876	1403C05	Z67182
88,692,274	88,953,127	1403D09	D14S0036i
88,692,274	88,953,127	1402C02	D14S0070i
88,692,274	88,953,127	1401A07	D14S0418i
88,692,274	88,953,127	1401D12	D14S0422i
90,768,629	90,789,977	1406B03	D14S0428i
90,768,629	90,789,977	1406F03	D14S0539i
92,239,907	92,284,765	1406D05	D14S0407i
92,239,907	92,284,765	1405D06	D14S0447i
92,718,294	92,721,002	1405F07	D14S0483i
93,587,019	93,617,311	1401D01	D14S0287i
93,587,019	93,617,311	1401E03	D14S0398i
93,900,404	93,914,178	1404B10	D14S0304i
93,900,404	93,914,178	1407B05	D14S0534i
95,740,950	95,780,542	1402G03	D14S0345i
95,740,950	95,780,542	1401F04	D14S0555i
99,220,407	99,263,391	1406C05	D14S0355i
99,220,407	99,263,391	9907H08	D14S0491i
99,774,855	99,814,557	1401B01	D14S0521i
99,774,855	99,814,557	1401B12	Z67128
22,619,887	23,215,702	1503D06	D15S0006i
22,619,887	23,215,702	1505B09	D15S0228i
22,619,887	23,215,702	1505C09	D15S0230i
22,619,887	23,215,702	1506E01	D15S122

22,619,887	23,215,702	1502G05	D15S128
31,945,720	32,118,595	1505D04	D15S0304i
31,945,720	32,118,595	1504E03	D15S0477i
31,945,720	32,118,595	1503A02	D15S1040
32,869,723	32,875,181	1504G07	D15S0246i
32,869,723	32,875,181	1504D04	D15S0470i
36,567,590	36,644,224	1501C10	D15S0487i
37,660,572	37,676,960	1504F10	D15S0084i
37,660,572	37,676,960	1501A07	D15S0247i
38,366,448	38,387,330	1501G07	D15S994
38774661	38811646	RAD51	new design
39,008,839	39,018,529	1503F08	D15S0093i
39,008,839	39,018,529	1505G10	D15S0265i
39,412,361	39,460,538	1505G11	D15S0289i
39,739,902	39,849,433	1505D09	D15S0231i
39,739,902	39,849,433	1506D12	D15S0236i
41,612,949	41,769,525	1504D10	D15S0232i
41,612,949	41,769,525	1505A07	D15S0354i
41825882	41852096	PDIA3	new design
42,790,977	42,797,649	1504A03	D15S0312i
42,790,977	42,797,649	1505E01	D15S0315i
47,502,751	47,566,815	1504C10	D15S0253i
47,502,751	47,566,815	1506D07	D15S0259i
48,321,436	48,345,218	1505A02	D15S0115i
49,288,961	49,418,086	1506H07	D15S0139i
49,288,961	49,418,086	1504E04	D15S0447i
50,098,739	50,145,754	1503H01	D15S982
50,189,114	50,192,264	1505E12	D15S0302i
54,998,125	55,368,008	463E02	chr15.fa.O7frz.53612467
54,998,125	55,368,008	1503C12	D15S0180i
54,998,125	55,368,008	1506H10	D15S0446i
54,998,125	55,368,008	1503B05	D15S648
54,998,125	55,368,008	9907G10	Z67030
56,675,802	56,829,469	1505C10	D15S0255i
56,675,802	56,829,469	1501F02	D15S148
57,184,612	57,204,536	1504C12	D15S0027i
57,718,358	57,736,991	1506D09	D15S0393i
58,084,427	58,085,434	1506G06	D15S0158i
58,084,427	58,085,434	1503F05	HUMUT1232
58,426,642	58,477,477	1506A11	D15S0479i
58,576,755	59,308,794	1502G07	D15S0042i
58,576,755	59,308,794	1502G11	D15S0154i
58,576,755	59,308,794	1503A12	D15S0176i
58,576,755	59,308,794	1505E09	D15S0234i
58,576,755	59,308,794	1506G12	D15S0240i
58,576,755	59,308,794	1506D03	D15S970
58,576,755	59,308,794	104G09	Z67427
61,986,288	62,125,574	1503A05	D15S644
61,986,288	62,125,574	1502H06	D15S993
61,986,288	62,125,574	738A07	DIJ28_10022026
62,235,067	62,242,407	1506B09	D15S0227i
62,995,046	63,038,086	1501D07	D15S0013i
62,995,046	63,038,086	1506D01	D15S1009
63,196,770	63,213,227	1501B07	D15S0182i
64,466,674	64,570,936	1505C01	D15S0168i
64,466,674	64,570,936	1505F02	D15S0177i

64,466,674	64,570,936	1506H08	HUMUT5980
65,145,249	65,274,587	1502G12	D15S0156i
65,145,249	65,274,587	1502B06	D15S988
65,622,075	65,886,506	1506H04	D15S0269i
65,622,075	65,886,506	1503A03	D15S1015
65,622,075	65,886,506	1503D04	Z66922
66,381,096	66,511,546	1504G09	D15S0187i
66,381,096	66,511,546	1504G02	D15S0386i
66,381,096	66,511,546	1502A11	D15S0455i
67,532,177	67,534,939	1502E12	D15S0371i
68,127,597	68,177,310	1502D03	D15S650
68,127,597	68,177,310	T003G12	D15S977
69,889,948	69,897,654	1506B05	D15S0033i
69,889,948	69,897,654	T001B03	D15S0327i
70,364,122	70,455,868	1505B08	D15S0282i
71,639,410	71,712,806	1506A07	D15S0423i
71,763,675	71,793,912	1504B10	HUMUT744
72,417,157	72,447,134	T001C05	D15S0332i
72,417,157	72,447,134	1506A10	Z67571
72,798,943	72,804,930	1505C11	D15S0280i
72,798,943	72,804,930	1504H04	D15S0392i
73,546,515	73,658,680	1502A01	D15S0481i
74,020,333	74,091,842	1506C10	D15S0104i
74,020,333	74,091,842	1504A07	D15S0352i
75,074,609	75,116,727	328H08	AC051643.2_53971
75,074,609	75,116,727	1502H10	D15S0350i
77,001,162	77,024,475	1505D11	D15S0281i
77,001,162	77,024,475	1506F04	D15S1023
78,040,290	78,050,698	1503B04	D15S1005
79,262,148	79,392,157	1503G12	D15S0200i
79,262,148	79,392,157	1504C11	D15S0207i
79,262,148	79,392,157	1502E08	D15S1041
83,578,821	84,093,590	464A06	chr15.fa.O7frz.83916193
83,578,821	84,093,590	1506A06	D15S0272i
83,578,821	84,093,590	045A06	D15S972
83,578,821	84,093,590	1501A02	D15S999
83,578,821	84,093,590	100B03	HUMUT1211
83,578,821	84,093,590	1502D07	Z66702
86,983,039	87,000,684	9907F09	D15S0049i
86,983,039	87,000,684	1501G08	D15S0506i
88,129,130	88,159,072	9907G11	D15S0329i
88,129,130	88,159,072	1506A04	HUMUT644B
89,061,606	89,159,688	1505F08	D15S0202i
89,061,606	89,159,688	9907G09	D15S0273i
89,061,606	89,159,688	1503H03	D15S127
89,212,889	89,227,691	9907F12	D15S0399i
94,674,950	94,683,048	1501H01	D15S0106i
94,674,950	94,683,048	9907A10	D15S0306i
97,010,288	97,319,034	1504D09	D15S0215i
97,010,288	97,319,034	1501H03	D15S0433i
97,010,288	97,319,034	1502D10	D15S120
97,010,288	97,319,034	1502C03	Z67468
1,696,222	1,760,319	1603B11	D16S0217i
1,968,919	1,971,441	1606F08	D16S0494i
10,867,648	10,926,341	046B02	D16S414
10,867,648	10,926,341	1606C03	D16S497

11,255,775	11,257,540	1603H09	D16S0155i
11,255,775	11,257,540	1606D07	HUMUT1334
11,549,357	11,588,823	1602G01	D16S0316i
11,549,357	11,588,823	1604C04	D16S0512i
11966465	11969426	TNFRSF171	new design
11966465	11969426	TNFRSF172	new design
15,704,493	15,858,388	1603D05	D16S0011i
15,704,493	15,858,388	9908F03	D16S0032i
15,704,493	15,858,388	1602G02	D16S3060
15,950,935	16,143,774	1604C07	D16S0180i
162,875	163,708	1601F11	D16S0102i
2,145,800	2,168,131	1601E07	D16S0452i
21,559,426	21,571,473	1604A11	D16S0160i
21,559,426	21,571,473	1603H10	D16S0179i
23,597,692	23,609,189	1606G10	D16S0444i
23,597,692	23,609,189	1603B03	D16S417
23,754,823	24,139,358	9908B02	D16S0020i
23,754,823	24,139,358	1603E10	D16S0169i
23,754,823	24,139,358	1604D11	D16S0178i
23,754,823	24,139,358	1601C11	D16S0558i
23,754,823	24,139,358	1605D03	D16S0560i
23,754,823	24,139,358	1602H04	D16S420
27,232,752	27,283,600	1605C07	D16S0091i
27,232,752	27,283,600	1601H07	D16S0519i
27,379,436	27,468,775	1601D08	D16S0048i
277,441	342,465	682C07	DISO7_12395103
28,418,184	28,425,656	663D02	chr16.fa.O7frz.38545966
28,418,184	28,425,656	1604C11	D16S0112i
29,581,801	29,589,688	1606F12	D16S0531i
29,731,591	29,766,842	1603B06	D16S0030i
3,010,343	3,012,385	1605B07	D16S0007i
3,010,343	3,012,385	1603F01	D16S3082
3,232,029	3,246,628	1603F06	D16S0040i
3,232,029	3,246,628	1604E08	D16S0211i
3,531,826	3,567,290	1605C12	D16S0002i
3,531,826	3,567,290	1602C08	D16S0103i
3,630,847	3,654,064	1606B08	D16S0120i
3,716,568	3,870,723	1605C11	D16S0023i
3,716,568	3,870,723	1603C08	D16S0101i
3,716,568	3,870,723	1601B06	D16S3065
30,362,453	30,364,725	1602E07	D16S0552i
30,391,551	30,442,007	1606G11	D16S0462i
30,815,429	30,822,382	1601F05	D16S0562i
31178789	31251714	ITGAM1	new design
31178789	31251714	ITGAM2	new design
31,274,010	31,301,819	1604F03	D16S0471i
4,466,426	4,500,349	1604E12	D16S0328i
45,746,798	46,052,519	1604B01	D16S0508i
45,746,798	46,052,519	1602G12	D16S0517i
45,746,798	46,052,519	1602G07	D16S3044
46,758,323	46,838,806	9908A08	D16S0425i
46,758,323	46,838,806	1601H10	D16S0427i
49,288,551	49,324,488	1604G06	D16S0350i
49,288,551	49,324,488	1601F09	D16S3035
52082693	52094671	AKTIP1	new design
52082693	52094671	AKTIP2	new design

54,070,589	54,098,104	493H04	chr16.fa.O7frz.65771871
54,070,589	54,098,104	9908A06	D16S0335i
54,394,264	54,424,576	1603A11	D16S0198i
55,180,768	55,182,501	9908H04	D16S0287i
55,180,768	55,182,501	1603D02	D16S3071
55,581,018	55,673,941	1606A04	D16S0356i
55,581,018	55,673,941	1605E10	D16S0377i
55,581,018	55,673,941	1601A06	D16S0380i
55,950,219	55,957,602	1605F06	D16S0364i
55,996,180	56,007,475	1601B10	D16S0158i
56,616,783	56,638,306	9908E04	D16S0281i
56,616,783	56,638,306	1601H11	HUMUT5103
64,958,064	64,996,190	1602C06	D16S0343i
64,958,064	64,996,190	1601G10	D16S0541i
65,143,967	65,170,463	1604E11	D16S0353i
65,620,551	65,692,462	1601B03	D16S0422i
65,620,551	65,692,462	1606E07	Z66903
65,745,605	65,751,306	1606H11	D16S0424i
65,765,371	65,767,127	1606D01	D16S421
66,525,908	66,528,254	1602F03	D16S0298i
66,525,908	66,528,254	1601D12	D16S0386i
66,676,845	66,818,338	1604A04	D16S0313i
66,902,446	66,948,663	T001E06	D16S0381i
67,018	75,845	1601C05	D16S521
67,328,696	67,426,945	1604C06	D16S0412i
68,156,498	68,296,054	1605A07	D16S0344i
68,156,498	68,296,054	1604E06	D16S0556i
68,890,573	68,925,232	1604C12	D16S0246i
70,685,116	70,704,312	1603D07	D16S0079i
70,685,116	70,704,312	047H01	D16S3106
71,378,456	71,639,775	1603C06	D16S0034i
71,378,456	71,639,775	1603E06	D16S0039i
71,378,456	71,639,775	1603D08	D16S0105i
71,378,456	71,639,775	1602H03	D16S0113i
71,378,456	71,639,775	1603A10	D16S0159i
71,378,456	71,639,775	9908B05	D16S0299i
73,885,109	74,024,888	9908D06	D16S0339i
73,885,109	74,024,888	1606E10	D16S0362i
73,885,109	74,024,888	1604H01	D16S0544i
76,613,992	76,623,499	1606E06	D16S518
78,185,732	78,192,112	9908G06	D16S0375i
78,185,732	78,192,112	1603B01	D16S3040
84,268,781	84,280,089	1601H09	D16S0565i
84,490,275	84,513,713	1601G09	D16S0414i
84,490,275	84,513,713	1601A01	D16S0487i
85,101,659	85,105,548	1601A02	D16S0526i
85,101,659	85,105,548	1606F05	D16S520
86,421,130	86,460,615	1602C05	D16S0554i
86,421,130	86,460,615	1602E01	D16S413
87,232,502	87,234,383	9908F02	D16S0251i
88,512,527	88,529,713	1604B08	D16S0252i
1,483,902	1,495,792	1706D12	D17S0145i
1,483,902	1,495,792	1702B07	D17S0440i
1,909,888	2,220,160	1701G08	D17S0205i
1,909,888	2,220,160	1704E11	D17S0208i
1,909,888	2,220,160	1703D10	D17S0211i

1,909,888	2,220,160	1702A12	D17S0496i
10,365,192	10,393,704	1705D12	D17S0038i
10,365,192	10,393,704	1706D04	D17S1852
11,864,860	11,987,865	1702E05	D17S0111i
15,616,046	15,629,130	1702E04	D17S0372i
15,616,046	15,629,130	1704F01	D17S0374i
15,875,983	16,059,570	1701G03	D17S0001i
15,875,983	16,059,570	1701F01	D17S1843
16,259,613	16,281,042	1701B01	D17S1857
16,783,123	16,816,127	1704E03	D17S0425i
17,655,794	17,681,050	1702D07	D17S0428i
17,932,008	17,952,017	1704F03	D17S0430i
17,932,008	17,952,017	1701B12	D17S0525i
18,028,014	18,053,993	1705G04	D17S0483i
18,516,347	18,516,964	9909F02	D17S0459i
19,221,659	19,227,445	1705F09	D17S0433i
2,443,686	2,535,638	1704A09	D17S0041i
2,443,686	2,535,638	1704E12	D17S0360i
2,443,686	2,535,638	1705E04	D17S0484i
21,128,581	21,159,118	1705F03	D17S0154i
22,980,951	23,000,711	1704C03	D17S0441i
23,107,919	23,151,682	1704E09	D17S0024i
23,107,919	23,151,682	1704C05	D17S0472i
23,718,425	23,721,844	9909C02	D17S0404i
23,875,086	23,889,302	1702H03	D17S0401i
24,424,663	24,531,556	1702D06	D17S0402i
24,424,663	24,531,556	9908E09	D17S0406i
24,424,663	24,531,556	1706B05	D17S0522i
24,424,663	24,531,556	1706H05	D17S841
25,549,032	25,586,831	1705B01	D17S0153i
25,549,032	25,586,831	1701E04	Z67368
26,133,828	26,175,826	1705G05	D17S0196i
26,133,828	26,175,826	1702A05	D17S0465i
29,606,409	29,608,335	1706H06	D17S1293
29,707,584	29,709,742	1706B04	D17S0493i
29,711,512	29,714,365	331G12	AC011193.2_31574
3,415,491	3,459,454	1701B06	D17S0309i
3,415,491	3,459,454	1701D09	D17S829
3,486,522	3,511,585	1701G07	D17S0090i
3,564,671	3,660,578	1701B04	D17S1298
3,746,634	3,766,709	1701E06	D17S1828
31,116,989	31,146,753	1701E01	D17S1833
31,222,611	31,231,490	1703A07	D17S0086i
31,811,186	31,816,297	1702F11	D17S0438i
32,516,040	32,841,015	1705A03	D17S0107i
32,516,040	32,841,015	1706D09	D17S0265i
32,516,040	32,841,015	1704D11	D17S0272i
32,924,064	32,947,709	1701B02	D17S0124i
33,046,526	33,077,600	1703E07	D17S0095i
35,097,919	35,138,441	1703B07	D17S0089i
35,097,919	35,138,441	1705D02	D17S0260i
35,425,214	35,427,592	303B05	AC007776.1_62510
35,472,589	35,503,646	303C05	AC007776.1_75537
35,502,567	35,510,499	9908H11	D17S0330i
35,502,567	35,510,499	1706D11	D17S0452i
35,718,972	35,767,420	1706E09	D17S0280i

35,798,321	35,827,695	1704G10	D17S0273i
35,963,547	35,975,250	1706D08	D17S0285i
35,963,547	35,975,250	1703E04	HUMUT186
36,787,447	36,792,181	1703A08	D17S0108i
36,886,467	36,891,194	1705D08	D17S0053i
36,886,467	36,891,194	1702F02	D17S0530i
37,222,727	37,232,995	1706B11	D17S0368i
37,222,727	37,232,995	1706B01	HUMUT8182
37,506,952	37,518,277	1703E12	D17S0266i
37,506,952	37,518,277	1702F01	HUMUT8184
37,604,721	37,681,950	1706C05	D17S0161i
37,604,721	37,681,950	048G02	D17S1801
37,604,721	37,681,950	1706G10	D17S1802
38,084,961	38,087,371	1701C11	D17S0521i
38,238,949	38,249,303	1702C05	G10143
38,916,860	38,957,206	1704H09	D17S0170i
38,916,860	38,957,206	1706G11	D17S0426i
38,916,860	38,957,206	092E08	HUMUT573
39,199,015	39,211,872	1705G11	D17S0007i
39,199,015	39,211,872	1706G03	D17S0173i
39,199,015	39,211,872	1702F06	D17S951
39,509,647	39,556,540	1703A09	D17S0134i
39,509,647	39,556,540	1706B10	D17S0320i
39,682,566	39,700,993	1702A11	D17S1860
39,805,076	39,822,399	1703D08	D17S0122i
4,480,963	4,491,709	1705A01	D17S0238i
4,560,533	4,571,544	1701A02	D17S0350i
4,646,397	4,648,756	607C09	chr17.fa.O7frz.5865115
4,683,351	4,742,135	331A03	AC015913.4_60812
4,776,372	4,779,067	571C11	chr17.fa.O7frz.5607732
4,789,692	4,793,067	1704H04	D17S0432i
40,392,587	40,401,170	1701G01	D17S0506i
40,392,587	40,401,170	738D08	DIJ28_10035753
40,696,278	40,750,148	1704C09	D17S0025i
40,696,278	40,750,148	1705C11	D17S0142i
40,696,278	40,750,148	1702D05	D17S950
41,217,449	41,268,973	9908C10	D17S0253i
41,217,449	41,268,973	1703F12	D17S0267i
41,217,449	41,268,973	1701E10	D17S0480i
42,196,855	42,251,081	9908C12	D17S0339i
42,196,855	42,251,081	1702C12	D17S791
42,196,855	42,251,081	1703D02	D17S920
42,686,207	42,745,076	332C05	AC064817.4_80427
42,686,207	42,745,076	1706A03	D17S0092i
42,686,207	42,745,076	9909B01	D17S0373i
43,165,609	43,178,484	1703E08	D17S0123i
43,165,609	43,178,484	1702D10	D17S0527i
43,165,609	43,178,484	1706F12	D17S806
43,480,720	43,493,841	1705D09	D17S0281i
43,565,804	43,862,551	9908F10	D17S0286i
43,565,804	43,862,551	1704G07	D17S0453i
43,565,804	43,862,551	1703B02	D17S958
44,007,868	44,010,742	1704D01	D17S1827
44,927,654	44,947,360	1702G03	D17S797
45,422,368	45,427,587	1705F05	D17S0188i
45,616,456	45,633,992	1703B09	D17S0135i

45,616,456	45,633,992	1704B09	D17S0358i
46,585,919	46,604,103	1705B02	D17S0004i
5,276,823	5,283,195	1704H11	D17S0113i
5,284,956	5,312,905	1701B10	D17S0224i
5,343,472	5,428,553	1702E08	D17S0517i
50,697,370	50,755,886	1706C06	D17S0021i
50,697,370	50,755,886	1704C06	D17S1799
52,320,269	52,346,408	1702E06	D17S0105i
52,320,269	52,346,408	1703A10	D17S0168i
53,625,088	53,636,783	1702F09	D17S0193i
53702201	53713295	MPO1	new design
53702201	53713295	MPO2	new design
54,997,668	55,040,484	9908B12	D17S0336i
54,997,668	55,040,484	9909G01	D17S0391i
58,058,494	58,124,629	1702C03	D17S1835
58,058,494	58,124,629	1701H10	D17S794
58,058,494	58,124,629	1701A07	D17S808
58,908,166	58,952,935	1705A06	D17S0349i
59,205,299	59,250,409	1704G02	D17S0271i
59,348,294	59,349,930	1705D06	D17S0278i
59,754,142	59,817,723	1704D06	D17S0439i
59,926,200	59,932,872	1706F11	D17S0390i
6,840,108	6,856,220	1705A02	D17S0158i
6,918,580	6,924,324	465E03	chr17.fa.O7frz.7725213
60,437,295	60,483,216	1702B05	D17S1792
60,437,295	60,483,216	1703A03	D17S1825
60,955,143	60,988,227	1701D12	D17S0486i
60,955,143	60,988,227	1702G04	D17S0519i
61,729,388	62,237,324	150E09	AC006263.1_34791
61,729,388	62,237,324	1704E08	D17S0011i
61,729,388	62,237,324	1703G06	D17S0075i
61,729,388	62,237,324	1704C07	D17S0454i
61,729,388	62,237,324	1703B04	D17S1291
61,729,388	62,237,324	048C10	D17S1816
61,729,388	62,237,324	1701E03	D17S942
64,922,433	65,051,067	1705G09	D17S0337i
64,922,433	65,051,067	1701A09	D17S1786
68,672,755	68,679,689	467B04	chr17.fa.O7frz.78835314
68,672,755	68,679,689	9908E12	D17S0343i
68,672,755	68,679,689	1706D05	D17S0399i
69,974,117	69,992,528	1704F10	D17S0297i
69,974,117	69,992,528	9908F12	D17S0345i
7,156,702	7,173,362	1701H07	D17S0478i
7,283,413	7,288,980	1704A01	D17S0479i
7,392,932	7,405,649	1701C05	Z67321
7,393,099	7,405,649	1704C12	D17S0018i
7,883,083	7,893,177	1706F05	D17S0446i
70,048,842	70,053,877	1706E01	HUMUT7429
70,087,099	70,100,017	1703B05	HUMUT1523
70,202,047	70,220,712	1702D04	D17S0394i
70,780,669	70,797,109	1702F07	D17S0356i
70,780,669	70,797,109	1705H03	D17S0383i
71,229,111	71,265,494	1706F07	D17S1839
71,644,009	71,648,966	303G08	AC015801.21_117665
71,644,009	71,648,966	303H08	AC015801.21_98885
71,892,297	71,895,536	049G01	D17S1817

71,892,297	71,895,536	1703G03	D17S785
72,220,514	72,234,158	9908A11	D17S0302i
73,721,872	73,733,311	1705E03	D17S0049i
73,721,872	73,733,311	1704B04	D17S0529i
73,864,454	73,867,753	T002C05	D17S0219i
73,864,454	73,867,753	1703G04	HUMUT952
74,181,727	74,289,971	1704E05	D17S0410i
74,181,727	74,289,971	1704G04	D17S0463i
74,360,654	74,433,067	1703A11	D17S0222i
75,723,612	75,735,533	1706H11	D17S0294i
75,723,612	75,735,533	1704B06	D17S0471i
76,580,274	76,588,528	1705B11	D17S0223i
76,705,160	76,754,467	1704A05	D17S0531i
77,091,594	77,094,422	1706B03	D17S0407i
77,418,886	77,422,527	9908H08	D17S0215i
77,866,035	77,868,769	1702E12	D17S928
77,872,189	77,884,930	1701E11	D17S0537i
78,070,883	78,153,743	1704A07	D17S0411i
78,070,883	78,153,743	1701D04	D17S0516i
8,722,953	8,756,559	1704D09	D17S0019i
8,722,953	8,756,559	1704B11	D17S0020i
8,722,953	8,756,559	1701A01	D17S786
11,679,263	11,871,922	1804E09	D18S0049i
11,679,263	11,871,922	1805C07	D18S0278i
11,679,263	11,871,922	1805C10	D18S0344i
11,679,263	11,871,922	9901C03	D18S0507i
11,679,263	11,871,922	1804D07	D18S482
12,775,480	12,874,334	573D07	chr18.fa.O7frz.16363530
12,775,480	12,874,334	1803F04	D18S0050i
13,716,680	13,754,554	1806G09	D18S0055i
13,716,680	13,754,554	1803A03	Z67649
13,815,543	13,816,861	1801D09	Z67345
16,787,533	16,944,869	1803D05	D18S0073i
16,787,533	16,944,869	1806D06	D18S0554i
18,003,414	18,036,225	1801B01	Z67399
19,523,560	19,789,028	1802H07	D18S0204i
19,523,560	19,789,028	1804H04	D18S0285i
19,523,560	19,789,028	1801C03	D18S0448i
20,294,591	20,313,919	1803E01	D18S1107
20,294,591	20,313,919	1802F09	D18S1108
204,522	258,049	1801D01	D18S0041i
23,784,933	24,011,189	1803A06	D18S0087i
23,784,933	24,011,189	1803B06	D18S0090i
23,784,933	24,011,189	1805H02	D18S0226i
23,784,933	24,011,189	1805A04	D18S0410i
23,784,933	24,011,189	1804H01	D18S0479i
3,402,072	3,448,409	123D10	AC006211.1_151493
3,402,072	3,448,409	113B09	AC006211.1_168801
3,402,072	3,448,409	1804B03	D18S0455i
309,356	490,685	1803B10	D18S0192i
309,356	490,685	1804H09	D18S0429i
37,789,197	37,915,446	1803D08	D18S0155i
37,789,197	37,915,446	1803H10	D18S0206i
37,789,197	37,915,446	1802E08	D18S0312i
41,558,155	41,585,297	1803E07	D18S0129i
41,558,155	41,585,297	1805H03	D18S0144i

41,659,543	41,678,045	1805F11	D18S0385i
44,700,221	44,731,079	1803D11	D18S0223i
44,700,221	44,731,079	1805F05	D18S0297i
46,340,482	46,512,194	1804G12	D18S0119i
46,340,482	46,512,194	1802D08	D18S0490i
46,340,482	46,512,194	1803D02	D18S479
51,045,967	51,406,858	418H01	AC018994.3_111068
51,045,967	51,406,858	1804B08	D18S0003i
51,045,967	51,406,858	1806D10	D18S0382i
51,045,967	51,406,858	1806G06	HUMUT7024B
54,489,598	54,568,350	1802D12	D18S0565i
54,489,598	54,568,350	1802C12	D18S0566i
55,085,251	55,091,605	1805D08	D18S0317i
55,085,251	55,091,605	1804E01	D18S0518i
55,148,088	55,177,463	1801A05	D18S1155
56,189,564	56,190,562	575A04	chr18.fa.O7frz.64410150
56,189,564	56,190,562	1802D01	D18S0244i
58,143,500	58,205,872	1803H08	D18S0168i
58,143,500	58,205,872	1802B02	D18S0441i
58,941,559	59,137,593	1803A12	D18S0241i
58,941,559	59,137,593	1804A02	D18S0321i
58,941,559	59,137,593	1803H03	HUMUT574
59,705,922	59,722,100	1806F01	D18S68
59,767,574	59,779,093	9901E05	HUMUT2039
6,931,885	7,107,813	1806E11	D18S0258i
6,931,885	7,107,813	1805D04	D18S0350i
6,931,885	7,107,813	1805B03	D18S0352i
647,619	663,492	573C03	chr18.fa.O7frz.941566
65,681,172	65,775,140	1805B09	D18S0327i
65,681,172	65,775,140	1803H02	Z67518
65,681,172	65,775,140	1801D07	Z67555
66,107,243	66,145,329	1804C08	D18S0407i
66,107,243	66,145,329	1806C07	D18S0510i
7,557,817	8,396,854	1805E01	D18S0045i
7,557,817	8,396,854	1803E04	D18S0047i
7,557,817	8,396,854	1804E06	D18S0193i
7,557,817	8,396,854	1803C10	D18S0194i
7,557,817	8,396,854	1806E02	D18S0196i
7,557,817	8,396,854	1803E10	D18S0199i
7,557,817	8,396,854	1801A08	D18S0202i
7,557,817	8,396,854	9901B06	D18S0478i
7,557,817	8,396,854	1801E06	D18S1163
711,592	802,547	1801H06	D18S0446i
711,592	802,547	9909H05	D18S0452i
72,819,777	72,973,762	9901H05	D18S0498i
72,819,777	72,973,762	1802H04	D18S1097
75,256,760	75,390,311	1805G11	D18S0394i
75,256,760	75,390,311	9909E05	D18S0439i
9,465,007	9,528,106	1806C11	D18S0075i
1,018,174	1,037,627	9909H06	D19S886
1,560,293	1,603,328	1903H09	D19S0054i
1,560,293	1,603,328	9901B09	D19S0081i
1,560,293	1,603,328	1904B07	D19S0190i
10,083,197	10,087,065	1901B03	D19S0008i
10,083,197	10,087,065	1901E07	D19S0395i
10,258,650	10,260,198	1904D05	D19S0206i

10,322,205	10,352,211	1903A01	D19S0093i
10,457,796	10,475,243	1903B01	HUMUT5187
10,673,106	10,803,579	T001E09	D19S0283i
10,843,253	10,894,448	1901H01	D19S0245i
10,932,606	11,033,953	9909C08	D19S0301i
11,061,132	11,105,490	1902C03	D19S0372i
11,296,093	11,311,321	305C09	AC020561.3_124319
11,348,883	11,356,019	9901E08	D19S0139i
11,477,744	11,500,972	1902A06	D19S0364i
12,763,286	12,765,129	1903A02	D19S914
12,910,423	12,916,303	9909E06	HUMUT8091
12,917,654	12,925,455	1903C05	D19S0195i
13,933,352	13,978,097	1901D09	D19S0311i
13,933,352	13,978,097	1902D12	D19S0390i
14,063,500	14,089,559	1904A11	D19S0196i
14,353,213	14,380,535	1902F02	D19S0198i
14,444,278	14,447,174	1901H10	D19S226
14,570,918	14,646,810	1903H02	D19S0352i
14,704,205	14,750,353	1904D10	D19S0086i
15,024,015	15,027,900	1903E12	D19S0009i
15,024,015	15,027,900	1901F09	D19S929
15,131,444	15,172,792	1901C08	D19S0048i
15,440,463	15,451,312	1901G10	G08034
15,587,421	15,601,445	1901E08	D19S588
15,612,707	15,634,634	1903H05	D19S0318i
15,849,834	15,869,885	1902E08	D19S0050i
15,884,181	15,906,326	9901C11	D19S0354i
16,105,838	16,130,381	467D12	chr19.fa.O7frz.17685171
16,105,838	16,130,381	1901D08	D19S0248i
16,105,838	16,130,381	1901D03	D19S885
16,296,648	16,299,345	9901D09	D19S917
16,489,705	16,514,248	1904A02	D19S0114i
17,203,694	17,217,151	1902E10	D19S410
17,203,694	17,217,151	1901H08	D19S593
17,374,755	17,377,457	1904F08	D19S0151i
17,374,755	17,377,457	1903A10	D19S0162i
17,766,658	17,785,385	1902C08	D19S0109i
17,766,658	17,785,385	1902D02	D19S0159i
17,788,322	17,819,800	1901F12	D19S0022i
18,031,371	18,058,702	1902H04	D19S0051i
18,125,016	18,142,343	1901C11	D19S212
18,357,968	18,360,987	1902F12	D19S0215i
18,357,968	18,360,987	1901G06	D19S898
18,503,568	18,515,383	1903G09	D19S0284i
18,891,494	18,900,436	1903H06	D19S0013i
19,164,008	19,173,678	9901A08	D19S0087i
2,427,135	2,429,257	1904A07	D19S0370i
2,427,135	2,429,257	1901H07	D19S565
3,545,504	3,557,658	9901D11	D19S0106i
3,927,054	3,936,461	1903B07	D19S0366i
3,958,748	3,990,383	1902F06	D19S0328i
34,994,741	35,007,059	1902B01	D19S0044i
34,994,741	35,007,059	1901D05	G08036
37,763,944	37,770,171	1903B05	D19S0035i
38,482,776	38,485,160	9909H08	D19S0332i
38,482,776	38,485,160	674H06	DISO7_10007438

38,482,776	38,485,160	093E04	HUMUT1974
4,041,319	4,075,126	1902A02	D19S0032i
4,180,495	4,188,525	1903D05	D19S0123i
4,180,495	4,188,525	1901D07	D19S0137i
4,608,557	4,621,415	9901F10	D19S0040i
4,608,557	4,621,415	1901B11	D19S0131i
4,766,944	4,782,716	9901G10	D19S0060i
4,766,944	4,782,716	9909D07	D19S0098i
40,451,721	40,462,558	1902A08	D19S0085i
40,451,721	40,462,558	1904F02	D19S0273i
40,895,670	40,899,780	1902F01	D19S0384i
41,070,983	41,085,025	1903C10	D19S0002i
41,070,983	41,085,025	1904F01	D19S0227i
41,070,983	41,085,025	1901B07	D19S876
41,191,863	41,196,981	1902B09	D19S224
43,770,121	43,800,471	T002D09	D19S0380i
43,770,121	43,800,471	1901E12	D19S422
43,984,155	43,995,422	1901F01	D19S0361i
44,082,455	44,091,374	9901E11	D19S0108i
44,082,455	44,091,374	1902C04	D19S417
44,082,455	44,091,374	1902H07	D19S881
44,426,033	44,427,609	1901F07	D19S0193i
44,450,997	44,452,572	9909G07	D19S0285i
44,589,293	44,591,885	1902B08	D19S0375i
44,785,004	44,789,954	1902A03	D19S0260i
44,886,786	44,891,928	1902B02	D19S0275i
44,913,735	44,920,508	1901G08	D19S0083i
447,490	456,342	1902G10	D19S0073i
447,490	456,342	1903A04	D19S0338i
45,389,491	45,413,314	1902H08	D19S0226i
45,389,491	45,413,314	1902E07	HUMUT5576
45,389,491	45,413,314	9901B10	HUMUT6385
45,645,541	45,663,516	1904H05	D19S0210i
45,645,541	45,663,516	1903F05	D19S0276i
46,041,284	46,226,008	9901F08	D19S223
46,041,286	46,226,008	1901B10	D19S0262i
46,041,286	46,226,008	1901G07	HUMUT5036
46,390,955	46,405,284	1904C05	D19S0214i
46528254	46551656	TGFB11	new design
46528254	46551656	TGFB12	new design
46,904,377	46,925,686	239F08	AC005794.1_22677
46,904,377	46,925,686	1904D09	D19S0223i
46,992,381	47,007,431	576F01	chr19.fa.O7frz.51175481
46,992,381	47,007,431	051H06	D19S423
47,394,592	47,416,115	1902A10	D19S0094i
47,394,592	47,416,115	9909A08	D19S0293i
47,577,500	47,579,250	1902C10	D19S872
47,703,298	47,724,479	1902G05	D19S0111i
47,776,235	47,790,890	1904E07	D19S0103i
47,776,235	47,790,890	1903F08	D19S0126i
48,063,198	48,075,711	239F05	AC005260.1_494
48,063,198	48,075,711	9901B07	D19S211
48,549,651	48,559,368	1904G12	D19S0280i
48,549,651	48,559,368	1903F02	D19S0350i
48,739,032	48,771,998	1901A08	D19S0295i
48,739,032	48,771,998	9909A07	D19S408

48,842,088	48,866,539	9901C08	D19S0107i
48,912,078	48,916,013	1903F09	D19S0029i
48,912,078	48,916,013	9909B07	D19S217
49,839,066	49,858,690	1904A03	D19S0229i
49,839,066	49,858,690	1903F04	D19S574
49,943,820	49,955,140	9901H08	D19S0164i
49,943,820	49,955,140	1901A03	HUMUT7544
5,157,379	5,237,399	1904E06	D19S0265i
5,157,379	5,237,399	1901F10	D19S0362i
5,793,902	5,802,482	1904F10	D19S0130i
5,793,902	5,802,482	9901B11	D19S0325i
5,944,175	6,061,554	1903D01	D19S0303i
5,944,175	6,061,554	1901B01	D19S0304i
50,196,539	50,233,292	468B12	chr19.fa.O7frz.55431947
50,546,686	50,565,669	1903E07	D19S0105i
50,546,686	50,565,669	9901D12	D19S0317i
50,604,712	50,619,017	9901D08	D19S0077i
50,784,865	50,797,294	1903G08	D19S0001i
51,059,358	51,068,895	1904D11	D19S0221i
51,059,358	51,068,895	1901A11	D19S0387i
51,059,358	51,068,895	1901E02	D19S0393i
51,214,255	51,218,163	1904E10	D19S0110i
51,869,413	51,911,597	1904B04	D19S0253i
52,356,000	52.367.000	9901A12	D19S0181i
52,415,921	52,427,863	1902F04	D19S0264i
52,504,971	52,517,173	1904H08	D19S0185i
52,544,386	52,577,795	1901A02	D19S606
53,310,515	53,365,372	1904C01	D19S0160i
53,403,325	53,450,955	1904D01	D19S0287i
53,520,441	53,525,623	1902H05	D19S0171i
53,814,360	53,825,474	1904D07	D19S0271i
53,943,080	53,950,459	9901A11	D19S0166i
53,950,628	53,953,395	1904G10	D19S0173i
53,950,628	53,953,395	1904H04	D19S0180i
54,149,929	54,156,867	1903F07	D19S0179i
54,211,049	54,212,159	1904A09	D19S0186i
54,217,939	54,244,212	1904G05	D19S0289i
54,280,277	54,303,682	1901C01	D19S0297i
54,530,240	54,535,675	1903C08	D19S0072i
54,530,240	54,535,675	1902D06	D19S604
54,530,240	54,535,675	1901D02	HUMUT2523
54708304	54721402	FCGRT1	new design
54708304	54721402	FCGRT2	new design
54,750,780	54,775,626	1903H03	D19S0300i
55,084,723	55,124,598	1902D07	D19S0337i
55,571,515	55,578,051	469B02	chr19.fa.O7frz.63753376
55,571,515	55,578,051	9901H06	D19S0165i
56,319,977	56,325,379	154C08	AF135024.2_4066
56,319,977	56,325,379	9901G12	D19S0353i
56,605,087	56,612,869	1901A06	D19S0254i
56,714,795	56,726,922	1902A09	D19S0324i
56,806,996	56,831,696	1903F12	D19S0068i
56,940,839	56,946,962	1903A07	D19S0027i
56,955,995	56,965,591	9901C10	D19S0014i
58,484,666	58,486,687	1903B11	D19S0291i
58,484,666	58,486,687	1902C05	D19S921

58,988,650	59,019,409	9909G06	D19S0058i
58,988,650	59,019,409	1904E05	D19S0288i
59,077,279	59,102,713	1904H09	D19S0244i
59,077,279	59,102,713	670G07	DISO7_10004464
59,289,745	59,297,806	1902G12	D19S0170i
59,289,745	59,297,806	1903D03	D19S0355i
59,412,549	59,418,709	1904G11	D19S0230i
59,491,666	59,496,077	1903H07	D19S0038i
59,557,047	59,568,533	1904G06	D19S0235i
59,618,417	59,639,882	1902F05	D19S0239i
59,738,595	59,748,862	1904F04	D19S0169i
59,911,791	59,916,501	664A03	DISO7_10004466
6,235,811	6,344,184	1902C06	D19S0334i
6,323,444	6,326,040	1901B12	D19S0274i
6,482,037	6,486,933	1904D06	D19S0391i
6,536,850	6,542,163	608H08	chr19.fa.O7frz.7699148
6,628,878	6,671,660	663A12	chr19.fa.O7frz.7846308
6,628,878	6,671,660	9901F09	D19S0146i
6,723,722	6,808,371	9901G11	D19S0132i
6,838,577	6,891,464	1901E09	D19S0144i
6,838,577	6,891,464	9909D08	D19S0313i
60,077,361	60,095,055	1903G03	D19S926
60,168,465	60,204,318	9909D06	D19S0453i
60,384,428	60,412,654	1903F01	D19S605
60,911,610	60,941,580	1904G09	D19S0241i
60,911,610	60,941,580	1901G05	Z66860
61,099,123	61,135,489	1902G03	D19S0389i
63,754,745	63,758,298	1903D11	D19S0290i
7,067,049	7,245,045	305B05	AC010606.5_70425
7,067,049	7,245,045	1903C01	D19S0340i
7,067,049	7,245,045	1903G04	D19S406
7,659,662	7,673,032	1904A01	D19S0117i
7,659,662	7,673,032	9901C07	D19S905
7,734,081	7,740,491	1901C06	D19S912
7,874,728	7,885,363	1903F03	D19S0351i
776,097	783,017	1902D05	D19S0342i
8,023,934	8,033,547	1902F07	D19S922
8,491,689	8,548,330	1902A11	D19S0343i
810,665	814,624	1903C09	D19S0011i
9,806,999	9,821,358	1902G06	D19S0279i
9,931,237	9,982,147	1902A05	D19S583
1,614,666	1,727,298	0201A07	D2S0869i
10,101,133	10,112,414	0205D06	D2S0137i
101,680,920	101,877,584	0207D10	D2S2264
101,974,738	102,011,317	0220C03	HUMUT1265
102,125,678	102,162,766	0217B09	D2S1275i
102,169,865	102,222,243	0217B11	D2S1036i
102294394	102334929	IL1RL11	new design
102,345,529	102,381,650	0211B05	D2S0556i
102,401,686	102,435,457	0208E03	D2S373
102,602,598	102,694,241	0208E11	D2S0123i
108,360,853	108,370,702	0216C04	D2S0211i
108,360,853	108,370,702	0205B09	D2S1889
108,702,369	108,767,683	0201A02	D2S0205i
108,877,361	108,972,260	0216C11	D2S1281i
11,239,229	11,402,162	0206B05	D2S1586i

11,239,229	11,402,162	0205G04	D2S168
11,239,229	11,402,162	0202G05	Z67467
111,597,781	111,641,058	0205G06	D2S0198i
111,597,781	111,641,058	0208A05	D2S1892
112,372,662	112,503,416	377B11	AC067761.2_149902
112,372,662	112,503,416	0221H11	D2S0532i
113,247,963	113,259,442	0212G11	D2S1051i
113303808	113310827	IL1B1	new design
113303808	113310827	IL1B2	new design
113303808	113310827	IL1B3	new design
113387017	113392930	IL1F71	new design
113387017	113392930	IL1F72	new design
113387017	113392930	IL1F73	new design
113,452,077	113,459,698	0202E11	D2S1276i
113,591,941	113,608,064	0201D01	D2S0193i
113,591,941	113,608,064	0210G06	D2S0321i
118,288,725	118,306,425	0217C04	D2S0886i
119,416,215	119,468,706	0215E06	D2S0233i
119,416,215	119,468,706	0202B11	D2S0627i
119,630,289	119,632,941	0211A06	D2S0582i
119,630,289	119,632,941	0205C04	D2S2254
119,905,950	119,911,486	0202A10	D2S0218i
119,905,950	119,911,486	0216B01	D2S0592i
120,233,677	120,451,507	0218G01	D2S0897i
120,233,677	120,451,507	0212H06	D2S0911i
120,233,677	120,451,507	0209A04	D2S1533i
120,819,469	120,825,444	0202F10	D2S2329
120,819,469	120,825,444	0204A07	D2S2341
121,266,327	121,466,321	0203G09	D2S2212
121,266,327	121,466,321	0206B07	D2S2258
121,266,327	121,466,321	0208B04	D2S283
121,266,327	121,466,321	0207C09	Z67547
121,811,825	122,123,522	278D01	AC013399.2_117318
121,811,825	122,123,522	378G07	AC018737.3_67168
121,811,825	122,123,522	502H02	chr2.fa.O7frz.125811119
121,811,825	122,123,522	0217D12	D2S1064i
121,811,825	122,123,522	0221E05	D2S343
127,130,154	127,170,716	0211E06	D2S0593i
127,130,154	127,170,716	0211C07	D2S0617i
127,130,154	127,170,716	0219H11	D2S1467i
127,778,609	127,817,240	0209E07	D2S1631i
127,778,609	127,817,240	0206B04	D2S2271
127,892,486	127,903,288	0218D08	D2S0214i
127,892,486	127,903,288	0216D05	D2S0596i
130,830,088	130,848,614	0209F03	D2S1522i
130,830,088	130,848,614	0209D04	D2S1536i
136,313,666	136,350,481	0201H08	D2S0632i
136,313,666	136,350,481	0201G05	Z67485
136,705,639	136,709,450	0203E04	D2S1714i
136,705,639	136,709,450	0221C09	D2S2196
138,438,278	138,490,404	0213D08	D2S1302i
138,438,278	138,490,404	0206F10	D2S1810i
15,648,753	15,688,676	0219E10	D2S1383i
15,648,753	15,688,676	0218C05	D2S1389i
15,998,134	16,004,580	0210A09	D2S0381i
15,998,134	16,004,580	0203C08	D2S1828i

151,835,231	151,854,620	0214E05	D2S0657i
151,835,231	151,854,620	0214D12	D2S1334i
153,216,334	153,283,014	0211F07	D2S0624i
153,216,334	153,283,014	0204D02	D2S2299
156,889,194	156,897,474	0202B07	D2S1807i
157,979,377	158,008,850	0216D06	D2S0717i
157,979,377	158,008,850	0211D12	D2S0724i
160,277,256	160,333,330	0221D09	D2S0708i
160,277,256	160,333,330	0206G12	D2S156
160,277,256	160,333,330	009G10	D2S306
160,368,118	160,469,493	0213E02	D2S1128i
160,505,506	160,627,367	0201H05	D2S1122i
160,664,438	160,765,009	0213C11	D2S1403i
161,701,712	161,800,928	0217B03	D2S0677i
161,701,712	161,800,928	0211E12	D2S0725i
162,557,001	162,639,298	0218F11	D2S0929i
162,557,001	162,639,298	0214G04	D2S0932i
162,831,835	162,883,285	0215E09	D2S0917i
170,149,096	170,202,500	0216G02	D2S0649i
170,149,096	170,202,500	0213E08	D2S1313i
172,487,204	172,556,846	9902F08	D2S0689i
172,487,204	172,556,846	0214H01	D2S1444i
173,000,616	173,079,256	0210A02	D2S0048i
173,129,025	173,172,108	0211H05	D2S0581i
174,481,504	174,538,676	381G03	AC055875.2_105198
174,481,504	174,538,676	504B05	chr2.fa.O7frz.181842884
174,921,124	174,968,689	0201D08	D2S0320i
174,921,124	174,968,689	0201E02	D2S1731i
175,132,548	175,255,873	0211G11	D2S0705i
175,132,548	175,255,873	0209H08	D2S1665i
176,689,738	176,692,916	0210G01	D2S0046i
176,689,738	176,692,916	0219H07	D2S0260i
177,965,731	178,112,411	0211F10	D2S0687i
177,965,731	178,112,411	0213B11	D2S1399i
177,965,731	178,112,411	0203E07	D2S2173
182,029,864	182,110,719	0210G05	D2S0253i
182,029,864	182,110,719	0215D10	D2S1147i
183,406,982	183,439,743	0216A09	D2S0735i
183,651,732	183,673,616	0215D06	D2S1380i
183,651,732	183,673,616	0220E12	D2S1462i
187,163,045	187,253,873	279F08	AC017026.5_11120
187,163,045	187,253,873	381G05	AC017026.6_146393
187,163,045	187,253,873	381A06	AC017101.8_55453
189,547,344	189,585,717	381G07	AC066694.2_218537
189,547,344	189,585,717	429C05	chr2.fa.O7frz.197184084
189,547,344	189,585,717	0219D03	D2S0774i
190,133,561	190,153,858	0215H10	D2S0739i
190,133,561	190,153,858	0219B09	D2S0746i
191,542,121	191,587,181	0212H02	D2S0775i
191,542,121	191,587,181	0215G02	D2S1178i
191,602,551	191,724,539	0214H03	D2S0745i
197,336,917	197,372,670	0209H06	D2S1614i
197,336,917	197,372,670	0207F02	D2S1621i
198,059,553	198,073,243	0214C08	D2S1664i
20,264,039	20,288,675	0210C08	D2S0359i
201,443,924	201,462,244	0204E09	D2S116

201,443,924	201,462,244	0207D04	D2S1707i
201,756,100	201,802,372	0209E04	D2S1539i
201,806,396	201,854,521	0212G01	D2S0749i
202,949,916	203,140,719	0217C11	D2S0201i
202,949,916	203,140,719	0218G11	D2S1768i
203,811,658	203,878,579	0217B01	D2S1174i
203,811,658	203,878,579	0213E04	D2S1183i
204,279,443	204,310,801	0219F06	G09915
204,279,443	204,310,801	0208F10	HUMUT426
204,440,754	204,446,928	169G12	AF225900.1_4678
204,440,754	204,446,928	0219C01	D2S1188i
204,440,754	204,446,928	0221H04	D2S307
207,653,323	207,738,859	0208A11	D2S0057i
207,653,323	207,738,859	0215A11	D2S0116i
207,653,323	207,738,859	0213H11	D2S1424i
208,102,931	208,171,818	0221A07	D2S1701i
211,050,678	211,252,076	340F03	AC021150.7_98846
211,050,678	211,252,076	0220A12	D2S0094i
211,050,678	211,252,076	0221D05	D2S0298i
211,050,678	211,252,076	0213A12	D2S1430i
215,933,409	216,009,041	0214G12	D2S0265i
215,933,409	216,009,041	0210H06	D2S0323i
216,680,435	216,779,248	0221F07	D2S0052i
216,680,435	216,779,248	0219G07	D2S0226i
216,680,435	216,779,248	0205G10	D2S0230i
216,985,441	217,056,021	0204D05	D2S0809i
216,985,441	217,056,021	0206B06	D2S1655i
216,985,441	217,056,021	0219C03	D2S1659i
217,206,372	217,237,404	0217D03	D2S0278i
217,206,372	217,237,404	0219F12	D2S1476i
218,698,991	218,710,220	0204C02	D2S1206i
218,955,161	218,968,994	0219D05	D2S0791i
218,955,161	218,968,994	0220A10	D2S1538i
219,354,745	219,388,259	0219F02	D2S0828i
219,354,745	219,388,259	011A01	D2S2250
219,354,745	219,388,259	0221D02	G08149
219,628,173	219,633,433	0210A07	D2S0336i
219,628,173	219,633,433	0210B07	D2S0340i
219,628,173	219,633,433	0205G11	D2S0790i
219,822,677	219,826,882	0220B12	D2S0090i
220,145,161	220,148,679	0204H01	D2S1338i
227,578,168	227,737,519	0214E03	D2S0276i
227,578,168	227,737,519	0221G02	D2S1349
227,737,525	227,887,751	0201C03	D2S1802i
228,045,286	228,130,548	0204E11	D2S1673i
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228,386,814	228,390,494	0214F12	HUMUT8098
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230,741,896	230,792,932	0206B11	D2S1813i
231,681,199	231,698,068	0215H09	D2S0292i
231,681,199	231,698,068	0215G01	D2S0794i
233,633,433	233,781,288	0221A06	D2S331
233,633,433	233,781,288	0220D03	HUMUT8067
234,191,030	234,346,695	0220E08	D2S0042i
234,191,030	234,346,695	0218C03	D2S0839i

234,191,030	234,346,695	0216F12	D2S1220i
234,191,030	234,346,695	082D06	Z67659
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237,143,182	237,155,730	0214B03	D2S1219i
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237,897,401	237,987,559	0207F06	D2S1806i
238,893,821	238,972,536	383C04	AC013400.4_10628
238,893,821	238,972,536	506H10	chr2.fa.O7frz.250246308
238,893,821	238,972,536	0207H02	D2S0335i
239,000,365	239,025,630	0220D04	D2S0841i
239,000,365	239,025,630	0204C09	D2S1221i
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239,635,319	239,987,580	0205H02	D2S1205i
239,635,319	239,987,580	0213F05	D2S1214i
239,635,319	239,987,580	0202H10	D2S1704i
24,126,075	24,140,055	0219E03	D2S0149i
24,126,075	24,140,055	0207A05	D2S1779i
241,148,144	241,152,104	0219G05	D2S0338i
241,148,144	241,152,104	0209D07	D2S1629i
241,903,396	241,942,115	0210C01	D2S0033i
241,903,396	241,942,115	0203H09	D2S1565i
242,146,865	242,162,226	0220G05	D2S1540i
242,440,711	242,449,731	0209G07	D2S1637i
25,237,226	25,245,063	0210D09	D2S0397i
25,237,226	25,245,063	0204C04	D2S171
27,383,769	27,384,634	0219A11	D2S1352i
29,269,144	29,997,936	0214G01	D2S0965i
29,269,144	29,997,936	0216E02	D2S1255i
29,269,144	29,997,936	0202A04	D2S146
29,269,144	29,997,936	0218A05	D2S1687i
29,269,144	29,997,936	0209E10	D2S1765i
29,269,144	29,997,936	0204E02	D2S2383
31,410,691	31,491,117	0215F01	D2S0437i
31,410,691	31,491,117	0210H11	D2S0446i
31,410,691	31,491,117	0202H07	D2S2203
31,410,691	31,491,117	0203H01	D2S352
32,303,022	32,344,427	0218E10	D2S0143i
32,303,022	32,344,427	0217C12	D2S1405i
32,435,234	32,697,470	0220B04	D2S0152i
32,435,234	32,697,470	0215D07	D2S0311i
33,025,896	33,478,080	0210G03	D2S0151i
33,025,896	33,478,080	0210D08	D2S0363i
33,025,896	33,478,080	0210F08	D2S0371i
33,025,896	33,478,080	0210C09	D2S0391i
33,025,896	33,478,080	0205C12	D2S0453i
33,025,896	33,478,080	0212B09	D2S0985i
33,025,896	33,478,080	0212D09	D2S0992i
33,025,896	33,478,080	0206B03	D2S2325
33,025,896	33,478,080	0205E12	D2S2347
33,514,920	33,643,162	0215D08	D2S0384i
37,331,149	37,398,541	0215H01	D2S0873i
37,331,149	37,398,541	0214A09	D2S0877i
37,331,149	37,398,541	0209E02	D2S1501i
38,148,154	38,156,796	0215H06	D2S0459i
38,148,154	38,156,796	0201A08	D2S0967i
38,878,375	38,956,525	0210F10	D2S0416i

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38,878,375	38,956,525	0208C01	D2S2331
39,066,469	39,201,067	0202D03	D2S0425i
39,066,469	39,201,067	0215C03	D2S0431i
39,329,911	39,517,946	0210D01	D2S0036i
39,329,911	39,517,946	0207E03	D2S0101i
39,329,911	39,517,946	0208D11	D2S0109i
43,717,916	43,848,630	0202F06	D2S119
45,732,547	46,268,633	0217F04	D2S0434i
45,732,547	46,268,633	0220B11	D2S1482i
45,732,547	46,268,633	0205E10	D2S2182
45,732,547	46,268,633	0203C09	D2S2240
45,732,547	46,268,633	T002B12	D2S2291
46,661,580	46,697,708	0210A11	D2S0423i
46,661,580	46,697,708	0220D06	D2S1719i
46,779,595	46,843,431	0220A09	D2S1717i
48,395,374	48,459,938	0215E08	D2S0988i
48,395,374	48,459,938	0209B06	D2S1595i
48,767,471	48,836,321	0218B03	D2S0420i
49,043,156	49,235,134	0209D02	D2S1500i
49,043,156	49,235,134	0209A03	D2S1509i
49,043,156	49,235,134	0205A01	D2S1510i
49,043,156	49,235,134	0209B03	D2S1513i
58,127,224	58,240,510	376B06	AC068193.5_165968
58,127,224	58,240,510	0220C10	D2S0443i
6,935,247	6,955,821	0210C07	D2S0343i
6,935,247	6,955,821	0215D11	D2S0351i
6,935,247	6,955,821	0212E07	D2S0936i
60,962,254	61,003,682	0211E03	D2S0524i
64,173,499	64,225,062	0212G09	D2S1003i
64,173,499	64,225,062	0212H09	D2S1008i
68,203,572	68,341,866	0214D03	D2S0182i
68,203,572	68,341,866	0217G12	D2S0305i
68,203,572	68,341,866	0202E04	D2S0484i
69,995,707	70,023,581	376H04	AC019206.3_137449
69,995,707	70,023,581	0221C01	D2S0183i
69,995,707	70,023,581	0216B12	D2S0313i
70,527,924	70,634,438	0214D07	D2S0039i
70,527,924	70,634,438	0206F08	D2S0076i
70,527,924	70,634,438	0206F02	D2S292
70,910,855	70,916,461	0202D01	D2S1464i
72,209,875	72,228,471	0208E02	D2S2112
73,842,837	73,860,756	0201A12	D2S1715i
74,598,766	74,606,826	0205B12	D2S0066i
74,598,766	74,606,826	0209A10	D2S1745i
74,634,795	74,638,181	0220E03	D2S0062i
85,737,951	85,748,823	0214B09	D2S0171i
85,737,951	85,748,823	0219B08	D2S0315i
85,919,782	85,969,648	0216E03	D2S0575i
85,919,782	85,969,648	0208C03	D2S388
86,521,954	86,573,350	377E03	AC068288.3_48784
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86,521,954	86,573,350	0219C02	D2S1437i
86,865,239	86,871,638	0214B05	D2S0560i
86,895,971	86,942,549	0206C05	D2S1847i
89,120,836	89,121,310	0212D06	D2S0889i

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9,463,264	9,481,127	0203H08	D2S2207
9,641,552	9,688,629	0203H02	D2S2169
96,172,638	96,174,906	0220F10	D2S1576i
96,365,211	96,405,001	0215F12	D2S0498i
97,696,461	97,722,755	377F07	AC017099.9_66660
97,696,461	97,722,755	0221B09	D2S2222
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99,225,141	99,238,002	0206E02	D2S1524i
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1,297,622	1,321,806	2005H10	D20S0258i
1,399,386	1,420,233	2004B05	D20S0382i
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1,822,813	1,868,543	2001B01	G09329
10,566,334	10,602,636	2005A09	D20S0238i
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155,899	158,527	2002E01	D20S864
2,224,647	2,269,725	245B06	AL031678.2_90137
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2,769,366	2,967,320	2002G03	D20S0337i
22,509,643	22,514,102	2001B05	D20S0179i
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22,974,270	22,978,301	2003A10	D20S0197i
23,007,995	23,014,977	2002F06	D20S0077i
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23,676,190	23,679,574	2002G05	D20S0428i
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29,565,892	29,621,031	2004C01	D20S0416i
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3,724,386	3,734,762	2001E02	D20S0131i
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31,541,589	31,701,503	2005E06	D20S0007i
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31,541,589	31,701,503	2004E02	D20S0399i
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36,867,762	36,985,081	9909D11	D20S0365i
37,024,409	37,101,778	2003F10	D20S0215i
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43,269,052	43,271,827	2005G06	D20S0335i
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17,887,842	17,907,136	2005G08	D20S0013i
17,887,842	17,907,136	2005B08	D20S0280i
25,933,460	26,009,106	2003H06	D20S0130i
25,933,460	26,009,106	2004F01	HUMUT278
29,831,125	30,234,153	2102G11	D21S0019i
29,831,125	30,234,153	2103H05	D21S0076i
29,831,125	30,234,153	2102C10	D21S0153i
29,831,125	30,234,153	2101E06	D21S0185i
29,831,125	30,234,153	2101C01	D21S0212i
29,831,125	30,234,153	9909B12	D21S0324i
31953806	31963115	SOD11	new design
31953806	31963115	SOD12	new design
33,320,023	33,323,374	2102A09	D21S0003i
33,524,076	33,559,839	2102F10	D21S0024i
33,524,076	33,559,839	718G09	DIJ28_10003558
33,619,079	33,654,038	2103E03	D21S0017i
33,697,072	33,731,698	2101E07	D21S0227i
35,081,968	35,343,511	157E06	AP001721.1_224451
35,081,968	35,343,511	2102B06	D21S0021i
35,081,968	35,343,511	2101D07	D21S0029i
35,081,968	35,343,511	2101E05	D21S0086i
35,081,968	35,343,511	2101G07	D21S0091i
35,081,968	35,343,511	9909G12	D21S0237i
36,679,559	36,710,995	2102A01	D21S0090i
36,679,559	36,710,995	2101F11	D21S0095i
37,661,729	37,809,347	2101E12	D21S0183i
37,661,729	37,809,347	2103C12	D21S0221i
37,661,729	37,809,347	2103E01	D21S270
38,675,671	38,955,488	2103F03	D21S0025i
38,675,671	38,955,488	2102E10	D21S0200i
38,675,671	38,955,488	2103G12	D21S0233i
38,675,671	38,955,488	2101E04	G08076
40,039,204	40,095,893	2102F09	D21S0089i
40,039,204	40,095,893	059F07	Z67428
40,306,213	41,140,909	2101G09	D21S0084i

40,306,213	41,140,909	2103E06	D21S0102i
40,306,213	41,140,909	2103D08	D21S0136i
40,306,213	41,140,909	2101H06	D21S0143i
40,306,213	41,140,909	2103C09	D21S0164i
40,306,213	41,140,909	2103H09	D21S0184i
40,306,213	41,140,909	2101D12	D21S0209i
40,306,213	41,140,909	2103E11	D21S0213i
40,306,213	41,140,909	2101F07	D21S1887
40,306,213	41,140,909	2101F03	D21S1906
41,655,820	41,702,739	2102H05	D21S0088i
41,655,820	41,702,739	2103C01	D21S266
41,720,024	41,753,008	2102D06	D21S0228i
42,599,751	42,608,775	2102F03	D21S0151i
43,963,406	44,006,608	2101F02	D21S0020i
43,963,406	44,006,608	2103B11	D21S0205i
43,963,406	44,006,608	2102G08	D21S0229i
44,467,313	44,485,262	2101B07	D21S1912
44,530,191	44,542,530	2101D06	D21S0097i
45,130,296	45,173,181	2101C05	D21S0241i
45737914	45786779	SLC19A1	new design
46,226,091	46,249,391	2102E07	D21S0007i
46,226,091	46,249,391	9909D12	D21S0206i
46,342,470	46,377,190	2101C12	D21S0262i
46,879,507	46,909,291	2102B10	D21S0245i
15,945,849	15,971,405	2202F03	D22S0091i
16,501,485	16,593,383	9910C08	D22S0210i
16,591,460	16,631,812	2202F12	D22S0026i
16,591,460	16,631,812	2201C06	D22S0231i
17,141,172	17,159,474	9910D07	D22S0216i
17,403,798	17,489,962	2201A09	D22S0151i
17,403,798	17,489,962	2202E04	D22S0205i
18,091,066	18,092,297	9910E02	D22S0041i
18,091,066	18,092,297	2201F09	D22S0206i
19,108,875	19,122,146	2202B03	D22S0089i
19,601,714	19,638,034	9910H02	D22S0046i
19,601,714	19,638,034	2201C11	D22S0128i
19,699,449	19,713,119	2202E03	D22S0228i
20,326,542	20,328,588	2201G07	D22S446
20,443,946	20,551,970	2201E11	D22S0109i
20,929,200	20,929,926	2202A11	D22S0119i
21,220,123	21,231,768	2201B10	D22S0232i
21,852,552	21,990,224	9910C03	D22S0055i
21,852,552	21,990,224	103C02	HUMUT8144
22,245,312	22,252,495	9910F03	D22S0068i
22,245,312	22,252,495	9910C05	D22S0156i
22,369,647	22,567,417	2201B11	D22S0163i
22,369,647	22,567,417	9910F06	D22S0186i
22,706,141	22,714,271	2202F02	D22S0169i
22,737,765	22,904,596	9910E06	D22S0184i
22,737,765	22,904,596	2202F01	D22S1174
23,153,537	23,168,325	2201B06	D22S0176i
23,309,718	23,354,972	9910B05	D22S0153i
26,474,265	26,527,486	2202D06	D22S0063i
26,474,265	26,527,486	2202G03	HUMUT7995
27,520,548	27,526,560	9910E07	D22S0218i
28,966,441	28,972,748	2202E07	D22S0018i

28,966,441	28,972,748	2201G01	HUMUT5900
29,333,161	29,353,047	2201B02	D22S0221i
29,388,039	29,393,872	2202B02	D22S0127i
30,125,539	30,160,438	2202C09	D22S0010i
30,125,539	30,160,438	9910H06	D22S0193i
31,526,802	31,589,028	2201G03	D22S0025i
31,526,802	31,589,028	251H05	Z17028.1_102
34,107,057	34,120,194	719C01	DIJ28_10030051
34,374,370	34,394,402	2201H11	D22S0042i
34,374,370	34,394,402	2202D10	D22S0132i
35,007,272	35,113,958	2201A02	D22S283
35,290,050	35,428,849	**252H05**	-H4251-
35,586,976	35,604,005	2202C02	D22S0165i
35,586,976	35,604,005	2201H09	D22S1177
35,851,824	35,875,908	2202E08	D22S0052i
35,906,152	35,914,276	T002D04	D22S0122i
35,906,152	35,914,276	2202F05	D22S0148i
35,951,238	35,970,251	2202G08	D22S0171i
36,216,346	36,245,193	2201C10	D22S0135i
36,216,346	36,245,193	9910B06	D22S0177i
36,837,448	36,907,763	2202C11	D22S0099i
36,837,448	36,907,763	2201F10	D22S0106i
37,209,389	37,232,262	2202G12	D22S0092i
37,209,389	37,232,262	9910F05	D22S0166i
37,460,681	37,481,928	2101D09	D21S1919
37,460,681	37,481,928	053B05	D21S267
37,949,310	37,971,006	2202F09	D22S0037i
38,125,692	38,163,078	2202G10	D22S0002i
38,246,515	38,248,637	2201B01	D22S428
38,627,032	38,698,204	2201G09	D22S0108i
38,627,032	38,698,204	2202G04	D22S284
39,817,736	39,906,024	2202C06	D22S0021i
40,664,687	40,673,094	2202B11	D22S0007i
40,664,687	40,673,094	2202A10	D22S0064i
40,852,445	40,856,827	2201D03	D22S0227i
40,885,963	40,941,389	**9910B07**	D22S0199i
41,108,917	41,158,340	2202H04	D22S0200i
41,108,917	41,158,340	2202H03	D22S0201i
41,309,671	41,340,906	252A05	Z93241.11_118962
41,418,071	41,446,820	2201D06	HUMUT1091
41,836,701	41,855,662	2201F05	D22S1151
41,836,701	41,855,662	054F01	D22S1179
44,925,163	45,018,317	2202F04	D22S1149
45,394,963	45,454,352	2201H01	D22S0202i
45,394,963	45,454,352	9910E08	D22S0225i
45,458,971	45,512,816	2202F10	D22S0173i
49,311,047	49,315,321	2202F07	D22S0096i
49,385,997	49,396,843	9910D08	D22S0222i
49,459,936	49,518,507	728A10	-
10,181,563	10,260,427	0304D05	D3S1329i
103,029,547	103,062,556	0301F10	D3S1228i
103,029,547	103,062,556	632E08	DISO7_10001184
106,568,403	106,778,434	0313F05	D3S1080i
106,568,403	106,778,434	0310D06	D3S1083i
106,568,403	106,778,434	0315A01	D3S1591
106,859,799	107,070,577	0310G09	D3S0029i

106,859,799	107,070,577	0309D06	D3S0668i
106,859,799	107,070,577	0301G07	D3S1493i
109,244,631	109,292,625	0310A05	D3S0548i
109,244,631	109,292,625	0309C01	D3S0552i
109,244,631	109,292,625	0302C06	Z67497
11,269,400	11,279,415	0314A07	D3S0216i
11,269,400	11,279,415	0301D05	D3S0835i
110,024,321	110,056,542	0303H10	D3S1302
112,273,555	112,395,063	0307C11	D3S0116i
112,273,555	112,395,063	0313B10	G08281
112,743,546	112,853,906	0309F05	D3S0644i
112,743,546	112,853,906	0302E07	D3S1443i
112,743,546	112,853,906	0306H04	D3S1572
113,522,943	113,564,349	0307C06	D3S1359i
113,522,943	113,564,349	0315D12	Z66960
113,667,463	113,701,066	0301F03	Z67725
114,017,246	114,047,487	0312E12	D3S0657i
114,017,246	114,047,487	0304C11	D3S1410i
114,122,746	114,176,650	0308F03	D3S0290i
12,169,568	12,175,851	393G02	AC015546.16_112255
12,169,568	12,175,851	396A05	AC026166.2_143575
12,169,568	12,175,851	0317H08	D3S1127i
12,304,359	12,450,843	0304H07	D3S0036i
12,304,359	12,450,843	0311H05	D3S0208i
12,304,359	12,450,843	0317C09	D3S1133i
120,102,167	120,347,588	0303G01	D3S0934i
120,102,167	120,347,588	0315H02	D3S3515
120,102,167	120,347,588	729D03	DIJ28_10010297
120,725,832	120,761,139	285H01	AC069519.8_29705
120,725,832	120,761,139	013E09	D3S3513
120,792,984	120,831,342	398B01	AC073352.7_5796
120,982,021	121,020,022	0306B04	D3S3620
121,028,233	121,295,954	0314D03	D3S0118i
121,937,926	121,984,605	0315B05	D3S1059i
123,256,911	123,322,673	0310G01	D3S1225i
123,256,911	123,322,673	0317A01	D3S1779i
123,256,911	123,322,673	0303B04	D3S3720
124,813,833	125,085,839	0316C06	D3S1322i
124,813,833	125,085,839	0306E04	D3S3552
125,964,485	126,088,842	0308E05	D3S0359i
125,964,485	126,088,842	0308G08	D3S0446i
125,964,485	126,088,842	0315D07	D3S0698i
128,190,192	128,238,922	0307B03	D3S1258i
128,190,192	128,238,922	0304D07	D3S1459i
128,799,943	128,823,969	0310H09	D3S0356i
128,799,943	128,823,969	013F11	D3S3607
129,253,902	129,273,216	0313A04	D3S0790i
129,253,902	129,273,216	0304C01	Z67486
129,680,960	129,694,718	0315F04	D3S0688i
130,262,300	130,263,941	0313E12	D3S0360i
130,756,708	130,808,351	0311E07	D3S0958i
130,756,708	130,808,351	0307G02	D3S1250i
131,176,253	131,179,470	0314E02	D3S0200i
131,176,253	131,179,470	0312B11	D3S0348i
131,176,253	131,179,470	0302B07	D3S1176i
131,880,468	131,948,340	0309F10	D3S0809i

131,880,468	131,948,340	0305B06	D3S1053i
133,798,784	133,804,072	0302G03	D3S1306i
135,996,950	136,461,999	390E07	AC016951.9_56629
135,996,950	136,461,999	0308D08	D3S0442i
135,996,950	136,461,999	0311C06	D3S0959i
135,996,950	136,461,999	0316E05	D3S1590
135,996,950	136,461,999	0315E10	D3S3641
135,996,950	136,461,999	0316A04	D3S3696
135,996,950	136,461,999	0303A05	Z67391
138,159,397	138,212,610	0308D05	D3S0357i
138,159,397	138,212,610	0301A12	D3S3617
139,856,921	139,960,875	0315F01	D3S0555i
139,856,921	139,960,875	0307E07	D3S1383i
14,161,648	14,195,143	0312A05	D3S0854i
14,964,240	15,065,784	0312G02	D3S0836i
14,964,240	15,065,784	0301H08	D3S0841i
140,145,756	140,148,491	0309D02	D3S0565i
140,145,756	140,148,491	0304C04	G09845
142,939,741	142,947,933	0308A05	D3S0345i
142,939,741	142,947,933	0301F12	D3S1451i
143,078,160	143,128,072	0305F10	D3S1061i
144,466,754	145,049,979	386E07	AC026673.12_150939
144,466,754	145,049,979	386D07	AC026673.12_52550
144,466,754	145,049,979	398G05	AC073242.3_44298
144,466,754	145,049,979	515D08	chr3.fa.O7frz.163941355
144,466,754	145,049,979	0305H03	D3S1171i
144,466,754	145,049,979	0307B04	D3S1276i
144,466,754	145,049,979	0317A12	D3S1281i
144,466,754	145,049,979	0305D08	D3S1536i
144,466,754	145,049,979	014E03	D3S3599
149,898,355	149,943,478	390F08	AF245699.1_60143
149,898,355	149,943,478	0312D03	D3S0592i
149,898,355	149,943,478	0317A09	D3S1131i
150,230,604	150,287,007	0313D08	D3S0585i
150,230,604	150,287,007	0303G02	D3S1555
150,330,061	150,373,995	0317H01	D3S0362i
152,412,595	152,478,847	387F12	AC024886.10_174359
152,412,595	152,478,847	0310E04	D3S1000i
152,637,167	152,659,187	0301B10	D3S1499i
154,035,426	154,038,535	0302G04	D3S0145i
154,035,426	154,038,535	0301F01	D3S1193i
155,476,152	155,524,971	0301D08	D3S3677
155,476,152	155,524,971	0305H05	D3S3710
156,280,153	156,384,186	0312E11	D3S0134i
156,280,153	156,384,186	0312G05	D3S1004i
158,637,301	158,644,071	0307A05	D3S1311i
16,949,586	17,107,089	0303C06	D3S1429i
16,949,586	17,107,089	0304D08	D3S1452i
161,189,323	161,196,500	388C05	AC026118.8_8957
161,189,323	161,196,500	0311D01	D3S2442
161,189,323	161,196,500	0303B05	D3S3580
161,427,938	161,650,320	0306C10	D3S0398i
161,427,938	161,650,320	0315C07	D3S0693i
161,427,938	161,650,320	0301E11	D3S1482i
162,284,365	162,305,854	0307B06	D3S1354i
168,884,388	168,935,345	0311G10	D3S0989i

168,884,388	168,935,345	0303D02	D3S1494i
170,285,244	170,347,054	0308E07	D3S0395i
170,285,244	170,347,054	T003G02	D3S1282
170,965,092	170,965,542	0309H08	D3S0726i
170,965,092	170,965,542	0302H04	D3S3523
171,422,919	171,506,459	0305D04	D3S1013i
171,422,919	171,506,459	0315B06	D3S1289i
173,706,158	173,723,963	0306B09	D3S0009i
173,706,158	173,723,963	0315C10	D3S0162i
178,221,867	178,397,734	0312D09	D3S1017i
178,221,867	178,397,734	0305A12	D3S1092i
178,221,867	178,397,734	0311D03	D3S1522i
180,349,005	180,435,194	0317F06	D3S1052i
180,349,005	180,435,194	0315D01	Z66727
184,322,697	184,363,317	0303C09	D3S1295i
184,322,697	184,363,317	0317D12	D3S1301i
185,572,467	185,578,626	389H02	AC068634.11_165297
185,572,467	185,578,626	0303D05	D3S3578
186,563,664	186,683,322	0317B09	D3S1132i
187,917,814	187,944,437	0311B11	D3S1037i
187,917,814	187,944,437	0306B12	D3S1093i
188,131,210	188,279,035	128G07	AC007488.15_56318
188,131,210	188,279,035	287H05	AC034190.2_77059
188,131,210	188,279,035	0311C01	D3S1030i
188,131,210	188,279,035	0305D10	D3S1397i
188,418,632	188,492,446	0316D10	D3S3600
188,568,862	188,572,066	0306E10	D3S0421i
188,568,862	188,572,066	706B03	DID22N_0041504
188,869,388	188,870,895	0311B08	D3S1021i
188,869,388	188,870,895	0315H11	D3S1293i
188,869,388	188,870,895	634E03	DISO7_10001334
190,831,910	191,097,759	389G03	AC063939.9_142349
190,831,910	191,097,759	0314C07	D3S0402i
190,831,910	191,097,759	0310H11	D3S1101i
191,714,585	191,858,537	0314A03	D3S0024i
191,714,585	191,858,537	0303B11	D3S0027i
191,714,585	191,858,537	0302F01	D3S1404i
193,342,413	193,928,066	389H04	AC026671.12_22466
193,342,413	193,928,066	389F04	AC027042.2_47409
193,342,413	193,928,066	0314H08	D3S0146i
193,342,413	193,928,066	0305C09	D3S0409i
193,342,413	193,928,066	0309D03	D3S0601i
193,342,413	193,928,066	0309F04	D3S0626i
193,342,413	193,928,066	0311F11	D3S1036i
193,342,413	193,928,066	0311F12	D3S1038i
193,342,413	193,928,066	076H08	D3S2418
193,342,413	193,928,066	015B03	D3S3663
193,342,413	193,928,066	0316F03	D3S3669
195,595,348	195,601,523	0311G12	D3S1039i
197,260,553	197,293,343	0305G02	D3S0165i
197,951,312	198,043,756	0313E04	D3S0161i
197,951,312	198,043,756	0310C11	D3S0163i
198,214,553	198,241,043	0313F11	D3S0158i
198,214,553	198,241,043	0302H08	D3S1464i
213,650	426,098	0311E11	D3S0597i
213,650	426,098	0317C07	D3S1067i

213,650	426,098	0307C01	D3S1206i
23,908,576	23,933,541	0310F04	D3S0837i
23,961,810	23,996,241	0311F04	D3S0472i
24,134,709	24,511,317	357H09	AC069214.5_236353
24,134,709	24,511,317	0307D10	D3S0003i
24,134,709	24,511,317	0312E08	D3S0048i
24,134,709	24,511,317	0314E04	D3S0223i
24,134,709	24,511,317	0307C08	D3S1469i
25,190,893	25,614,424	0313B08	D3S0234i
25,190,893	25,614,424	0317G01	D3S0238i
25,190,893	25,614,424	0308A10	D3S0479i
25,190,893	25,614,424	0308D10	D3S0486i
25,190,893	25,614,424	0301C01	D3S1583
27,732,872	27,738,807	0315D06	D3S1439i
3,086,421	3,127,031	0307F12	D3S0205i
3,086,421	3,127,031	0310C06	D3S0213i
30,622,998	30,710,638	0314B04	D3S0204i
30,622,998	30,710,638	0314E07	D3S0228i
31,549,495	31,652,560	0308A12	D3S0518i
32,255,175	32,386,817	0314B07	D3S0752i
32,255,175	32,386,817	0305F08	D3S1150i
32,255,175	32,386,817	0301B04	D3S1531i
32,408,167	32,471,337	384E06	AC026763.10_85474
32,408,167	32,471,337	384A06	AC046140.9_14929
32,497,808	32,519,869	393A07	AC010742.3_125628
32,497,808	32,519,869	384C06	AC046140.9_123741
32,968,070	32,972,840	0315B10	D3S1457i
33,512,741	33,734,852	0313B04	D3S0254i
33,814,561	33,886,198	282A02	AC078780.1_24631
33,814,561	33,886,198	084G01	Z66622
37,468,817	37,836,285	0315F10	D3S0073i
37,468,817	37,836,285	0304A01	D3S0246i
37,468,817	37,836,285	T001F01	D3S0438i
37,468,817	37,836,285	0315C04	D3S0453i
37,468,817	37,836,285	0315H04	D3S0776i
37,468,817	37,836,285	0313D07	D3S1400i
37,468,817	37,836,285	0303H02	D3S3623
37,878,129	38,000,964	0317G08	D3S1123i
37,878,129	38,000,964	9902F12	D3S1349i
38155009	38159517	MyD881	new design
38155009	38159517	MyD882	new design
39,279,989	39,298,190	0303H03	D3S0070i
39,279,989	39,298,190	0306F01	D3S3527
39,279,989	39,298,190	0303F12	D3S3593
39,346,219	39,351,077	0303H11	D3S0063i
4,510,136	4,864,081	0306E09	D3S0180i
4,510,136	4,864,081	0311G03	D3S0214i
4,510,136	4,864,081	0309D11	D3S0846i
4,510,136	4,864,081	0303A02	D3S1122i
4,510,136	4,864,081	0304F04	D3S1470i
4,510,136	4,864,081	0304H11	Z67067
41,216,004	41,256,938	0301C04	D3S1526i
41,216,004	41,256,938	0303G05	HUMUT2543
42,617,151	42,665,237	0302C09	D3S3687
42,825,980	42,883,779	0312F12	D3S1081i
42,888,688	42,892,637	0314E08	D3S0061i

45,098,773	45,162,918	0307F10	D3S0012i
45,098,773	45,162,918	0312D07	D3S0065i
45,098,773	45,162,918	9903A01	D3S1392i
45,240,962	45,242,758	0310D07	D3S1151i
45,903,023	45,919,671	0313A06	D3S0445i
46,037,295	46,043,983	0312E10	D3S0869i
46,218,204	46,224,836	0303B09	Z67705
46,227,186	46,283,166	0313C02	D3S0004i
46,423,725	46,426,018	0307E10	D3S0010i
46,452,500	46,481,657	0309F03	D3S0605i
46,894,240	46,926,585	0313G02	D3S0884i
46,894,240	46,926,585	0306E07	G08276
47,397,528	47,429,935	0316D11	D3S0236i
47,819,625	47,866,687	0317F02	D3S0840i
48,420,266	48,446,464	0301A03	D3S1313i
49,369,613	49,370,795	0306C07	D3S2409
49,371,582	49,424,530	0301D04	D3S1507i
49,482,595	49,548,048	0315F03	D3S0075i
49,482,595	49,548,048	0316C09	D3S3629
49,696,391	49,701,099	0304A11	D3S1378i
49,899,439	49,916,074	0317E01	D3S0077i
49,899,439	49,916,074	0315C03	D3S2449
49,899,439	49,916,074	0304F07	D3S3667
52,059,799	52,065,329	581B10	chr3.fa.O7frz.59298456
52,059,799	52,065,329	611B01	chr3.fa.O7frz.59596281
52,230,138	52,248,223	0317G04	D3S0058i
52,230,138	52,248,223	0304C07	D3S3561
52,504,396	52,533,551	0305E10	D3S1159i
52,504,396	52,533,551	0317G12	D3S1341i
53,170,263	53,201,773	0305F02	D3S0882i
53,855,612	53,874,867	0315G12	D3S1117i
53,855,612	53,874,867	0305G12	D3S1449i
55,474,783	55,496,371	0301B09	D3S3719
55,517,376	56,477,431	341H03	AC021129.3_44166
55,517,376	56,477,431	0313C08	D3S0261i
55,517,376	56,477,431	0309H03	D3S0609i
55,517,376	56,477,431	0309B12	D3S0885i
55,517,376	56,477,431	0310D08	D3S1416i
55,517,376	56,477,431	0303E05	D3S3588
55,517,376	56,477,431	0316B06	D3S3721
55,517,376	56,477,431	0304G05	D3S3724
55,517,376	56,477,431	076B07	G08284
55,517,376	56,477,431	0315H10	Z67483
57,103,316	57,179,374	0308C11	D3S0511i
57,103,316	57,179,374	0312H08	D3S0866i
57,103,316	57,179,374	0315G09	D3S1173i
61,522,285	62,255,613	0306C09	D3S0016i
61,522,285	62,255,613	0308D02	D3S0251i
61,522,285	62,255,613	0308B03	D3S0264i
61,522,285	62,255,613	0310H05	D3S0637i
61,522,285	62,255,613	0311D09	D3S0760i
61,522,285	62,255,613	0313G01	D3S0763i
61,522,285	62,255,613	0317B06	D3S1044i
61,522,285	62,255,613	0301F11	D3S1045i
69,216,780	69,237,929	0315E12	D3S0263i
69,871,323	70,100,177	611H02	chr3.fa.O7frz.81730591

69,871,323	70,100,177	0306D04	D3S1296
69,871,323	70,100,177	0316G02	D3S1366i
69,871,323	70,100,177	0307B07	D3S1373i
71,087,426	71,715,830	283C05	AC069204.3_182407
71,087,426	71,715,830	0316G01	D3S0080i
71,087,426	71,715,830	0311H11	D3S0095i
71,087,426	71,715,830	0313A01	D3S0098i
71,087,426	71,715,830	0309G05	D3S0645i
71,087,426	71,715,830	0314G12	D3S0651i
71,087,426	71,715,830	0309D12	D3S0887i
71,087,426	71,715,830	0309G12	D3S0892i
71,087,426	71,715,830	T003A02	D3S1562
71,087,426	71,715,830	0302B09	D3S3516
71,087,426	71,715,830	0303E09	D3S3568
85,858,322	86,200,641	430G11	chr3.fa.O7frz.92701960
85,858,322	86,200,641	430H11	chr3.fa.O7frz.92800740
85,858,322	86,200,641	0312E03	D3S0089i
85,858,322	86,200,641	9903F01	D3S1472i
85,858,322	86,200,641	0313H07	D3S1595
87,359,140	87,387,339	0312C11	D3S0289i
87,359,140	87,387,339	0315E08	D3S0894i
87,359,140	87,387,339	0301C12	D3S1513i
9,919,150	9,933,086	0301E06	D3S0050i
9,933,782	9,950,314	0311A03	D3S0179i
95,074,647	95,175,412	0305G09	D3S1471i
1,764,832	1,780,396	0415D12	D4S1055i
101,088,265	101,090,535	0411D02	D4S1218i
102,163,610	102,487,376	343G09	AP001963.1_82726
102,163,610	102,487,376	0402G08	D4S0206i
102,163,610	102,487,376	0411B03	D4S0343i
102,163,610	102,487,376	0415F08	D4S0796i
102,163,610	102,487,376	0413D09	D4S0802i
102,163,610	102,487,376	0414H05	D4S0966i
102,930,919	103,214,918	0410C06	D4S0099i
102,930,919	103,214,918	0409E09	D4S0514i
102,930,919	103,214,918	0406D09	D4S2961
103,641,518	103,757,507	0404D06	D4S0013i
103,641,518	103,757,507	0403C10	D4S0107i
107,456,302	107,489,097	0415A12	D4S0535i
107,456,302	107,489,097	0416C09	D4S0886i
109,072,166	109,094,062	0404F07	D4S0088i
109,072,166	109,094,062	0410A11	D4S0516i
11,009,086	11,040,487	0415G12	D4S0064i
11,009,086	11,040,487	0405G12	D4S2949
110,881,301	110,942,590	0416E04	D4S0738i
111,053,499	111,152,868	0411B01	D4S0023i
111,053,499	111,152,868	0405E10	D4S0035i
111,053,499	111,152,868	0410F08	D4S0091i
111,053,499	111,152,868	0411F06	D4S1217i
111,616,697	111,702,872	0406F09	D4S0877i
111,616,697	111,702,872	0407B11	D4S0961i
114,190,319	114,524,337	0406H08	D4S0048i
114,190,319	114,524,337	0401E03	D4S0096i
114,190,319	114,524,337	0409A10	D4S0524i
114,190,319	114,524,337	0415H11	D4S1250i
114,593,021	114,902,177	172G04	AC004168.2_12092

114,593,021	114,902,177	0401H01	D4S0003i
114,593,021	114,902,177	0408F09	D4S0066i
114,593,021	114,902,177	9911E01	D4S0112i
114,593,021	114,902,177	0402B05	D4S1611
121,200,029	121,207,411	0406A02	D4S0548i
121,200,029	121,207,411	0409B11	D4S0559i
122,808,598	122,837,626	0405C05	D4S0358i
122,957,975	122,964,505	0403B08	D4S1246i
123,592,075	123,597,339	0405G03	D4S1051i
123,753,221	123,761,662	0410A05	D4S0753i
123,967,313	124,038,840	583E05	chr4.fa.O7frz.130586887
123,967,313	124,038,840	0406D05	D4S0540i
129,021,551	129,039,377	0416B06	D4S0804i
14,950,658	15,056,887	0408H03	D4S1104i
14,950,658	15,056,887	0402G05	D4S2362
140,156,393	140,186,543	0415A01	D4S0352i
142,777,204	142,874,062	0411A07	D4S0680i
142,777,204	142,874,062	0414D10	D4S0778i
144,654,066	144,694,017	0416D04	D4S0734i
144,654,066	144,694,017	0404B05	D4S1292i
145,136,707	145,159,946	0401G07	D4S1279i
145,249,906	145,281,294	0404G04	D4S1223i
146,622,401	146,699,778	0403F04	Z67626
148,646,691	148,647,812	0416A01	-
148,646,691	148,647,812	0403F02	D4S0821i
148,646,691	148,647,812	0415G09	D4S1131i
149,219,370	149,582,973	0412A09	D4S0381i
149,219,370	149,582,973	0409H03	D4S0386i
149,219,370	149,582,973	0412G03	D4S0658i
149,219,370	149,582,973	0411G08	D4S0681i
149,219,370	149,582,973	0413E04	D4S0687i
15,313,738	15,343,508	0414G06	D4S1084i
15,313,738	15,343,508	0406F04	Z67830
15,388,999	15,460,167	0407E01	D4S2960
15,578,955	15,686,664	129E03	AC005598.6_64773
15,578,955	15,686,664	0402D10	D4S0060i
153,461,860	153,675,622	0408B12	D4S0270i
153,461,860	153,675,622	0401E09	D4S0599i
153,461,860	153,675,622	0401B11	D4S0610i
153,461,860	153,675,622	0406H01	D4S1057i
154,824,891	154,846,693	0408C05	D4S1132i
154,824,891	154,846,693	0402D08	D4S1179i
155,703,596	155,711,688	0416C03	D4S0101i
156,349,231	156,357,678	0404D12	D4S0183i
159,849,729	159,864,002	0415A07	D4S2997
159,849,729	159,864,002	129F08	D63861.1_4468
166,519,538	166,638,926	0414F01	D4S1252i
166,519,538	166,638,926	0415G01	D4S2952
175,647,955	175,680,213	292F09	AC009887.5_114826
175,647,955	175,680,213	292A10	AC021528.3_90278
175,647,955	175,680,213	0411C03	D4S0773i
175,647,955	175,680,213	0414E03	HUMUT880B
177,841,685	177,950,889	0413D08	D4S0874i
185,545,909	185,632,697	0402F07	D4S1535
185,545,909	185,632,697	0415A04	D4S3047
185,545,909	185,632,697	695E08	DISD22_0004409

187,227,303	187,243,246	0416E08	D4S0875i
187,349,668	187,371,606	0411G02	D4S0225i
187,349,668	187,371,606	0411D01	D4S0824i
2,440,605	2,487,382	0416H09	D4S0908i
2,815,382	2,901,587	0402A11	D4S0001i
24,138,185	24,195,282	0401D06	D4S0045i
24,138,185	24,195,282	0409C06	D4S0460i
24,405,153	24,411,562	0415H01	D4S0009i
24,405,153	24,411,562	0414H03	D4S0039i
24,844,751	24,889,811	T003B03	D4S2970
25,930,430	26,045,851	343F03	AC044869.2_137286
25,930,430	26,045,851	0404G01	D4S0451i
25,930,430	26,045,851	0407F06	Z67448
25,930,430	26,045,851	0415F02	Z67691
38450255	38460984	TLR101	new design
38450255	38460984	TLR102	new design
38,504,618	38,507,555	0405F09	D4S1050i
38,965,471	39,044,390	0402H07	D4S0279i
38,965,471	39,044,390	0402H02	D4S0805i
38,965,471	39,044,390	0414B11	D4S1181i
39,874,965	39,922,663	0413G01	D4S0288i
39,874,965	39,922,663	0403H10	D4S0292i
47,762,988	47,831,030	0403B03	D4S0441i
47,762,988	47,831,030	0411H11	D4S0449i
47,762,988	47,831,030	0416B08	D4S0864i
5,067,214	5,072,100	518E04	chr4.fa.O7frz.5109115
5,067,214	5,072,100	0415C05	HUMUT5936
54,790,204	54,859,171	0411E10	D4S0176i
54,790,204	54,859,171	0402D06	D4S1630
55,218,842	55,301,638	0413A08	D4S0005i
55,218,842	55,301,638	0405G02	D4S428
55,218,842	55,301,638	0401C09	G08377
55,639,401	55,686,519	0406C03	D4S1274i
68,107,041	68,155,206	0404H09	D4S0180i
68,107,041	68,155,206	0412H01	D4S0481i
68,285,688	68,304,399	0414H02	D4S3018
68,369,189	68,432,311	0409E01	D4S0303i
68,369,189	68,432,311	0410F09	D4S0332i
69,085,497	69,116,840	0414C07	D4S1323i
69,996,782	70,013,293	0408C07	D4S1288i
70,180,783	70,323,496	0414E07	D4S0082i
70,180,783	70,323,496	0414B07	D4S1245i
70,928,761	70,936,836	0414G12	D4S0723i
70,928,761	70,936,836	694C08	DISD22_0003744
71,740,548	71,751,128	0406F06	D4S0330i
74825139	74828297	IL81	new design
74,921,277	74,923,341	0408E11	D4S0196i
75,065,660	75,066,541	0406F05	D4S0494i
75,121,170	75,123,354	9903B03	D4S1308i
75,449,724	75,473,341	0409A07	D4S0471i
75,529,717	75,539,590	0413D04	D4S0475i
75,529,717	75,539,590	0416E10	D4S0942i
75,889,001	75,938,853	0407F10	D4S0951i
75,889,001	75,938,853	0414G02	D4S1558
77,141,523	77,147,665	0407D02	D4S3042
77,298,918	77,354,059	0403E10	D4S1291i

77,298,918	77,354,059	0407H01	D4S2990
78,651,931	78,752,010	0407H10	D4S0955i
78,651,931	78,752,010	0407A11	D4S0959i
78,651,931	78,752,010	0402A08	D4S1165i
81,406,766	81,431,195	0413C05	D4S0175i
81,406,766	81,431,195	0415C11	D4S0937i
82,171,143	82,193,749	0410A06	D4S0187i
82,171,143	82,193,749	0409E07	D4S0484i
84,432,639	84,475,330	0407H02	D4S395
87,156,656	87,593,307	0401E04	D4S0197i
87,156,656	87,593,307	0409F09	D4S0517i
87,156,656	87,593,307	0416F12	D4S1110i
87,156,656	87,593,307	9903A03	D4S1255i
87,156,656	87,593,307	0415F10	Z67188
87,734,909	87,955,326	0408F10	D4S0152i
87,734,909	87,955,326	0406G11	D4S1542
87,734,909	87,955,326	0408A08	G08379
89,115,826	89,123,592	0412B08	D4S0314i
89,115,826	89,123,592	0403E03	D4S1158i
89,230,440	89,299,035	0415F07	D4S0898i
89,518,915	89,583,272	0415A09	D4S0900i
89,518,915	89,583,272	0414D05	D4S0901i
89,518,915	89,583,272	0413F07	D4S1171i
9,055,358	9,061,338	0411H02	D4S0709i
95,438,730	95,483,050	0407H11	D4S0976i
95,898,151	96,295,099	0407C07	D4S0054i
95,898,151	96,295,099	0413H02	D4S0198i
95,898,151	96,295,099	0409A09	D4S0506i
95,898,151	96,295,099	0405G06	D4S0960i
95,898,151	96,295,099	0406A08	D4S0982i
		0514C01	D5S1480
		0504A06	D5S647
1,306,282	1,348,162	0515A11	D5S2005
1,306,282	1,348,162	018D04	D5S678
10,732,343	10,814,344	0513D06	D5S0309i
10,732,343	10,814,344	0507B01	D5S432
110,433,677	110,441,623	0503D08	D5S0383i
110,433,677	110,441,623	0509F12	D5S0676i
110,587,968	110,858,483	0506H08	D5S0122i
110,587,968	110,858,483	0512F03	D5S0345i
110,587,968	110,858,483	0509C11	D5S0643i
110,587,968	110,858,483	0511B01	D5S0649i
112,101,483	112,209,835	0502C01	D5S0048i
112,101,483	112,209,835	0509G12	D5S0677i
114,942,247	114,989,610	0514F09	D5S0658i
114,942,247	114,989,610	0510F07	D5S0873i
115,168,329	115,180,304	0508B12	D5S0358i
122,386,977	122,400,324	9903E11	D5S1319i
122,386,977	122,400,324	0502E08	Z67521
131,424,121	131,426,796	0501A03	D5S1174i
131,658,035	131,707,798	0509C01	D5S0386i
131,658,035	131,707,798	0515E01	D5S1984
131,658,035	131,707,798	661B02	DISO7_10004993
131,733,343	131,759,205	0512B12	D5S0822i
131,845,200	131,854,389	0511E05	D5S0707i
131,920,529	132,007,651	0513B07	D5S0868i

132,235,913	132,238,637	0507F07	D5S0004i
132,235,913	132,238,637	0507C11	D5S1011i
132,415,561	132,468,608	0501B03	D5S1016i
134,122,360	134,194,710	0506H11	D5S0021i
134,122,360	134,194,710	0501G10	D5S458
134,934,274	134,942,868	0501H01	D5S0829i
135,255,834	135,259,415	0508F06	D5S0085i
135,255,834	135,259,415	0513B12	D5S0780i
135,255,834	135,259,415	0504A05	D5S816
137,503,358	137,542,257	0514E07	D5S0182i
137,503,358	137,542,257	0503B06	D5S0421i
137,503,358	137,542,257	0501F02	D5S414
137,829,080	137,832,903	0507A12	D5S1032i
137,829,080	137,832,903	0502C06	D5S500
139,207,444	139,403,063	0513D01	D5S0272i
139,207,444	139,403,063	0509B02	D5S0415i
139,207,444	139,403,063	0511H07	D5S0694i
139,692,612	139,706,359	0501A06	D5S0273i
139,692,612	139,706,359	0503C09	D5S1305i
139,991,501	139,993,439	0504G03	D5S0084i
140,005,142	140,007,424	0511D07	D5S0704i
140,494,984	140,497,888	0506C07	D5S658
140,541,164	140,545,980	0504F08	D5S0116i
140,980,627	140,996,596	0506D11	D5S1267i
141,951,927	142,046,134	368A06	AC016560.6_172920
141,951,927	142,046,134	0506E12	D5S0125i
142,637,689	142,795,270	0514B11	D5S0041i
142,637,689	142,795,270	0510C02	D5S0500i
143,171,919	143,180,477	0509E05	D5S0505i
143,171,919	143,180,477	0511C05	D5S0699i
148,734,023	148,739,031	347A08	AC012613.5_58125
148,734,023	148,739,031	0506C06	D5S1196i
148,855,038	148,911,200	0514C02	D5S0717i
149,413,051	149,473,128	0514B07	D5S0162i
149,413,051	149,473,128	0508F09	D5S0264i
149,473,595	149,515,615	0508E08	D5S0157i
149,473,595	149,515,615	0503D05	D5S2015
149,761,393	149,772,685	0514H09	D5S0879i
150,207,879	150,260,488	0502E10	D5S1023i
150,380,112	150,388,747	0503E02	D5S0266i
156,445,421	156,468,716	0506H05	D5S0445i
156,540,432	156,614,687	369H02	AC009185.4_71677
156,540,432	156,614,687	0514G07	D5S0196i
158,058,006	158,459,347	254D05	AC007200.1_36545
158,058,006	158,459,347	369D03	AC011376.2_79673
158,058,006	158,459,347	0505E11	D5S0002i
158,058,006	158,459,347	0508B07	D5S0097i
158,058,006	158,459,347	0515G06	D5S2038
158,058,006	158,459,347	0506F06	D5S412
158,674,369	158,690,059	295G10	AC011376.2_147332
158,674,369	158,690,059	0511A09	D5S0722i
158,674,369	158,690,059	058F03	Z67033
159,707,339	159,730,207	0508A03	D5S1138i
159,707,339	159,730,207	0501A01	D5S403
162,797,155	162,804,600	0507G05	D5S2093
162,820,241	162,851,525	0513A12	D5S0091i

168,996,871	169,442,959	0514A07	D5S0160i
168,996,871	169,442,959	0510D07	D5S0277i
168,996,871	169,442,959	0508F11	D5S0341i
168,996,871	169,442,959	0511C06	D5S0726i
168,996,871	169,442,959	0505C10	D5S1456
168,996,871	169,442,959	0504B01	D5S1961
168,996,871	169,442,959	0505H02	D5S1973
168,996,871	169,442,959	0506E04	D5S504
169,465,495	169,469,305	0506A03	D5S0063i
169,607,666	169,657,400	0513H10	D5S0169i
169,607,666	169,657,400	0506H01	HUMUT7277
172,127,707	172,130,809	0511E06	D5S0736i
172,504,130	172,523,989	0511G07	D5S0747i
172,504,130	172,523,989	0514C05	D5S1088i
172,504,130	172,523,989	0503D09	D5S394
175,017,637	175,045,847	0514D06	D5S0066i
175,017,637	175,045,847	0508C08	D5S0155i
176,446,493	176,457,733	0513H04	D5S0448i
176,871,184	176,876,573	0513F09	D5S0512i
176,871,184	176,876,573	0506D09	D5S1078i
179,058,536	179,091,248	021C07	D5S2073
179,595,388	179,640,218	0504E02	D5S0752i
179,945,812	180,009,172	348F06	AC022095.4_12069
179,945,812	180,009,172	0513A04	D5S0755i
179,945,812	180,009,172	021D07	D5S408
180,458,383	180,460,484	9903F04	D5S1069i
180,458,383	180,460,484	0501E06	Z66649
324,739	488,225	672C05	chr5.fa.O7frz.1514538
324,739	488,225	0514G10	D5S1178i
324,739	488,225	0514A01	D5S392
34,022,040	34,160,396	0510G04	D5S0562i
34,022,040	34,160,396	0511B11	D5S0798i
34,022,040	34,160,396	0508B01	D5S1079i
35,084,621	35,266,334	0504H10	D5S0580i
35,084,621	35,266,334	0508F01	D5S1093i
35,084,621	35,266,334	0506E10	D5S1213i
35,084,621	35,266,334	0503C11	D5S493
35,892,748	35,915,462	0508H03	D5S1173i
35,892,748	35,915,462	0515F05	D5S2025
36,187,946	36,219,904	0508H10	D5S0326i
36,187,946	36,219,904	0506H06	D5S1268i
36,187,946	36,219,904	0504F02	Z66972
38,510,822	38,631,253	0501A09	D5S1071i
38,510,822	38,631,253	0511E02	D5S1197i
38,510,822	38,631,253	0503C05	Z67436
39,141,114	39,255,432	0507H07	D5S0146i
39,141,114	39,255,432	0508G08	D5S0217i
39,141,114	39,255,432	0505D06	D5S0573i
39,320,061	39,400,412	0510C03	D5S1073i
40,715,789	40,729,594	0505A02	D5S0954i
40,715,789	40,729,594	0505C08	D5S1061i
40,877,043	40,896,025	0513C07	D5S0566i
40,945,356	41,018,798	0507E06	D5S1457
41,178,093	41,297,297	597A07	chr5.fa.O7frz.46786737
41,178,093	41,297,297	0515A07	D5S0081i
42,459,783	42,757,736	0509H07	D5S0583i

42,459,783	42,757,736	0507E08	D5S0927i
42,459,783	42,757,736	0505H03	D5S1264i
42,459,783	42,757,736	0506A10	D5S1297i
43,229,915	43,448,250	0514G11	D5S0180i
43,229,915	43,448,250	9903A09	D5S0986i
43,229,915	43,448,250	0514F05	D5S1251i
44,340,854	44,424,541	0513G03	D5S0483i
44,340,854	44,424,541	0502D10	D5S2063
52,119,531	52,285,242	0515H02	D5S1202i
52,119,531	52,285,242	0503F10	D5S623
52,119,531	52,285,242	667F02	DISO7_10995141
52,321,014	52,423,947	0501E09	D5S1184i
52,321,014	52,423,947	0505F03	D5S1239i
54,355,838	54,366,155	0501H05	D5S1191i
54,434,230	54,441,837	667B03	DISO7_11025103
54,587,830	54,639,278	0508A01	D5S1056i
55,069,609	55,148,362	0508H08	D5S0225i
55,069,609	55,148,362	0513H06	D5S0578i
55,069,609	55,148,362	0503F03	D5S664
55,183,091	55,248,922	0504A01	D5S645
55,266,680	55,326,529	0502A11	D5S1340i
56,146,022	56,227,736	0509D08	D5S0591i
56,146,022	56,227,736	0505A09	D5S1237i
58,302,468	59,320,301	293D08	AC026095.3_41930
58,302,468	59,320,301	526B08	chr5.fa.O7frz.64839304
58,302,468	59,320,301	0508B05	D5S0012i
58,302,468	59,320,301	0508E06	D5S0079i
58,302,468	59,320,301	0513E01	D5S0585i
58,302,468	59,320,301	0510F04	D5S0785i
58,302,468	59,320,301	0511F12	D5S0843i
58,302,468	59,320,301	019A06	D5S2000
58,302,468	59,320,301	0502E03	D5S2080
58,302,468	59,320,301	0515B04	D5S2091
58,302,468	59,320,301	0501F04	D5S431
58,302,468	59,320,301	0507B02	D5S468
58,302,468	59,320,301	0504E06	HUMUT2092
58,302,468	59,320,301	0504G04	HUMUT5438
66,513,872	66,528,368	0512C10	D5S0188i
66,513,872	66,528,368	0508D11	D5S0336i
66,513,872	66,528,368	0503F08	D5S1210i
67,547,360	67,633,405	0512B10	D5S0235i
67,547,360	67,633,405	0509E08	D5S0593i
68,498,593	68,509,828	367A02	AC010273.3_156905
68,498,593	68,509,828	294A03	AC022107.5_95947
68,498,593	68,509,828	0501E07	HUMUT1151
68,682,567	68,701,596	9903G08	D5S0934i
68,682,567	68,701,596	0514E05	D5S1177i
7,922,217	7,954,237	0507B09	D5S0943i
7,922,217	7,954,237	0514B05	D5S0949i
72,777,839	72,780,108	0509H04	D5S0493i
72,777,839	72,780,108	0504F06	D5S1140i
73,958,990	73,973,005	0514D09	D5S0610i
73,958,990	73,973,005	0509A10	D5S0618i
73,958,990	73,973,005	0505G07	D5S0623i
74,668,790	74,693,685	0513C04	D5S0144i
74,668,790	74,693,685	0510E04	D5S0148i

74,702,684	74,843,719	0501G04	D5S0840i
75,947,063	75,954,996	0508D08	D5S0156i
75,947,063	75,954,996	0512B06	D5S0338i
76,047,542	76,067,054	0503F05	D5S1284i
76,150,610	76,166,896	0507E03	D5S424
77,816,794	77,841,979	0508F07	D5S0124i
77,816,794	77,841,979	0509D10	D5S0629i
79,957,801	79,986,556	0510G12	D5S1057i
79,957,801	79,986,556	0502C07	D5S1120i
82,803,339	82,912,737	0513F03	D5S0194i
82,803,339	82,912,737	9903D06	D5S0778i
82,803,339	82,912,737	9903C05	Z67581
86,599,461	86,723,489	0511E11	D5S0615i
86,599,461	86,723,489	0513G02	D5S1205i
86,599,461	86,723,489	0515D09	D5S1248i
92,944,799	92,956,077	0508G11	D5S0342i
96,122,277	96,169,559	0514G12	D5S0053i
96,122,277	96,169,559	0511F01	D5S0633i
96,122,277	96,169,559	0509H10	D5S0638i
		0606D01	D6S426
		0606F12	D6S461
1,257,675	1,259,983	9904D01	D6S0367i
1,257,675	1,259,983	0609F06	D6S0630i
1,335,068	1,340,831	0605B06	Z67528
1,555,206	1,559,131	0603H06	D6S0303i
1,569,040	2,190,845	0614H01	D6S0280i
1,569,040	2,190,845	0611G01	D6S0641i
1,569,040	2,190,845	0609A07	D6S0645i
1,569,040	2,190,845	0613H03	D6S0649i
10,636,575	10,737,587	0605F02	D6S0656i
10,636,575	10,737,587	0605H07	D6S1025i
100,939,606	101,019,494	0602F10	D6S0792i
100,939,606	101,019,494	0612F12	D6S0996i
101,953,385	102,624,651	**0602B03**	D6S1642
105,282,661	105,414,867	0609F11	D6S0772i
105,282,661	105,414,867	0605D02	D6S1254i
106,640,888	106,664,507	0614C09	D6S1049i
106,640,888	106,664,507	0606G07	D6S1241i
106,739,044	106,880,388	0612B08	D6S0031i
106,739,044	106,880,388	0606G05	D6S0779i
107,918,010	108,089,195	0608B04	D6S0085i
107,918,010	108,089,195	0613B04	D6S0999i
108,593,955	108,616,706	0613D02	D6S0043i
108,593,955	108,616,706	023G09	D6S1594
108,593,955	108,616,706	0604A01	Z67377
108,987,719	109,108,661	0607F07	D6S0497i
108,987,719	109,108,661	0605D07	D6S1167i
109,794,412	109,810,353	0607H09	D6S1050i
109,820,624	109,868,524	0604H03	D6S0905i
11,291,517	11,490,535	531B10	chr6.fa.O7frz.12034704
11,291,517	11,490,535	0608C04	D6S0089i
11,291,517	11,490,535	0603E10	D6S0103i
11,291,517	11,490,535	0610F08	D6S0283i
11,291,517	11,490,535	0608F12	D6S0386i
110,527,715	110,607,900	0609G05	D6S0605i
110,527,715	110,607,900	0602E08	HUMUT893

111,409,984	111,453,487	0603A07	D6S1698
112,088,228	112,301,348	0612G11	D6S0766i
112,088,228	112,301,348	0601A09	D6S0768i
112,088,228	112,301,348	023D10	D6S302
112,088,228	112,301,348	175G07	Z97989.1_71410
112,536,654	112,682,605	0608B06	D6S0172i
112,536,654	112,682,605	0612E09	D6S0394i
112,536,654	112,682,605	0612E02	D6S0775i
114,368,571	114,399,029	0609G11	D6S0776i
114,368,571	114,399,029	0601B03	D6S401
116,369,386	116,488,614	0605E06	D6S0428i
116,369,386	116,488,614	0602F07	D6S0878i
117,305,068	117,360,008	0606A01	D6S1206i
118,892,932	119,137,924	0614G08	D6S0282i
118,892,932	119,137,924	0602D01	D6S0548i
118,892,932	119,137,924	0612B04	D6S0784i
118,892,932	119,137,924	0601H06	D6S0790i
119,540,965	119,712,625	0607G06	D6S0273i
119,540,965	119,712,625	0609G02	D6S0461i
12,398,582	12,405,413	0602E02	D6S0100i
12,398,582	12,405,413	0614F03	D6S0144i
12,825,819	13,396,624	0601D05	D6S0371i
124,166,768	125,188,502	**0602D11**	D6S0559i
126,144,000	126,293,950	0612D02	D6S0930i
127,813,023	127,879,540	0613G06	D6S0573i
128,331,625	128,883,453	0613F06	D6S0077i
128,331,625	128,883,453	0613E04	D6S0270i
128,331,625	128,883,453	0603D01	D6S0536i
128,331,625	128,883,453	0605F03	D6S0822i
128,331,625	128,883,453	0607A05	D6S1030
128,331,625	128,883,453	0604D06	D6S1033
129,246,035	129,879,407	0612B06	D6S0589i
129,246,035	129,879,407	0604B10	D6S0798i
129,246,035	129,879,407	0611A06	D6S0833i
129,246,035	129,879,407	0601H03	D6S1047i
129,246,035	129,879,407	0601E03	D6S1075i
129,246,035	129,879,407	0605C03	D6S1226i
129,246,035	129,879,407	0602G07	D6S1244i
131,202,180	131,426,017	0607B08	D6S0834i
131,202,180	131,426,017	0607A04	D6S1572
131,508,154	131,646,366	0612E11	D6S0068i
131,508,154	131,646,366	0609D12	D6S0799i
131,935,977	131,947,165	9903D12	D6S1622i
131,935,977	131,947,165	024D02	D6S457
131,935,977	131,947,165	0605F01	HUMUT5174B
132,000,135	132,110,243	207D10	AC005587.1_83579
132,000,135	132,110,243	183F08	AL135904.11_38895
132,310,199	132,314,206	0612F06	D6S0028i
132,310,199	132,314,206	0614D03	D6S0041i
132,658,887	132,764,357	0608A09	D6S0271i
132,658,887	132,764,357	0614H07	D6S0998i
133,044,422	133,076,881	0605C07	D6S0407i
133,044,422	133,076,881	0613C10	D6S1171i
134,532,081	134,680,889	0614C07	D6S0807i
134,532,081	134,680,889	0601G06	D6S270
134,532,081	134,680,889	0601H01	D6S976

136,705,565	136,913,485	0611B10	D6S0835i
136,919,878	137,155,349	0604A08	D6S0422i
136,919,878	137,155,349	T001A12	D6S0478i
136,919,878	137,155,349	0602E11	D6S0800i
136,919,878	137,155,349	0613B07	D6S1003i
137,362,801	137,407,991	0613F11	D6S0808i
137,362,801	137,407,991	0606A06	D6S1009
137,506,650	137,536,478	0611G10	D6S0813i
138,230,274	138,246,142	0610B03	D6S0907i
138,230,274	138,246,142	0611A05	D6S0915i
139,158,950	139,266,900	0609B05	D6S0590i
139,158,950	139,266,900	0605F05	D6S0801i
139,497,942	139,543,639	0601C06	D6S0561i
139,497,942	139,543,639	0604A12	D6S0564i
139,735,089	139,737,478	0604A05	D6S1109i
14,225,715	14,245,128	0602A09	D6S0879i
14,225,715	14,245,128	0614A02	D6S429
143,114,297	143,308,031	0608G07	D6S0229i
143,114,297	143,308,031	0603H11	D6S0337i
143,114,297	143,308,031	094F12	HUMUT525
143,114,297	143,308,031	087H02	HUMUT7700
143,788,765	143,813,517	0605H11	D6S0094i
143,788,765	143,813,517	0610G11	D6S0560i
143,971,010	144,194,014	0608F07	D6S0228i
143,971,010	144,194,014	0603B06	D6S0552i
143,971,010	144,194,014	0614A01	D6S1704
144,513,356	144,551,200	0613D08	D6S0830i
144,513,356	144,551,200	0614G07	D6S0987i
144,513,356	144,551,200	0601E10	D6S1003
144,654,566	145,215,863	**0603G05**	D6S0836i
147,566,565	147,748,588	0609D06	D6S0626i
147,566,565	147,748,588	0609E06	D6S0627i
147,566,565	147,748,588	0607G07	D6S0628i
148,313	151,392	0603H10	D6S1086i
148,313	151,392	0610A01	D6S1139i
149,680,756	149,774,442	9903A12	-
149,680,756	149,774,442	187B08	AL031056.1_26387
149,680,756	149,774,442	183B02	AL031056.1_52627
149,680,756	149,774,442	0611H09	D6S0203i
149,680,756	149,774,442	0606G03	D6S0241i
149,680,756	149,774,442	024D06	D6S1553
149,867,324	149,908,864	9904A01	D6S0831i
150,112,273	150,174,249	0610B02	D6S1117i
150,251,294	150,253,863	0607G05	HUMUT5779
150,304,829	150,312,064	0601A08	D6S0841i
151,603,202	151,719,602	0612E04	D6S0933i
151,603,202	151,719,602	0601H08	D6S476
152,170,379	152,466,099	0603C04	D6S0027i
152,170,379	152,466,099	0609G01	D6S0433i
152,170,379	152,466,099	0609A03	D6S0468i
152,170,379	152,466,099	0610C09	D6S0846i
152,484,515	153,000,227	0610C11	D6S0117i
152,484,515	153,000,227	0605G05	D6S0226i
152,484,515	153,000,227	0611E12	D6S0853i
152,484,515	153,000,227	0611A12	D6S0935i
153,113,626	153,122,593	0613B10	D6S0593i

154,402,136	154,609,693	0611H10	D6S0346i
155,620,488	155,686,932	0601B01	D6S0937i
155,620,488	155,686,932	0604A11	D6S1162i
155,758,194	155,818,729	183G06	AL133474.9_33793
155,758,194	155,818,729	176F12	AL133474.9_63821
155,758,194	155,818,729	0609D02	D6S0453i
157,140,756	157,572,094	0605A09	D6S0470i
157,140,756	157,572,094	0610A03	D6S0838i
158,164,282	158,286,097	0613F01	D6S0044i
158,164,282	158,286,097	0606C02	D6S0582i
158,509,372	158,535,008	586F01	chr6.fa.O7frz.168445622
158,509,372	158,535,008	537F05	chr6.fa.O7frz.168477401
158,509,372	158,535,008	0611C07	D6S0863i
16,407,322	16,869,700	**0609D04**	D6S0516i
160,020,138	160,034,343	0611E08	D6S0970i
160,066,607	160,097,341	0601G02	D6S1581
160,310,121	160,447,573	0606F04	D6S0005i
160,310,121	160,447,573	0601E08	D6S0260i
160,310,121	160,447,573	0605C10	D6S0279i
160,462,853	160,499,740	0604G11	D6S0445i
160,462,853	160,499,740	0602B01	D6S0553i
160,462,853	160,499,740	0614D07	D6S0854i
161,471,047	161,615,097	0608C10	D6S0324i
161,471,047	161,615,097	0606E02	D6S0330i
161,471,047	161,615,097	0602G08	D6S0351i
161,688,442	163,068,793	**T001G10**	D6S1011i
163,068,154	163,656,514	**0611G12**	D6S0934i
165,660,766	165,995,578	**0602G06**	D6S0459i
166,742,844	167,195,761	0601C05	D6S1585
167,332,660	167,473,174	0613F09	D6S0086i
167,332,660	167,473,174	0606B11	D6S0566i
167,332,660	167,473,174	0612F07	D6S0859i
167,928,066	167,940,388	0608H03	D6S0075i
167,928,066	167,940,388	0606E10	D6S0218i
170,457,769	170,556,162	0608G04	D6S0105i
170,457,769	170,556,162	0608G10	D6S0331i
170,457,769	170,556,162	0601E11	D6S1590
170,686,134	170,704,312	0606D10	D6S0204i
170,686,134	170,704,312	0612B01	D6S0249i
18,236,521	18,263,353	0613H08	D6S0037i
2,710,665	2,731,926	0607F09	D6S1039i
2,832,499	2,848,513	0612B11	D6S0116i
20,642,667	21,340,614	**0603B10**	D6S0153i
22,395,459	22,405,709	0602C09	D6S0373i
22,395,459	22,405,709	0607C05	Z67232
22,677,657	22,679,871	0605B12	D6S0136i
22,677,657	22,679,871	0611F05	D6S0958i
237,053	296,355	0611C05	D6S0887i
237,053	296,355	0601E05	D6S1090i
24,758,184	24,775,240	135B03	AL031230.1_102019
24,758,184	24,775,240	0601B07	D6S0676i
25,387,285	25,728,737	**0606D09**	G08569
26,195,427	26,205,038	T002G03	D6S0284i
26,510,460	26,523,445	0607H08	D6S1026i
26,510,460	26,523,445	0602G12	D6S1248i
27,323,487	27,332,327	0603C01	D6S0243i

27,323,487	27,332,327	0613A05	D6S1155i
28,217,695	28,233,215	0611G03	D6S0111i
28,217,695	28,233,215	0610F02	D6S0660i
28,301,046	28,309,239	0606C06	D6S0147i
29,631,368	29,778,041	181A05	AC006162.1_38368
29,631,368	29,778,041	186A07	AL050328.24_38345
29,732,755	29,748,128	174B01	AL050328.24_40038
29,798,531	29,803,052	180G06	AF055066.1_308034
29799096	29803052	D6S2770	D6S2770
29799096	29803052	D6S2872	D6S2872
29799096	29803052	D6S2910	D6S2910
29799096	29803052	D6S2911	D6S2911
29,802,425	29,802,895	613G10	chr6.fa.O7frz.33382117
29,902,723	30,021,633	0610D04	D6S0668i
3,009,212	3,060,420	0607A11	D6S1088i
30018310	30021633	D6S2704	D6S2704
30018310	30021633	D6S2707	D6S2707
30018310	30021633	D6S2838	D6S2838
30018310	30021633	D6S2847	D6S2847
30018310	30021633	697B02	DISD22_0011489
30018310	30021633	022G02	-
30018310	30021633	186B05	-
30,030,962	30,031,390	0607C02	D6S265
30,107,469	30,109,633	0603F12	D6S0509i
30,212,487	30,224,491	733H11	DIJ28_10010194
30,227,701	30,236,690	0610D05	D6S0014i
30,420,877	30,422,649	0609C04	D6S0505i
30,561,651	30,562,700	0612D01	D6S0493i
30565250	30569077	C3_2_11, D6S2840	C3_2_11, D6S2840
30565250	30569077	D6S2799	D6S2799
30,621,633	30,632,987	0609G04	D6S0525i
30,775,563	30,793,645	0605H05	D6S1124i
30888622	30906415	C4_2_12, D6S2827	C4_2_12, D6S2827
30,983,956	30,989,859	0607D12	D6S1128i
31,059,474	31,065,654	0606D05	D6S0076i
31344505	31432935	C1_2_5, D6S2811	C1_2_5, D6S2811
31344505	31432935	C1_2_A, D6S2793	C1_2_A, D6S2793
31344505	31432935	C1_4_3, D6S2930	C1_4_3, D6S2930
31344505	31432935	C1_4_4, D6S2931	C1_4_4, D6S2931
31344505	31432935	D6S2792	D6S2792
31429628	31432914	C1_3_2a, D6S2902	C1_3_2a, D6S2902
31429628	31432914	C2_4_3, D6S2938	C2_4_3, D6S2938
31429628	31432914	C4_2_7, D6S2825	C4_2_7, D6S2825
31,475,540	31,491,069	186H03	AB031008.1_2319
31,538,938	31,541,565	0602G01	D6S0517i
31,604,718	31,605,987	0612H04	D6S1220i
31,648,042	31,650,080	TNFa	Udalova
31,648,042	31,650,080	TNFb	Udalova
31,648,042	31,650,080	TNFc	Udalova
31,648,042	31,650,080	TNFd	Udalova
31,648,042	31,650,080	TNFe	Udalova
31648072	31650077	S2780, D6S1615, D6S27	6S2780, D6S1615, D6S278
31651329	31654091	D6S2924	D6S2924
31,690,984	31,692,781	022F03	D6S273
31696429	31713533	BAT2CA, D6S2787	BAT2CA, D6S2787
31,752,440	31,759,796	186A04	AF134726.1_179024
31,129,963	**31,135,632**	134E07	-

32003473	32021428	D6S2740	D6S2740
32003473	32021428	D6S2913	D6S2913
32084175	32185131	3-3, D6S2920	3-3, D6S2920
32,204,462	32,206,045	0603B07	D6S1255i
32,266,521	32,299,822	0613G11	D6S0267i
32,266,521	32,299,822	079C09	D6S1014
32270598	32299822	D6S2894	new design
32368453	32460310	3-7, D6S2892	3-7, D6S2892
32,368,464	32,447,662	0609D03	D6S0483i
32,515,597	32,520,943	0610H04	D6S0518i
32515625	32520801	DRA_CA, D6S2883	DRA_CA, D6S2883
32,654,524	32,665,603	310G03	AC026010.3_134784
32,713,112	32,719,407	022B04	D6S1666
32735222	32754296	D6S2818	D6S2818
32735222	32754296	G511525	new design
32,735,225	32,742,572	9903E12	D6S0067i
32,831,445	32,839,446	697A03	DISD22_0000187
32,888,518	32,892,803	132A02	X87344.1_184861
32,897,588	32,914,525	0602A04	D6S1104i
33,044,415	33,057,075	0614C04	D6S0274i
33,188,206	33,204,868	0602F11	D6S0512i
33238447	33268223	M2_2_9, D6S2731	M2_2_9, D6S2731
33238447	33268223	M2_4_25, D6S2822	M2_4_25, D6S2822
33238447	33268223	186C02	-
33,276,631	33,280,192	0609A04	D6S0498i
33,326,027	33,347,640	186G05	Z97183.1_16345
33,375,449	33,390,142	0608H06	D6S0196i
33,648,307	33,655,997	133F12	Z93017.6_2832
33,696,500	33,772,329	0601H07	D6S1165i
34,541,883	34,610,984	0601A01	HUMUT2253
34,541,883	34,610,984	0607F05	HUMUT6615
35,418,313	35,503,933	0613A02	D6S0990i
35,649,345	35,804,338	0614D11	D6S1211i
35,649,345	35,804,338	0603G11	D6S1645
35,908,789	35,996,942	0608H02	D6S0036i
35,908,789	35,996,942	0601G04	D6S0664i
36,103,551	36,186,513	0602C10	G10173
36,129,769	36,215,820	0611B04	D6S0035i
36,129,769	36,215,820	T002C03	D6S0078i
36,569,647	36,623,234	0611H01	D6S0234i
36,569,647	36,623,234	0605A03	D6S0992i
36,754,413	36,763,094	0605C05	D6S0335i
36,754,413	36,763,094	0605B02	D6S1051
36,930,581	36,950,778	0603H03	D6S0508i
36,930,581	36,950,778	9904H01	D6S1010i
37,245,957	37,251,182	0609A08	D6S0682i
37,895,285	38,230,375	0601A12	D6S0233i
37,895,285	38,230,375	0603C11	D6S0312i
37,895,285	38,230,375	0612F05	D6S0670i
38,250,711	38,673,848	0613D06	D6S0347i
38,250,711	38,673,848	0609H07	D6S0679i
38,792,313	39,106,545	0611A09	D6S0017i
38,792,313	39,106,545	0608B12	D6S0370i
38,792,313	39,106,545	0610E02	D6S0524i
38,792,313	39,106,545	0614F07	D6S0895i
39,868,120	39,980,622	0605E03	D6S1168i

39,868,120	39,980,622	0604D12	D6S1641
41,102,749	41,114,906	0614E03	D6S0047i
41,102,749	41,114,906	0603A10	D6S0302i
41,224,979	41,230,048	0607D02	D6S1575
41,284,270	41,298,360	9904A02	D6S1012i
41,411,505	41,426,603	0608G08	D6S0263i
41,622,142	41,678,100	0602D03	D6S0379i
41,622,142	41,678,100	0609B08	D6S0683i
41,622,142	41,678,100	0608H01	D6S1672
42,010,649	42,124,404	0608C12	D6S0372i
42,010,649	42,124,404	0604H07	D6S1552
42,300,647	42,527,767	0608A10	D6S0320i
42,300,647	42,527,767	0612H08	D6S0671i
42,300,647	42,527,767	0603C02	D6S1237i
42,300,647	42,527,767	0602A07	HUMUT2081
43,039,586	43,054,936	0601G12	D6S0294i
43,039,586	43,054,936	0606H05	D6S1209i
43,152,007	43,237,435	0605D03	D6S1582
43,845,924	43,862,202	0609E07	D6S0662i
43,845,924	43,862,202	0610H01	D6S1031i
44,322,802	44,329,598	0607A09	D6S1027i
44,322,802	44,329,598	0607A02	D6S1650
44,333,881	44,341,503	0607G08	D6S1024i
45,404,032	45,626,797	0611D06	D6S0918i
46,625,404	46,728,482	0608C03	D6S0060i
46,625,404	46,728,482	0603D10	D6S1541
46,625,404	46,728,482	0610D01	D6S1638
46,779,897	46,811,389	0604B11	D6S0691i
47,307,227	47,385,639	0605G11	D6S0290i
47,307,227	47,385,639	0604G10	D6S0489i
47,307,227	47,385,639	0604H02	Z66926
47,553,899	47,702,620	0611G07	D6S0874i
47,553,899	47,702,620	0604E03	D6S0978i
47,953,998	48,144,384	0609C08	D6S0686i
47,953,998	48,144,384	0610E07	D6S0715i
47,953,998	48,144,384	0604B07	HUMUT596
49,680,830	49,712,511	0613H10	D6S0299i
49,680,830	49,712,511	0613F02	HUMUT6326
50,035,964	50,039,777	0606D11	D6S0598i
50,084,810	50,097,607	0605D01	D6S0602i
51,588,104	52,060,382	0608F10	D6S0327i
51,588,104	52,060,382	0603C07	D6S0487i
51,588,104	52,060,382	0611H05	D6S0919i
51,588,104	52,060,382	0605H09	HUMUT7510
52,159,144	52,163,395	0612D03	D6S0702i
52,209,438	52,217,257	0605H02	D6S0250i
52,209,438	52,217,257	0604F04	D6S1195i
52,392,953	52,468,540	0609F02	D6S0460i
52,470,159	52,549,821	0610H02	D6S0709i
52,764,183	52,776,616	0606B02	D6S0115i
53,470,098	53,517,790	0610D03	D6S0692i
53,470,098	53,517,790	0606C07	D6S1623
55,300,226	55,375,250	0606D06	D6S1636
55,300,226	55,375,250	0607H02	D6S294
55,726,402	55,848,334	134G03	AL137178.7_78870
55,726,402	55,848,334	0602A06	D6S1236i

55,726,402	55,848,334	T003B05	D6S1661
55,726,402	55,848,334	058C03	G10114
56,029,347	56,366,851	181F03	AL034452.8_92704
56,029,347	56,366,851	0614F04	D6S0369i
56,029,347	56,366,851	0605A10	D6S1189i
56,927,732	57,000,099	0602H10	D6S1115i
57,019,470	57,143,057	0613H01	D6S0309i
57,145,083	57,157,694	0603F10	D6S0710i
6,533,340	6,600,215	174G08	AL031123.14_110913
6,533,340	6,600,215	0602C02	D6S0311i
6,533,340	6,600,215	0613E01	D6S0579i
62,447,824	63,054,091	**0614G09**	D6S1212i
63,964,538	63,980,909	0607D11	D6S1093i
63,964,538	63,980,909	0601E02	D6S1120i
64,339,879	64,351,448	0607A03	D6S1658
66,095,895	66,473,839	**0608A05**	D6S0119i
69,401,980	70,156,124	**0609B03**	D6S0469i
7,486,869	7,531,945	133H08	AL390026.1_29062
7,486,869	7,531,945	598G03	chr6.fa.O7frz.8505863
7,486,869	7,531,945	0605E10	D6S0377i
7,672,009	7,826,752	0603G03	D6S0225i
7,672,009	7,826,752	0609B07	D6S0647i
73,388,241	73,965,295	**0611F04**	D6S0927i
74,161,192	74,184,013	0609H05	D6S0609i
74,161,192	74,184,013	0610E01	D6S1228i
74,282,194	74,288,344	0612G07	D6S0726i
74,282,194	74,288,344	0613B11	D6S0882i
74,462,548	74,591,509	0605D09	D6S0741i
74,462,548	74,591,509	0614G05	D6S1596
74,462,548	74,591,509	0603D04	D6S406
78,228,641	78,229,900	0601D09	D6S1066i
78,228,641	78,229,900	0602G10	Z66785
79,633,908	79,665,039	0606C04	D6S1192i
79,633,908	79,665,039	0603F05	D6S1243i
79,967,681	80,001,174	585F07	chr6.fa.O7frz.86184415
79,967,681	80,001,174	0607C08	D6S0920i
80,873,083	81,112,706	0610G04	D6S0574i
80,873,083	81,112,706	0609E09	D6S0728i
80,873,083	81,112,706	0602A08	D6S1181i
86,216,528	86,262,215	0601A04	D6S0734i
86,216,528	86,262,215	0612G08	D6S1141i
87,597,028	87,709,921	0608C09	D6S0297i
87,597,028	87,709,921	0608H11	D6S0357i
87,851,935	87,861,569	0608C01	D6S1182i
9,813,644	**10,168,908**	**0607H07**	D6S0639i
90,199,616	90,400,123	0603B12	D6S0248i
90,199,616	90,400,123	0605A04	D6S0254i
90,199,616	90,400,123	0611C12	D6S0883i
90,596,349	90,640,876	0607F03	D6S1613
91,280,013	91,353,628	0612E06	D6S0738i
91,280,013	91,353,628	0607H03	D6S1570
94,007,860	94,185,993	0612F03	D6S0584i
94,007,860	94,185,993	0614B03	D6S1056
97,479,217	97,695,351	0608B09	D6S0288i
97,479,217	97,695,351	0611E07	D6S0884i
97,479,217	97,695,351	0601B05	D6S1246i

100,156,359	100,159,259	0710D03	D7S0053i
100325551	100331651	ACHE1	new design
100325551	100331651	ACHE2	new design
100325551	100331651	ACHE3	new design
100,557,172	100,569,026	0714E11	D7S1170i
100,557,172	100,569,026	0704D01	D7S1273i
101,715,172	101,748,898	0710E04	D7S0272i
101,883,690	101,892,293	0712D11	D7S0888i
101,883,690	101,892,293	026D09	D7S2448
102,899,473	103,417,199	0711C12	D7S0034i
102,899,473	103,417,199	0707B11	D7S0064i
102,899,473	103,417,199	0710H02	D7S1125i
102,899,473	103,417,199	T003G05	D7S2504
102,899,473	103,417,199	0701G09	D7S818
102,899,473	103,417,199	0706D06	Z66799
104,544,059	104,816,577	0711F08	D7S0303i
104,544,059	104,816,577	0708D07	D7S0399i
104,544,059	104,816,577	0702A04	D7S0732i
104,544,059	104,816,577	0705B08	D7S1841
104,544,059	104,816,577	0706G04	D7S2545
105,677,892	105,712,603	0702A08	D7S0255i
105,677,892	105,712,603	0711H05	D7S0358i
105,677,892	105,712,603	0702F12	D7S1083i
106,292,977	106,334,828	0712A03	D7S0621i
106,292,977	106,334,828	0705H07	D7S0909i
107,351,499	107,431,040	206C07	AC005048.2_36985
107,351,499	107,431,040	0709H10	D7S0882i
107,451,232	107,558,036	0701B12	D7S0018i
111,850,462	111,903,483	0702H02	D7S0267i
111,850,462	111,903,483	0709B08	D7S0811i
113,842,288	114,117,391	0706F08	D7S0095i
113,842,288	114,117,391	0701F03	D7S0693i
113,842,288	114,117,391	0713F02	D7S0983i
113,842,288	114,117,391	0707C08	D7S1244i
115,952,075	115,988,466	137G11	AJ133269.1_180046
115,952,075	115,988,466	0708C09	D7S0455i
115,952,075	115,988,466	0709D01	D7S0554i
116,099,695	116,225,676	0701D08	D7S0551i
116,099,695	116,225,676	0709C06	D7S0741i
116,099,695	116,225,676	0703E09	D7S2460
121,300,395	121,489,326	139C09	AC006020.2_128904
121,300,395	121,489,326	0702E11	D7S0384i
121,300,395	121,489,326	0705G12	D7S0404i
121,300,395	121,489,326	0701D09	D7S0566i
124,250,549	124,357,110	0702H07	D7S0017i
124,250,549	124,357,110	0708B05	D7S0322i
124,250,549	124,357,110	0710H04	D7S0939i
127,668,567	127,684,917	0705B05	D7S1166i
127,668,567	127,684,917	0707G06	D7S1171i
128,365,230	128,377,325	0704B10	D7S1076i
128,365,230	128,377,325	0705G02	D7S1278i
128,615,949	128,640,622	0712D01	D7S0936i
128,615,949	128,640,622	0712B09	D7S1068i
129,038,791	129,184,158	541E08	chr7.fa.O7frz.134016965
129,038,791	129,184,158	0712C01	D7S0929i
129,038,791	129,184,158	0706A06	D7S530

13,897,379	13,995,289	0707D12	D7S0119i
13,897,379	13,995,289	0702D09	D7S0199i
13,897,379	13,995,289	0702H04	D7S0211i
13,897,379	13,995,289	0702B05	D7S0679i
130,663,175	130,831,931	0713E11	D7S0800i
130,663,175	130,831,931	0705E02	D7S0816i
130,663,175	130,831,931	0701B02	D7S1235i
130,663,175	130,831,931	0707F08	D7S1255i
138,786,805	138,818,998	0713H09	D7S0374i
139,124,668	139,366,560	0713F06	D7S0049i
139,124,668	139,366,560	0714G01	D7S0143i
139,124,668	139,366,560	0713D02	D7S0323i
139,124,668	139,366,560	0704A03	D7S0327i
139,124,668	139,366,560	0711B10	D7S0995i
139,124,668	139,366,560	0705F10	D7S1003i
139,753,916	139,772,419	0707C04	D7S1107i
141,273,626	141,293,252	0712C04	D7S0948i
141,273,626	141,293,252	0711B11	D7S0950i
141,645,314	142,221,097	0713E03	D7S0604i
141,645,314	142,221,097	0709G05	D7S0727i
141,645,314	142,221,097	0711E09	D7S0972i
141,645,314	142,221,097	0707F04	D7S1113i
141,645,314	142,221,097	0701C09	D7S1193i
141,645,314	142,221,097	0711C03	D7S1199i
141,645,314	142,221,097	0704G05	D7S2473
142,348,323	142,369,625	0711C10	D7S0957i
142,348,323	142,369,625	0704F09	D7S1104i
142,695,524	142,714,907	0714D07	D7S0996i
142,798,327	142,816,107	0711H10	D7S1004i
148,135,408	148,212,347	0712D02	D7S0960i
148,135,408	148,212,347	9904G04	D7S1052i
148,135,408	148,212,347	0712D07	D7S1056i
149,666,351	149,669,696	9904E04	D7S0793i
149,666,351	149,669,696	0712F08	D7S0812i
150,319,080	150,342,609	542A05	chr7.fa.O7frz.157560056
150,319,080	150,342,609	T003A06	D7S636
150,381,832	150,385,929	0705C05	D7S1277i
155,288,319	155,297,728	0701D07	D7S0446i
155,288,319	155,297,728	0706C06	D7S550
157,024,516	158,073,179	0710A07	D7S0968i
157,024,516	158,073,179	0711A05	D7S1039i
157,024,516	158,073,179	0707D06	D7S1159i
157,024,516	158,073,179	0707F06	D7S1167i
157,024,516	158,073,179	0704H03	D7S1196i
157,024,516	158,073,179	0704A05	D7S1232i
157,024,516	158,073,179	0701H08	D7S2423
18,501,894	19,003,518	204F10	AC002433.1_139651
18,501,894	19,003,518	0707E11	D7S0073i
18,501,894	19,003,518	0710G04	D7S0086i
18,501,894	19,003,518	0701D02	D7S0163i
18,501,894	19,003,518	0714H01	D7S0186i
18,501,894	19,003,518	0705C09	D7S0578i
18,501,894	19,003,518	0709D04	D7S0651i
18,501,894	19,003,518	0709E04	D7S0655i
18,501,894	19,003,518	0709A09	D7S0832i
18,501,894	19,003,518	0702B07	D7S638

19,121,616	19,123,820	0708F10	D7S0488i
19,121,616	19,123,820	025E01	D7S2495
2,912,308	3,050,025	0701D10	D7S2484
2,912,308	3,050,025	0701D04	D7S2521
20,337,250	20,421,907	0707G12	D7S0132i
20,337,250	20,421,907	0714D08	D7S0200i
20,337,250	20,421,907	0713A03	D7S0208i
22,732,028	22,738,141	0703F04	D7S0667i
22,732,028	22,738,141	0701C07	D7S629
23,252,841	23,281,254	0712H01	D7S0842i
24,290,332	24,298,002	0706E08	D7S0088i
24,290,332	24,298,002	0714C11	D7S0644i
25,124,800	25,131,480	0703E04	D7S1791
27,147,521	27,149,812	0708B10	D7S0477i
27,147,521	27,149,812	0708E10	D7S0486i
30,430,672	30,484,833	0708H08	D7S0440i
30,658,725	30,706,244	0713F04	D7S0077i
30,658,725	30,706,244	0714C03	G09471
30,917,993	30,931,656	0705H03	D7S0658i
30,917,993	30,931,656	0706G01	D7S526
32,963,577	33,013,067	0709E06	D7S0749i
32,963,577	33,013,067	0713D07	D7S0843i
38,246,150	38,374,181	0710E10	D7S0036i
38,246,150	38,374,181	0706G08	D7S0106i
38,246,150	38,374,181	0706H08	D7S0176i
38,246,150	38,374,181	0705D09	D7S2497
4,688,456	4,777,600	0712A06	D7S1022i
4,688,456	4,777,600	0705C08	D7S511
41,695,126	41,709,231	9904A03	-
41,695,126	41,709,231	0706H02	D7S2548
41,970,196	42,241,712	0705A12	D7S0643i
41,970,196	42,241,712	0709C04	D7S0647i
41,970,196	42,241,712	0705G05	D7S0797i
41,970,196	42,241,712	0702E08	D7S671
43,589,251	43,632,247	0708F05	D7S0336i
43,589,251	43,632,247	0708D10	D7S0484i
43,589,251	43,632,247	0709C10	D7S0866i
44,150,395	44,195,563	0701H07	D7S1249i
44,150,395	44,195,563	0701C05	G09840
44,571,928	44,581,175	0708H01	D7S0167i
44,571,928	44,581,175	0704G06	D7S2488
44,802,777	44,809,240	0704H05	D7S0180i
44,802,777	44,809,240	0706A03	D7S478
44,968,786	44,985,203	0703D03	D7S2427
5,533,312	5,536,747	0706E07	G08627
50,314,924	50,438,053	0701A11	D7S1189i
50,625,259	50,828,652	0704F10	D7S0624i
50,625,259	50,828,652	0709F07	D7S0785i
50,625,259	50,828,652	0707F01	D7S0786i
55,054,219	55,242,525	0714A08	D7S0988i
55,716,261	55,748,439	0710H01	D7S1153i
6,380,651	6,410,123	0710A02	D7S1024i
6,380,651	6,410,123	0701C01	D7S1186i
65,063,110	65,084,635	0707B07	D7S1181i
65,063,110	65,084,635	0706B03	D7S2549
7,643,100	7,724,763	0709H04	D7S0680i

7,643,100	7,724,763	0702F03	G10238
72,486,045	72,488,386	0705D10	Z67541
72,821,263	72,822,536	0710C03	D7S1124i
73,262,023	73,282,100	0712C10	D7S1213i
73,262,023	73,282,100	0706B08	HUMUT623
73,341,741	73,458,201	0712A12	D7S0104i
73,341,741	73,458,201	0711F03	D7S0116i
73,506,056	73,654,853	0713C03	D7S0360i
73,506,056	73,654,853	0706H04	D7S2472
73,709,966	73,812,958	0706E03	D7S1870
73,826,245	73,841,595	138B07	AC004883.2_46325
73,848,420	73,905,777	9904G03	D7S1175i
74,975,005	74,995,389	0712G09	D7S0670i
74,975,005	74,995,389	0713A02	D7S1122i
75,236,778	75,257,150	0708B11	D7S0501i
75,236,778	75,257,150	0713C08	HUMUT533B
75,769,859	75,771,548	0711G01	D7S1218i
76,662,535	76,667,080	0713E12	D7S0900i
76,662,535	76,667,080	0701C03	D7S1077i
77,004,351	77,107,324	0706C09	D7S0240i
77,004,351	77,107,324	0707E07	D7S1210i
79,602,076	79,686,661	0708H11	D7S0519i
79,602,076	79,686,661	0702D06	D7S2443
80,069,459	80,144,262	0711G12	D7S0999i
80,069,459	80,144,262	0711B09	D7S1007i
81,166,258	81,237,388	0705H02	D7S0495i
81,166,258	81,237,388	0709F04	D7S0674i
82,831,158	83,116,260	0714A12	D7S0227i
82,831,158	83,116,260	0714F08	D7S0232i
82,831,158	83,116,260	0704A08	D7S0249i
82,831,158	83,116,260	0704F12	D7S0415i
82,831,158	83,116,260	0714B02	D7S0597i
82,831,158	83,116,260	0714G05	D7S0894i
82,831,158	83,116,260	0705D06	D7S1015i
82,831,158	83,116,260	0705G10	D7S2540
86,970,884	87,180,500	0702H08	D7S0121i
86,970,884	87,180,500	0708B04	D7S0275i
86,970,884	87,180,500	0713G07	D7S1228i
86,970,884	87,180,500	713C11	DIJ28_10004693
91,579,402	91,601,946	0714C04	D7S0248i
91,579,402	91,601,946	0708F03	D7S0250i
91,579,402	91,601,946	0705B11	D7S0677i
92,072,171	92,301,148	0714D04	D7S0251i
92,072,171	92,301,148	0704B06	D7S0278i
92,072,171	92,301,148	0714H04	D7S0522i
93,861,809	93,898,480	0710G11	D7S0123i
93,861,809	93,898,480	0703H05	D7S0302i
93,861,809	93,898,480	0711E01	D7S0640i
96,156,015	96,177,139	586G07	chr7.fa.O7frz.98288632
96,156,015	96,177,139	0702B01	D7S1274i
97,199,311	97,207,720	0706G11	D7S0543i
97,199,311	97,207,720	0703A11	HUMUT901
97,760,007	97,868,316	0710C04	D7S0022i
97,760,007	97,868,316	0710G07	D7S0057i
989,361	995,802	0703C09	D7S1263i
989,361	995,802	0703D12	D7S2474

99,083,437	99,219,744	0712C12	D7S0916i
99,083,437	99,219,744	0705C10	D7S647
99,263,572	99,302,109	540B09	chr7.fa.O7frz.102029376
99,499,406	99,517,299	698C04	DISD22_0005257
99,771,673	99,803,388	0710A06	D7S0755i
99,771,673	99,803,388	0702B11	D7S2480
6,825,000	6,900,000	0804G07	D8S1706
6,825,000	6,900,000	0801D07	D8S1819
10,659,883	10,734,796	0805A11	D8S0730i
10,659,883	10,734,796	0811A07	D8S0894i
10,659,883	10,734,796	0802G05	D8S520
102,000,090	102,034,745	350B05	AC027373.2_36983
102,000,090	102,034,745	0808G03	D8S0336i
103,730,188	103,737,128	0807F02	D8S0305i
103,730,188	103,737,128	0803B02	D8S1834
104,222,097	104,311,709	0809A10	D8S0324i
104,222,097	104,311,709	0811D06	D8S0643i
105,421,228	105,438,092	0802B08	D8S1738
105,421,228	105,438,092	0808D03	HUMUT5342
108,330,886	108,579,459	0804E04	D8S0323i
108,330,886	108,579,459	0807E12	D8S0566i
108,330,886	108,579,459	0801H01	D8S0781i
108,330,886	108,579,459	9904E09	D8S0787i
108,330,886	108,579,459	0804A11	D8S0797i
11,388,919	11,459,522	0804A05	D8S1695
11,388,919	11,459,522	0805C01	D8S1759
11,388,919	11,459,522	0801D03	D8S265
11,599,122	11,654,920	0806E02	D8S0813i
11,868,871	11,869,517	0811G09	D8S1033i
110,168,900	110,200,989	0801F10	D8S0907i
110,168,900	110,200,989	0808C03	D8S0923i
12,212,843	12,220,196	0807C07	D8S0411i
120,004,977	120,033,492	0801C12	D8S0421i
120,004,977	120,033,492	9904F09	D8S0793i
120,497,882	120,505,776	0802B04	D8S0048i
120,497,882	120,505,776	0805F04	D8S1823
121,206,533	121,453,454	9904G09	D8S0809i
121,206,533	121,453,454	0808B03	D8S0937i
121,206,533	121,453,454	0806G06	D8S1000i
128,817,498	128,822,856	0810G01	D8S0020i
128,817,498	128,822,856	0811F10	D8S0988i
141,590,586	141,596,434	0808G02	D8S0596i
141,590,586	141,596,434	0808D05	D8S0705i
141,590,586	141,596,434	030H03	D8S1717
141,737,683	142,080,514	T002F06	D8S0710i
141,737,683	142,080,514	0803F07	D8S1035i
141,737,683	142,080,514	0803F06	D8S1704
142,501,189	142,510,802	0803F08	D8S0822i
143,950,775	143,958,238	0811D08	D8S0811i
144,171,274	144,175,199	0808C05	D8S1011i
144,870,498	144,876,619	0811D03	D8S0722i
16,009,761	16,094,595	0806C12	D8S0211i
16,009,761	16,094,595	0801C07	D8S0449i
16,009,761	16,094,595	733H01	DIJ28_10036995
16,894,049	16,904,061	256D03	AB020858.1_88789
16,894,049	16,904,061	405D08	AC072058.1_86060

16,894,049	16,904,061	645F10	DISO7_10002436
18,293,035	18,303,003	0810E12	D8S0455i
18,293,035	18,303,003	T002A03	D8S1145
21,822,330	21,827,151	0805H08	D8S0073i
21,822,330	21,827,151	0802D07	D8S1025i
21,955,883	21,962,266	0811F05	D8S0467i
21,955,883	21,962,266	0803E08	HUMUT5312
22,354,541	22,454,583	0806D11	D8S0186i
22,354,541	22,454,583	0806D03	D8S0839i
22,601,117	22,606,760	0805A09	D8S0190i
22,601,117	22,606,760	0803B12	D8S0654i
22,601,117	22,606,760	0803F05	D8S1733
22,933,591	22,982,637	0801A07	D8S0005i
22,933,591	22,982,637	0802C01	D8S1008i
23016377	23030895	TNFRSF10C	new design
23049046	23077488	TNFRSF10D1	new design
23049046	23077488	TNFRSF10D2	new design
23104009	23138584	TNFRSF10A1	new design
23104009	23138584	TNFRSF10A2	new design
23,157,114	23,175,452	0808F06	D8S0452i
25,332,693	25,338,087	0806D12	D8S0213i
25,757,490	25,958,292	0806E11	D8S0187i
25,757,490	25,958,292	0802F05	D8S0929i
25,757,490	25,958,292	0804B09	D8S1031i
25,757,490	25,958,292	713C09	DIJ28_10000970
26,296,331	26,326,562	0806A04	D8S0850i
27,224,916	27,372,824	0806B11	D8S0182i
27,224,916	27,372,824	0803H08	D8S0438i
27,224,916	27,372,824	0809H04	D8S0457i
27,510,351	27,528,288	0807G08	D8S0461i
27,510,351	27,528,288	0802H02	D8S1839
27,547,304	27,590,211	9904A09	D8S0690i
27,783,655	27,906,117	0806E03	D8S0841i
29,249,530	29,264,104	0811C03	D8S0718i
29,249,530	29,264,104	0809A02	D8S0891i
30,555,422	30,635,274	9904A06	-
30,555,422	30,635,274	543G11	chr8.fa.O7frz.33849047
30,555,422	30,635,274	0810C11	D8S0636i
33,568,393	33,577,043	544G01	chr8.fa.O7frz.37049102
33,568,393	33,577,043	028F04	D8S1845
38,153,263	38,189,966	0811H03	D8S0008i
38,153,263	38,189,966	0811A02	D8S1791
38,389,406	38,445,296	406A04	AC011237.4_133993
38,389,406	38,445,296	0804H08	D8S1038i
38,389,406	38,445,296	0811B08	D8S1821
38,734,008	38,829,703	349E03	AC016813.3_111110
38,734,008	38,829,703	0811A11	G10158
39,890,485	39,905,120	0810F05	D8S0218i
39,890,485	39,905,120	0809B01	D8S0924i
41,629,901	41,873,437	614G08	chr8.fa.O7frz.46429060
41,629,901	41,873,437	0808G04	D8S0083i
41,629,901	41,873,437	0809H02	D8S0240i
41,629,901	41,873,437	0808C02	D8S0687i
42,247,986	42,309,130	0808H08	D8S0250i
42,247,986	42,309,130	0802A05	D8S0742i
48,848,222	49,035,296	0804A12	D8S0897i

54,300,829	54,326,747	0811B03	D8S0712i
54,300,829	54,326,747	0811F11	D8S0716i
56,954,926	57,086,493	587G05	chr8.fa.O7frz.62681686
56,954,926	57,086,493	0802D09	D8S0902i
56,954,926	57,086,493	028C09	D8S1828
59,565,292	59,575,275	9904F08	D8S0253i
59,565,292	59,575,275	0805F02	D8S1723
59,658,617	59,734,940	0808C08	D8S0948i
6,344,580	6,408,338	543B01	chr8.fa.O7frz.7433403
6,344,580	6,408,338	0809G08	D8S0184i
65,671,246	65,873,902	0810F07	D8S0493i
65,671,246	65,873,902	0801F03	D8S544
65,671,246	65,873,902	064D05	G08709
67,251,166	67,253,380	0806F10	D8S0174i
71,648,227	71,683,158	0811E09	D8S0714i
75,066,141	75,103,859	0802G10	D8S0070i
75,066,141	75,103,859	0803C06	D8S526
76,482,826	76,641,623	0811A05	D8S0294i
76,482,826	76,641,623	0801C09	D8S0746i
76,482,826	76,641,623	0805E12	D8S0765i
78,057,713	78,074,994	0806E05	D8S0898i
78,057,713	78,074,994	0802G06	D8S0899i
79,807,560	79,880,313	407D09	AC048363.3_2317
79,807,560	79,880,313	T001A11	D8S0679i
79,807,560	79,880,313	056A04	Z67101
8,597,076	8,599,026	0802G07	D8S0827i
8,597,076	8,599,026	0808C07	D8S0830i
82,042,600	82,186,858	0806H08	D8S0101i
82,042,600	82,186,858	0808C11	D8S0296i
82,355,326	82,359,563	0806C08	D8S0062i
82,355,326	82,359,563	0809E03	D8S0085i
82,553,481	82,558,023	0808E09	D8S0081i
82,807,243	82,834,305	0807H10	D8S0496i
82,807,243	82,834,305	029C03	D8S525
89,118,576	89,408,892	0806A09	D8S0107i
89,118,576	89,408,892	0810D07	D8S0298i
89,118,576	89,408,892	0807E02	D8S0304i
89,118,576	89,408,892	0809G02	D8S0413i
89,118,576	89,408,892	0810E02	D8S0913i
90,839,110	90,872,433	0806A01	D8S0779i
90,839,110	90,872,433	0806F01	D8S0791i
91,014,740	91,066,075	0811C11	D8S0997i
93,040,328	93,176,619	0801D02	D8S0780i
93,040,328	93,176,619	0806D01	D8S0785i
93,040,328	93,176,619	0806H01	D8S0795i
95,330,657	95,343,733	0803B05	D8S1083
95,330,657	95,343,733	0805D07	Z66605
95,961,628	95,976,660	0807G11	D8S0545i
95,961,628	95,976,660	0802H07	D8S1042i
97,343,340	97,415,950	314B04	AC068091.3_100690
97,343,340	97,415,950	0804A07	D8S0102i
97,343,340	97,415,950	0804E08	D8S0944i
97,343,340	97,415,950	029A05	D8S1772
97,575,058	97,693,213	0810E10	D8S0108i
97,575,058	97,693,213	0803A10	D8S0796i
97,575,058	97,693,213	698H11	DISD22_0005839

99,199,244	99,239,816	0810H02	D8S0560i
99,199,244	99,239,816	0804B04	D8S1778
99,199,244	99,239,816	0805B04	D8S506
99,536,041	99,907,085	0810A08	D8S0103i
99,536,041	99,907,085	9904D10	D8S0852i
99,536,041	99,907,085	0806B04	D8S0855i
99,536,041	99,907,085	0811B07	D8S0926i
99,536,041	99,907,085	0803G04	D8S1749
91,883,383	91,884,738	0901B04	D9S1797
91,883,383	91,884,738	0902F09	D9S1820
100,907,233	100,956,406	0904E12	D9S0215i
100,907,233	100,956,406	0905H11	D9S0532i
101,024,380	101,032,722	0909D02	D9S0086i
101,623,958	101,668,994	0905H03	D9S0313i
101,623,958	101,668,994	0906C02	D9S0726i
103,393,718	103,397,104	0905A11	D9S0506i
103,393,718	103,397,104	9905A09	D9S0724i
107,046,724	107,241,273	9905H09	D9S0793i
107,046,724	107,241,273	0903C07	D9S1784
107,464,599	107,465,214	0908H02	D9S0219i
110,656,692	110,659,068	0909G09	D9S0390i
110,656,692	110,659,068	0901A05	D9S0830i
111,177,800	111,300,407	0906A07	D9S0748i
111,177,800	111,300,407	0904C04	D9S1835
112,045,912	112,058,741	0907H11	D9S0629i
112,045,912	112,058,741	031D09	D9S1675
112,431,057	112,431,557	0902C11	D9S1828
113,364,678	113,401,917	0908E06	D9S0213i
113,364,678	113,401,917	9905D06	D9S0608i
113,698,867	113,737,470	0909D11	D9S0513i
113,698,867	113,737,470	9905F06	D9S0616i
113,698,867	113,737,470	0907C03	D9S0802i
114,967,620	115,024,010	9905B09	D9S0754i
114,967,620	115,024,010	0903G02	D9S262
115,209,336	115,212,773	0904G11	D9S0165i
115,209,336	115,212,773	0907E10	D9S0510i
116,125,157	116,128,578	081G08	D9S302
116,131,890	116,135,357	0903A01	D9S0172i
116,591,421	116,608,229	0901C10	D9S0116i
116,591,421	116,608,229	0908H11	D9S0840i
116,704,945	116,732,591	0904G07	D9S0015i
116,822,634	116,920,260	0904F02	D9S155
116,822,634	116,920,260	0904H04	D9S1776
119,506,405	119,519,589	9905G04	D9S0554i
119,506,405	119,519,589	0909G10	D9S1864
122,704,492	122,730,868	0906A10	D9S0050i
122,704,492	122,730,868	0904E04	D9S1823
122,754,434	122,852,375	0904C08	D9S0039i
124,173,050	124,197,802	0907D12	D9S0318i
124,173,050	124,197,802	9905C07	D9S0649i
126,155,565	126,217,542	0905D12	D9S0545i
126,155,565	126,217,542	0904H06	HUMUT7968
126,283,336	126,309,530	0904B05	D9S1840
126,319,380	126,573,410	0908E08	D9S0176i
126,319,380	126,573,410	0902G04	Z67401
127,036,953	127,043,430	0904E05	D9S1825

129,587,898	129,592,887	414B02	AL162586.7_116830
129,587,898	129,592,887	0901F06	D9S0133i
129,617,112	129,656,856	317C02	AL157935.6_74493
129,951,171	129,956,333	0908A09	D9S0735i
130,485,844	130,498,488	0902H06	D9S0546i
130,913,050	130,951,046	0907C01	D9S0200i
131,540,433	131,555,165	352H04	AC007936.2_31251
131,540,433	131,555,165	0909H05	D9S0091i
131,855,526	131,942,264	0909E12	D9S0020i
131,855,526	131,942,264	0906F04	D9S0720i
131,855,526	131,942,264	9905H08	D9S0723i
132,874,325	132,958,267	0906C05	D9S0761i
132,874,325	132,958,267	0906G05	D9S0767i
133,441,978	133,605,282	0901H04	D9S0547i
133,441,978	133,605,282	0907G03	D9S0550i
134,458,205	134,535,609	0906G08	D9S0198i
134,458,205	134,535,609	9905H03	HUMUT6781
134,895,897	134,923,709	0903H01	D9S0032i
134,895,897	134,923,709	0906C09	D9S0045i
135,120,384	135,140,451	0909E11	D9S0620i
135,276,941	135,314,329	0906E04	D9S0785i
135,276,941	135,314,329	T003D07	D9S164
135,616,837	135,847,547	0906G09	D9S0049i
135,616,837	135,847,547	9904F12	D9S0052i
135,616,837	135,847,547	9904G12	D9S0057i
135,616,837	135,847,547	9905A01	D9S0062i
135,616,837	135,847,547	0902H08	D9S0858i
136,673,473	136,876,510	0901D02	D9S0634i
136,940,837	136,949,630	9905C03	D9S0548i
138,508,717	138,560,135	0909A08	D9S0347i
138,900,786	138,940,888	0901D04	D9S0734i
139437668	139448679	NOXA11	new design
139437668	139448679	NOXA12	new design
15,454,064	15,501,017	0909D05	D9S0187i
15,454,064	15,501,017	0909C04	D9S0668i
2,005,342	2,183,624	9905G02	D9S0348i
2,005,342	2,183,624	0905A06	D9S0367i
2,005,342	2,183,624	0903F01	D9S0371i
2,794,152	2,834,095	0908E02	D9S0561i
2,794,152	2,834,095	0908B06	D9S0566i
21,067,104	21,067,962	0907F05	D9S0224i
21,067,104	21,067,962	0901B03	D9S0783i
21,130,213	21,132,144	0905H05	D9S0366i
21,191,234	21,229,990	9905G09	D9S0786i
21,357,423	21,358,961	0909B09	D9S0369i
21,470,838	21,472,312	0906G10	D9S0122i
21,470,838	21,472,312	0901H02	D9S0373i
21,957,751	21,984,490	0909G05	D9S0018i
21,957,751	21,984,490	0906A11	D9S0115i
21,992,902	21,999,312	0904D01	D9S1870
26,894,081	26,937,461	0907G06	D9S0788i
27,099,236	27,220,173	9905F02	D9S0285i
27,099,236	27,220,173	0909B05	D9S0749i
27,099,236	27,220,173	0909E10	D9S169
27,514,302	27,516,496	0906F06	D9S0708i
3,208,297	3,515,983	0906G11	D9S0191i

3,208,297	3,515,983	0908D07	D9S0406i
3,208,297	3,515,983	0903D08	D9S0424i
3,208,297	3,515,983	T001F11	D9S0571i
3,208,297	3,515,983	0904B07	HUMUT537
32,445,300	32,516,322	0907G02	D9S0582i
32,445,300	32,516,322	0903D09	D9S0842i
33,242,469	33,254,744	0908H09	D9S0673i
33,254,167	33,271,525	0904D12	D9S0188i
34,636,635	34,651,884	0906H03	D9S0812i
34,636,635	34,651,884	063E02	Z67043
35,599,976	35,608,753	0906H07	D9S0693i
35,687,334	35,722,369	411A07	AL133410.26_90374
35,687,334	35,722,369	0909E02	D9S0363i
36,562,873	36,667,679	470C11	chr9.fa.O7frz.39457705
36,562,873	36,667,679	0905C08	D9S0435i
37,909,131	38,059,249	0908D03	D9S0445i
37,909,131	38,059,249	0906H01	D9S0683i
4,975,245	5,118,183	0905H06	D9S0413i
4,975,245	5,118,183	0902B02	D9S0838i
5,440,525	5,460,547	0902A05	D9S0755i
5,440,525	5,460,547	0901G11	D9S0762i
5,500,570	5,561,252	0906H04	D9S0768i
6,205,809	6,247,983	0909B08	D9S0235i
6,205,809	6,247,983	0904A01	D9S1852
70,817,241	70,818,849	0902C05	D9S0147i
74,956,493	74,975,129	0905H01	D9S0260i
74,956,493	74,975,129	0907C07	D9S0584i
76,302,072	76,491,937	0905E09	D9S0465i
76,302,072	76,491,937	0905F09	D9S0469i
76,302,072	76,491,937	9905F07	D9S0656i
78,824,391	78,825,689	0901H06	D9S0489i
8,304,246	9,008,735	0907D07	D9S0242i
8,304,246	9,008,735	0908H01	D9S0247i
8,304,246	9,008,735	0909F08	D9S0408i
8,304,246	9,008,735	0903B11	D9S0417i
8,304,246	9,008,735	0905E07	D9S0420i
8,304,246	9,008,735	T003G06	D9S1676
88,749,098	88,751,924	0902A09	D9S1680
89,301,963	89,513,369	0908F04	D9S0487i
89,301,963	89,513,369	0907B08	D9S0493i
89,301,963	89,513,369	0907F12	D9S0501i
89,301,963	89,513,369	0906G01	D9S257
91,115,925	91,121,438	412F07	AL160054.5_63624
91,181,972	91,302,708	0901C01	D9S906
92,603,890	92,700,652	0905F03	D9S0311i
92,603,890	92,700,652	0902C09	D9S1836
93,211,148	93,225,965	352B02	AL353645.3_94104
93,211,148	93,225,965	0908F11	D9S0194i
97,245,083	97,318,923	472F02	chr9.fa.O7frz.96923615
97,245,083	97,318,923	9905G01	D9S0585i
97,245,083	97,318,923	0904D03	D9S1816
99,477,012	99,499,460	0907G08	D9S0800i
99,655,357	99,658,818	472C04	chr9.fa.O7frz.100149745
99,785,462	99,818,046	0906E03	D9S0832i
100,491,091	100,527,839	2304C07	DXS0684i
100,491,091	100,527,839	2308F02	DXS0923i

103,697,652	104,898,478	2306D03	DXS0001i
103,697,652	104,898,478	2310B01	DXS0151i
103,697,652	104,898,478	2306H08	DXS0208i
103,697,652	104,898,478	2304G05	DXS0433i
103,697,652	104,898,478	2307D04	DXS0438i
103,697,652	104,898,478	2307E04	DXS0442i
103,697,652	104,898,478	2307H04	DXS0450i
103,697,652	104,898,478	2309D05	DXS0629i
103,697,652	104,898,478	2311B07	DXS0741i
103,697,652	104,898,478	2303A01	DXS0964i
103,697,652	104,898,478	2304D04	DXS0979i
103,697,652	104,898,478	2308C05	DXS8112
103,697,652	104,898,478	2304E10	Z67212
105,823,724	105,926,902	2301B07	DXS8048
105,823,724	105,926,902	055B11	DXS8097
105,823,724	105,926,902	2301A10	HUMUT1690
106,843,107	106,905,858	2306G07	DXS0175i
106,843,107	106,905,858	2307F04	DXS0443i
107,103,687	107,105,431	2307G04	DXS0447i
107,285,493	107,569,383	2301H07	DXS0140i
107,285,493	107,569,383	2301D09	DXS0141i
107,285,493	107,569,383	2311D11	DXS0640i
107,285,493	107,569,383	2304B01	DXS6797
107,569,810	107,827,431	2311H11	DXS0641i
107,569,810	107,827,431	2303D11	DXS0716i
110,226,244	110,350,816	2301G11	DXS0968i
114,144,794	114,159,792	2308A06	DXS0727i
115,216,003	115,220,253	552C03	chrX.fa.O7frz.114508264
117,745,563	117,812,530	2311B02	DXS0287i
117,745,563	117,812,530	2306B11	DXS0308i
119,446,367	119,487,189	2304F06	DXS0156i
119,446,367	119,487,189	2307H10	DXS0622i
12,795,123	12,818,420	2307D09	DXS0567i
12,834,679	12,851,209	2309E08	DXS0246i
12,903,148	12,905,267	2306A10	DXS0244i
122,821,558	122,875,510	2311B11	DXS0634i
122,821,558	122,875,510	2305H07	DXS8098
123,307,875	123,334,686	2305F09	DXS0171i
123,307,875	123,334,686	2310D06	DXS0613i
128,408,159	128,485,158	2303D04	DXS0835i
128,408,159	128,485,158	2304C10	DXS0839i
128,408,159	128,485,158	2301B08	DXS0843i
128,607,006	128,616,595	2305C02	DXS0166i
128,607,006	128,616,595	2307D11	DXS0635i
129,091,018	129,127,489	2306G08	DXS0205i
129,091,018	129,127,489	2310F07	DXS0483i
130,235,161	130,361,358	2306A09	DXS0212i
130,235,161	130,361,358	2307A11	DXS0624i
134,482,215	134,544,100	2305F03	DXS0701i
134,895,264	134,957,089	9910E12	DXS0735i
134,895,264	134,957,089	2301E05	DXS0826i
135,558,002	135,570,215	2307H06	DXS0495i
135,558,002	135,570,215	2301G06	DXS0829i
137,541,401	137,894,912	2308H11	DXS0042i
137,541,401	137,894,912	2302H08	DXS0173i
137,541,401	137,894,912	2308H10	DXS0184i

137,541,401	137,894,912	2308G10	DXS0199i
137,541,401	137,894,912	2309C05	DXS0869i
137,541,401	137,894,912	2306G02	HUMUT1537
149,685,467	149,817,837	260E03	AF002223.1_128496
149,685,467	149,817,837	2306C08	DXS0189i
15,273,639	15,312,498	721B09	DIJ28_10038784
15,273,639	15,312,498	2307G09	DXS0575i
15,273,639	15,312,498	258F05	U75931.1_14164
15,392,290	15,484,573	2303G09	DXS1053
15,489,077	15,530,199	2310A08	DXS0008i
152,413,591	152,428,206	2307F07	DXS0516i
152,413,591	152,428,206	2307A08	DXS0524i
152,561,182	152,569,975	2303G03	DXS8087
152,780,163	152,804,802	2310E04	DXS0638i
152,929,145	152,938,625	2311H05	HUMUT2234
153,412,800	153,428,981	2302B07	DXS1073
153,644,229	153,659,158	2309H10	DXS0494i
18,167,355	18,282,768	2305G08	DXS0133i
18,167,355	18,282,768	2304H09	DXS0667i
19,288,095	19,443,363	2310G03	DXS0240i
19,288,095	19,443,363	9911B02	DXS0782i
19,288,095	19,443,363	2305B08	DXS7592
19,462,014	19,815,640	2305D08	DXS0248i
19,462,014	19,815,640	2308B03	DXS0789i
19,462,014	19,815,640	2308E03	DXS0885i
2,680,115	2,743,968	9911C02	DXS0787i
22,927,999	22,931,627	2308E02	DXS0064i
22,927,999	22,931,627	2308E07	DXS0746i
22,927,999	22,931,627	2301F09	DXS7110
23,592,300	23,614,437	2311F06	DXS0350i
28,515,437	29,884,761	2306E04	DXS0044i
28,515,437	29,884,761	2306F05	DXS0094i
28,515,437	29,884,761	2309B08	DXS0339i
28,515,437	29,884,761	2304B12	DXS0343i
28,515,437	29,884,761	2306G12	DXS0348i
28,515,437	29,884,761	2307A01	DXS0351i
28,515,437	29,884,761	2310H06	DXS0361i
28,515,437	29,884,761	2307H09	DXS0576i
28,515,437	29,884,761	2308G07	DXS0783i
28,515,437	29,884,761	9911B03	DXS0936i
28,515,437	29,884,761	2306H01	Z67237
30,232,244	30,237,636	125G12	AC005185.1_116697
30,232,244	30,237,636	2310E11	DXS0063i
30,232,244	30,237,636	257A12	U31929.1_4333
37,429,931	37,476,322	2305G07	DXS0078i
37,524,208	37,557,658	2302D10	DXS0873i
38,305,553	38,433,118	2307H01	DXS0369i
38,305,553	38,433,118	2301G10	DXS0539i
41,077,595	41,108,669	2311B05	DXS0705i
41,077,595	41,108,669	2302D05	DXS993
44,588,193	44,589,078	2309D03	DXS0585i
44,588,193	44,589,078	2302H02	DXS0943i
46,349,697	46,503,434	2308C01	DXS0019i
46,349,697	46,503,434	2301A05	DXS1003
46,349,697	46,503,434	2308H03	DXS1055
47,326,634	47,331,134	2311C01	DXS0084i

47,368,557	47,374,648	2310D01	DXS0396i
48,427,112	48,434,762	2306H03	DXS0016i
48,439,930	48,452,347	2306F04	DXS0059i
48,529,906	48,537,662	2303D07	DXS0753i
48,545,170	48,568,336	2310B07	DXS0020i
48,993,841	49,008,232	2306E01	DXS1208
49,856,156	50,111,653	2308F07	DXS0765i
49,856,156	50,111,653	2302E07	DXS0803i
53,128,274	53,134,447	2301A07	DXS8017
53,128,274	53,134,447	055E03	DXS8062
53,238,059	53,271,329	2308B07	DXS0780i
53,238,059	53,271,329	2305H10	DXS988
55,052,213	55,074,136	665B12	DISO7_10004639
55,052,213	55,074,136	2308C02	DXS0807i
57,719,936	57,723,438	2301D01	DXS0074i
66,680,599	66,867,186	2311A06	DXS0033i
66,680,599	66,867,186	2303G11	DXS0108i
68,752,636	69,176,047	2308C10	DXS0109i
68,752,636	69,176,047	2307B04	DXS0425i
68,752,636	69,176,047	2305G12	DXS0841i
69,394,741	69,396,379	2308A02	DXS0724i
69,394,741	69,396,379	2302D02	DXS983
70,232,772	70,240,110	2302B01	DXS0830i
70,243,979	70,248,188	2310D04	DXS0553i
70,752,491	70,755,092	2310B10	DXS0421i
70,752,491	70,755,092	2303G06	DXS8101
71,341,232	71,375,602	2310A06	DXS0409i
71,341,232	71,375,602	2303A09	DXS0978i
71,341,232	71,375,602	257H02	U07360.1_98
71,466,091	71,709,623	2302H01	DXS0114i
71,466,091	71,709,623	2302C06	DXS0118i
71,466,091	71,709,623	2307F09	DXS0574i
76,596,303	76,598,669	2309F09	DXS0281i
76,596,303	76,598,669	072E09	G10119
77,413,617	77,469,743	2309G08	DXS0252i
77,413,617	77,469,743	2303A12	Z67046
9,391,369	9,647,778	2309A09	DXS0017i
9,391,369	9,647,778	2306A06	DXS0105i
9,391,369	9,647,778	2309A04	DXS0324i
9,391,369	9,647,778	2305G03	DXS8051
95,826,365	96,746,652	2311A01	DXS0012i
95,826,365	96,746,652	2308C12	DXS0146i
95,826,365	96,746,652	2307A05	DXS0454i
95,826,365	96,746,652	2301B12	DXS0458i
95,826,365	96,746,652	T001C06	DXS0588i
95,826,365	96,746,652	2304G12	DXS0649i
95,826,365	96,746,652	2305D03	DXS0651i
95,826,365	96,746,652	2303B12	DXS0653i
95,826,365	96,746,652	2307A12	DXS0655i
95,826,365	96,746,652	2307B12	DXS0657i
95,826,365	96,746,652	2301C06	DXS0818i
99,984,969	100,015,990	2304C06	DXS0191i
99,984,969	100,015,990	2309H09	DXS0592i
13,322,554	13,482,162	9911D06	DYS0039i
13525413	13541784	DDX3Y1	new design
13525413	13541784	DDX3Y2	new design

13,869,653	14,101,947	9911A06	DYS0035i
13,869,653	14,101,947	9911F11	DYS0083i
14,324,841	14,327,298	9911C12	DYS0088i
19,611,898	19,614,093	9911D12	DYS0089i
2769527	2794997	RPS4Y11	new design
2769527	2794997	RPS4Y12	new design
20,326,689	20,366,212	9911H09	DYS0069i
6,838,727	7,019,724	9911B10	DYS0071i
6,838,727	7,019,724	9911F10	DYS0075i

Marker Start Position	Marker End Position	Marker start - gene start	Marker end - gene end
1118517	1118699	10234	13253
1377882	1378152	117,361	103,529
1674131	1674253	116,794	51,144
1965222	1965610	-6,547	-141,084
10480824	10481227	41,658	26,027
100984474	100984814	26,589	7,625
101457925	101458128	-17,107	-21,534
107413661	107414087	12,837	10,648
107942872	107943023	27,567	-366,085
108359820	108360046	444,515	50,938
107995615	107995824	80,310	-313,284
108101217	108101367	185,912	-207,741
109482692	109482919	76,048	62,772
109925706	109926123	32,882	-12,375
109854474	109854584	-38,350	-83,914
11024850	11025217	15,683	-4,660
10916159	10916533	-93,008	-113,344
11206544	11206940	117,365	-38,236
11275250	11275466	186,071	30,290
11136881	11137209	47,702	-107,967
11813253	11813518	44,886	24,816
11843587	11843676	15,234	12,687
110244279	110244430	-10,499	-30,714
111259436	111259863	44,092	15,782
111215883	111216019	539	-28,062
111576226	111576568	4,422	-11,017
111951031	111951504	123,538	43,397
111801431	111801622	-26,062	-106,485
112076662	112076907	190,299	16,071
113057162	113057354	11,911	5,775
114042643	114042849	-50,338	-173,055
114203304	114203593	110,323	-12,311
114891669	114891958	-20,032	-33,830
115021860	115022030	-26,753	-80,117
115380627	115380776	6,689	2,312
115626587	115626756	-3,473	-55,624
116813768	116814047	-44,912	-101,137
117015268	117015647	96,714	3,749
117126586	117126967	28,056	13,593
117222284	117222492	-31,918	-112,011
117358295	117358401	104,093	23,898
117554280	117554477	66,548	-602
117477252	117477671	-10,480	-77,408
119888983	119889236	37,627	30,036
12107161	12107554	61,140	-19,297
12156704	12156927	7,057	-34,945
120395204	120395554	139,505	-18,245
120698748	120698903	29754	38557
120724753	120724985	-3749	-12475
144243331	144243536	7,083	-11,689
144341864	144342095	-65,291	-84,876
146398562	146398665	-19,973	-23,709
146482484	146482839	-84,877	-94,308
148224704	148224871	57,536	49,475
148862649	148862853	48,991	44,093

149005432	149005676	36,257	619
149074817	149074986	39,506	27,550
149126523	149126710	91,212	79,274
149243779	149244097	-31,891	-42,603
149568202	149568358	37,165	1,543
15592470	15592659	-63,341	-97,823
15743102	15743307	87,291	52,825
150124005	150124257	84,641	53,285
150321738	150321938	50,132	45,803
151509676	151510156	-27,286	-39,662
151679764	151680119	66,956	65,370
151741386	151741558	-32,313	-33,786
151815693	151816092	32,980	26,856
151903033	151903133	2,128	-7,015
151981475	151981706	80,570	71,558
152254939	152255252	25,086	24,002
152311055	152311181	81,202	79,931
152640133	152640283	4160	68267
152689113	152689266	-44820	19284
153167546	153167951	-46,207	-50,397
153368540	153368689	1,980	-5,321
153695008	153695274	270,084	265,944
154674287	154674388	-25,856	-62,856
155099951	155100256	57,292	46,986
155091484	155091672	48,825	38,402
155821590	155821916	71,799	32,982
155907593	155907785	97,430	73,291
155968421	155968850	-13,724	-44,696
156053140	156053528	70,995	39,982
156491097	156491389	74,736	70,079
156581636	156581790	55,436	51,746
157182878	157183052	-53,504	-108,517
157343650	157343800	107,268	52,231
157436866	157437022	28,843	-5,892
157529540	157529738	3,412	-14,900
157905533	157905683	-43,170	-45,320
158026403	158026552	9,057	7,595
158110214	158110363	-53,239	-71,647
158339075	158339223	11,321	4,120
158611823	158611977	8,342	2,715
158710267	158710590	-11,177	-49,086
158994467	158994763	79,307	46,498
159042070	159042242	9,518	-22,427
159241305	159241641	9,680	-33,763
159289844	159289978	58,219	14,574
159476005	159476157	24,312	19,044
159547782	159547902	81,703	73,312
159718090	159718302	23754	37682
159925743	159926078	66,133	58,458
16068553	16068848	21,607	-70,694
160680728	160680994	49,048	32,442
163670101	163670279	33,323	-10,778
165776202	165776309	109,701	21,838
165742032	165742474	75,531	-11,997
165996572	165996681	38,740	-30,003
166760192	166760479	-16,434	-19,380

166847127	166847541	34,792	29,602
167782019	167782189	31,991	-40,261
167839015	167839240	14,354	-26,791
167888112	167888292	63,451	22,261
167934170	167934404	7,738	-13,059
17538987	17539227	31,710	-23,859
170879507	170879676	-15,270	-22,961
170974676	170975097	79,899	72,460
171297482	171297762	21,759	11,083
171264445	171264712	-11,278	-21,967
171384999	171385262	-34,494	-57,832
171509854	171509987	90,361	66,893
171743126	171743355	30,098	18,786
172228252	172228588	88,690	75,449
173372906	173373307	69,289	-10,518
173789361	173789708	230,803	-189,821
173663383	173663770	104,825	-315,759
173551440	173551669	-7,118	-427,860
173979342	173979564	420,784	35
173943745	173943862	385,187	-35,667
173783268	173783512	224,710	-196,017
177098271	177098441	12,978	-8,397
177222734	177223120	-95,001	-110,533
177468156	177468492	150,421	134,839
178439502	178439869	48,911	81
178371799	178371991	-18,792	-67,797
179291903	179292263	22,141	-49
18558257	18558663	251,430	-18,900
18453893	18454062	147,066	-123,501
18306011	18306145	-816	-271,418
18640976	18641135	334,149	63,572
181023651	181023751	-51,476	-99,759
181140182	181140466	65,055	16,956
181453066	181453438	31,044	-27,224
181485371	181485534	63,349	4,872
181778627	181778785	-12,693	-47,849
184498645	184499049	-33,389	-51,268
184973466	184973772	65,920	57,593
190964044	190964300	92,139	68,241
190826568	190826757	-45,337	-69,302
194983594	194984042	95,963	785
194917054	194917353	29,423	-65,904
195153322	195153523	142,751	-863
195259589	195259868	80,069	64,889
196859008	196859237	-15,416	-133,798
198427146	198427367	163,793	14,192
198979477	198979894	119,830	74,145
198766750	198766850	-92,897	-138,899
2521865	2522093		
2530030	2530401	-50880	-43788
20310948	20311409	-71	-7,228
20246759	20246900	-64,260	-71,737
20383149	20383327	72,130	64,690
20807260	20807633	19,232	-10,355
20755451	20755747	-32,577	-62,241
200184737	200184971	-58,959	-67,968

200450701	200450807	67,937	53,475
200498563	200498816	94,761	73,712
201426851	201427023	100,446	23,867
201387330	201387616	60,925	-15,540
201338325	201338509	11,920	-64,647
201635202	201635518	58,827	48,278
201989619	201989975	-11,338	-22,148
202348103	202348336	39,237	-15,158
202327292	202327557	18,426	-35,937
202692591	202692790	34,212	-33,385
202816750	202817052	64,616	23,181
203304684	203304960	25,721	-8,801
203220013	203220180	-58,950	-93,581
203891616	203892025	58,286	23,402
204741554	204741703	31,140	4,857
204833379	204833538	-42,125	-90,843
205013527	205013705	88,615	39,454
N/A	N/A	N/A	N/A
205048253	205048519	9,415	-34,430
205078640	205078851	-26,682	-30,340
205158514	205158736	21,103	14,629
205303798	205304022	-25,012	-35,939
205441979	205442426	97,749	57,486
205647276	205647722	85,800	46,788
205687370	205687674	-6,828	-42,189
205947729	205947928	211,633	66,195
205883859	205883961	147,763	2,228
205826044	205826169	89,948	-55,564
206056498	206056664	64,473	21,183
206137789	206138080	20,847	-13,290
206105499	206105697	-11,443	-45,673
206221446	206221542	104,504	70,172
207864747	207865168	9,909	-27,275
207949877	207950139	95,039	57,696
207783865	207784057	-70,973	-108,386
208036528	208036697	10,869	-9,405
209669985	209670146	103,405	55,235
209471360	209471602	-95,220	-143,309
210736987	210737439	-68,387	-123,303
210927833	210928181	122,459	67,439
212795947	212796130	198,473	4,865
212604688	212604861	7,214	-186,404
212919548	212919946	76,393	15,409
215300678	215300839	557,467	-76,881
214943506	214943765	200,295	-433,955
214784611	214784751	41,400	-592,969
214880392	214880547	137,181	-497,173
215160267	215160455	417,056	-217,265
215361062	215361182	617,851	-16,538
215216213	215216336	473,002	-161,384
216654129	216654315	67,929	-30,269
219115070	219115257	-4,296	-9,765
219201032	219201262	81,666	76,240
219906078	219906406	-35,311	-75,735
219865643	219865801	-75,746	-116,340
220066424	220066770	125,035	84,629

22081456	22081556	60,132	-54,821
22393746	22394082	75,569	51,885
22808779	22809269	-26,926	-29,493
22822726	22822865	-12,979	-15,897
22897463	22897645	61,758	58,883
23141418	23141558	231,373	27,153
221394688	221394784	44,418	11,537
224053319	224053540	-11,140	-46,344
224133098	224133270	68,639	33,386
224579194	224579455	-35,821	-82,959
224715979	224716073	100,964	53,659
225001629	225002044	115,615	8,397
224922112	224922501	36,098	-71,146
226712934	226713078	1,631	881
227588826	227589226	-44,789	-47,242
227637808	227638013	4,193	1,545
233985087	233985489	94,123	-128,074
234092495	234092797	201,531	-20,766
233918710	233919094	27,746	-194,469
233960402	233960594	69,438	-152,969
234369444	234369756	163,691	66,050
234215458	234215755	9,705	-87,951
234756938	234757107	132,635	42,458
234635612	234635898	11,309	-78,751
234697293	234697439	72,990	-17,210
234988436	234988869	72,014	-5,685
24365214	24365363	46,366	23,165
24284111	24284522	-34,737	-57,676
24327532	24327681	8,684	-14,517
240059211	240059445	-18,894	-60,419
241879146	241879476	160,988	-200,577
241929347	241929516	211,189	-150,537
241980312	241980412	262,154	-99,641
242132500	242132680	414,342	52,627
241757649	241757909	39,491	-322,144
245668817	245669049	20,843	-9,984
245753885	245754055	105,911	75,022
25083878	25084302	-14,718	-79,760
25156255	25156713	57,659	-7,349
25489580	25489690	18,012	-39,833
25605276	25605382	43,949	-23,888
26125160	26125617	-33,685	-71,618
26208532	26208633	49,687	11,398
26523553	26523675	6,555	4,074
27063369	27063469	-26,198	-36,080
27161953	27162115	51,387	49,068
27284905	27285150	-12,988	-80,909
27406448	27406579	108,555	40,520
27826445	27826654	15,283	-7,721
27810008	27810268	-1,154	-24,107
28304800	28304978	-41,464	-87,993
28390511	28390738	44,247	-2,233
29515207	29515334	79,596	-10,565
29594202	29594459	158,591	68,560
3713783	3714235	-49,922	-77,618
31104317	31104509	-10,584	-61,792

31184208	31184506	69,307	18,205
31579705	31579970	-30,982	-38,540
31691178	31691327	80,491	72,817
32160735	32161040	16,126	-15,538
32217659	32218079	73,050	41,501
32319158	32319636	67,141	20,599
32431626	32431870	-57,854	-92,483
32598999	32599175	109,519	74,822
32582337	32582751	52,063	10,928
36750332	36750555	46,101	29,089
36661487	36661961	-42,744	-59,505
37880392	37880591	75,388	46,482
39946153	39946337	-30,964	-55,836
40031816	40032000	54,699	29,827
40155002	40155420	21,317	15,146
40932954	40933281	3,125	-76,583
41048818	41049032	118,989	39,168
41152667	41152942	-65,284	-97,873
41431703	41431992	166,242	-48,383
41273561	41273803	8,100	-206,572
42533358	42533792	118,561	-40,343
42458163	42458359	43,366	-115,776
42869889	42870274	-26,746	-44,742
43008557	43008657	-46,806	-74,590
43127420	43127586	72,057	44,339
43537628	43537883	-38,434	-54,839
43534013	43534296	-63,200	-67,165
43834710	43835035	65,576	-26,889
43729147	43729375	-39,987	-132,549
44199795	44200229	28,216	24,730
45032172	45032449	-6,451	-17,030
46345335	46345508	66,936	-25,546
46969602	46969764	-67,703	-87,908
47134127	47134555	96,822	76,883
47346835	47346984	85,008	57,974
47518034	47518204	63,484	48,230
47416796	47416956	-37,754	-53,018
47658013	47658114	3,682	1,803
47717197	47717366	42,921	38,416
50870539	50870957	192,801	-327,567
51227256	51227512	549,518	28,988
50840440	50840693	162,702	-357,831
50614475	50614898	-63,263	-583,626
51062311	51062566	384,573	-135,958
50946157	50946278	268,419	-252,246
56865797	56865983	133,270	48,138
56704450	56704849	-28,077	-112,996
56794815	56795091	62,288	-22,754
56982831	56982992	99,248	29,396
57157156	57157372	64,091	890
59040129	59040337	21,081	17,750
6451748	6451891	7,950	-50,817
6552569	6552780	108,771	50,072
60193176	60193646	61,608	28,596
63594563	63594850	33,263	31,465
65266692	65266955	195,192	62,180

65098573	65098960	27,073	-105,815
65047672	65047939	-23,828	-156,836
65749437	65749865	90,579	-129,965
65868877	65869147	210,019	-10,683
65610383	65610582	-48,475	-269,248
66629082	66629540	598,301	16,690
66123732	66124206	92,951	-488,644
66279960	66280185	249,179	-332,665
66399431	66399713	368,650	-213,137
66030154	66030296	-627	-582,554
67522012	67522314	117,341	24,064
67422737	67423039	18,066	-75,211
67640744	67640896	95,109	5,725
7889010	7889252	-13,484	-34,261
7978140	7978428	75,646	54,915
71167018	71167270	76,394	-118,809
71269404	71269634	178,780	-16,445
71173779	71174035	83,155	-112,044
70958653	70958962	-131,971	-327,117
78505947	78506207	-36,209	-272,767
78679341	78679503	137,185	-99,471
78756727	78756953	214,571	-22,021
78913609	78913851	25,505	11,500
78833428	78833809	-54,676	-68,542
79149764	79149943	21,727	-129,162
79296770	79297183	168,733	18,078
84503775	84503929	187,446	27,160
84308970	84309145	-7,359	-167,624
85473216	85473695	-31,303	-42,664
85541131	85541346	36,612	24,987
85574178	85574426	17,422	-128,989
85702827	85703016	146,071	-399
89086765	89086983	-4,438	-42,906
89278228	89278608	33,280	17,476
89426234	89426486	81,831	12,175
89570050	89570158	71,197	59,039
9693234	9693397	58,844	-18,167
91852607	91852865	-65,881	-291,282
91967265	91967485	48,777	-176,662
92219475	92219731	300,987	75,584
988762	988968	50,096	49,185
94083562	94083798	-39,787	-63,802
94827241	94827552	59,872	47,608
102047157	102047636	147,316	68,270
101876767	101877235	-23,074	-102,131
103081011	103081184	-22,799	-225,884
103282436	103282643	178,626	-24,425
103186239	103186527	82,429	-120,541
103458963	103459149	-60,914	-66,668
104183819	104184212	39,499	31,941
104578855	104579053	52,859	13,042
104622910	104623111	42,632	35,831
11415824	11416266	328,534	-2,414
11136346	11136564	49,056	-282,116
11044923	11045394	-42,367	-373,286
11405372	11405511	318,082	-13,169

11230768	11230868	143,478	-187,812
11308543	11308703	221,253	-109,977
112213182	112213522	-34,404	-47,770
112437722	112438107	120,283	83,723
112381801	112381926	64,362	27,542
115398137	115398286	-30,788	-82,368
12315190	12315371	103,548	63,405
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121442456	121442757	41,584	15,436
123119005	123119448	645,628	-228,514
122456224	122456679	-17,153	-891,283
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123260196	123260544	786,819	-87,418
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123340429	123340702	867,052	-7,260
122634709	122634881	161,332	-713,081
123044495	123044666	571,118	-303,296
122923502	122923945	450,125	-424,017
122493370	122493470	19,993	-854,492
122956331	122956574	482,954	-391,388
122772594	122772780	299,217	-575,182
124310913	124311313	742	-81,929
124402715	124402918	92,544	9,676
124863927	124864289	-39,856	-50,587
125000685	125000816	96,902	85,940
127371251	127371500	-73,761	-82,880
127590942	127591112	76,046	16,095
127882368	127882572	191,428	-184,483
127989618	127989813	298,678	-77,242
128093957	128094069	403,017	27,014
127669764	127669864	-21,176	-397,191
129430152	129430372	4,648	932
129643468	129643725	48,153	-130,430
129532723	129532934	-62,592	-241,221
131176113	131176333	20,657	-279,025
131345857	131346011	190,401	-109,347
131534323	131534438	378,867	79,080
133656190	133656439	25,009	10,989
134980088	134980242	54,190	39,880
135205989	135206368	15,132	-18,346
14950401	14950560	-28,963	-85,877
15100482	15100739	121,118	64,302
15516539	15516781	-79,415	-285,349
15642982	15643419	47,028	-158,711
15863327	15863513	267,373	61,383
15717867	15718069	121,913	-84,061
16622065	16622206	26,317	18,196
16559201	16559433	-36,547	-44,577
17365771	17366154	54,488	46,556
17935391	17935717	44,023	-57,467
18281120	18281283	142,762	41,186
22622833	22622987	-27,313	-37,207
26880805	26881255	113,667	-15,483
26737714	26738072	-29,424	-158,666

26801475	26801569	34,337	-95,169
30761817	30761974	-1,055	-28,794
30856805	30856995	93,933	66,227
31788555	31788912	141,125	-69,836
31856227	31856469	208,797	-2,279
31859304	31859717	211,874	969
31602801	31603020	-44,629	-255,728
31720106	31720285	72,676	-138,463
31787228	31787345	139,798	-71,403
33306963	33307354	77,637	20,150
33203437	33203802	-25,889	-83,402
33559442	33559664	53,016	-105,532
33484703	33484876	-21,723	-180,320
35519919	35520311	64,112	-21,581
35448262	35448663	-7,545	-93,229
35598142	35598320	142,335	56,428
44277379	44277528	91,768	76,980
45135539	45135859	-54,096	-125,712
45246939	45247383	57,304	-14,188
49078072	49078274	151,856	45,252
49291720	49292060	106,981	-25,349
49173610	49173915	-11,129	-143,494
54251939	54252109	56,793	50,643
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59827471	59827581	62,726	27,066
6102858	6103019	68,518	42,863
6162899	6163377	70,241	19,083
6549064	6549479	39,953	-112,790
6486119	6486280	-22,992	-175,989
6668019	6668169	158,908	5,900
61519163	61519332	60,998	-300,162
61820415	61820639	362,250	1,145
61766240	61766389	308,075	-53,105
61406911	61407069	-51,254	-412,425
61701830	61701989	243,665	-117,505
62198756	62198925	-6,934	-25,691
64180823	64181149	-60,939	-64,984
64312963	64313152	71,201	67,019
70356451	70356625	25,411	-19,984
70589837	70590132	72,003	55,559
72065347	72065494	38,237	32,973
74921438	74921888	55,246	-3,877
74830893	74831188	-35,299	-94,577
75407328	75407563	66,432	60,302
75601437	75601688	20,466	-537,379
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76125105	76125467	544,134	-13,600
76006821	76006993	425,850	-132,074
75772150	75772617	191,179	-366,450
76170406	76170578	589,435	31,511
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79286180	79286359	65,623	-70,025
79346447	79346849	125,890	-9,535
8065595	8066046	-71,067	-91,124
8180349	8180566	43,687	23,396
80850406	80850658	73,180	65,562

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81638448	81638647	-49,028	-60,194
83847088	83847379	222,302	-889,534
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83719442	83719602	94,656	-1,017,311
83685373	83685725	60,587	-1,051,188
84031913	84032082	407,127	-704,831
84521953	84522351	897,167	-214,562
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88575128	88575545	68,752	-99,380
89591521	89591700	-21,329	-129,967
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91165956	91166186	202,650	1,892
90922229	90922428	-41,077	-241,866
94854112	94854543	43,101	36,099
96414616	96414782	-18,752	-71,155
96600924	96601325	-88553	1682
96616024	96616357	-103653	-13350
96754217	96754382	-65799	-15245
96815763	96815961	29,244	-3,283
97404709	97405004	-56,817	-214,438
97518155	97518364	56,629	-101,078
97676529	97676681	215,003	57,239
97939396	97939567	-2,049	-81,749
98037615	98037775	-16,460	-50,536
98113222	98113486	59,147	25,175
1700761	1701110	-29,797	-40,688
1811459	1811748	80,901	69,950
1918252	1918425	87,476	48,356
10344350	10344812	61,178	59,313
100348362	100348532	-65,951	-157,933
100436054	100436203	21,741	-70,262
101668113	101668513	-25,291	-45,162
101888016	101888260	-8,433	-18,428
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102097115	102097340	29,490	15,662
102147724	102147929	1,280	-8,640
102258351	102258583	46,613	39,031
102293049	102293484	-25,885	-38,188
102336786	102336969	17,852	5,297
104249491	104249665	-12,385	-24,942
104320257	104320527	1,453	-24,846
104381250	104381373	11,070	-3,536
104609328	104609428	95,449	93,765
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106786937	106787219	-91,727	-154,418
106906426	106906608	27,762	-35,029

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107729808	107730105	131,039	-14,931
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108177867	108178016	136,853	-138,850
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109643389	109643531	38,013	-29,116
110687039	110687495	-41,151	-68,132
110820084	110820297	91,894	64,670
111587200	111587444	68,014	47,394
111495994	111496143	-23,192	-43,907
112504798	112505030	167,430	-148,751
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112393437	112393626	56,069	-260,155
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114834170	114834546	283,943	-45,779
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114630455	114630551	80,228	-249,774
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117421158	117421352	58,839	43,948
117321983	117322360	-40,336	-55,044
117700389	117700722	19,727	8,622
117710065	117710464	-410	-8,205
118198233	118198689	72,610	31,607
118140629	118140811	15,006	-26,271
118302331	118302484	42,554	30,303
118294141	118294291	34,364	22,110
118770905	118771288	86,461	78,238
119059296	119059573	45,278	-45,072
119177944	119178053	163,926	73,408
119585098	119585541	-31,158	-110,322
119723000	119723254	106,744	27,391
119637040	119637172	20,784	-58,691
120769755	120769894	-58,375	-235,727
121040925	121041033	212,795	35,412
125333610	125333823	54,060	35,608
125216965	125217304	-62,585	-80,911
125734783	125734933	76,591	62,250
125585523	125585702	-72,669	-86,981
13409041	13409169	-61,136	-64,974
133254024	133254494	-36,371	-72,827
133323661	133323811	33,266	-3,510
133365279	133365517	74,884	38,196
133524030	133524139	80,000	-2,722
133559866	133560110	115,836	33,249
133778960	133779196	25,352	-7,826
14884514	14884663	28,383	14,336
17113699	17113909	45,838	-33,955
17002331	17002575	-65,530	-145,289
18093321	18093663	2,725	-1,032
18229909	18230280	6,544	3,522
18297333	18297482	73,968	70,724
18378499	18378623	77,780	33,470

18658608	18658789	-23,827	-45,564
18855689	18855901	149,638	85,936
2156353	2156501	49,435	30,885
2420074	2420260	64,978	45,035
2283799	2283921	-71,297	-91,304
2792169	2792522	-68,850	-71,055
20299960	20300129	-65,719	-187,275
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22598011	22598324	-48,219	-192,799
22741651	22741808	95,421	-49,315
22816598	22816863	170,368	25,740
255428	255888	-13,142	-19,416
287487	287636	18,917	12,332
27637704	27637859	4,688	-62,013
27695872	27696148	62,856	-3,724
3640770	3640991	17,833	-1,231
33715142	33715474	34,010	874
33649572	33649789	-31,560	-64,811
34338576	34338725	-78,478	-111,458
35262509	35262746	145,516	52,221
35189696	35189866	72,703	-20,659
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36450016	36450216	-17,283	-38,182
36588787	36589004	42,648	31,127
405192	405367	-9476	2030
413520	413946	-17804	-6549
4812943	4813113	67,867	-157,122
4975673	4976118	230,597	5,883
4874800	4875272	129,724	-94,963
4724509	4724721	-20,567	-245,514
43243236	43243507	-46,873	-79,148
43927725	43928112	68,754	29,720
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44536919	44537277	-6,798	-60,638
45860353	45860453	-3,425	-24,139
45933382	45933561	69,604	48,969
46807925	46808037	110,594	90,406
46634982	46635131	-62,349	-82,500
47332639	47332808	105,556	85,836
47223856	47224048	-3,227	-22,924
47566731	47567132	23,267	4,442
47460024	47460448	-83,440	-102,242
47658692	47659143	90,900	78,627
48137208	48137396	178,519	-8,850
47979419	47979563	20,730	-166,683
5127935	5128105	-75,335	-84,349
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5640602	5641025	-26,893	-47,644
5685349	5685820	17,854	-2,849
5776756	5777027	109,261	88,358
56766568	56766738	8,938	5,249
56813022	56813215	-49,503	-80,910
56922052	56922231	11,220	7,525
57005540	57005740	-70,165	-86,593
57117326	57117551	-4,277	-21,351
57222126	57222292	100,523	83,390

59601726	59602151	21,049	6,987
59945379	59945684	-8,259	-26,157
6556371	6556806	-25,169	-31,871
6582930	6583317	1,390	-5,360
6644378	6644852	62,838	56,175
60310130	60310329	-64,853	-69,691
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61119711	61119869	80,350	14,995
61376985	61377415	60,259	56,129
62284965	62285163	-31,254	-44,366
62458815	62458918	78,721	45,989
62993108	62993250	-37,024	-47,565
63719113	63719554	-39,533	-43,281
63794870	63795098	29,881	26,836
63927537	63927929	97,921	87,143
64249526	64249691	-1,433	-19,813
64524878	64525231	66,359	65,295
64462810	64462937	4,291	3,001
64807919	64808269	21,913	-13,395
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65222246	65222415	44,597	35,456
65462513	65462963	83,655	79,501
65346967	65347136	-31,891	-36,326
65854507	65854868	15,973	13,777
65975563	65975718	-15,411	-25,664
66132595	66133021	61,628	45,648
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66600844	66601220	19,947	5,160
66526118	66526306	-54,779	-69,754
66871457	66871897	-16,758	-25,885
66948890	66949039	60,675	51,257
67069719	67069901	62,622	54,751
67168673	67168902	60,811	58,201
67457480	67457688	-57,671	-70,481
67624326	67624698	61,267	49,756
67855692	67855935	19,018	-117,382
68013498	68013891	176,824	40,574
67888234	67888517	51,560	-84,800
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69149669	69149895	-15,385	-28,528
69324892	69325079	27,914	25,727
69751899	69752017	24,982	20,873
7017138	7017337	765	-31,996
7096246	7096473	79,873	47,140
7867613	7867973	-69,934	-73,807
8027665	8027909	90,118	86,129
71155608	71155807	-66,286	-70,449
71429082	71429258	41,495	34,849
72666465	72666905	59,473	41,860
72539761	72539886	-67,231	-85,159
72616021	72616121	9,029	-8,924
72815181	72815466	50,128	29,299
73007538	73007678	-16,054	-43,834

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74649816	74649977	-4,314	-90,544
75441946	75442301	238,023	-89,041
75563087	75563342	359,164	32,000
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75339935	75340147	136,012	-191,195
75724913	75725164	-13,739	-44,364
75822080	75822524	83,428	52,996
76713339	76713605	2,631	-148,976
76646166	76646333	-64,542	-216,248
77819086	77819508	215,096	13,094
77653879	77654097	49,889	-152,317
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86300226	86300600	-34,143	-43,481
86416124	86416387	81,755	72,306
88608867	88609333	58,599	-59,141
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88575395	88575564	25,127	-92,910
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93885648	93885921	95,534	19,233
93792191	93792340	2,077	-74,348
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10087332	10087531	72,051	58,070
10171994	10172269	58,573	29,397
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10429073	10429350	77,389	69,367
10537837	10538291	81,656	73,830
10622662	10622872	-10,377	-20,559
10740104	10740529	-2,851	-26,642
101316913	101317109	3,107	-81,362
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101913847	101914133	38,253	35,712
101880231	101880528	4,637	2,107
102562239	102562561	57,058	-122,074
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102538509	102538726	33,328	-145,909
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102963757	102964206	-71,231	-91,964
103065571	103065835	30,583	9,665
103360732	103361193	155,875	93,001
105442833	105443296	-58,330	-237,415
105605002	105605216	103,839	-75,495
105703670	105703837	202,507	23,126
107227972	107228172	19,172	-29,046
107546197	107546409	6,397	-5,390
108055338	108055655	44,959	39,995
108083845	108084082	73,466	68,422
108248621	108248864	48,454	17,456
108195877	108196139	-4,290	-35,269
109352563	109352725	-71,825	-101,549
109439729	109440012	15,341	-14,262

11685531	11685738	-8,524	-253,865
11718773	11718949	24,718	-220,654
11793396	11793617	99,341	-145,986
11990747	11990978	296,692	51,375
111309260	111309377	-31,659	-122,723
111459825	111460188	118,906	28,088
111799546	111799692	-29,576	-54,682
112103089	112103288	123,044	83,072
112051097	112051240	71,052	31,024
115731355	115731467	-52,055	-72,148
115839045	115839149	55,635	35,534
116283881	116284210	148,519	245
116073014	116073216	-62,348	-210,749
116360490	116360689	225,128	76,724
118111422	118111554	10,444	-5,380
118081112	118081313	-19,866	-35,621
120041329	120041603	98,851	80,439
119906036	119906229	-36,442	-54,935
12146717	12147053	31,572	-108,161
12293759	12293984	178,614	38,770
12341197	12341421	176,244	30,408
12569802	12570166	49,704	-36,418
12605068	12605244	84,970	-1,340
12530591	12530790	10,493	-75,794
12923727	12923938	153,597	49,756
120085304	120085687	30,243	-22,572
120098187	120098601	43,126	-9,658
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121504494	121504896	182,560	31,827
121379039	121379484	57,105	-93,585
121704586	121704690	-60,670	-62,607
122610261	122610730	-42,364	-60,705
122785607	122785735	101,274	74,162
123487252	123487709	112,338	-81,084
123335726	123336092	-39,188	-232,701
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123551451	123551625	176,537	-17,168
123478494	123478745	103,580	-90,048
123785839	123785947	-42,290	-128,399
123912323	123912419	84,194	-1,927
124113254	124113485	115,929	73,865
128051485	128051693	-12,320	-15,947
129137593	129137752	-75,364	-78,486
129286415	129286564	73,458	70,326
129903550	129903765	-18,971	-23,551
131664912	131665106	-40,564	-43,939
14919482	14919661	45,970	31,981
14874634	14874948	1,122	-12,732
14992281	14992518	6,064	-13,352
15056240	15056476	70,023	50,606
15300249	15300411	-66,505	-341,191
15674320	15674532	307,566	32,930
15426311	15426470	59,557	-215,132
15524891	15525092	158,137	-116,510
18686865	18687129	381,124	-5,488
18740430	18740725	434,689	48,108

18263410	18263511	-42,331	-429,106
18360074	18360183	54,333	-332,434
18449572	18449809	143,831	-242,808
2828263	2828442	53,849	45,057
2873844	2874055	99,430	90,670
25168001	25168287	-81,446	-126,834
25269412	25269582	19,965	-25,539
26314493	26314662	-62,700	-562,736
26813119	26813273	435,926	-64,125
26939529	26939766	562,336	62,368
26609551	26609775	232,358	-267,623
26693892	26694063	316,699	-183,335
26557884	26558019	180,691	-319,379
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26495532	26495631	118,339	-381,767
28008328	28008607	6,044	-7,576
28091917	28092066	89,633	75,883
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29352779	29352968	-28,777	-72,442
29431238	29431647	49,682	6,237
3645701	3645871	175,015	72,471
3538279	3538526	67,593	-34,874
3457675	3457844	-13,011	-115,556
31111945	31112104	-6,116	-36,888
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4315826	4315989	62,627	31,212
4508240	4508410	94,671	83,369
4605075	4605250	35,570	11,948
4566036	4566290	-3,469	-27,012
42438703	42438812	-344	-29,354
42557887	42558129	118,840	89,963
44546904	44547358	-54,555	-123,257
44703079	44703522	101,620	32,907
46490799	46490990	28,027	-8,934
46556248	46556348	93,476	56,424
47544321	47544518	34,515	12,294
47583832	47584131	74,026	51,907
47684743	47684960	26,240	22,214
47770522	47770962	1,051	-3,907
47893345	47893701	28,498	24,548
48065378	48065631	52,911	48,393
48262703	48262971	24,351	14,793
49402209	49402647	-41,919	-97,681
49489767	49490229	45,639	-10,099
49591028	49591174	146,900	90,846
5978723	5978991	50,422	-125,106
6035146	6035410	106,845	-68,687
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5945674	5945835	17,373	-158,262
5837039	5837319	-91,262	-266,778
50000958	50001096	-7,536	-25,634
51157078	51157229	-10,153	-16,060
51654720	51654947	77,482	69,820
51557334	51557446	-19,904	-27,681
51830228	51830548	-41,146	-56,719
51902241	51902398	11,620	-9,855

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52659623	52659825	6,446	3,355
53019917	53020186	47,755	39,128
53066185	53066285	94,023	85,227
53175440	53175857	100,128	76,540
53390512	53390893	65,870	62,477
53329249	53329539	4,607	1,123
54398484	54398764	33,865	10,815
54337267	54337416	-27,352	-50,533
54612617	54612828	1,404	-21,246
54675920	54676089	41,764	29,324
55099487	55099575	80,561	79,114
55442274	55442554	49,790	35,306
55498736	55498853	106,252	91,605
55791940	55792334	22,783	16,808
55950121	55950516	-40302	-35535
55951465	55951629	-41646	-36648
56022483	56022632	-92,327	-108,244
56231892	56232105	96,529	94,047
56377877	56378037	-50,393	-54,394
56589563	56589732	89,586	62,718
6235483	6235761	56,349	18,073
6324780	6324991	16,596	3,469
6288126	6288299	-20,058	-33,223
6439131	6439549	75,536	68,555
6587061	6587187	73,189	69,390
6597357	6597553	83,485	79,756
6792176	6792404	23,264	-7,833
6904463	6904614	84,827	77,795
64942912	64943311	73,642	14,627
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66365842	66366077	36,821	25,667
66415802	66416056	86,781	75,646
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66904234	66904403	69,418	64,613
66838693	66838991	3,877	-799
N/A	N/A	N/A	N/A
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67603158	67603380	114,911	82,899
69244866	69245030	43,635	-72,439
69299051	69299293	97,820	-18,176
69481619	69481905	163,490	-118,948
69673344	69673504	355,215	72,651
7170247	7170547	31,956	17,478
7709589	7709738	-63,689	-83,598
7794552	7794931	21,274	1,595
78562872	78563350	52,996	-45,571
79310149	79310458	-8,448	-287,641
79475665	79476124	157,068	-121,975
79557911	79558131	239,314	-39,968
8126572	8126744	49,946	27,359
8048872	8049081	-27,754	-50,304
8252748	8252849	85,255	70,379
8654797	8654971	97,394	88,742

8933305	8933450	66,821	12,804
87529479	87529893	118,782	31,524
87486164	87486560	75,467	-11,809
88226691	88227034	-39,277	-43,393
88320166	88320357	54,198	49,930
9046735	9046934	13,251	-7,676
9553148	9553304	92,254	61,212
9376108	9376310	-84,786	-115,782
9497176	9497448	36,282	5,356
9739603	9739784	101,188	88,020
9876479	9876698	5,135	-12,173
90039212	90039461	-23,954	-61,476
90073419	90073672	10,253	-27,265
91115769	91115992	54,739	52,241
91679397	91679629	-13,860	-167,509
91915912	91916032	222,655	68,894
92373939	92374337	47,720	14,180
92496455	92496742	8,726	2,633
92465871	92466225	-21,858	-27,884
92619073	92619331	23,791	-149,332
92574243	92574702	-21,039	-193,961
92781427	92781596	186,145	12,933
92708679	92708878	113,397	-59,785
93115238	93115652	48,608	-107,704
93037033	93037253	-29,597	-186,103
93294493	93294682	227,863	71,326
93844675	93845073	-95,127	-146,414
94863903	94864025	-54,839	-89,471
94989229	94989364	70,487	35,868
97476068	97476460	42,541	8,210
97392901	97393045	-40,626	-75,205
97592308	97592639	29,099	-60,703
97633038	97633348	69,829	-19,994
97528647	97529019	-34,562	-124,323
99472130	99472380	80,320	-9,394
99461304	99461632	69,494	-20,142
99423743	99424039	31,933	-57,735
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101019349	101019512	116,492	-149,634
101405021	101405170	235,713	-446,986
101656393	101656559	487,085	-195,597
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101318212	101318481	148,904	-533,675
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107736868	107737038	79,077	68,321
107844860	107845093	124,882	86,267
109801351	109801759	202,040	44,254
109648396	109648570	49,085	-108,935
109978018	109978413	220,386	15,038
112983609	112983911	-15,948	-41,835

20257883	20258180	82,404	62,943
20643000	20643381	30,350	22,160
20557425	20557629	-55,225	-63,592
21173783	21173991	30,613	-2,646
21215397	21215842	72,227	39,205
23139163	23139311	96,440	-8,921
23243644	23243795	200,921	95,563
23083142	23083346	40,419	-64,886
25963459	25963901	237,183	86,526
25834146	25834547	107,870	-42,828
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26078404	26078846	48,564	-82,239
26805545	26805847	-91,136	-101,976
26957206	26957639	60,525	49,816
27358433	27358626	-75,840	-82,691
27478401	27478570	2,990	-94,159
27618297	27618554	142,886	45,825
27953530	27953699	179,740	-13,533
27869868	27870023	96,078	-97,209
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29970494	29970820	39,610	-118,909
29906396	29906794	-24,488	-182,935
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30244427	30244579	36,782	8,023
31922785	31923197	135,168	51,388
35835464	35835578	-69,031	-79,430
36317134	36317436	25,795	15,696
40132897	40133162	105,096	-5,572
39975108	39975292	-52,693	-163,442
41970551	41970720	-64,321	-109,428
42092311	42092485	57,439	12,337
44821373	44821567	228,723	65,330
44496186	44496554	-96,464	-259,683
44713243	44713628	120,593	-42,609
44830757	44830862	21,749	17,357
46302100	46302455	-3,414	-65,724
46345241	46345710	39,727	-22,469
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47997390	47997628	114,220	109,681
48196230	48196355	17,538	14,856
52255232	52255509	79,832	43,561
94559555	94559705	89,471	-191,983
94698049	94698332	227,965	-53,356
94480217	94480614	10,133	-271,074
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98749659	98749833	4,869	-7,875
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101709325	101709631	92,186	33,855
101822811	101823084	60,436	-18,200
102307652	102308130	-5,917	-134,251
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103312211	103312378	78,504	60,829
104341507	104341623	50,978	44,587
104670447	104670755	83,665	67,956

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19826086	19826246	-23,281	-45,051
19906719	19906868	57,352	35,571
20276160	20276537	-42,890	-43,927
20618135	20618406	37,884	36,180
22182690	22182915	1,022,793	92,000
21479279	21479478	319,382	-611,437
22028150	22028453	868,253	-62,462
21328896	21329186	168,999	-761,729
21875450	21875599	715,553	-215,316
21577795	21577963	417,898	-512,952
21186185	21186349	26,288	-904,566
21757385	21757515	597,488	-333,400
21270918	21271150	111,021	-819,765
22439738	22439902	64,105	53,259
22280814	22281202	-94,819	-105,441
22535821	22536096	76,248	67,595
22656227	22656373	-128	-2,292
22814584	22814823	-31,282	-35,975
22962373	22962572	50,515	47,120
23630109	23630242	-31,098	-47,774
23839637	23839920	91,010	84,900
23943961	23944294	36,867	25,644
24044148	24044344	-68,416	-70,962
24121670	24121860	48330	51453
24192338	24192541	-22338	-19228
28330240	28330505	25,439	21,884
28257603	28257879	-47,198	-50,742
29435297	29435499	319,861	-31,152
29262603	29262789	147,167	-203,862
29526109	29526368	410,673	59,717
29016263	29016467	-99,173	-450,184
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34231541	34231758	-17,857	-21,891
34918147	34918589	-22,321	-25,114
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37116005	37116456	-12,935	-17,784
37232711	37233184	103,771	98,944
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37824490	37824956	77,535	72,937
44710536	44710892	55,677	36,620
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49928543	49928979	-26,450	-140,147
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51890305	51890758	39,442	25,684
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53436482	53436805	-49,725	-56,557
53593304	53593509	107,097	100,147
53938580	53938926	5,157	-17,756
54629121	54629387	65,527	43,427
55811442	55811671	156,596	-26,113
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61143560	61143747	285,374	56,296
60800266	60800425	-57,920	-287,026
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62818684	62818896	-30,711	-35,420
62892243	62892460	42,848	38,144
63585561	63585992	-35,827	-289,078
63876107	63876504	254,719	1,434
63720780	63720959	99,392	-154,111
64441002	64441427	-34,623	-37,857
68362589	68363050	-48,204	-152,697
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70246928	70247317	-17,677	-98,324
70370762	70370929	106,157	25,288
74852031	74852209	36,747	33,524
75038385	75038685	-20,152	-44,401
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75464406	75464680	-29,789	-52,562
75527214	75527586	33,019	10,344
75942526	75942991	35,047	-93,970
76025446	76025619	117,967	-11,342
75863464	75863650	-44,015	-173,311
77174362	77174469	-34,140	-69,640
77293976	77294208	85,474	50,099
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80471349	80471808	-20,179	-210,591
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87457690	87457886	-11,421	-71,774
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88059646	88059898	55,779	-30,978
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92208560	92209028	-31,347	-75,737
92301822	92301976	61,915	17,211
92665583	92665684	-52,711	-55,318
93664936	93665155	77,917	47,844
93521287	93521445	-65,732	-95,866
94013907	94014188	113,503	100,010
93907101	93907324	6,697	-6,854
95781905	95782117	40,955	1,575
95664504	95664706	-76,446	-115,836
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99275129	99275290	54,722	11,899
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99765742	99765988	-9,113	-48,569
23078354	23078568	458,467	-137,134
23155553	23155754	535,666	-59,948
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23231137	23231291	611,250	15,589

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32012936	32013103	67,216	-105,492
31913669	31913869	-32,051	-204,726
32820177	32820560	-49,546	-54,621
32973028	32973177	103,305	97,996
36508001	36508150	-59,589	-136,074
37776157	37776513	115,585	99,553
37660967	37661197	395	-15,763
38369373	38369590	2,925	-17,740
38739331	38739549	35330	72097
39052668	39052839	43,829	34,310
38931987	38932186	-76,852	-86,343
39544355	39544546	131,994	84,008
39752196	39752437	12,294	-96,996
39865926	39866373	126,024	16,940
41622051	41622403	9,102	-147,122
41706981	41707307	94,032	-62,218
41806120	41806270	19762	45826
42718636	42718849	-72,341	-78,800
42800986	42801377	10,009	3,728
47550841	47551198	48,090	-15,617
47657612	47658032	154,861	91,217
48393580	48394030	72,144	48,812
49407764	49408106	118,803	-9,980
49303014	49303192	14,053	-114,894
50146217	50146340	47,478	586
50215465	50215681	26,351	23,417
55019891	55020323	21,766	-347,685
55244562	55244793	246,437	-123,215
55368974	55369156	370,849	1,148
55165601	55165839	167,476	-202,169
54898634	54898816	-99,491	-469,192
56666269	56666486	-9,533	-162,983
56830252	56830385	154,450	916
57249332	57249720	64,720	45,184
57689592	57689840	-28,766	-47,151
58001826	58002255	-82,601	-83,179
58139383	58139534	54,956	54,100
58478125	58478377	51,483	900
58604444	58604688	27,689	-704,106
59297551	59297816	720,796	-10,978
58782555	58782724	205,800	-526,070
58877671	58877885	300,916	-430,909
58977946	58978364	401,191	-330,430
59087521	59087774	510,766	-221,020
59076470	59076626	499,715	-232,168
62073587	62073798	87,299	-51,776
62004907	62005089	18,619	-120,485
61905971	61906120	-80,317	-219,454
62317691	62317867	82,624	75,460
63127006	63127286	131,960	89,200
62942725	62942862	-52,321	-95,224
63239929	63240121	43,159	26,894
64414983	64415400	-51,691	-155,536
64646079	64646530	179,405	75,594

64540767	64540965	74,093	-29,971
65320336	65320572	175,087	45,985
65113637	65113910	-31,612	-160,677
65835777	65836140	213,702	-50,366
65626435	65626525	4,360	-259,981
65669136	65669238	47,061	-217,268
66422171	66422538	41,075	-89,008
66518358	66518512	137,262	6,966
66297190	66297339	-83,906	-214,207
67488489	67488729	-43,688	-46,210
68044119	68044251	-83,478	-133,059
68241434	68241634	113,837	64,324
69940758	69941117	50,810	43,463
69841475	69841628	-48,473	-56,026
70313328	70313733	-50,794	-142,135
71725492	71725884	86,082	13,078
71857694	71858093	94,019	64,181
72387628	72387823	-29,529	-59,311
72477905	72478090	60,748	30,956
72794409	72794608	-4,534	-10,322
72841471	72841726	42,528	36,796
73573462	73573611	26,947	-85,069
73935516	73935815	-84,817	-156,027
74102486	74102604	82,153	10,762
75018571	75018934	-56,038	-97,793
75079805	75080007	5,196	-36,720
77055934	77056165	54,772	31,690
76928739	76929010	-72,423	-95,465
78111951	78112070	71,661	61,372
79182433	79182589	-79,715	-209,568
79231537	79231915	-30,611	-160,242
79452215	79452352	190,067	60,195
83706160	83706564	127,339	-387,026
84166314	84166691	587,493	73,101
83712649	83712876	133,828	-380,714
84046409	84046579	467,588	-47,011
83678213	83678322	99,392	-415,268
83787882	83788129	209,061	-305,461
86956758	86957203	-26,281	-43,481
87096274	87096437	113,235	95,753
88099167	88099366	-29,963	-59,706
88188346	88188631	59,216	29,559
89007946	89008196	-53,660	-151,492
89079156	89079608	17,550	-80,080
89198746	89198873	137,140	39,185
89313939	89314196	101,050	86,505
94659259	94659444	-15,691	-23,604
94715440	94715645	40,490	32,597
96961037	96961440	-49,251	-357,594
97077023	97077172	66,735	-241,862
97409689	97409850	399,401	90,816
97249155	97249292	238,867	-69,742
1715132	1715300	18,910	-45,019
1941711	1941861	-27,208	-29,580
10960331	10960485	92,683	34,144
10988018	10988179	120,370	61,838

11253513	11253680	-2,262	-3,860
11325274	11325545	69,499	68,005
11545405	11545633	-3,952	-43,190
11498224	11498376	-51,133	-90,447
11952949	11953116	13516	16310
11968282	11968434	-1817	992
15946157	15946367	241,664	87,979
15832715	15832958	128,222	-25,430
15767606	15767801	63,113	-90,587
16039379	16039743	88,444	-104,031
160809	161082	-2,066	-2,626
2153935	2154221	8,135	-13,910
21639956	21640295	80,530	68,822
21491146	21491448	-68,280	-80,025
23634635	23635014	36,943	25,825
23684673	23684800	86,981	75,611
23807914	23808291	53,091	-331,067
24101554	24101749	346,731	-37,609
23742470	23742824	-12,353	-396,534
23995989	23996138	241,166	-143,220
24048207	24048621	293,384	-90,737
24143725	24143913	388,902	4,555
27332776	27333207	100,024	49,607
27222751	27222900	-10,001	-60,700
27491142	27491338	111,706	22,563
298680	298785	21,239	-43,680
28489310	28489545	71,126	63,889
28446611	28447003	28,427	21,347
29585304	29585508	3,503	-4,180
29717086	29717245	-14,505	-49,597
2973215	2973608	-37,128	-38,777
3057182	3057379	46,839	44,994
3270186	3270361	38,157	23,733
3174454	3174788	-57,575	-71,840
3463581	3464011	-68,245	-103,279
3548459	3548687	16,633	-18,603
3627974	3628208	-2,873	-25,856
3917284	3917686	200,716	46,963
3813919	3814095	97,351	-56,628
3762270	3762427	45,702	-108,296
30376915	30377064	14,462	12,339
30489388	30489681	97,837	47,674
30890227	30890376	74,798	67,994
31181102	31181270	-2313	70444
31253195	31253600	-74406	-1886
31345326	31345504	71,316	43,685
4473129	4473511	6,703	-26,838
45855925	45856074	109,127	-196,445
45755306	45755468	8,508	-297,051
45995121	45995315	248,323	-57,204
46689476	46689676	-68,847	-149,130
46924887	46925148	166,564	86,342
49384477	49384823	95,926	60,335
49215118	49215388	-73,433	-109,100
52131630	52131781	-48937	-37110
52126699	52126852	-44006	-32181

54106207	54106515	35,618	8,411
54032176	54032462	-38,413	-65,642
54433324	54433573	39,060	8,997
55183484	55183683	2,716	1,182
55222408	55222493	41,640	39,992
55651348	55651538	70,330	-22,403
55584461	55584781	3,443	-89,160
55709932	55710210	128,914	36,269
55911803	55912204	-38,416	-45,398
56024812	56025048	28,632	17,573
56590591	56590793	-26,192	-47,513
56552978	56553146	-63,805	-85,160
64882417	64882654	-75,647	-113,536
65094021	65094170	135,957	97,980
65191351	65191682	47,384	21,219
65689391	65689580	68,840	-2,882
65589309	65589450	-31,242	-103,012
65767425	65767574	21,820	16,268
65853212	65853417	87,841	86,290
66578451	66578711	52,543	50,457
66506488	66506719	-19,420	-21,535
66801026	66801324	124,181	-17,014
66883087	66883253	-19,359	-65,410
34295	34446	-32,723	-41,399
67515184	67515304	186,488	88,359
68100934	68101404	-55,564	-194,650
68218683	68218832	62,185	-77,222
68942004	68942399	51,431	17,167
70593921	70594124	-91,195	-110,188
70745261	70745460	60,145	41,148
71474329	71474502	95,873	-165,273
71600267	71600426	221,811	-39,349
71522743	71522918	144,287	-116,857
71647224	71647436	268,768	7,661
71565950	71566111	187,494	-73,664
71388652	71388936	10,196	-250,839
73875778	73875977	-9,331	-148,911
74082377	74082765	197,268	57,877
73955171	73955392	70,062	-69,496
76695528	76695807	81,536	72,308
78139168	78139367	-46,564	-52,745
78209120	78209232	23,388	17,120
84191615	84191780	-77,166	-88,309
84557968	84558256	67,693	44,543
84425825	84425974	-64,450	-87,739
85168301	85168450	66,642	62,902
85073645	85073835	-28,014	-31,713
86537558	86537707	116,428	77,092
86451405	86451551	30,275	-9,064
87174014	87174176	-58,488	-60,207
88523669	88524048	11,142	-5,665
1416045	1416342	-67,857	-79,450
1487303	1487473	3,401	-8,319
1916267	1916502	6,379	-303,658
2033583	2034001	123,695	-186,159
2139892	2140157	230,004	-80,003

2234574	2234733	324,686	14,573
10385987	10386367	20,795	-7,337
10456232	10456433	91,040	62,729
11939704	11940004	74,844	-47,861
15598218	15598513	-17,828	-30,617
15690829	15691057	74,783	61,927
16108494	16108764	232,511	49,194
16005240	16005438	129,257	-54,132
16355951	16356133	96,338	75,091
16748940	16749186	-34,183	-66,941
17664978	17665246	9,184	-15,804
17974790	17974994	42,782	22,977
17910409	17910576	-21,599	-41,441
18014334	18014766	-13,680	-39,227
18561196	18561412	44,849	44,448
19250890	19251272	29,231	23,827
2601331	2601728	157,645	66,090
2391141	2391510	-52,545	-144,128
2529345	2529750	85,659	-5,888
21176961	21177417	48,380	18,299
23056581	23056867	75,630	56,156
23154137	23154468	46,218	2,786
23225251	23225444	117,332	73,762
23684176	23684376	-34,249	-37,468
23874781	23874996	-305	-14,306
24379049	24379308	-45,614	-152,248
24505188	24505310	80,525	-26,246
24434601	24434751	9,938	-96,805
24566594	24566862	141,931	35,306
25564795	25565234	15,763	-21,597
25678162	25678329	129,130	91,498
26105502	26105934	-28,326	-69,892
26037647	26037843	-96,181	-137,983
29584279	29584562	-22,130	-23,773
29764758	29764899	57,174	55,157
29792535	29792972	81,023	78,607
3373807	3373992	-41,684	-85,462
3492018	3492267	76,527	32,813
3548917	3549166	62,395	37,581
3613299	3613543	48,628	-47,035
3757216	3757422	10,582	-9,287
31148163	31148318	31,174	1,565
31282300	31282469	59,689	50,979
31895852	31896098	84,666	79,801
32534609	32535044	18,569	-305,971
32834762	32835086	318,722	-5,929
32711674	32712041	195,634	-128,974
32956258	32956455	32,194	8,746
33158937	33159143	112,411	81,543
35105436	35105592	7,517	-32,849
35228291	35228766	130,372	90,325
35417890	35418210	-7,324	-9,382
35430632	35431010	-41,957	-72,636
35603899	35604099	101,332	93,600
35550014	35550259	47,447	39,760
35724808	35725225	5,836	-42,195

35779043	35779443	-19,278	-48,252
35892219	35892436	-71,328	-82,814
35943289	35943434	-20,258	-31,816
36715377	36715553	-72,070	-76,628
36795531	36795960	-90,936	-95,234
36963799	36964015	77,332	72,821
37200413	37200655	-22,314	-32,340
37147056	37147228	-75,671	-85,767
37462949	37463196	-44,003	-55,081
37552518	37552777	45,566	34,500
37658510	37658750	53,789	-23,200
37669310	37669548	64,589	-12,402
37607045	37607194	2,324	-74,756
38033506	38033655	-51,455	-53,716
38322089	38322316	83,140	73,013
38951249	38951561	34,389	-5,645
38891056	38891233	-25,804	-65,973
39002730	39002865	85,870	45,659
39300407	39300768	101,392	88,896
39268247	39268501	69,232	56,629
39175619	39175792	-23,396	-36,080
39566265	39566482	56,618	9,942
39480891	39481330	-28,756	-75,210
39725896	39726104	43,330	25,111
39790593	39790867	-14,483	-31,532
4460580	4461030	-20,383	-30,679
4517980	4518234	-42,553	-53,310
4689816	4690139	43,419	41,383
4696976	4697334	13,625	-44,801
4836563	4836811	60,191	57,744
4891427	4891649	101,735	98,582
40292502	40292652	-100,085	-108,518
40429552	40429701	36,965	28,531
40832522	40832863	136,244	82,715
40650583	40650997	-45,695	-99,151
40615954	40616143	-80,324	-134,005
41355644	41355844	138,195	86,871
41163611	41163780	-53,838	-105,193
41224893	41225048	7,444	-43,925
42280260	42280459	83,405	29,378
42211549	42211725	14,694	-39,356
42170071	42170171	-26,784	-80,910
42666508	42666979	-19,699	-78,097
42640875	42641066	-45,332	-104,010
42822486	42822768	136,279	77,692
43217422	43217588	51,813	39,104
43133649	43133803	-31,960	-44,681
43166868	43167022	1,259	-11,462
43434380	43434831	-46,340	-59,010
43688485	43688684	122,681	-173,867
43908084	43908198	342,280	45,647
43604048	43604148	38,244	-258,403
43993483	43993614	-14,385	-17,128
44909381	44909580	-18,273	-37,780
45465137	45465591	42,769	38,004
45714467	45714640	98,011	80,648

45676226	45676554	59,770	42,562
46642809	46643228	56,890	39,125
5217527	5217929	-59,296	-65,266
5398877	5399128	113,921	86,223
5499787	5499937	156,315	71,384
50660637	50660937	-36,733	-94,949
50795628	50795719	98,258	39,833
52385101	52385333	64,832	38,925
52310353	52310633	-9,916	-35,775
53541902	53542131	-83,186	-94,652
53676373	53676538	25828	36757
53748178	53748434	-45977	-35139
55075140	55075342	77,472	34,858
54982977	54983164	-14,691	-57,320
58100137	58100399	41,643	-24,230
58170985	58171216	112,491	46,587
58025847	58026005	-32,647	-98,624
59049850	59050293	141,684	97,358
59224879	59225107	19,580	-25,302
59430647	59431054	82,353	81,124
59731034	59731158	-23,108	-86,565
59967269	59967418	41,069	34,546
6878488	6878922	38,380	22,702
6936589	6936982	18,009	12,658
60490000	60490278	52,705	7,062
60458409	60458625	21,114	-24,591
60990600	60990816	35,457	2,589
60881229	60881381	-73,914	-106,846
61877737	61878096	148,349	-359,228
62261110	62261431	531,722	24,107
62309476	62309723	580,088	72,399
61711640	61711743	-17,748	-525,581
62080968	62081112	351,580	-156,212
61851099	61851367	121,711	-385,957
61919796	61919965	190,408	-317,359
64855856	64856266	-66,577	-194,801
65006332	65006492	83,899	-44,575
68671760	68672214	-995	-7,475
68732511	68732808	59,756	53,119
68655234	68655507	-17,521	-24,182
69882746	69883135	-91,371	-109,393
70021387	70021603	47,270	29,075
7198529	7198678	41,827	25,316
7284908	7285058	1,495	-3,922
7372005	7372151	-20,927	-33,498
7489622	7489957	96,523	84,308
7931173	7931386	48,090	38,209
70073050	70073218	24,208	19,341
70105487	70105785	18,388	5,768
70222075	70222326	20,028	1,614
70702761	70703017	-77,908	-94,092
70786563	70786985	5,894	-10,124
71313458	71313703	84,347	48,209
71694392	71694802	50,383	45,836
71713182	71713612	69,173	64,646
71993688	71993888	101,391	98,352

71942968	71943164	50,671	47,628
72178971	72179170	-41,543	-54,988
73725524	73725934	3,652	-7,377
73676900	73677071	-44,972	-56,240
73941484	73941691	77,030	73,938
73819950	73820073	-44,504	-47,680
74344438	74344538	162,711	54,567
74225834	74225976	44,107	-63,995
74531344	74531515	170,690	98,448
75761616	75761765	38,004	26,232
75677867	75677982	-45,745	-57,551
76576971	76577374	-3,303	-11,154
76681319	76681547	-23,841	-72,920
77007114	77007246	-84,480	-87,176
77477110	77477286	58,224	54,759
77846169	77846317	-19,866	-22,452
77876155	77876304	3,966	-8,626
78124664	78124790	53,781	-28,953
78031404	78031553	-39,479	-122,190
8828321	8828649	105,368	72,090
8699019	8699354	-23,934	-57,205
8752505	8752653	29,552	-3,906
11711693	11712033	32,430	-159,889
11658519	11658718	-20,744	-213,204
11744816	11745091	65,553	-126,831
11958362	11958526	279,099	86,604
11836214	11836512	156,951	-35,410
12887634	12888027	112,154	13,693
12727818	12728101	-47,662	-146,233
13777416	13777790	60,736	23,236
13839885	13839973	123,205	85,419
13884019	13884238	68,476	67,377
16805085	16805339	17,552	-139,530
16977216	16977636	189,683	32,767
18058126	18058326	54,712	22,101
19723502	19723775	199,942	-65,253
19578820	19579205	55,260	-209,823
19877984	19878126	354,424	89,098
20381987	20382104	87,396	68,185
20351017	20351251	56,426	37,332
280401	280685	75,879	22,636
23965447	23965692	180,514	-45,497
24000036	24000201	215,103	-10,988
24107196	24107651	322,263	96,462
23872009	23872476	87,076	-138,713
23793800	23794039	8,867	-217,150
3497155	3497572	95,083	49,163
3479862	3480208	77,790	31,799
3364217	3364349	-37,855	-84,060
312106	312275	2,750	-178,410
487260	487643	177,904	-3,042
37770662	37770882	-18,535	-144,564
37988134	37988309	198,937	72,863
37866368	37866652	77,171	-48,794
41524565	41524743	-33,590	-60,554
41585396	41585871	27,241	574

41676289	41676494	16,746	-1,551
44716381	44716621	16,160	-14,458
44753251	44753718	53,030	22,639
46532715	46532914	192,233	20,720
46428295	46428518	87,813	-83,676
46315429	46315724	-25,053	-196,470
51332534	51332775	286,567	-74,083
51404172	51404547	358,205	-2,311
51024679	51025142	-21,288	-381,716
51180270	51180704	134,303	-226,154
54396910	54397059	-92,688	-171,291
54506404	54506563	16,806	-61,787
55129037	55129236	43,786	37,631
55037573	55037818	-47,678	-53,787
55214674	55214878	66,586	37,415
56155298	56155498	-34,266	-35,064
56230893	56231162	41,329	40,600
58047669	58047838	-95,831	-158,034
58202155	58202421	58,655	-3,451
58946489	58946749	4,930	-190,844
59205218	59205463	263,659	67,870
59099824	59100129	158,265	-37,464
59688675	59688958	-17,247	-33,142
59837986	59838224	70,412	59,131
7127958	7128430	196,073	20,617
6997737	6998212	65,852	-109,601
6899223	6899685	-32,662	-208,128
581817	582320	-65,802	-81,172
65690141	65690343	8,969	-84,797
65752472	65752567	71,300	-22,573
65859492	65859736	178,320	84,596
66132759	66133155	25,516	-12,174
66169136	66169490	61,893	24,161
7778992	7779434	221,175	-617,420
8464921	8465102	907,104	68,248
7984004	7984360	426,187	-412,494
8013729	8013894	455,912	-382,960
8334247	8334531	776,430	-62,323
7666605	7666793	108,788	-730,061
7865967	7866267	308,150	-530,587
8115829	8116086	558,012	-280,768
7462347	7462548	-95,470	-934,306
776450	776582	64,858	-25,965
835049	835319	123,457	32,772
72997931	72998145	178,154	24,383
72908932	72909136	89,155	-64,626
75237085	75237284	-19,675	-153,027
75349212	75349491	92,452	-40,820
9433959	9434326	-31,048	-93,780
949793	949945	-68,381	-87,682
1593054	1593369	32,761	-9,959
1644992	1645289	84,699	41,961
1499518	1499954	-60,775	-103,374
10152253	10152466	69,056	65,401
10059407	10059556	-23,790	-27,509
10350483	10350898	91,833	90,700

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10556822	10557079	99,026	81,836
10765925	10766099	92,819	-37,480
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11032661	11032951	100,055	-1,002
11063825	11063974	2,693	-41,516
11356276	11356548	60,183	45,227
11372470	11372718	23,587	16,699
11525302	11525497	47,558	24,525
12802814	12802908	39,528	37,779
12933953	12934229	23,530	17,926
12971199	12971526	53,545	46,071
14051727	14052020	118,375	73,923
13906216	13906471	-27,136	-71,626
14154954	14155153	91,454	65,594
14353051	14353242	-162	-27,293
14494401	14494643	50,123	47,469
14563688	14563793	-7,230	-83,017
14748665	14748915	44,460	-1,438
14968243	14968433	-55,772	-59,467
15021462	15021719	-2,553	-6,181
15194816	15195102	63,372	22,310
15543228	15543409	102,765	92,097
15589231	15589400	1,810	-12,045
15714939	15715309	102,232	80,675
15891264	15891465	41,430	21,580
15953695	15953983	69,514	47,657
16193930	16194348	88,092	63,967
16037651	16037932	-68,187	-92,449
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16222045	16222265	-74,603	-77,080
16531141	16531564	41,436	17,316
17258423	17258592	54,729	41,441
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17326770	17327165	-47,985	-50,292
17390091	17390415	15,336	12,958
17864321	17864558	97,663	79,173
17673806	17674044	-92,852	-111,341
17899279	17899516	110,957	79,716
18057973	18058108	26,602	-594
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18334781	18334960	-23,187	-26,027
18596135	18596500	92,567	81,117
18907905	18908245	16,411	7,809
19244455	19244606	80,447	70,928
2359629	2360065	-67,506	-69,192
2518233	2518400	91,098	89,143
3520176	3520412	-25,328	-37,246
3815090	3815483	-111,964	-120,978
4056047	4056223	97,299	65,840
34949852	34949994	-44,889	-57,065
35108867	35109072	114,126	102,013
37753523	37753848	-10,421	-16,323
38551264	38551463	68,488	66,303
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38490143	38490435	7,367	5,275
4114285	4114447	72,966	39,321
4203947	4204292	23,452	15,767
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4566051	4566324	-42,506	-55,091
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4715221	4715370	-51,723	-67,346
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43685112	43685348	-85,009	-115,123
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44409308	44409582	-16,725	-18,027
44501732	44501959	50,735	49,387
44640675	44640827	51,382	48,942
44744928	44745192	-40,076	-44,762
44908211	44908484	21,425	16,556
45006026	45006179	92,291	85,671
563308	563498	115,818	107,156
415846	415954	-31,644	-40,388
45455194	45455466	65,703	42,152
45343168	45343343	-46,323	-69,971
45301489	45301656	-88,002	-111,658
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46181119	46181300	139,833	-44,708
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46844822	46845254	-59,555	-80,432
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47031766	47032110	39,385	24,679
47035576	47035771	43,195	28,340
47498973	47499133	104,381	83,018
47378082	47378339	-16,510	-37,776
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47723378	47723598	20,080	-881
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47863332	47863642	87,097	72,752
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48075856	48076050	12,658	339
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48821392	48821629	82,360	49,631
48739218	48739421	186	-32,577

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49007465	49007833	95,387	91,820
48973247	48973399	61,169	57,386
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5235146	5235587	77,767	-1,812
5197861	5198012	40,482	-39,387
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5753600	5753858	-40,302	-48,624
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50627258	50627479	80,572	61,810
50685568	50685742	80,856	66,725
50867727	50868112	82,862	70,818
51149907	51150106	90,549	81,211
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54550003	54550147	19,763	14,472
54706541	54706771	1763	14631
54681901	54682127	26403	39275
54855017	54855117	104,237	79,491
55136560	55136746	51,837	12,148
55639157	55639562	67,642	61,511
55635317	55635535	63,802	57,484
56256138	56256518	-63,839	-68,861
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56557148	56557371	-47,939	-55,498
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56824270	56824469	17,274	-7,227
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56936254	56936533	-19,741	-29,058
58539617	58539988	54,951	53,301
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59183053	59183531	105,774	80,818
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59337936	59338050	48,191	40,244
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59507806	59508124	16,140	12,047
59609115	59609561	52,068	41,028
59639965	59640165	21,548	283
59816713	59817046	78,118	68,184
60001566	60001704	89,775	85,203
6280318	6280497	44,507	-63,687
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6483239	6483667	1,202	-3,266
6581806	6582257	44,956	40,094
6727274	6727663	98,396	56,003
6728177	6728469	99,299	56,809
6806715	6806976	82,993	-1,395
6847573	6847856	8,996	-43,608
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60180648	60180748	103,287	85,693
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60443648	60443764	59,220	31,110
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60832939	60833146	-78,671	-108,434
61134017	61134166	34,894	-1,323
63727333	63727711	-27,412	-30,587
7051801	7052153	-15,248	-192,892
7175922	7176033	108,873	-69,012
7325847	7326057	258,798	81,012
7703903	7704314	44,241	31,282
7575875	7576090	-83,787	-96,942
7777648	7777826	43,567	37,335
7862364	7862479	-12,364	-22,884
814977	815110	38,880	32,093
8043740	8043981	19,806	10,434
8579977	8580270	88,288	31,940
857763	858141	47,098	43,517
9823019	9823311	16,020	1,953
9919343	9919575	-11,894	-62,572
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101786053	101786292	105,133	-91,292
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108316120	108316326	-44,733	-54,376
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112425429	112425722	52,767	-77,694
113252155	113252325	4,192	-7,117
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113368629	113368782	18388	24148
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119641557	119641741	11,268	8,800
119705324	119705531	75,035	72,590
119934392	119934620	28,442	23,134
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130827865	130827965	-2,223	-20,649
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136303743	136304012	-9,923	-46,469
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136727093	136727249	21,454	17,799
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138527183	138527354	88,905	36,950
138395897	138396179	-42,381	-94,225
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16063652	16063939	65,518	59,359
15947097	15947246	-51,037	-57,334

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156968251	156968423	79,057	70,949
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160815133	160815302	150,695	50,293
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170257037	170257509	107,941	55,009
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172455198	172455581	-32,006	-101,265
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174636743	174637092	155,239	98,416
175027967	175028235	106,843	59,546
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176667247	176667426	-22,491	-25,490
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191590367	191590753	48,246	3,572
191754776	191755181	152,225	30,642
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20230058	20230279	-33,981	-58,396
201376547	201376682	-67,377	-85,562

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201918390	201918559	111,994	64,038
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204319505	204319838	40,062	9,037
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204502851	204503305	62,097	56,377
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207724573	207724826	71,250	-14,033
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219688036	219688304	59,863	54,871
219612951	219613155	-15,222	-20,278
219573217	219573489	-54,956	-59,944
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227518054	227518321	-60,114	-219,198
227913019	227913180	175,494	25,429
228215209	228215360	169,923	84,812
228489886	228490260	103,072	99,766
228326339	228326699	-60,475	-63,795
230880789	230881058	138,893	88,126
230683311	230683483	-58,585	-109,449
230779461	230779629	37,565	-13,303
231755697	231755981	74,498	57,913
231619056	231619433	-62,143	-78,635
233552171	233552434	-81,262	-228,854
233659011	233659174	25,578	-122,114
234373969	234374118	182,939	27,423
234103483	234103910	-87,547	-242,785

234200801	234201279	9,771	-145,416
234264123	234264352	73,093	-82,343
237237672	237237861	94,490	82,131
237130467	237130772	-12,715	-24,958
237833843	237833992	-63,558	-153,567
237970209	237970467	72,808	-17,092
238925101	238925372	31,280	-47,164
238914010	238914471	20,189	-58,065
238882796	238883068	-11,025	-89,468
239090060	239090330	89,695	64,700
238976211	238976375	-24,154	-49,255
239635109	239635283	-210	-352,297
239758861	239759001	123,542	-228,579
240006107	240006256	370,788	18,676
239792233	239792387	156,914	-195,193
24184569	24184994	58,494	44,939
24088439	24088593	-37,636	-51,462
241248039	241248393	99,895	96,289
241121772	241121874	-26,372	-30,230
242004021	242004266	100,625	62,151
241784903	241785040	-118,493	-157,075
242146093	242146193	-772	-16,033
242515176	242515277	74,465	65,546
25229075	25229259	-8,151	-15,804
25271916	25272190	34,690	27,127
27359989	27360211	-23,780	-24,423
29283052	29283387	13,908	-714,549
29769672	29770144	500,528	-227,792
29445625	29445814	176,481	-552,122
29674360	29674791	405,216	-323,145
29971108	29971271	701,964	-26,665
30023269	30023475	754,125	25,539
31540002	31540341	129,311	49,224
31503570	31503810	92,879	12,693
31460330	31460583	49,639	-30,534
31354662	31354853	-56,029	-136,264
32296968	32297365	-6,054	-47,062
32411629	32412052	108,607	67,625
32707262	32707535	272,028	10,065
32673028	32673350	237,794	-24,120
33546531	33546691	520,635	68,611
33072497	33072647	46,601	-405,433
33182059	33182228	156,163	-295,852
33444125	33444284	418,229	-33,796
33280505	33280757	254,609	-197,323
33139067	33139288	113,171	-338,792
33360568	33360737	334,672	-117,343
33008934	33009129	-16,962	-468,951
33230300	33230581	204,404	-247,499
33643406	33643706	128,486	544
37275397	37275725	-55,752	-122,816
37379955	37380285	48,806	-18,256
37476967	37477095	145,818	78,554
38122920	38123241	-25,234	-33,555
38200775	38201036	52,621	44,240
39025472	39025631	147,097	69,106

38949294	38949683	70,919	-6,842
38797912	38798042	-80,463	-158,483
39265227	39265473	198,758	64,406
39186598	39186955	120,129	-14,112
39414513	39414683	84,602	-103,263
39475878	39476172	145,967	-41,774
39539072	39539253	209,161	21,307
43927500	43927723	209,584	79,093
46015353	46015816	282,806	-252,817
46231850	46231999	499,303	-36,634
46119173	46119410	386,626	-149,223
45897619	45897801	165,072	-370,832
45677512	45677730	-55,035	-590,903
46599373	46599542	-62,207	-98,166
46757023	46757216	95,443	59,508
46852045	46852194	72,450	8,763
48306665	48307044	-88,709	-152,894
48434165	48434286	38,791	-25,652
48747046	48747468	-20,425	-88,853
49110881	49110981	67,725	-124,153
48962781	48962881	-80,375	-272,253
49144683	49144836	101,527	-90,298
49234049	49234150	190,893	-984
58071245	58071703	-55,979	-168,807
58162400	58162586	35,176	-77,924
6994376	6994656	59,129	38,835
6963679	6963891	28,432	8,070
6894594	6894784	-40,653	-61,037
61024210	61024456	61,956	20,774
64100707	64100861	-72,792	-124,201
64179780	64180013	6,281	-45,049
68419257	68419661	215,685	77,795
68188178	68188626	-15,394	-153,240
68334128	68334399	130,556	-7,467
70005546	70006003	9,839	-17,578
70029761	70029990	34,054	6,409
69973877	69974356	-21,830	-49,225
70592440	70592767	64,516	-41,671
70649299	70649563	121,375	15,125
70555511	70555694	27,587	-78,744
70946526	70946787	35,671	30,326
72233266	72233397	23,391	4,926
73832042	73832250	-10,795	-28,506
74650343	74650585	51,577	43,759
74556566	74556774	-42,200	-50,052
74734382	74734584	99,587	96,403
85695372	85695693	-42,579	-53,130
85766676	85767120	28,725	18,297
86014326	86014777	94,544	45,129
85930443	85930702	10,661	-38,946
86481806	86482255	-40,148	-91,095
86607160	86607620	85,206	34,270
86662286	86662672	140,332	89,322
86841440	86841786	-23,799	-29,852
86908869	86909126	12,898	-33,423
89172886	89173170	52,050	51,860

89092632	89092736	-28,204	-28,574
9545244	9545477	81,980	64,350
9770787	9771039	129,235	82,410
96131524	96131764	-41,114	-43,142
96391129	96391330	25,918	-13,671
97648370	97648747	-48,091	-74,008
97665848	97666066	-30,613	-56,689
99248226	99248576	23,085	10,574
99198421	99198671	-26,720	-39,331
1075701	1075850	33,762	-21,172
1042062	1042169	123	-54,853
1278444	1278902	-19,178	-42,904
1414174	1414553	14,788	-5,680
1627603	1628002	136,035	79,347
1453576	1453824	-37,992	-94,831
1852526	1852809	29,713	-15,734
1915834	1915981	93,021	47,438
10468619	10469073	-97,715	-133,563
10647962	10648232	81,628	45,596
86338	86655	-30,189	-31,609
146257	146482	-9,642	-12,045
2243002	2243484	18,355	-26,241
2246502	2246660	21,855	-23,065
2885175	2885486	115,809	-81,834
2975709	2976093	206,343	8,773
2739652	2739854	-29,714	-227,466
22500092	22500389	-9,551	-13,713
22926217	22926435	-48,053	-51,866
23011100	23011259	36,830	32,958
23072431	23072641	64,436	57,664
23632827	23633072	-43,363	-46,502
23710443	23710602	34,253	31,028
29276254	29276633	-32,874	-34,463
29531589	29531787	64,877	51,143
29675979	29676128	110,087	55,097
29817890	29818039	101,974	43,673
29963244	29963452	64,142	41,241
30041477	30041705	45,058	38,149
3538319	3538503	-77,298	-97,272
3665638	3665883	50,021	30,108
3624718	3624988	9,101	-10,787
3807269	3807548	82,883	72,786
30177456	30177729	73,741	24,409
30144920	30145081	41,205	-8,239
31765768	31766217	224,179	64,714
31516174	31516542	-25,415	-184,961
31580139	31580333	38,550	-121,170
31929789	31929994	67,009	24,163
32523119	32523324	108,417	-39,535
32619207	32619328	204,505	56,469
33236471	33236781	24,340	7,953
33292497	33292779	80,366	63,951
33238509	33238874	26,378	10,046
33372401	33372550	94,306	44,332
34915492	34915592	-38,269	-97,998
35492476	35492649	85,974	25,410

35427085	35427236	20,583	-40,003
36321601	36321804	-44,390	-77,517
36454505	36454815	46,206	15,748
36969201	36969461	101,439	-15,620
36782486	36782761	-85,276	-202,320
37158641	37158802	134,232	57,024
39219224	39219373	19,933	-18,402
4597602	4597960	-17,394	-32,276
4706071	4706483	91,075	76,247
41150140	41150578	1,015,334	-101,446
41165683	41165948	1,030,877	-86,076
40231755	40231923	96,949	-1,020,101
40388945	40389228	254,139	-862,796
40508545	40508736	373,739	-743,288
40639843	40640123	505,037	-611,901
40768118	40768461	633,312	-483,563
41295115	41295398	1,160,309	43,374
40079904	40080130	-54,902	-1,171,894
40263871	40264054	129,065	-987,970
40903636	40903786	768,830	-348,238
40582810	40583087	448,004	-668,937
41384612	41384811	91,811	91,296
42343696	42343949	-74,159	-149,495
42469679	42469878	51,824	-23,566
42714600	42714852	33,023	1,055
42610838	42610995	-70,739	-102,802
42973139	42973586	-55,390	-168,428
43082466	43082583	53,937	-59,431
43128045	43128526	99,516	-13,488
43201734	43201901	16,254	15,381
43287293	43287673	18,241	15,846
43501370	43501723	114,028	91,245
43413351	43413737	26,009	3,259
43838223	43838449	-65,545	-80,993
43946095	43946254	-6,095	-14,612
44070803	44070923	-151	-7,684
44086162	44086318	15,208	7,711
44089440	44089828	-90,873	-276,429
44260258	44260495	79,945	-105,762
44373780	44373923	193,467	7,666
47462308	47462501	-91,510	-155,613
47597297	47597699	43,479	-20,415
47642731	47642937	88,913	24,823
47912603	47913082	49,946	-29,097
47824925	47825188	-37,732	-116,991
48163425	48163888	32,357	-39,790
48255969	48256203	124,901	52,525
48556244	48556641	-4,050	-78,065
48511333	48511761	-48,961	-122,945
48680433	48680690	120,139	45,984
49658775	49659075	217,692	66,410
49426684	49427092	-14,399	-165,573
49541678	49541893	100,595	-50,772
54255131	54255383	-2,064	-2,895
54317486	54317726	60,291	59,448
54701984	54702428	64,219	54,682

55241252	55241401	64,041	-33,690
55185102	55185276	7,891	-89,815
55141904	55142124	-35,307	-132,967
55406692	55406914	47,157	19,296
56963064	56963445	-27,533	-52,252
57058409	57058747	67,812	43,050
57241425	57241563	-67,452	-92,879
57408573	57408815	99,696	74,373
6625316	6625613	-70,995	-83,314
6739349	6739609	43,038	30,682
60168671	60168920	-54,750	-59,798
60337796	60337928	20,286	-37,835
60558269	60558438	86,321	74,017
60892936	60893230	-86,599	-146,513
61313485	61313944	-24,195	-28,355
61564795	61564907	-25,015	-36,042
61832661	61832866	73,054	32,371
61716515	61716673	-43,092	-83,822
62262741	62262890	80,809	47,843
10043338	10043640	625	-77,158
9989532	9989791	-53,181	-131,007
17849118	17849521	-38,724	-57,615
17983081	17983527	95,239	76,391
25851098	25851338	-82,362	-157,768
26038537	26038759	105,077	29,653
29900811	29901057	69,686	-333,096
30005976	30006392	174,851	-227,761
30182244	30182610	351,119	-51,543
30061909	30062119	230,784	-172,034
30272600	30272811	441,475	38,658
29948759	29948908	117,634	-285,245
31916276	31916427	37530	46688
32011915	32012170	-58109	-49055
33376373	33376722	56,350	53,348
33613191	33613533	89,115	53,694
33545939	33546338	21,863	-13,501
33661983	33662397	42,904	8,359
33741795	33742055	44,723	10,357
35265334	35265781	183,366	-77,730
35146018	35146410	64,050	-197,101
35005633	35005935	-76,335	-337,576
35189018	35189185	107,050	-154,326
35370855	35371031	288,887	27,520
35068535	35068771	-13,433	-274,740
36748728	36748907	69,169	37,912
36580779	36580938	-98,780	-130,057
37789223	37789394	127,494	-19,953
37615962	37616430	-45,767	-192,917
37752385	37752576	90,656	-56,771
39018313	39018754	342,642	63,266
38931371	38931761	255,700	-23,727
38648399	38648600	-27,272	-306,888
38811931	38812147	136,260	-143,341
40027996	40028375	-11,208	-67,518
40143204	40143396	104,000	47,503
40450061	40450313	143,848	-690,596

40555208	40555687	248,995	-585,222
40663023	40663237	356,810	-477,672
40267494	40267744	-38,719	-873,165
40746724	40746965	440,511	-393,944
40826561	40826826	520,348	-314,083
40378111	40378422	71,898	-762,487
40941939	40942140	635,726	-198,769
41137140	41137282	830,927	-3,627
41050684	41050855	744,471	-90,054
41649699	41650054	-6,121	-52,685
41606447	41606596	-49,373	-96,143
41812064	41812435	92,040	59,427
42536581	42536760	-63,170	-72,015
43880390	43880659	-83,016	-125,949
43996255	43996486	32,849	-10,122
44086865	44087171	123,459	80,563
44402316	44402488	-64,997	-82,774
44543483	44543743	13,292	1,213
45169636	45169867	39,340	-3,314
45691473	45691724	46441	95055
46224207	46224587	-1,884	-24,804
46145961	46146257	-80,130	-103,134
46361189	46361360	18,719	-15,830
46862014	46862352	-17,493	-46,939
15927772	15928021	-18,077	-43,384
16492436	16492647	-9,049	-100,736
16729284	16729487	137,824	97,675
16662641	16662798	71,181	30,986
17257781	17257992	116,609	98,518
17470252	17470477	66,454	-19,485
17430236	17430344	26,438	-59,618
18028865	18029187	-62,201	-63,110
18112524	18112689	21,458	20,392
19103184	19103404	-5,691	-18,742
19670598	19670976	68,884	32,942
19572504	19572679	-29,210	-65,355
19740853	19741038	41,404	27,919
20349158	20349359	22,616	20,771
20499076	20499254	55,130	-52,716
20890510	20890709	-38,690	-39,217
21261707	21261856	41,584	30,088
21878997	21879366	26,445	-110,858
21802539	21802905	-50,013	-187,319
22264873	22265321	19,561	12,826
22190160	22190641	-55,152	-61,854
22562953	22563211	193,306	-4,206
22377136	22377493	7,489	-189,924
22686745	22686893	-19,396	-27,378
22930381	22930811	192,616	26,215
22818525	22818750	80,760	-85,846
23222216	23222470	68,679	54,145
23337671	23338080	27,953	-16,892
26381581	26381950	-92,684	-145,536
26498810	26498919	24,545	-28,567
27519538	27519979	-1,010	-6,581
28956158	28956473	-10,283	-16,275

29029236	29029413	62,795	56,665
29341951	29342126	8,790	-10,921
29456612	29456883	68,573	63,011
30031450	30031827	-94,089	-128,611
30176682	30177150	51,143	16,712
31450148	31450450	-76,654	-138,578
31539392	31539625	12,590	-49,403
34058547	34058702	-48,510	-61,492
34415920	34416143	41,550	21,741
34302410	34302609	-71,960	-91,793
35080895	35081028	73,623	-32,930
35424938	35425370	134,888	-3,479
35557645	35557887	-29,331	-46,118
35593050	35593232	6,074	-10,773
35820296	35820671	-31,528	-55,237
35851391	35851592	-54,761	-62,684
35895899	35896251	-10,253	-18,025
36007306	36007695	56,068	37,444
36238295	36238522	21,949	-6,671
36120693	36121162	-95,653	-124,031
36906045	36906244	68,597	-1,519
36871605	36871832	34,157	-35,931
37247357	37247577	37,968	15,315
37183761	37184191	-25,628	-48,071
37486599	37486745	25,918	4,817
37389271	37389447	-71,410	-92,481
37919400	37919746	-29,910	-51,260
38219510	38219805	93,818	56,727
38284898	38285044	38,383	36,407
38712192	38712382	85,160	14,178
38646869	38646966	19,837	-51,238
39919883	39920230	102,147	14,206
40704695	40704916	40,008	31,822
40619325	40619533	-45,362	-53,561
40815249	40815400	-37,196	-41,427
40981112	40981560	95,149	40,171
41105397	41105499	-3,520	-52,841
41177565	41177665	68,648	19,325
41383433	41383663	73,762	42,757
41434402	41434575	16,331	-12,245
41870833	41870965	34,132	15,303
41922461	41922636	85,760	66,974
45051566	45051682	126,403	33,365
45299040	45299191	-95,923	-155,161
45413605	45413804	18,642	-40,548
45509532	45509786	50,561	-3,030
49234813	49235130	-76,234	-80,191
49460533	49460726	74,536	63,883
49460474	49460728	538	-57,779
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102968116	102968245	-61,431	-94,311
103063330	103063443	33,783	887
106551569	106552022	-16,834	-226,412
106647987	106648346	79,584	-130,088
106807881	106808123	239,478	29,689
106851878	106852192	-7,921	-218,385

107048902	107049121	189,103	-21,456
106952798	106952981	92,999	-117,596
109209127	109209520	-35,504	-83,105
109250569	109250846	5,938	-41,779
109333834	109334104	89,203	41,479
11197378	11197837	-72,022	-81,578
11254679	11254947	-14,721	-24,468
110035267	110035399	10,946	-21,143
112338828	112339040	65,273	-56,023
112445269	112445591	171,714	50,528
112868680	112868834	125,134	14,928
112655521	112655677	-88,025	-198,229
112748266	112748509	4,720	-105,397
113554037	113554143	31,094	-10,206
113449323	113449472	-73,620	-114,877
113692065	113692250	24,602	-8,816
114081491	114081928	64,245	34,441
114005884	114006128	-11,362	-41,359
114223163	114223318	100,417	46,668
12123407	12123628	-46,161	-52,223
12101709	12102085	-67,859	-73,766
12204119	12204322	34,551	28,471
12378958	12379239	74,599	-71,604
12498126	12498519	193,767	47,676
12279897	12280164	-24,462	-170,679
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131274401	131274623	98,148	95,153
131843700	131843869	-36,768	-104,471

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136438745	136438953	441,795	-23,046
136252285	136252508	255,335	-209,491
136188036	136188314	191,086	-273,685
135992348	135992576	-4,602	-469,423
138243465	138243644	84,068	31,034
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139948493	139948794	91,572	-12,081
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14249625	14250066	87,977	54,923
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140135455	140135609	-10,301	-12,882
140178488	140178621	32,732	30,130
142922442	142922615	-17,299	-25,318
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152716121	152716270	78,954	57,083
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155589179	155589445	113,027	64,474
156407786	156408228	127,633	24,042
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16961643	16961799	12,057	-145,290
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171020671	171020869	55,579	55,327
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173724754	173724981	18,596	1,018
173812150	173812389	105,992	88,426
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188317899	188318222	186,689	39,187
188312881	188313124	181,671	34,089
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188634626	188634924	65,764	62,858
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188900192	188900343	30,804	29,448
191144735	191145104	312,825	47,345
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191898171	191898346	183,586	39,809
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193828174	193828524	485,761	-99,542
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193799704	193799798	457,291	-128,268
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198252634	198252993	38,081	11,950
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77124888	77125098	-16,635	-22,567
77388926	77389112	90,008	35,053

77309459	77309619	10,541	-44,440
78790555	78790655	138,624	38,645
78824160	78824260	172,229	72,250
78753926	78754076	101,995	2,066
81440222	81440617	33,456	9,422
81336012	81336161	-70,754	-95,034
82154182	82154482	-16,961	-39,267
82071273	82071442	-99,870	-122,307
84465266	84465396	32,627	-9,934
87122526	87122759	-34,130	-470,548
87451125	87451294	294,469	-142,013
87163936	87164088	7,280	-429,219
87243136	87243335	86,480	-349,972
87496152	87496301	339,496	-97,006
88030621	88030782	295,712	75,456
87892055	87892269	157,146	-63,057
87820478	87820651	85,569	-134,675
89068189	89068667	-47,637	-54,925
89200552	89200710	84,726	77,118
89342337	89342585	111,897	43,550
89433693	89433842	-85,222	-149,430
89465513	89465701	-53,402	-117,571
89534671	89535042	15,756	-48,230
9112896	9113268	57,538	51,930
95515379	95515479	76,649	32,429
96009126	96009407	110,975	-285,692
96260569	96261012	362,418	-34,087
96125625	96125794	227,474	-169,305
95901519	95901686	3,368	-393,413
95847326	95847547	-50,825	-447,552
144123911	144124141	N/A	N/A
66283133	66283274	N/A	N/A
1395107	1395278	88,825	47,116
1418748	1418999	112,466	70,837
10786178	10786565	53,835	-27,779
10746187	10746304	13,844	-68,040
110508891	110509177	75,214	67,554
110380391	110380561	-53,286	-61,062
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110771375	110771838	183,407	-86,645
110629720	110629906	41,752	-228,577
110716110	110716457	128,142	-142,026
112183702	112183861	82,219	-25,974
112056138	112056374	-45,345	-153,461
114990414	114990773	48,167	1,163
114846596	114846964	-95,651	-142,646
115156987	115157287	-11,342	-23,017
122431585	122431784	44,608	31,460
122319834	122320020	-67,143	-80,304
131338683	131338839	-85,438	-87,957
131703037	131703208	45,002	-4,590
131622621	131622837	-35,414	-84,961
131642903	131643015	-15,132	-64,783
131779645	131780068	46,302	20,863
131862517	131862730	17,317	8,341
132039199	132039604	118,670	31,953

132206059	132206177	-29,854	-32,460
132276372	132276496	40,459	37,859
132568945	132569078	153,384	100,470
134220212	134220476	97,852	25,766
134044966	134045251	-77,394	-149,459
134896997	134897277	-37,277	-45,591
135256253	135256409	419	-3,006
135181575	135181956	-74,259	-77,459
135329409	135329651	73,575	70,236
137446099	137446559	-57,259	-95,698
137537642	137537892	34,284	-4,365
137606326	137606517	102,968	64,260
137753326	137753424	-75,754	-79,479
137874849	137875060	45,769	42,157
139126532	139126966	-80,912	-276,097
139403699	139403933	196,255	870
139224463	139224732	17,019	-178,331
139611679	139611963	-80,933	-94,396
139764668	139764823	72,056	58,464
139949412	139949666	-42,089	-43,773
140007688	140007888	2,546	464
140353100	140353373	-141,884	-144,515
140597349	140597601	56,185	51,621
141014799	141015032	34,172	18,436
141984877	141985233	32,950	-60,901
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142616498	142616665	-21,191	-178,605
142728153	142728455	90,464	-66,815
143103771	143103930	-68,148	-76,547
143191724	143191923	19,805	11,446
148635071	148635474	-98,952	-103,557
148766227	148766376	32,204	27,345
148918316	148918621	63,278	7,421
149351180	149351524	-61,871	-121,604
149436051	149436308	23,000	-36,820
149591133	149591407	117,538	75,792
149558530	149558702	84,935	43,087
149781333	149781782	19,940	9,097
150164772	150164958	-43,107	-95,530
150332712	150332911	-47,400	-55,836
156456397	156456677	10,976	-12,039
156615269	156615669	74,837	982
156652504	156652969	112,072	38,282
158477374	158477733	419,368	18,386
158338144	158338484	280,138	-120,863
158511682	158511889	453,676	52,542
158229060	158229320	171,054	-230,027
158315566	158315783	257,560	-143,564
158135261	158135438	77,255	-323,909
158600565	158600870	-73,804	-89,189
158683574	158683778	9,205	-6,281
158599281	158599499	-75,088	-90,560
159663198	159663369	-44,141	-66,838
159818253	159818409	110,914	88,202
162766478	162766599	-30,677	-38,001
162917627	162918055	97,386	66,530

169018539	169018879	21,668	-424,080
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169282985	169283149	286,114	-159,810
168965098	168965291	-31,773	-477,668
169170475	169170654	173,604	-272,305
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169139843	169140023	142,972	-302,936
169540021	169540310	74,526	71,005
169581504	169581924	-26,162	-75,476
169726873	169727127	119,207	69,727
172124463	172124666	-3,244	-6,143
172599952	172600152	95,822	76,163
172491159	172491458	-12,971	-32,531
172525566	172525712	21,436	1,723
175084968	175085300	67,331	39,453
174951020	174951287	-66,617	-94,560
176398313	176398781	-48,180	-58,952
176945493	176945863	74,309	69,290
176850177	176850409	-21,007	-26,164
179112656	179112905	54,120	21,657
179718756	179718997	123,368	78,779
179933101	179933472	-12,711	-75,700
180029755	180030095	83,943	20,923
179920845	179921099	-24,967	-88,073
180485942	180486278	27,559	25,794
180522400	180522620	64,017	62,136
479256	479633	154,517	-8,592
570961	571185	246,222	82,960
355164	355260	30,425	-132,965
34111560	34111932	89,520	-48,464
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34200645	34200758	178,605	40,362
35117563	35117808	32,942	-148,526
35189548	35189656	104,927	-76,678
35286579	35286824	201,958	20,490
34987917	34988196	-96,704	-278,138
35954991	35955133	62,243	39,671
36008337	36008544	115,589	93,082
36103624	36103791	-84,322	-116,113
36189035	36189184	1,089	-30,720
36319363	36319496	131,417	99,592
38729405	38729644	218,583	98,391
38603334	38603723	92,512	-27,530
38477427	38477589	-33,395	-153,664
39331462	39331679	190,348	76,247
39283567	39283799	142,453	28,367
39160686	39160938	19,572	-94,494
39472776	39473114	152,715	72,702
40635439	40635613	-80,350	-93,981
40821647	40821800	105,858	92,206
40957586	40958030	80,543	62,005
41069616	41069726	124,260	50,928
41166889	41167162	-11,204	-130,135
41381487	41381646	203,394	84,349
42817338	42817533	357,555	59,797

42459948	42460130	165	-297,606
42686198	42686487	226,415	-71,249
42603582	42603731	143,799	-154,005
43270004	43270157	40,089	-178,093
43313584	43313733	83,669	-134,517
43404843	43405143	174,928	-43,107
44476023	44476493	135,169	51,952
44294841	44295066	-46,013	-129,475
52286904	52287082	167,373	1,840
52321314	52321460	201,783	36,218
52071399	52071556	-48,132	-213,686
52367539	52367688	46,525	-56,259
52452062	52452213	131,048	28,266
54399325	54399474	43,487	33,319
54521287	54521362	87,057	79,525
54711128	54711244	123,298	71,966
55081967	55082127	12,358	-66,235
55233101	55233548	163,492	85,186
55009464	55009584	-60,145	-138,778
55341573	55341756	158,482	92,834
55401779	55401928	135,099	75,399
56232907	56233089	86,885	5,353
56130442	56130591	-15,580	-97,145
58411116	58411568	108,648	-908,733
58396439	58396906	93,971	-923,395
58718072	58718365	415,604	-601,936
58758848	58759110	456,380	-561,191
59394412	59394857	1,091,944	74,556
58940879	58941237	638,411	-379,064
59144945	59145157	842,477	-175,144
58650709	58650934	348,241	-669,367
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58658547	58658779	356,079	-661,522
58836457	58836637	533,989	-483,664
58547117	58547216	244,649	-773,085
58351415	58351623	48,947	-968,678
58218602	58218898	-83,866	-1,101,403
66447680	66448151	-66,192	-80,217
66516806	66516975	2,934	-11,393
66577175	66577328	63,303	48,960
67566652	67567078	19,292	-66,327
67692297	67692467	144,937	59,062
68423173	68423476	-75,420	-86,352
68432709	68432907	-65,884	-76,921
68549960	68550208	51,367	40,380
68780870	68781111	98,303	79,515
68742475	68742616	59,908	41,020
8011177	8011277	88,960	57,040
7940759	7941050	18,542	-13,187
72810180	72810334	32,341	30,226
72766794	72767076	-11,045	-13,032
73899600	73899983	-59,390	-73,022
73993056	73993295	34,066	20,290
74064408	74064581	105,418	91,576
74683673	74683972	14,883	-9,713
74736577	74736926	67,787	43,241

74859004	74859218	156,320	15,499
75914313	75914489	-32,750	-40,507
75979075	75979548	32,012	24,552
76087034	76087184	39,492	20,130
76193683	76193804	43,073	26,908
77839474	77839676	22,680	-2,303
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79893408	79893741	-64,393	-92,815
79966232	79966428	8,431	-20,128
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82987070	82987224	183,731	74,487
86527996	86528232	-71,465	-195,257
86616588	86616991	17,127	-106,498
86741172	86741321	141,711	17,832
92967674	92967861	22,875	11,784
96145216	96145401	22,939	-24,158
96235335	96235731	113,058	66,172
96027674	96027845	-94,603	-141,714
40750185	40750393	N/A	N/A
23689621	23689880	N/A	N/A
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1291534	1291703	33,859	31,720
1362983	1363179	27,915	22,348
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1764964	1765120	195,924	-425,725
1959022	1959399	389,982	-231,446
2107768	2107968	538,728	-82,877
2213166	2213628	644,126	22,783
10746001	10746196	109,426	8,609
10693184	10693317	56,609	-44,270
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101005179	101005379	65,573	-14,115
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105202933	105203167	-79,728	-211,700
105406658	105406836	123,997	-8,031
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106852107	106852401	113,063	-27,987
108084109	108084360	166,099	-4,835
107949600	107949976	31,590	-139,219
108583332	108583656	-10,623	-33,050
108616334	108616467	22,379	-239
108515507	108515709	-78,448	-100,997
109146251	109146511	158,532	37,850
109014806	109015042	27,087	-93,619
109762832	109762933	-31,580	-47,420
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11587673	11588033	296,156	97,498
11385084	11385253	93,567	-105,282
11441121	11441357	149,604	-49,178
11198485	11198798	-93,032	-291,737
11318907	11319078	27,390	-171,457
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112105969	112106159	17,741	-195,189
112082075	112082266	-6,153	-219,082
112578044	112578213	41,390	-104,392
112630046	112630462	93,392	-52,143
112761184	112761648	224,530	79,043
114299456	114299626	-69,115	-99,403
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116489219	116489425	119,833	811
117303398	117303578	-1,670	-56,430
118995007	118995176	102,075	-142,748
118918991	118919212	26,059	-218,712
118873276	118873676	-19,656	-264,248
119212984	119213280	320,052	75,356
119694333	119694588	153,368	-18,037
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12430249	12430479	31,667	25,066
13287520	13287714	461,701	-108,910
124649327	124649565	482,559	-538,937
126327274	126327689	183,274	33,739
127955309	127955758	142,286	76,218
128797557	128798028	465,932	-85,425
128589350	128589677	257,725	-293,776
128866494	128866763	534,869	-16,690
128278260	128278482	-53,365	-604,971
128737875	128737978	406,250	-145,475
128392399	128392583	60,774	-490,870
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129887281	129887463	641,246	8,056
129705017	129705231	458,982	-174,176
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131379267	131379380	177,087	-46,637
131746406	131746622	238,252	100,256
131487729	131488019	-20,425	-158,347
132016887	132017110	80,910	69,945
131896863	131897055	-39,114	-50,110
131844837	131845193	-91,140	-101,972
132082141	132082454	82,006	-27,789
132079887	132080322	79,752	-29,921
132275863	132276322	-34,336	-37,884
132244830	132245088	-65,369	-69,118
132663965	132664181	5,078	-100,176
132760308	132760778	101,421	-3,579
133147851	133148105	103,429	71,224
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137565287	137565499	58,637	29,021
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138281966	138282176	51,692	36,034
139325903	139326076	166,953	59,176
139167175	139167474	8,225	-99,426
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139476054	139476284	-21,888	-67,355
139771105	139771310	36,016	33,832
14255105	14255391	29,390	10,263
14182432	14182667	-43,283	-62,461
143188002	143188185	73,705	-119,846
143239562	143239830	125,265	-68,201
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143119565	143119738	5,268	-188,293
143875476	143875698	86,711	62,181
143788365	143788756	-400	-24,761
144114581	144114758	143,571	-79,256
144066879	144067132	95,869	-126,882
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144555294	144555698	41,938	4,498
144502984	144503437	-10,372	-47,763
144635990	144636295	122,634	85,095
145032603	145032881	378,037	-182,982
147568161	147568310	1,596	-180,278
147683319	147683487	116,754	-65,101
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138278	138481	-10,035	-12,911
175129	175297	26,816	23,905
149696454	149696628	15,698	-77,814
149647323	149647646	-33,433	-126,796
149621150	149621373	-59,606	-153,069
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149812637	149812866	131,881	38,424
149932908	149933057	65,584	24,193
150123828	150123960	11,555	-50,289
150264691	150264844	13,397	10,981
150370947	150371181	66,118	59,117
151757233	151757652	154,031	38,050
151635296	151635475	32,094	-84,127
152397002	152397299	226,623	-68,800
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152244388	152244779	74,009	-221,320
152780109	152780421	295,594	-219,806
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152604307	152604506	119,792	-395,721
152949445	152949667	464,930	-50,560
153150729	153151153	37,103	28,560

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155893582	155893858	135,388	75,129
155863580	155864011	105,386	45,282
155789784	155789943	31,590	-28,786
157524121	157524387	383,365	-47,707
157267984	157268385	127,228	-303,709
158254185	158254646	89,903	-31,451
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158584828	158585237	75,456	50,229
158555320	158555779	45,948	20,771
158484231	158484466	-25,141	-50,542
16593127	16593309	185,805	-276,391
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160196855	160197081	130,248	99,740
160239411	160239629	-70,710	-207,944
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160409020	160409197	-53,833	-90,543
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160519187	160519548	56,334	19,808
161574009	161574229	102,962	-40,868
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161622111	161622284	151,064	7,187
162643942	162644142	955,500	-424,651
163377802	163378085	309,648	-278,429
165782129	165782332	121,363	-213,246
167030450	167030633	287,606	-165,128
167409422	167409870	76,762	-63,304
167355649	167355816	22,989	-117,358
167506629	167507105	173,969	33,931
167926871	167927049	-1,195	-13,339
167965406	167965699	37,340	25,311
170432845	170433032	-24,924	-123,130
170485524	170485694	27,755	-70,468
170601790	170602006	144,021	45,844
170677634	170677846	-8,500	-26,466
170761646	170762073	75,512	57,761
18259657	18260013	23,136	-3,340
2667715	2667828	-42,950	-64,098
2779403	2779870	-53,096	-68,643
20862105	20862340	219,438	-478,274
22419518	22419782	24,059	14,073
22472950	22473076	77,491	67,367
22713240	22713472	35,583	33,601
22637790	22637989	-39,867	-41,882
254547	254760	17,494	-41,595
345685	345874	108,632	49,519
24666439	24666704	-91,745	-108,536
24854231	24854406	96,047	79,166
25405006	25405194	17,721	-323,543
26245803	26246097	50,376	41,059
26411190	26411300	-99,270	-112,145
26518884	26519041	8,424	-4,404
27301166	27301398	-22,321	-30,929

27342916	27343329	19,429	11,002
28276700	28277070	59,005	43,855
28200881	28201258	-16,814	-31,957
28388134	28388412	87,088	79,173
29736234	29736446	104,866	-41,595
29751702	29751902	120,334	-26,139
29753266	29753582	20,511	5,454
29802123	29802482	3,592	-570
29550333	29550545	-248,763	-252,507
29476083	29476238	-323,013	-326,814
29670244	29670434	-128,852	-132,618
29644100	29644264	-154,996	-158,788
29831719	29832103	29,294	29,208
30027185	30027486	124,462	5,853
3103508	3103611	94,296	43,191
30284629	30284792	266,319	263,159
29822664	29822810	-195,646	-198,823
29930636	29930880	-87,674	-90,753
30396299	30396607	377,989	374,974
30238657	30238758	220,347	217,125
30127492	30127613	109,182	105,980
30170485	30170689	152,175	149,056
30127492	30127613	96,530	96,223
30170485	30170689	63,016	61,056
30213749	30213943	1,262	-10,548
30321166	30321536	93,465	84,846
30456329	30456500	35,452	33,851
30519687	30520097	-41,964	-42,603
30515634	30515830	-49,616	-53,247
30583169	30583395	17,919	14,318
30716816	30716971	95,183	83,984
30889107	30889213	113,544	95,568
30889030	30889254	408	-17,161
30967250	30967351	-16,706	-22,508
31145725	31146018	86,251	80,364
31367081	31367280	22,576	-65,655
31579685	31579894	235,180	146,959
31317048	31317463	-27,457	-115,472
31312116	31312543	-32,389	-120,392
31643332	31643497	298,827	210,562
31203290	31203573	-226,338	-229,341
31169575	31169993	-260,053	-262,921
30967161	30967384	-462,467	-465,530
31565689	31566052	90,149	74,983
31579571	31579777	40,633	38,212
31648097	31648514	43,379	42,527
N/A	N/A	N/A	N/A
N/A	N/A	N/A	N/A
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31817063	31817216	168,991	167,139
31944497	31944649	293,168	290,558
31791664	31791799	100,680	99,018
31685318	31685519	-11,111	-28,014
31814672	31814942	62,232	55,146
31145725	31146018	15,762	10,386

32327802	32328124	324,329	306,696
32434558	32434788	431,085	413,360
32153714	32153926	69,539	-31,205
32256603	32256752	52,141	50,707
32351960	32352307	85,439	52,485
32299615	32299751	33,094	-71
32299495	32299838	28,897	16
32377666	32377882	9,213	-82,428
32442933	32443084	74,469	-4,578
32505292	32505607	-10,305	-15,336
32511329	32511466	-4,296	-9,335
32707394	32707854	52,870	42,251
32721587	32721719	8,475	2,312
32845242	32845375	110,020	91,079
32778014	32778233	42,792	23,937
32785483	32785908	50,258	43,336
32825072	32825180	-6,373	-14,266
32845249	32845491	-43,269	-47,312
32961904	32962066	64,316	47,541
33074668	33074896	30,253	17,821
33232052	33232277	43,846	27,409
33281628	33281840	43,181	13,617
32961890	32962094	-276,557	-306,129
33232052	33232277	-6,395	-35,946
33281662	33281841	5,031	1,649
33410105	33410512	84,078	62,872
33485439	33485663	109,990	95,521
33571139	33571410	-77,168	-84,587
33790555	33790704	94,055	18,375
34598233	34598378	56,350	-12,606
34539204	34539322	-2,679	-71,662
35347923	35348320	-70,390	-155,613
35802250	35802399	152,905	-1,939
35690784	35691025	41,439	-113,313
35902460	35902742	-6,329	-94,200
35991821	35992093	83,032	-4,849
36098858	36099012	-4,693	-87,501
36178949	36179320	49,180	-36,500
36249771	36250032	120,002	34,212
36631575	36631969	61,928	8,735
36474795	36474972	-94,852	-148,262
36777970	36778156	23,557	15,062
36740976	36741204	-13,437	-21,890
36935456	36935633	4,875	-15,145
37035946	37036145	105,365	85,367
37239036	37239280	-6,921	-11,902
37940375	37940615	45,090	-289,760
38247153	38247408	351,868	17,033
38090015	38090486	194,730	-139,889
38493309	38493755	242,598	-180,093
38661618	38661787	410,907	-12,061
39001022	39001277	208,709	-105,268
39139577	39139747	347,264	33,202
38942886	38943198	150,573	-163,347
38780924	38781334	-11,389	-325,211
39725403	39725562	-142,717	-255,060

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41082755	41083006	-19,994	-31,900
41134037	41134248	31,288	19,342
41255583	41255684	30,604	25,636
41318854	41319059	34,584	20,699
41446952	41447121	35,447	20,518
41731825	41732017	109,683	53,917
41595883	41596064	-26,259	-82,036
41645731	41645924	23,589	-32,176
42214527	42214696	203,878	90,292
42063121	42063306	52,472	-61,098
42338104	42338355	37,457	-189,412
42560864	42561334	260,217	33,567
42468577	42468726	167,930	-59,041
42264562	42264712	-36,085	-263,055
42985652	42985811	-53,934	-69,125
43126184	43126373	86,598	71,437
43206691	43206837	54,684	-30,598
43874446	43874606	28,522	12,404
43778399	43778514	-67,525	-83,688
44355441	44355541	32,639	25,943
44238027	44238145	-84,775	-91,453
44420063	44420165	86,182	78,662
45550048	45550262	146,016	-76,535
46660973	46661151	35,569	-67,331
46759985	46760114	134,581	31,632
46578524	46578719	-46,880	-149,763
46873386	46873573	93,489	62,184
47278333	47278554	-28,894	-107,085
47413291	47413588	106,064	27,949
47321028	47321230	13,801	-64,409
47641939	47642107	88,040	-60,513
47533166	47533390	-20,733	-169,230
48083547	48083706	129,549	-60,678
48000731	48001102	46,733	-143,282
48167659	48167944	213,661	23,560
49759145	49759464	78,315	46,953
49648096	49648436	-32,734	-64,075
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50121866	50122132	37,056	24,525
51889875	51890101	301,771	-170,281
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51774300	51774499	186,196	-285,883
52031461	52031628	443,357	-28,754
52103872	52104329	-55,272	-59,066
52312123	52312346	102,685	95,089
52194684	52194833	-14,754	-22,424
52386698	52386917	-6,255	-81,623
52498562	52498997	28,403	-50,824
52730587	52730812	-33,596	-45,804
53396387	53396728	-73,711	-121,062
53513334	53513603	43,236	-4,187
55363604	55363871	63,378	-11,379
55252250	55252341	-47,976	-122,909
55793444	55793854	67,042	-54,480
55916401	55916573	189,999	68,239

55746215	55746424	19,813	-101,910
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56026393	56026795	-2,954	-340,056
56363233	56363421	333,886	-3,430
56256568	56256729	227,221	-110,122
56907259	56907424	-20,473	-92,675
57111380	57111746	91,910	-31,311
57229312	57229578	84,229	71,884
6593132	6593306	59,792	-6,909
6695688	6695945	162,348	95,730
6515650	6516052	-17,690	-84,163
62715703	62715852	267,879	-338,239
64025660	64025763	61,122	44,854
63943648	63943828	-20,890	-37,081
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66242287	66242460	146,392	-231,379
69583839	69584018	181,859	-572,106
7572898	7573321	86,029	41,376
7588877	7589345	102,008	57,400
7527288	7527559	40,419	-4,386
7870600	7870798	198,591	44,046
7768079	7768240	96,070	-58,512
73622850	73623097	234,609	-342,198
74179707	74179889	18,515	-4,124
74098291	74098441	-62,901	-85,572
74215696	74216093	-66,498	-72,251
74307562	74308009	25,368	19,665
74600600	74600791	138,052	9,282
74447747	74447957	-14,801	-143,552
74527430	74527633	64,882	-63,876
78324298	78324448	95,657	94,548
78161782	78162024	-66,859	-67,876
79706873	79707064	72,965	42,025
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79895682	79896029	-71,999	-105,145
80004636	80004806	36,955	3,632
81110285	81110678	237,202	-2,028
80845205	80845354	-27,878	-267,352
81015266	81015415	142,183	-97,291
86217486	86217749	958	-44,466
86306353	86306776	89,825	44,561
87541626	87541795	-55,402	-168,126
87683307	87683476	86,279	-26,445
87893303	87893521	41,368	31,952
10027074	10027329	213,430	-141,579
90500971	90501238	301,355	101,115
90194376	90194670	-5,240	-205,453
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90652391	90652509	56,042	11,633
91342569	91342989	62,556	-10,639
91250703	91250837	-29,310	-102,791
94015023	94015428	7,163	-170,565
94154229	94154474	146,369	-31,519
97699568	97699739	220,351	4,388
97607534	97607736	128,317	-87,615
97475110	97475259	-4,107	-220,092

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100350198	100350399	-24647	-18748
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100520648	100520797	-36,524	-48,229
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101847243	101847689	-36,447	-44,604
101894447	101894688	10,757	2,395
103461676	103461883	562,203	44,684
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103252229	103252441	352,756	-164,758
103290070	103290220	390,597	-126,979
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104675130	104675331	131,071	-141,246
104633136	104633297	89,077	-183,280
104751564	104751762	207,505	-64,815
104851797	104851997	307,738	35,420
104504496	104504626	-39,563	-311,951
105597520	105597727	-80,372	-114,876
105726552	105726909	48,660	14,306
105778845	105779011	100,953	66,408
106243511	106243926	-49,466	-90,902
106396984	106397237	104,007	62,409
107470518	107470694	119,019	39,654
107378539	107378707	27,040	-52,333
107592145	107592427	140,913	34,391
111824685	111824903	-25,777	-78,580
111900209	111900439	49,747	-3,044
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114127081	114127410	284,793	10,019
113776818	113777080	-65,470	-340,311
115950216	115950625	-1,859	-37,841
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116023121	116023293	71,046	34,827
116059115	116059287	-40,580	-166,389
116097894	116098063	-1,801	-127,613
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121567185	121567481	266,790	78,155
121319883	121320093	19,488	-169,233
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124262464	124262696	11,915	-94,414
124156271	124156444	-94,278	-200,666
124399535	124399874	148,986	42,764
127688775	127688924	20,208	4,007
127775947	127776057	107,380	91,140
128353257	128353540	-11,973	-23,785
128285748	128285919	-79,482	-91,406
128557089	128557523	-58,860	-83,099
128623235	128623641	7,286	-16,981
129246648	129247097	207,857	62,939
129158656	129159071	119,865	-25,087
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13987603	13987762	90,224	-7,527
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13926485	13926682	29,106	-68,607
13956965	13957128	59,586	-38,161
130901037	130901516	237,862	69,585
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130704200	130704377	41,025	-127,554
130802097	130802266	138,922	-29,665
138849100	138849459	62,295	30,461
139194175	139194611	69,507	-171,949
139097659	139097964	-27,009	-268,596
139225945	139226387	101,277	-140,173
139135339	139135585	10,671	-230,975
139305170	139305370	180,502	-61,190
139405578	139405792	280,910	39,232
139789996	139790107	36,080	17,688
141221537	141221992	-52,089	-71,260
141335286	141335486	61,660	42,234
141688394	141688757	43,080	-532,340
141721025	141721174	75,711	-499,923
141998654	141998853	353,340	-222,244
142251063	142251161	605,749	30,064
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141653645	141653800	8,331	-567,297
142320091	142320290	-28,232	-49,335
142405627	142405843	57,304	36,218
142689296	142689668	-6,228	-25,239
142867776	142868015	69,449	51,908
148276290	148276712	140,882	64,365
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148187213	148187634	51,805	-24,713
149580075	149580254	-86,276	-89,442
149753800	149754258	87,449	84,562
150238918	150239214	-80,162	-103,395
150330368	150330582	11,288	-12,027
150440354	150440514	58,522	54,585
155325692	155325944	37,373	28,216
155210379	155210571	-77,940	-87,157
157042797	157043142	18,281	-1,030,037
158157657	158158010	1,133,141	84,831
157699810	157699923	675,294	-373,256
157995826	157995950	971,310	-77,229
157748493	157748669	723,977	-324,510
157192583	157192811	168,067	-880,368
157290561	157290805	266,045	-782,374
18597557	18597727	95,663	-405,791
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18553785	18554173	51,891	-449,345
18496813	18497048	-5,081	-506,470
18805042	18805336	303,148	-198,182
19033712	19033951	531,818	30,433
18654457	18654629	152,563	-348,889
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18938784	18939049	436,890	-64,469
18734483	18734687	232,589	-268,831

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2951804	2951964	39,496	-98,061
3064503	3064632	152,195	14,607
20314699	20314890	-22,551	-107,017
20430187	20430336	92,937	8,429
20472026	20472374	134,776	50,467
22686506	22686666	-45,522	-51,475
22780505	22780763	48,477	42,622
23289662	23290111	36,821	8,857
24250716	24250982	-39,616	-47,020
24337173	24337322	46,841	39,320
25109167	25109342	-15,633	-22,138
27214588	27214796	67,067	64,984
27117510	27117680	-30,011	-32,132
30526941	30527100	96,269	42,267
30725605	30726020	66,880	19,776
30677886	30678096	19,161	-28,148
30991310	30991535	73,317	59,879
30915257	30915388	-2,736	-16,268
33054279	33054543	90,702	41,476
32983800	32984208	20,223	-28,859
38340284	38340671	94,134	-33,510
38428541	38428821	182,391	54,640
38305055	38305266	58,905	-68,915
38228183	38228384	-17,967	-145,797
4783375	4783779	94,919	6,179
4667320	4667540	-21,136	-110,060
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41710718	41710920	15,592	1,689
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42273776	42274081	303,580	32,369
41929666	41929811	-40,530	-311,901
43631796	43631966	42,545	-281
43706557	43706793	117,306	74,546
43536588	43536856	-52,663	-95,391
44142667	44142830	-7,728	-52,733
44241919	44242154	91,524	46,591
44632387	44632558	60,459	51,383
44516225	44516452	-55,703	-64,723
44852100	44852281	49,323	43,041
44898728	44898851	95,951	89,611
44931275	44931510	-37,511	-53,693
5597181	5597288	63,869	60,541
50488473	50488623	173,549	50,570
50630675	50630926	5,416	-197,726
50763329	50763515	138,070	-65,137
50912977	50913250	287,718	84,598
55252760	55252931	198,541	10,406
55712576	55712864	-3,685	-35,575
6499210	6499465	118,559	89,342
6356712	6356865	-23,939	-53,258
65153022	65153136	89,912	68,501
65032022	65032259	-31,088	-52,376
7753015	7753187	109,915	28,424

7699383	7699518	56,283	-25,245
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72778377	72778776	-42,886	-43,760
73316412	73316839	54,389	34,739
73210018	73210124	-52,005	-71,976
73442297	73442641	100,556	-15,560
73472849	73473242	131,108	15,041
73702238	73702551	196,182	47,698
73520909	73521007	14,853	-133,846
73764718	73764835	54,752	-48,123
73779045	73779342	-47,200	-62,253
73997109	73997229	148,689	91,452
75050782	75051117	75,777	55,728
74924184	74924558	-50,821	-70,831
75293282	75293451	56,504	36,301
75257210	75257573	20,432	423
75693799	75694184	-76,060	-77,364
76697690	76698131	35,155	31,051
76601014	76601169	-61,521	-65,911
77176283	77176536	171,932	69,212
77004432	77004581	81	-102,743
79592066	79592297	-10,010	-94,364
79725585	79725727	123,509	39,066
80052425	80052625	-17,034	-91,637
80114473	80114720	45,014	-29,542
81227817	81228070	61,559	-9,318
81157943	81158229	-8,315	-79,159
83060391	83060632	229,233	-55,628
82749886	82750035	-81,272	-366,225
83007031	83007204	175,873	-109,056
83104217	83104369	273,059	-11,891
83150878	83151184	319,720	34,924
82884169	82884441	53,011	-231,819
82835248	82835533	4,090	-280,727
82954921	82955123	123,763	-161,137
87209744	87209965	238,860	29,465
86930460	86930671	-40,424	-249,829
87095596	87095934	124,712	-84,566
86997875	86998319	26,991	-182,181
91485569	91485814	-93,833	-116,132
91700349	91700641	120,947	98,695
91595624	91595882	16,222	-6,064
92092362	92092622	20,191	-208,526
92059629	92059887	-12,542	-241,261
92374977	92375168	302,806	74,020
93959064	93959397	97,255	60,917
93808120	93808314	-53,689	-90,166
93848657	93849063	-13,152	-49,417
96214944	96215331	58,929	38,192
96124060	96124209	-31,955	-52,930
97215408	97215667	16,097	7,947
97156808	97156953	-42,503	-50,767
97820947	97821303	60,940	-47,013
97871759	97872068	111,752	3,752
1070211	1070400	80,850	74,598
946405	946553	-42,956	-49,249

99001411	99001719	-82,026	-218,025
99106619	99106785	23,182	-112,959
99372196	99372582	108,624	70,473
99567451	99567565	68,045	50,266
99699860	99700229	-71,813	-103,159
99893639	99893859	121,966	90,471
6928203	6928471	103,203	28,471
6737377	6737597	-87,623	-162,403
10775389	10775489	115,506	40,693
10647006	10647407	-12,877	-87,389
10593772	10593964	-66,111	-140,832
101916022	101916387	-84,068	-118,358
102077256	102077611	77,166	42,866
103687505	103687722	-42,683	-49,406
103782232	103782461	52,044	45,333
104199534	104199829	-22,563	-111,880
104330863	104331321	108,766	19,612
105463228	105463438	42,000	25,346
105418932	105419286	-2,296	-18,806
108530678	108530942	199,792	-48,517
108639973	108640146	309,087	60,687
108295178	108295324	-35,708	-284,135
108415285	108415494	84,399	-163,965
108447214	108447385	116,328	-132,074
11387131	11387403	-1,788	-72,119
11515272	11515400	126,353	55,878
11317148	11317364	-71,771	-142,158
11657410	11657521	58,288	2,601
11896720	11896963	27,849	27,446
110146515	110146664	-22,385	-54,325
110238742	110239130	69,842	38,141
12277692	12277903	64,849	57,707
120032851	120033006	27,874	-486
119960673	119960872	-44,304	-72,620
120496958	120497185	-924	-8,591
120571321	120571545	73,439	65,769
121379855	121380093	173,322	-73,361
121487832	121488185	281,299	34,731
121169546	121169693	-36,987	-283,761
128831342	128831784	13,844	8,928
128738756	128738905	-78,742	-83,951
141580849	141581181	-9,737	-15,253
141502803	141503133	-87,783	-93,301
141631901	141632083	41,315	35,649
142079255	142079454	341,572	-1,060
142021823	142021972	284,140	-58,542
141720546	141720714	-17,137	-359,800
142536386	142536574	35,197	25,772
143921569	143921744	-29,206	-36,494
144169637	144170010	-1,637	-5,189
144799831	144799961	-70,667	-76,658
16052635	16052794	42,874	-41,801
15969566	15969745	-40,195	-124,850
16149300	16149451	139,539	54,856
16976421	16976768	82,372	72,707
16959613	16959877	65,564	55,816

16808197	16808365	-85,852	-95,696
18348129	18348454	55,094	45,451
18396794	18397013	103,759	94,010
21786803	21787029	-35,527	-40,122
21883796	21883949	61,466	56,798
21992576	21992958	36,693	30,692
22024661	22024894	68,778	62,628
22457030	22457199	102,489	2,616
22271221	22271353	-83,320	-183,230
22664958	22665199	63,841	58,439
22621327	22621551	20,210	14,791
22576582	22576836	-24,535	-29,924
22877189	22877449	-56,402	-105,188
22988344	22988515	54,753	5,878
22988349	22988557	28028	42338
23006985	23007135	42061	70353
23091332	23091506	-42286	-14018
23053800	23053961	50209	84623
23164037	23164144	-60028	-25560
23231860	23232223	74,746	56,771
25324253	25324459	-8,440	-13,628
25903546	25903705	146,056	-54,587
25786048	25786197	28,558	-172,095
25677104	25677260	-80,386	-281,032
26008411	26008844	250,921	50,552
26341334	26341468	45,003	14,906
27404034	27404230	179,118	31,406
27175459	27175647	-49,457	-197,177
27325382	27325791	100,466	-47,033
27566834	27567081	56,483	38,793
27438478	27438658	-71,873	-89,630
27651900	27652181	104,596	61,970
27905106	27905372	121,451	-745
29333818	29334040	84,288	69,936
29275807	29276226	26,277	12,122
30638173	30638286	82,751	3,012
30494188	30494669	-61,234	-140,605
30597094	30597515	41,672	-37,759
33574897	33575183	6,504	-1,860
33597800	33597900	29,407	20,857
38135122	38135485	-18,141	-54,481
38273218	38273456	119,955	83,490
38428745	38429115	39,339	-16,181
38423741	38423890	34,335	-21,406
38470657	38470800	81,251	25,504
38664547	38664985	-69,461	-164,718
38759699	38759848	25,691	-69,855
39963127	39963528	72,642	58,408
39912039	39912459	21,554	7,339
41679897	41680317	49,996	-193,120
41580307	41580646	-49,594	-292,791
41891541	41892002	261,640	18,565
41781623	41782012	151,722	-91,425
42180570	42180936	-67,416	-128,194
42279680	42279890	31,694	-29,240
48902172	48902351	53,950	-132,945

54273953	54274171	-26,876	-52,576
54236344	54236519	-64,485	-90,228
56878048	56878318	-76,878	-208,175
57014504	57014694	59,578	-71,799
56962552	56962755	7,626	-123,738
59498129	59498379	-67,163	-76,896
59579881	59580119	14,589	4,844
59779361	59779703	120,744	44,763
6331020	6331443	-13,560	-76,895
6462561	6463031	117,981	54,693
65668245	65668691	-3,001	-205,211
65753949	65754082	82,703	-119,820
65892255	65892470	221,009	18,568
67239580	67239810	-11,586	-13,570
71677981	71678184	29,754	-4,974
75026266	75026563	-39,875	-77,296
75089449	75089681	23,308	-14,178
76578720	76579194	95,894	-62,429
76482989	76483122	163	-158,501
76651602	76651729	168,776	10,106
78101362	78101487	43,649	26,493
78159151	78159299	101,438	84,305
79915926	79916400	108,366	36,087
79797810	79798011	-9,750	-82,302
79890586	79890857	83,026	10,544
8543660	8543916	-53,416	-55,110
8628444	8628823	31,368	29,797
81952954	81953128	-89,646	-233,730
82096153	82096502	53,553	-90,356
82356935	82357085	1,609	-2,478
82431027	82431467	75,701	71,904
82516244	82516636	-37,237	-41,387
82897681	82897943	90,438	63,638
82722795	82722947	-84,448	-111,358
89110896	89111061	-7,680	-297,831
89247886	89248270	129,310	-160,622
89337958	89338137	219,382	-70,755
89212552	89212980	93,976	-195,912
89463510	89463913	344,934	55,021
90917942	90918042	78,832	45,609
90858901	90859006	19,791	-13,427
91152169	91152323	137,429	86,248
93141896	93142035	101,568	-34,584
93200803	93200970	160,475	24,351
93040796	93040973	468	-135,646
95266645	95266936	-64,012	-76,797
95319278	95319375	-11,379	-24,358
96012888	96013065	51,260	36,405
95915699	95915848	-45,929	-60,812
97383890	97384321	40,550	-31,629
97420239	97420486	76,899	4,536
97267772	97267921	-75,568	-148,029
97358290	97358436	14,950	-57,514
97716363	97716772	141,305	23,559
97497725	97497852	-77,333	-195,361
97637410	97637623	62,352	-55,590

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99237264	99237469	38,020	-2,347
99314722	99314844	115,478	75,028
99877084	99877508	341,043	-29,577
99489084	99489283	-46,957	-417,802
99572518	99572728	36,477	-334,357
99674116	99674491	138,075	-232,594
99995842	99995977	459,801	88,892
91916978	91917217	33,595	32,479
91786989	91787168	-96,394	-97,570
100993879	100994048	86,646	37,642
100874975	100875255	-32,258	-81,151
101098178	101098397	73,798	65,675
101718461	101718612	94,503	49,618
101629262	101629510	5,304	-39,484
103485871	103486076	92,153	88,972
103424966	103425174	31,248	28,070
107241482	107241633	194,758	360
107078566	107078751	31,842	-162,522
107422684	107423090	-41,915	-42,124
110630541	110630850	-26,151	-28,218
110705868	110706031	49,176	46,963
111282970	111283094	105,170	-17,313
111092789	111092904	-85,011	-207,503
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112128955	112129173	83,043	70,432
112372536	112372710	-58,521	-58,847
113366245	113366636	1,567	-35,281
113272714	113272919	-91,964	-128,998
113683712	113683930	-15,155	-53,540
113830419	113830619	131,552	93,149
113622923	113623296	-75,944	-114,174
114982313	114982586	14,693	-41,424
115062577	115062731	94,957	38,721
115227413	115227573	18,077	14,800
115154388	115154722	-54,948	-58,051
116120936	116121193	-4,221	-7,385
116227615	116227889	95,725	92,532
116668752	116668979	77,331	60,750
116563365	116563680	-28,056	-44,549
116738516	116738733	33,571	6,142
116938283	116938406	115,649	18,146
116999255	116999373	176,621	79,113
119488179	119488441	-18,226	-31,148
119526784	119527053	20,379	7,464
122689596	122689918	-14,896	-40,950
122740185	122740291	35,693	9,423
122827363	122827582	72,929	-24,793
124198661	124198964	25,611	1,162
124127623	124127822	-45,427	-69,980
126152527	126152697	-3,038	-64,845
126236287	126236485	80,722	18,943
126327340	126327451	44,004	17,921
126589533	126589982	270,153	16,572
126482075	126482261	162,695	-91,149
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129681037	129681437	93,139	88,550
129495867	129496149	-92,031	-96,738
129704568	129704898	87,456	48,042
129906842	129907203	-44,329	-49,130
130452455	130452746	-33,389	-45,742
131034543	131034982	121,493	83,936
131568037	131568281	27,604	13,116
131540451	131540610	18	-14,555
131981878	131982283	126,352	40,019
131868460	131868560	12,934	-73,704
131813132	131813407	-42,394	-128,857
132809082	132809187	-65,243	-149,080
132877228	132877328	2,903	-80,939
133469875	133470149	27,897	-135,133
133666409	133666820	224,431	61,538
134580977	134581315	122,772	45,706
134449296	134449448	-8,909	-86,161
134863769	134863988	-32,128	-59,721
134820916	134821281	-74,981	-102,428
135136149	135136394	15,765	-4,057
135355839	135355943	78,898	41,614
135245604	135245870	-31,337	-68,459
135840148	135840462	223,311	-7,085
135577518	135577837	-39,319	-269,710
135657141	135657317	40,304	-190,230
135621569	135621804	4,732	-225,743
135783008	135783198	166,171	-64,349
136964438	136964659	290,965	88,149
137036356	137036780	95,519	87,150
138653439	138653835	144,722	93,700
138995119	138995332	94,333	54,444
139457459	139457662	-19791	-8983
139420470	139420671	17198	28008
15506863	15507114	52,799	6,097
15360887	15361174	-93,177	-139,843
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2232821	2233002	227,479	49,378
2105279	2105468	99,937	-78,156
2752251	2752615	-41,901	-81,480
2912066	2912378	117,914	78,283
20935741	20936171	-131,363	-131,791
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21356211	21356638	-1,212	-2,323
21565208	21565532	94,370	93,220
21473210	21473413	2,372	1,101
21906019	21906249	-51,732	-78,241
21980434	21980763	22,683	-3,727
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26949029	26949436	54,948	11,975
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27046819	27046987	-52,417	-173,186
27228648	27228922	129,412	8,749
27468780	27468881	-45,522	-47,615
3281142	3281541	72,845	-234,442

3544644	3544980	336,347	28,997
3498882	3499045	290,585	-16,938
3400069	3400257	191,772	-115,726
3186982	3187226	-21,315	-328,757
32600144	32600521	154,844	84,199
32359022	32359212	-86,278	-157,110
33216433	33216792	-26,036	-37,952
33363102	33363251	108,935	91,726
34561479	34561628	-75,156	-90,256
34680403	34680591	43,768	28,707
35637621	35637723	37,645	28,970
35760341	35760701	73,007	38,332
35789354	35789592	102,020	67,223
36601472	36601839	38,599	-65,840
36484101	36484319	-78,772	-183,360
38111829	38112209	202,698	52,960
37910069	37910382	938	-148,867
4958776	4959028	-16,469	-159,155
5118035	5118336	142,790	153
5380164	5380319	-60,361	-80,228
5457161	5457445	16,636	-3,102
5565247	5565348	64,677	4,096
6257328	6257643	51,519	9,660
6225983	6226204	20,174	-21,779
70858087	70858318	40,846	39,469
74973531	74973701	17,038	-1,428
74937484	74937956	-19,009	-37,173
76459038	76459207	156,966	-32,730
76521849	76522049	219,777	30,112
76285354	76285597	-16,718	-206,340
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8735688	8736162	431,442	-272,573
9009034	9009506	704,788	771
8848518	8848945	544,272	-159,790
8444760	8445059	140,514	-563,676
8556011	8556175	251,765	-452,560
8360163	8360362	55,917	-648,373
88811412	88811618	62,314	59,694
89237568	89238025	-64,395	-275,344
89352169	89352615	50,206	-160,754
89531653	89532080	229,690	18,711
89480562	89480826	178,599	-32,543
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91324552	91324696	142,580	21,988
92619901	92620084	16,011	-80,568
92726100	92726294	122,210	25,642
93238292	93238774	27,144	12,809
93229630	93230091	18,482	4,126
97220242	97220584	-24,841	-98,339
97382350	97382577	137,267	63,654
97316684	97316834	71,601	-2,089
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99580034	99580220	-75,323	-78,598
99763255	99763404	-22,207	-54,642
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104974501	104974747	1,276,849	76,269
104456682	104456960	759,030	-441,518
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103769044	103769435	71,392	-1,129,043
103979556	103979822	281,904	-918,656
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105823227	105823410	-497	-103,492
105909211	105909333	85,487	-17,569
105972467	105972746	148,743	45,844
106975337	106975491	132,230	69,633
106872121	106872323	29,014	-33,535
107105415	107105574	1,728	143
107278299	107278503	-7,194	-290,880
107439543	107439823	154,050	-129,560
107632123	107632510	346,630	63,127
107367721	107367989	82,228	-201,394
107730307	107730623	160,497	-96,808
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110248276	110248425	22,032	-102,391
114207848	114207961	63,054	48,169
115212733	115213144	-3,270	-7,109
117879004	117879437	133,441	66,907
117739651	117739764	-5,912	-72,766
119453980	119454186	7,613	-33,003
119561339	119561516	114,972	74,327
12736292	12736478	-58,831	-81,942
12867195	12867544	32,516	16,335
12954091	12954250	50,943	48,983
122900720	122901135	79,162	25,625
122741956	122742205	-79,602	-133,305
123328200	123328482	20,325	-6,204
123238456	123238924	-69,419	-95,762
128330566	128330715	-77,593	-154,443
128491461	128491649	83,302	6,491
128543441	128543590	135,282	58,432
128592496	128592759	-14,510	-23,836
128696418	128696596	89,412	80,001
129065849	129066022	-25,169	-61,467
129183759	129184182	92,741	56,693
130150441	130150625	-84,720	-210,733
130362360	130362565	127,199	1,207
134537294	134537474	55,079	-6,626
134878912	134879135	-16,352	-77,954
134804730	134804881	-90,534	-152,208
135578308	135578507	20,306	8,292
135646407	135646556	88,405	76,341
137964497	137964874	423,096	69,962
137891004	137891269	349,603	-3,643
137728137	137728516	186,736	-166,396

137604666	137605004	63,265	-289,908
137564241	137564631	22,840	-330,281
137823373	137823635	281,972	-71,277
149632934	149633307	-52,533	-184,530
149876389	149876567	190,922	58,730
15326688	15326837	53,049	14,339
15198039	15198215	-75,600	-114,283
15355548	15355957	81,909	43,459
15478660	15478863	86,370	-5,710
15588538	15588942	99,461	58,743
152489599	152489748	76,008	61,542
152373131	152373302	-40,460	-54,904
152547564	152547852	-13,618	-22,123
152891940	152892419	111,777	87,617
153019904	153020179	90,759	81,554
153482102	153482322	69,302	53,341
153731409	153731887	87,180	72,729
18122986	18123230	-44,369	-159,538
18240921	18241213	73,566	-41,555
19224446	19224800	-63,649	-218,563
19357725	19357924	69,630	-85,439
19393734	19393958	105,639	-49,405
19754666	19754953	292,652	-60,687
19562040	19562267	100,026	-253,373
19910542	19910801	448,528	95,161
2808176	2808375	128,061	64,407
22857504	22857710	-70,495	-73,917
22895583	22895669	-32,416	-35,958
23021461	23021609	93,462	89,982
23538321	23538572	-53,979	-75,865
28588079	28588250	72,642	-1,296,511
29289511	29289680	774,074	-595,081
28794377	28794842	278,940	-1,089,919
28899808	28900047	384,371	-984,714
28961875	28962037	446,438	-922,724
29149530	29149756	634,093	-735,005
29490005	29490392	974,568	-394,369
29377719	29377891	862,282	-506,870
29757165	29757273	1,241,728	-127,488
28472648	28472797	-42,789	-1,411,964
29864516	29864640	1,349,079	-20,121
30226367	30226663	-5,877	-10,973
30328327	30328645	96,083	91,009
30234459	30234841	2,215	-2,795
37431232	37431480	1,301	-44,842
37639576	37639775	115,368	82,117
38424695	38424853	119,142	-8,265
38277921	38278106	-27,632	-155,012
41208756	41209117	131,161	100,448
41032627	41032932	-44,968	-75,737
44668655	44668973	80,462	79,895
44590422	44590571	2,229	1,493
46552780	46553089	203,083	49,655
46419355	46419539	69,658	-83,895
46311318	46311404	-38,379	-192,030
47353138	47353526	26,504	22,392

47454008	47454427	85,451	79,779
48374977	48375152	-52,135	-59,610
48462114	48462312	22,184	9,965
48578101	48578249	48,195	40,587
48674053	48674492	128,883	106,156
48979085	48979333	-14,756	-28,899
50182301	50182401	326,145	70,748
49842981	49843116	-13,175	-268,537
53048169	53048317	-80,105	-86,130
53095822	53095913	-32,452	-38,534
53254276	53254406	16,217	-16,923
53369759	53369896	131,700	98,567
54953808	54954092	-98,405	-120,044
55133388	55133663	81,175	59,527
57620180	57620347	-99,756	-103,091
66656193	66656458	-24,406	-210,728
66698869	66699073	18,270	-168,113
69046787	69047173	294,151	-128,874
68739704	68739875	-12,932	-436,172
68792255	68792404	39,619	-383,643
69331909	69332152	-62,832	-64,227
69364800	69364978	-29,941	-31,401
70209546	70209695	-23,226	-30,415
70309061	70309439	65,082	61,251
70784226	70784649	31,735	29,557
70680132	70680406	-72,359	-74,686
71446806	71447248	105,574	71,646
71391726	71391911	50,494	16,309
71285268	71285510	-55,964	-90,092
71603641	71603839	137,550	-105,784
71525068	71525326	58,977	-184,297
71687566	71687728	221,475	-21,895
76680233	76680680	83,930	82,011
76602179	76602564	5,876	3,895
77337821	77338182	-75,796	-131,561
77463255	77463486	49,638	-6,257
9564271	9564682	172,902	-83,096
9420805	9420968	29,436	-226,810
9722847	9723231	331,478	75,453
9459372	9459530	68,003	-188,248
96011001	96011437	184,636	-735,215
96142112	96142440	315,747	-604,212
96278822	96278995	452,457	-467,657
95916941	95917169	90,576	-829,483
96471479	96471643	645,114	-275,009
96776973	96777104	950,608	30,452
96381455	96381605	555,090	-365,047
96413437	96413629	587,072	-333,023
96543841	96543954	717,476	-202,698
96642364	96642533	815,999	-104,119
95815805	95815960	-10,560	-930,692
100049656	100049911	64,687	33,921
99895129	99895569	-89,840	-120,421
13419282	13419497	96,728	-62,665
13491144	13491474	34269	50310
13495975	13496187	29438	45597

13814930	13815340	-54,723	-286,607
14058204	14058304	188,551	-43,643
14261984	14262176	-62,857	-65,122
19577511	19577613	-34,387	-36,480
2748518	2748678	21009	46319
2768356	2768506	1171	26491
20388814	20389033	62,125	22,821
6921204	6921332	82,477	-98,392
7001434	7001541	162,707	-18,183

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	all_152_ind	all_152_10	all_152_20	all_152_40	all_156_ind	all_156_10	all_156_20	all156_40
D01	1	0	0	0	1	0	0	0
D24	1	0	0	0	0	0	0	0
P01	0	0	0	0	0	0	0	0
P24	0	0	0	0	1	0	0	0

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	all_152_ind	all_152_10	all_152_20	all_152_40	all_156_ind	all_156_10	all_156_20	all156_40
D01	1	0	0	0	1	0	0	0
D24	1	0	0	0	0	0	0	0
P01	0	0	0	0	0	0	0	0
P24	0	0	0	0	1	0	0	0

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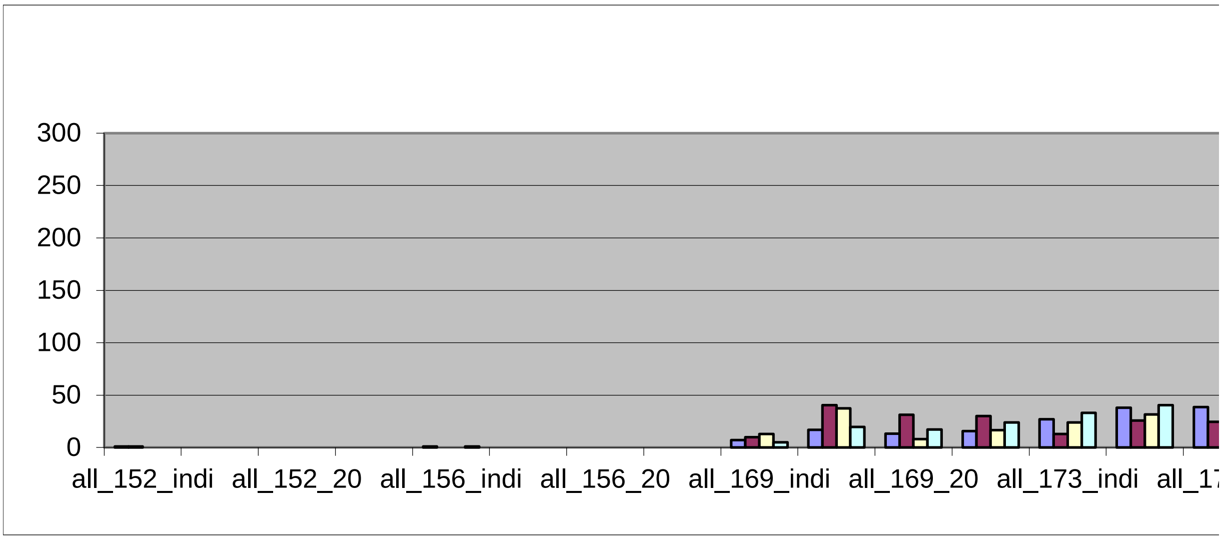
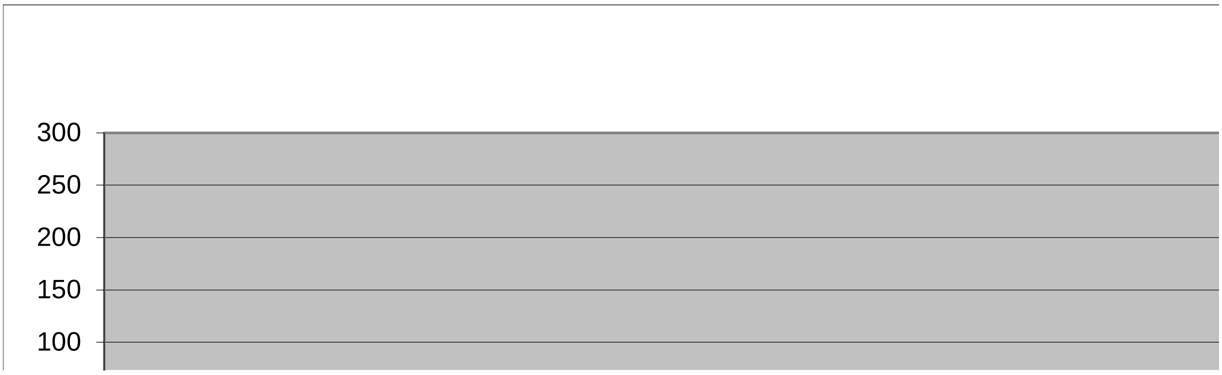
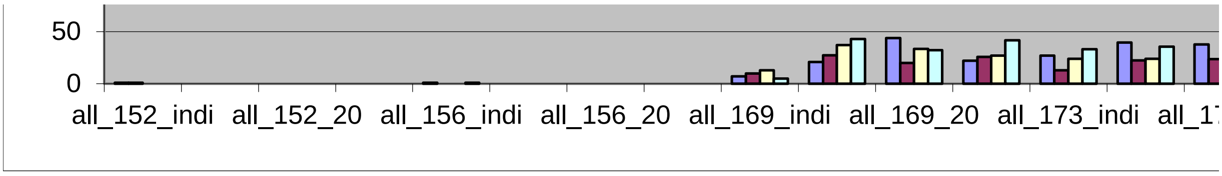
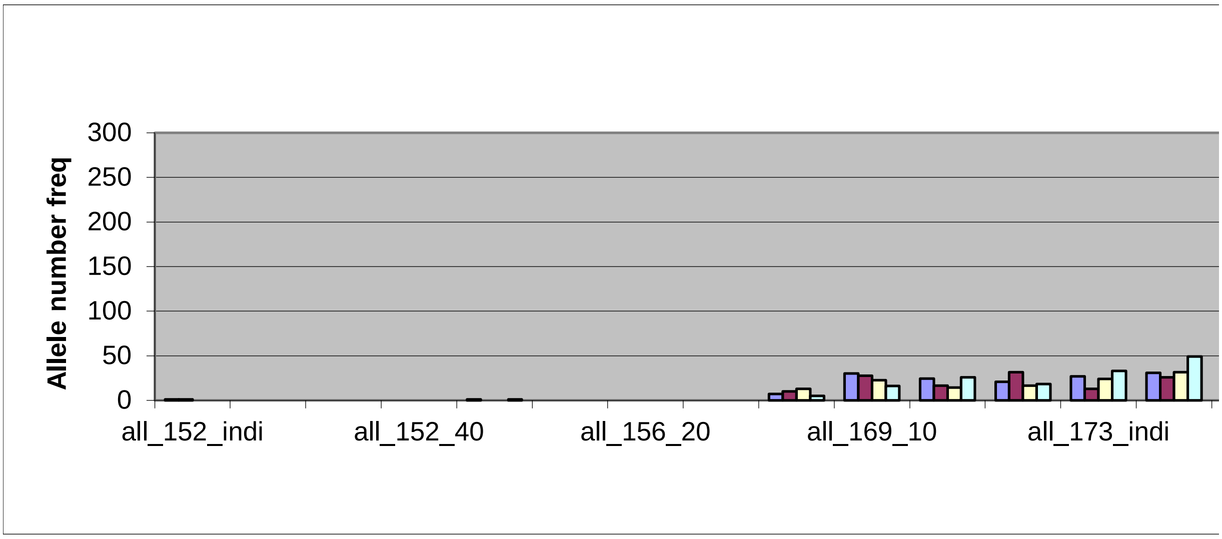
	all_152_ind	all_152_10	all_152_20	all_152_40	all_156_ind	all_156_10	all_156_20	all156_40
D01	1	0	0	0	1	0	0	0
D24	1	0	0	0	0	0	0	0
P01	0	0	0	0	0	0	0	0
P24	0	0	0	0	1	0	0	0






50
0
all_152_indi
all_152_20
all_156_indi
all_156_20
all_169_indi
all_169_20
all_173_indi
all_17

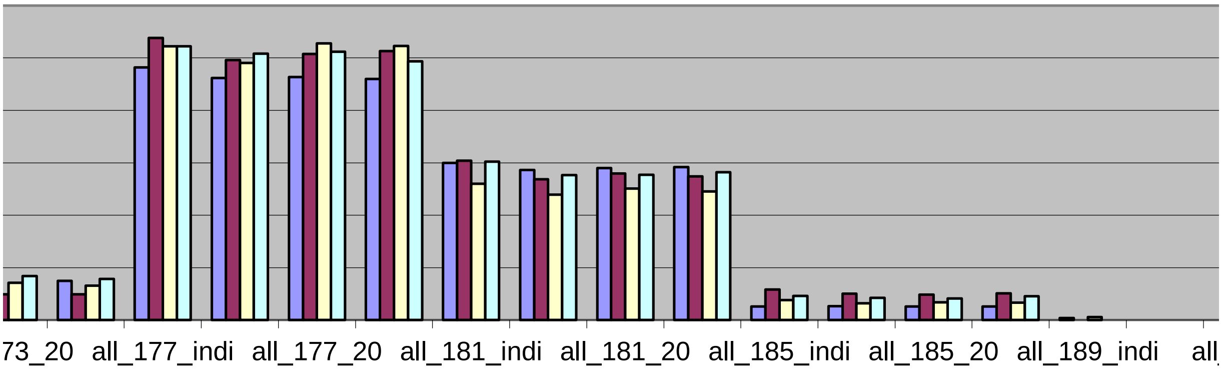

Allele number freq
300
250
200
150
100
50
0
all_152_indi
all_152_40
all_156_20
all_169_10
all_173_indi

all_169_in	all_169_10	all_169_20	all_169_40	all_173_in	all_173_10	all_173_20	all_173_40	all_177_in
7	16.84735	13.25337	15.84178	27	37.90654	38.65567	37.39232	241
10	40.50675	31.4152	30.2175	13	25.72534	24.55138	24.5295	269
13	37.54609	8.151417	16.54119	24	31.58542	35.42731	32.88308	261
5	19.73258	17.15352	24.05867	33	40.55213	42.07973	39.17811	261

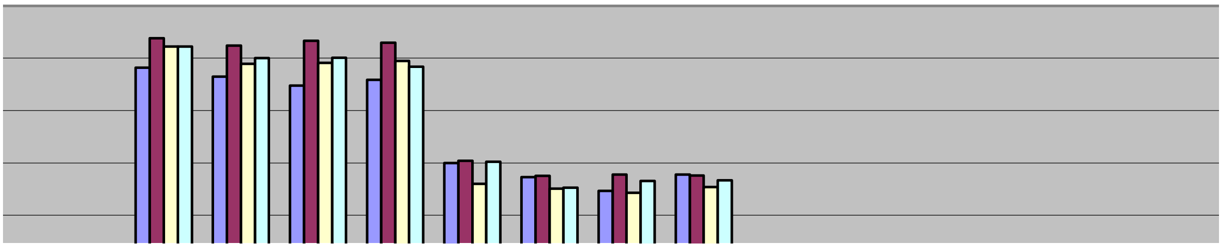
all_169_in	all_169_10	all_169_20	all_169_40	all_173_in	all_173_10	all_173_20	all_173_40	all_177_in
7	20.81844	43.84921	22.22143	27	39.45429	37.7834	39.34286	241
10	27.31143	19.92455	25.64863	13	22.42095	23.70511	21.98454	269
13	37.21922	33.43653	26.8886	24	23.89866	31.46285	32.26633	261
5	42.80465	32.28724	41.59516	33	35.62134	39.09479	37.89782	261

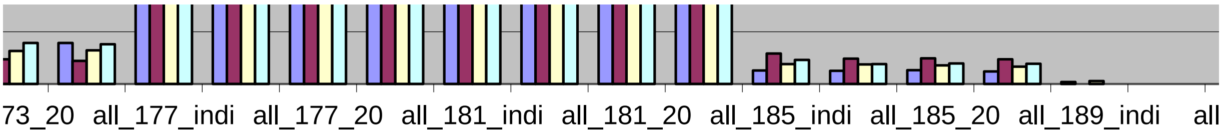
all_169_in	all_169_10	all_169_20	all_169_40	all_173_in	all_173_10	all_173_20	all_173_40	all_177_in
7	30.13636	24.48507	20.83099	27	31.00988	31.20896	33.76056	241
10	27.72346	16.51871	31.69862	13	25.73305	24.51724	27.89478	269
13	22.4442	14.33121	16.37622	24	31.49628	37.83439	31.13788	261
5	16.28648	25.77068	18.2372	33	49.28246	40.81193	44.67279	261

066B03_H

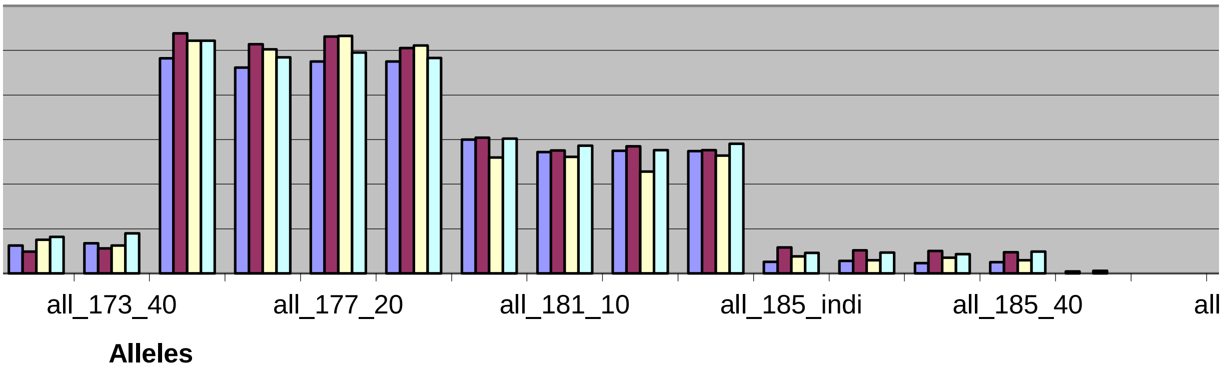


066B03_M




73_20
all_177_indi
all_177_20
all_181_indi
all_181_20
all_185_indi
all_185_20
all_189_indi
all

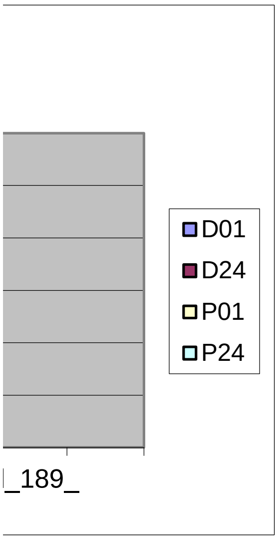
066B03_L

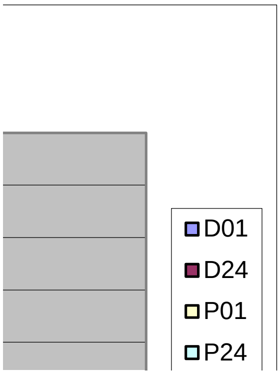

all_173_40
all_177_20
all_181_10
all_185_indi
all_185_40
all
Alleles

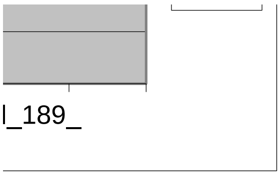
all_177_10	all_177_20	all_177_40	all_181_in	all_181_10	all_181_20	all_181_40	all_185_in	all_185_10
230.8411	231.934	229.9199	150	143.2025	145.1244	145.8586	13	13.20249
248.0861	253.8296	256.671	152	134.3829	139.9165	137.1045	29	25.29895
245.1249	263.9805	261.4703	130	119.7665	125.5109	122.5642	19	15.97706
254.0988	255.8287	246.7669	151	138.2953	138.4343	141.1516	23	21.32122

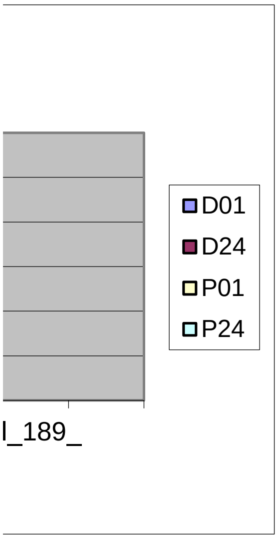
all_177_10	all_177_20	all_177_40	all_181_in	all_181_10	all_181_20	all_181_40	all_185_in	all_185_10
232.4166	223.704	229.3786	150	136.551	123.4355	138.9143	13	12.75969
262.2048	266.7847	264.8138	152	137.6857	138.961	137.903	29	24.37714
244.7066	245.6656	247.3752	130	125.37	121.5557	126.9526	19	18.8055
250.235	250.4206	241.9914	151	126.2491	132.65	133.2894	23	19.08989

all_177_10	all_177_20	all_177_40	all_181_in	all_181_10	all_181_20	all_181_40	all_185_in	all_185_10
230.8271	237.4925	237.5211	150	136.0504	137.2687	137.1972	13	13.97628
256.7618	265.3426	252.7436	152	137.9064	142.4087	137.9947	29	25.87522
250.9782	266.2739	255.5613	130	130.4492	114.0764	132.163	19	14.63213
242.1821	247.4787	241.6011	151	142.9826	138.2792	145.2284	23	23.2664






l_189_


D01
D24
P01
P24
l_189_

all_185_20	all_185_40	all_189_in	all_189_	all_189_	all_189_
13.03248	12.98741	2	0	0	0
24.28739	25.4775	0	0	0	0
16.92987	16.54119	3	0	0	0
20.50382	22.8447	0	0	0	0

all_185_20	all_185_40	all_189_in	all_189_	all_189_	all_189_
13.22784	12.14286	2	0	0	0
24.6247	23.65004	0	0	0	0
17.87926	16.51729	3	0	0	0
19.54739	19.22621	0	0	0	0

all_185_20	all_185_40	all_189_in	all_189_	all_189_	all_189_
11.54478	12.69014	2	0	0	0
25.21277	23.6683	0	0	0	0
17.48408	14.76166	3	0	0	0
21.6594	24.2605	0	0	0	0