Clonal Genomics In Autoreactive T-Cells In Type 1 Diabetes And Celiac Disease

by
Maha Zakariya Al-Riyami

Department of Medicine,
Division of Experimental Medicine
McGill University, Montreal

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“Discovery consists of looking at the same thing as everyone else and thinking something different.”

— Albert Szent-Györgyi
Nobel Prize in Physiology and Medicine in 1937

To my wonderful parents,
To my amazing siblings,
With Love…

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Abstract

Autoimmune diseases are caused by the immune system attacking self-antigens. Autoimmunity is known to depend on both inherited susceptibility and environmental factors. However, these alone may not explain all of the diseases. Current knowledge does not explain the discordance of autoimmunity in monozygotic twins living in a shared environment or the discordance in some inbred-strain animal models kept in a controlled environment. These could be explained by stochastic events and one plausible, never explored, such event is post-zygotic mutations (PZMs) in the expanding antigen-specific autoreactive T-cell lineages.

For my Ph.D. project, I investigated the potential causal role of PZMs in two autoimmune diseases for which the autoantigens are well known: Type 1 diabetes (T1D) and Celiac disease (CD).

I started by testing this hypothesis in NOD mice, the mouse model for T1D. Using a whole-genome scan, by high-resolution comparative genomic hybridization (CGH), of DNA from memory CD4+ T-cells from pancreatic lymph nodes of diabetic NOD mice (n=25), we identified eight recurrent mosaic copy-number aberrations (CNA) that occurred exclusively in self-reactive lymphocytes and independently in different mice. Some of these CNAs involve the same gene(s) across different mice, many with an immune or proliferation function and/or an association with autoimmune diseases such as *Ilf3* and *Dgka.*

Moreover, I showed that 66.6% of newly diagnosed patients in my study with T1D (n=17) harbor somatic mutations in their *ex vivo* insulin-reactive T-cells. I also, identified

recurrent affected genes in these patients, some with T-cell proliferation and differentiation regulatory functions such as *CASZ1* and *E2f1.*

In both human and mice with T1D, I identified CNAs in non-auto-reactive lymphocytes expanded during the normal process of host defense; however, these were significantly smaller (2 folds smaller) than those found in autoreactive cells. Moreover, the low T-cell clonality determined by T- cell receptor (TCR) sequencing suggested a pre-thymic formation for most of the CNAs, although post thymic clones had high enough mosaicism to be detected.

I also tested the hypothesis in CD as another autoimmune condition. I isolated the lymphocytes of CD patients (n=10) using an *ex vivo* expansion of gluten-peptide reactive cells and examined them for somatic CNAs. Using the same CGH approach I found that 70% of tested patients harbored somatic mutations in their gluten-reactive T-cells with three recurrent genes *CHD7, C8orf33, and LOC339685.* Moreover, I identified recurrent genes between T1D (Human and NOD mice) and CD that have previously been reported to be associated with celiac autoimmunity such as the *UBE2E3* gene.

My data have provided evidence for a potential causal role for PZMs in autoreactive T-cells in the pathogenesis of autoimmunity and suggested a putative mechanistic overlap between autoimmunity and cancer. These findings offer novel avenues for decrypting autoimmunity and its future individualized treatment through targeting disease-causing cells.

RÉSUMÉ

Les maladies auto-immunes sont causées par une attaque des antigènes du soi par le système immunitaire. Il est connu que l'auto-immunité dépend à la fois d'une susceptibilité héréditaire et de facteurs environnementaux. Cependant, ceux-ci, à eux seuls, ne suffisent pas à expliquer toutes ces maladies. L'état actuel de nos connaissances ne permet pas d'expliquer la discordance au niveau de l'auto-immunité entre des jumeaux monozygotes qui passent leur enfance dans un environnement partagé ou entre individus des modèles animaux de lignée consanguine élevés dans un environnement contrôlé. Cela pourrait être expliqué par des événements stochastiques. Une possibilité encore inexplorée, serait qu'un tel évènement stochastique soit des mutations post-zygotiques (PZMs) dans des lignées de cellules T auto-réactives à un antigène spécifique, au cours de leur expansion.

Pour mon projet doctoral, j'ai examiné le rôle causal potentiel des PZMs dans deux maladies auto-immunes pour lesquelles les auto-antigènes sont bien connus: le diabète de type I (T1D) et la maladie Cœliaque (CD).

J'ai commencé à tester cette hypothèse dans les souris NOD, le modèle de souris pour le T1D. En utilisant une analyse du génome entier, par hybridation génomique comparative à haute résolution (CGH) d'ADN de cellules T CD4+ mémoires provenant de ganglions lymphatiques pancréatiques de souris diabétiques NOD (n=25), j'ai identifié huit aberrations mosaïques du nombre de copies (CNA) récurrentes exclusivement dans les lymphocytes auto-réactifs et indépendamment dans différentes souris. Pour certains de ces CNAs, le ou les mêmes gènes sont impliqués entre les différentes souris, dont

beaucoup ont une fonction immunitaire ou proliférative et/ou une association avec des maladies auto-immunitaires comme *Ilf3* et *Dgka*.

De plus, j'ai montré que 66.6% des patients nouvellement diagnostiqués avec le T1D (n=17) présentent des mutations somatiques dans leurs cellules T réactives à l'insuline *ex vivo*. J'ai aussi identifié des gènes récurrents impliqués indépendement chez plus qu'un patient, certains ayant des fonctions régulatrices de la prolifération et différentiation des cellules T tels que les gènes *CASZ1* et *E2f1*.

Aussi bien chez l'homme que chez les souris diabétiques, j'ai identifié des CNAs dans des lymphocytes non auto-réactifs en expansion au cours du processus normal de défense de l'hôte; cependant, ces CNAs étaient significativement plus petites (2 fois plus petits) que ceux identifiés dans les cellules auto-réactives. De plus, la faible clonalité des cellules T déterminée par séquençage du récepteur des cellules T (TCR) suggérent une origine pré-thymique pour la plupart de ces CNAs, bien que des clones avec une clonalité post-thymique assez élevé pour expliquer le mosaicisme était aussi présents. J'ai aussi testé l'hypothèse dans la CD comme autre condition auto-immune. J'ai isolé des lymphocytes de patients avec la CD (n=10) en utilisant une expansion *ex vivo* de cellules réactives au peptide gluten et testé ces cellules afin de déceler la présence de CNAs somatiques. En utilisant la même approche par CGH, j'ai trouvé que 70% des patients testés présentaient des mutations somatiques dans leurs cellules T réactives au gluten avec trois gènes indépendemnt récurrents chez différents patients, *CHD7*, *C8orf33*, et *LOC339685*. De plus, j'ai identifié des gènes récurrents entre les maladies T1D (chez l'Homme et la souris NOD) et CD déjà rapportés comme étant associés à une auto-immunité cœliaque tel que le gène *UBE2E3*.

Mes données ont démontré un rôle causal des PZMs dans les cellules T auto-réactives dans la pathogenèse de l’auto-immunité et suggèrent un mécanisme possiblement chevauchant l'auto-immunité et lecancer. Ces résultats ouvrent de nouvelles perspectives de recherche dans le décryptage de l’auto-immunité et de son futur traitement individualisé en ciblant les cellules causant la maladie.

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Finally, I would like to thank and acknowledge Sultan Qaboos University, Oman for supporting my education with a doctoral-studies scholarship.

Contribution to Original Knowledge

The following are original contributions I have made in exploring the potential role of somatic mutations in autoreactive cells in the pathogenicity of autoimmunity:

Chapter Three: In this chapter, I developed an original working protocol to test the never explored somatic mutations hypothesis in Type 1 Diabetes in the animal model NOD mice. I have identified lymphocyte-exclusive mosaic somatic copy number aberrations (CNAs) with highly non-random independent involvement of the same gene(s) across different mice, some with an immune function and some have an association with autoimmune diseases such as *Ilf3* and *Dgka.* I also showed that CNAs in control samples consisting of lymphocytes expanded during standard host defense (*Leishmania major)* are fewer and significantly smaller in size. I have also determined a pre-thymic stage for the formation of these CNAs by sequencing their TCRs.

Chapter Four: In this chapter, I have explored the potential role of somatic mutations in autoreactive cells in human T1D. In this chapter since I do not have access to the inflammation site, I used an *ex vivo* protocol to activate the autoreactive cells by exposing PBMCs from newly diagnosed patients with T1D to Insulin as an antigen. By sorting the autoreactive clones and examining them for CNAs I showed that about 70% of patients carry somatic CNAs in their Insulin reactive clones. Moreover, I tested our protocol for specificity by a re-stimulation test of the sorted reactive cells and showed that our protocol is specific in obtaining antigen-reactive cells. Also, I identified recurrent genes in two or three newly diagnosed T1D patients including genes with an immune and/or a proliferative function such as *IKZF1* and *CUX1.* Moreover, I identified recurrent genes among newly diagnosed diabetic patients and the previously tested diabetic NOD mice in chapter three such as (*CASZ1* and *E2f1*) that have a T-cell proliferation and differentiation regulatory function. Finally, I showed the lymphocytes involved in host defense also harbored somatic mutations but similar to what was found in NOD mice; these are significantly smaller in size.

Chapter Five: In this chapter, I extended my investigation to Celiac disease (CD) as another autoimmune disease. I developed an *In Vitro* protocol to stimulate the autoreactive lymphocytes obtained from CD patients after undergoing a gluten challenge. Here, I presented preliminary data supporting our somatic mutations hypothesis. I showed the existence of copy number somatic mutations in gluten-reactive lymphocytes of 70% of tested patients with three recurrent genes (*CHD7*, *C8orf33*, and *LOC339685*). Interestingly, I was able to identify recurrent genes among NOD, T1D and CD diabetic cases that are known to be associated with autoimmunity in general and CD in particular, such as *UBE2E3* and *NFIA.*

Contributions of Authors

Chapter One: Statement of purpose

Maha Alriyami: Organization and writing of text.

Chapter two: Comprehensive Literature review

Maha Alriyami: Reviewing relevant literature, organization and writing of text.

Chapter Three: Clonal copy-number mosaicism in autoreactive T-lymphocytes in diabetic NOD mice

Maha Alriyami: Designed and executed the experiments, results analysis and interpretation, writing and preparation of manuscript.

Luc Marchand: Technical expertise and preforming the multiplex ligation-dependent probe amplification and CBS analysis.

Quan Li: Bioinformatics CBS analysis and MiSeq analysis.

Xiaoyu Du: Technical expertise and executing of the TCR sequencing.

Martin Olivier: Research collaborator, Technical expertise and conducting the *Leishmania major* mouse infection and contribution with providing BALB/c mice.

Constantin Polychronakos: Research supervisor and mentor, results interpretation, manuscript editing and corresponding author.

Chapter Four: Somatic mutations in clonally expanded memory T-lymphocytes in newly diagnosed patients with Type 1 diabetes

Maha Alriyami: Designed and executed the experiments, results analysis and interpretation, writing and preparation of manuscript.

Luc Marchand: Bioinformatics CBS analysis.

Xiaoyu Du: Technical expertise and executing of the TCR sequencing.

Khalid Bawazeer: Helped with the re-stimulation experiment and in making Figures 4.3 and 4.4.

Yao Wang: Originally developed the T- cell culture proliferation protocol for another project.

Constantin Polychronakos: Research supervisor and mentor, result interpretation, manuscript editing and corresponding author.

Chapter Five: Somatic mutations in clonally expanded memory T-lymphocytes in newly diagnosed patients with Celiac disease

Maha Alriyami: Designed and executed the experiments, results analysis and interpretation, writing and preparation of manuscript.

Luc Marchand: Bioinformatics CBS analysis.

Jonathan Wyse: Patients recruitment.

Brent Richards: Research collaborator, patient recruitment and ethics.

Constantin Polychronakos: Research supervisor and mentor, result interpretation, manuscript editing and corresponding author.

Chapter Six: Discussion and final conclusions

Maha Alriyami Organization and writing of text.

Ethics Statement

Research presented in this dissertation was approved by:

- **Animal Studies:** RI-MUHC Facility Animal Care Committee (FACC), following the guidelines established by the Canadian Council on Animal Care and the McGill University Animal Care Committee. Animal Authorization Protocol number: 7517 entitled “Post zygotic mutation in auto-reactive lymphocytes of NOD mice”.

- **Human Studies:** The MUHC Research Ethics Board and the Lady Davis Ethics board.

  Protocol number: 1230- PED entitled “A cell-lineage based approach to the immune dysregulation in type 1 diabetes”.

  Protocol number: A09-M86-14B entitled “The identification of driver mutations in celiac disease”.

Other Contributions

M Alriyami, C Polychronakos, Book review: Scientific Writing for Impact Factor Journals, J Med Genet-2015-103182 (2015).

Polychronakos, C. & **Alriyami, M**. Diabetes in the post-GWAS era. Nat. Genet. 47, 1373–1374 (2015).

Abbreviations

25(OH)D	25-hydroxyvitamin D (vitamin D metabolic active form)
AGA	Antigliadin antibodies
AICD	Activating-induced-cell-death
AIRE	Autoimmune-regulator AIRE
ALPS	Autoimmune lymphoproliferative syndrome
APC	Antigen presenting cell
APS1	Autoimmune polyendocrinopathy syndrome type 1
BAFF	B-cell activating factor
BBDP	Bio-breeding diabetes prone rat
BCR	B-cell receptor
C region	TCRs constant region
CBS	Binary segmentation algorithm
CD	Celiac disease
CGH	Comparative genomic hybridization
Chr	Chromosome
CNA	Copy number aberrations
CNV	Copy number variation
CTL	Cytotoxic T cell
CTLA4	Cytotoxic T-lymphocyte-associated protein 4
CTS	Cataract Shionogi mouse strain
DGV	The Database of Genomic Variants
DLRS	Derivative log ratio spread
DM	Diabetes Mellitus
DN	Double negative thymocyte
DP	Double positive thymocyte
DSBs	Double-strand breaks
EMA	Antiendomysial antibody
FACS	Fluorescence activated cell sorting
FoSTeS	Fork Stalling and Template Switching
GAA/ GAD	Glutamic acid decarboxylase
GCK	Glucokinase

GDM	Gestational diabetes mellitus
GFD	Gluten-free diet
GFD	Gluten free diet
GWA	Genome wide association studies
GWAS	Genome wide association studies
H-chain	Heavy chain of the B-cell receptor
HEV	Human Enterovirus
HLA	Human leukocyte antigen
HNF	Hepatocyte nuclear factor
Hsp70	Heat shock protein
IA-2/ ICA512	Protein tyrosine phosphatase
IAA	Insulin autoantibodies
ICA	Islet cell autoantibodies
IDF	The international diabetes federation
IFH1	Interferon-induced helicase c domain-containing protein 1
IL-1β	interleukin-1β
IL2RA	Interleukin 2 receptor alpha
INS	Insulin
IPEX	Immunodysregulation polyendocrinopathy enteropathy X-linked syndrome
J segment	TCRs joining segment
JRA	Juvenile rheumatoid arthritis
L sequence	TCRs leader sequence
L-chain	Light chain of the B-cell receptor
L. major	*Leishmania major*
LADA	Latent autoimmune diabetes in adults
LD	Linkage disequilibrium
LIEs	Intraepithelial lymphocytosis
LRR	Base-2 log ratio
MHC	Major histocompatibility complex
MIDD	Maternally inherited diabetes and deafness
MLPA	Multiplex Ligation-dependent Probe Amplification
MODY	Maturity-Onset-Diabetes of the Young

mTDNA	Mitochondrial DNA
mTEC	Medullary thymic epithelial cells
NAHR	Non-allelic homologous recombination
NDM	Neonatal diabetes mellitus
NGS	Next generation sequencing
NHEJ	Non-homologous end-joining
NK	Natural-killer T-cells
NOD	Non-obese diabetic mice
nsSNPs	Nonsynonymous SNPs
OGT	Oxford Gene Technologies
PAMPs	Pathogen-associated molecular patterns
PBMCs	Peripheral blood mononuclear cells
PD1	Programmed death 1
PLNs	Pancreatic lymph nodes
PNDM	Permanent neonatal diabetes mellitus
PRR	Pattern recognition receptor
PTPN22	Non-receptor type 22
PZM	Post zygotic mutation
R	Arginine
Rh-PI	Recombinant human Proinsulin
RSS	Recombination signal sequences
SCID	Severe combined immunodeficiency
SLE	Systemic lupus erythematosus
SP	Single positive lymphocyte
T1D	Type 1 diabetes
T1DGC	The T1D Genetics Consortium
T2D	Type 2 Diabetes
TCM	Central memory T cells
TCR	T- cell receptor
TEM	Effector memory T cells
TEMRA	CD45RA-reverted effector memory
Tfh	Follicular helper T cells

Th	T-helper cells
TLR	Toll-like receptor
TNDM	Transient neonatal diabetes mellitus
TNF	Tumour-necrosis factor
Treg	Regulatory T- cells
TT	Tetanus toxoid
tTG	Tissue Transglutaminase IgA antibody
V region	TCRs and BCRs variable region
VNTR	Variable number of tandem repeats
W	Tryptophan
WGA	Whole genome amplification
β-cells	Pancreatic beta cells
λs	The sibling relative risk

CHAPTER ONE Introduction and statement of purpose

Autoimmune diseases are among the most common chronic health problems. Close to 5% of the general population develops some form of autoimmunity, yet its underlying causes although intensively studied are still not fully known. It is known that autoimmune diseases have common mechanisms and are caused by both genetic and non-genetic risk factors. In the current genomic era, the genetic part of the equation is well established with the major risk loci having been identified, unlike the environmental part that is still unclear. Moreover, current knowledge does not explain the discordance of autoimmunity in monozygotic twins living in a shared environment or in some animal models kept in a controlled environment. These could be explained by stochastic events.

Here, we test the hypothesis that somatic mutations in expanding autoimmune cells represent such a stochastic event and are a common pathogenetic mechanism. In this hypothesis, the persistent proliferation of self-reactive lymphocytes that is usually hindered by a series of checkpoints is allowed due to somatic mutations in these cells that permit the cell to bypass multiple regulatory checkpoints, causing autoimmunity. This hypothesis proposes similar pathogenic mechanisms between autoimmunity and cancer. We set out to test this hypothesis in Type 1 diabetes and celiac disease, but it is likely that the same mechanisms operate in all or most other autoimmune diseases. Our findings show that this somatic mutation hypothesis perhaps is the missing piece of the autoimmunity puzzle.

CHAPTER TWO Comprehensive Literature review

2.1 The Immune system

The immune system is contemplated as the body's sixth sense that evolved in multi-cellular organisms over years of infection and selective pressure with a sole function of safeguarding the host from a universe of pathogenic microorganisms that likewise is continually evolving. Moreover, it also eliminates toxins and allergens that pass into the body through mucosal surfaces (Chaplin, 2010).

The immune system operates, by detecting structural hallmarks of pathogens or toxins, distinguishing them from host cells and subsequently eliminating them to maintain normal homeostasis. The mechanisms of the immune system consist of two general arms: The innate immune response and the adaptive immune response. The major distinction between the two systems is the specificity of receptors used to recognize pathogens (Medzhitov, 2007).

2.1.1 The Innate Immune Response

The innate immune system is the first line of defense with all its' signaling mechanisms are through receptors encoded in the host's germline. These receptors consist of a limited repertoire and react by recognizing molecular prints that are not unique to particular exogenous agents and antigens (Chaplin, 2010). The innate immune system comprises physical barriers (epithelial layers), secreted mucus layer, soluble proteins and small bioactive molecules (defensins, ficolins, cytokines, and chemokines) and membrane receptors (Chaplin, 2010). The constant availability of these barriers and receptors before the exposure to exogenous agents facilitates the prompt response of the innate system. Cells of the innate immunity ubiquitously express pattern recognition receptor (PRR) molecules that recognize molecular structures unique to the specific pathogens and therefore mediate the activation of antimicrobial defenses and trigger the adaptive immune response. The PRR include the scavenger receptors (reviewed in (Canton, Neculai, & Grinstein, 2013)) and the trans-membrane Toll-like receptors (TLRs) family (reviewed in (Tobias & Curtiss, 2005)). These receptors are primarily present on monocytes/macrophages and dendritic cells, which also act as antigen-presenting cells (APC). PRRs has a comprehensive specificity and recognize a wide spectrum of pathogenic trademark prints known as pathogen-associated molecular patterns (PAMPs), such as bacterial lipopolysaccharide, peptidoglycan, lipoteichoic acids, cell-wall lipoproteins, viral double-stranded RNA and fungal β-glucan (a component of fungal cell walls) (reviewed in (Medzhitov, 2007)). Fascinatingly, although PRRs do not differentiate between pathogenic microorganisms from symbiotic ones, the immune system manages to maintain homeostasis under normal conditions (Rakoff-Nahoum, Paglino, Eslami-Varzaneh, Edberg, & Medzhitov, 2004).

When the PRRs are provoked by their ligand, they induce an inflammatory response by producing pro-inflammatory cytokines such as tumor-necrosis factors (TNF), interleukin-1β (IL-1β) and IL-6. These induce vasodilation and elevate blood vessel permeability facilitating the recruitment of serum proteins and leukocytes to the site of infection (Medzhitov, 2007). If the innate response fails to clear the invading pathogen, the adaptive immune system gets enabled to assist via more sophisticated mechanisms.

2.1.2 The Adaptive Immune Response

The adaptive immune system consists of a small number of cell types that unlike the innate system recognize unique processed antigens from specific pathogens. These bone-marrow derived cells proliferate after encountering an antigen to generate a sufficient response to fight it. Cells of the adaptive immunity are categorized into two major divisions of lymphocytes: T-cells (mostly αβ T-cells) and B-cells. These cell types identify antigens with a high degree of specificity, in different manners (T-cells cell-mediated responses and B-cell humoral responses); nevertheless, they cooperate through networks of signaling pathways to clear antigens. Other minor classes of lymphocytes also exist: γδ T-cells and innate-like lymphocytes include B1 cells and natural-killer T-cells (NK-cells). These minor subsets have receptors with conserved structures and restricted diversity (Bendelac, Bonneville, & Kearney, 2001).

In adaptive immunity pathogen recognition is mediated by antigen receptors that are clonally diversified on the lymphocytes: T- cell receptors (TCRs) expressed on the surface of T-cells and B-cell receptors (BCRs) on the surface of B-cells.

2.1.2.1 T-cells

TCRs expressed on the surface of T-cells recognize antigenic peptides bound to major histocompatibility complex (MHC) molecules (a set of surface molecules that binds to antigenic peptides and display them on their surface), discussed in section 2.4.2.1.1). T-cells (αβ) are further categorized into two major classes: T-helper cells (Th); marked by the co-receptor CD4+, and cytotoxic T cells (CTLs), marked by CD8+.

The Th class (also called CD4+ cells) recognizes antigenic peptides bound to MHC class II molecules that are exclusively expressed on the surface of APCs in the context of appropriate co-stimulatory molecules. MHC molecules present peptides that result from protein degradation inside the APCs. Naïve CD4+ cells (never encountered an antigen, discussed below) differentiate into several subsets that differ by their cytokines profile (Th1, Th2, Th9, Th17, Th22, regulatory T-cells (Treg) and follicular helper T cells (Tfh)) (reviewed in (Golubovskaya & Wu, 2016)). The differentiation of a naïve cells into these subsets is triggered by specific cytokines. For example, a naïve CD4+ cell differentiates into a Th1 by IL-12 and IFN- γ, whereas, Th2 by IL-2. Treg cells are unlike other Th cells as they do not induce an immune response; on the contrary, they suppress T-cell action to protect components of self. This suppressive function of Treg cells is crucial in the context of autoimmunity, in which they maintain peripheral self-tolerance (further discussed in section 2.2.2).

The CTLs class expresses CD8+ and monitors all nucleated cells in the body for the presence of intracellular pathogens. CTLs identify antigenic peptides bound to MHC class I molecules that are expressed on the surface of nucleated host cells. Cytotoxicity exerted by CD8+ cells destroys the infected cell either directly through Fas signaling (Nagata, 1996) or perforin signaling (Trapani & Smyth, 2002) pathways and/or indirectly via releasing cytokines (Andersen, Schrama, Thor Straten, & Becker, 2006; Tomiyama, Matsuda, & Takiguchi, 2002). Moreover, CTLs are capable of detecting quantitative and qualitative antigenic variations and have a protective role against spontaneous malignant tumors (Castelli et al., 2000; van der Bruggen et al., 1991).

T-cells can further be categorized into two subgroups, naïve and memory, based on their prior exposure to a cognate antigen that determines their migrational patterns and functional capacities. In humans, distinguishing these two subgroups is based on their expression of isoforms of CD45 (a phosphatase involved in cell signaling): CD45RO+ on memory T-cells and CD45RA+ on naive T-cells (Akbar, Terry, Timms, Beverley, & Janossy, 1988; Merkenschlager, Terry, Edwards, & Beverley, 1988; Yamada, Kaneyuki, Hara, Rothstein, & Yokoyama, 1992).

Naïve T-cells, those that never encountered an antigen, express homing receptors (L-selectin and CCR7) that mediate their circulation between blood and secondary lymphoid organs (lymph nodes and spleen) (Sallusto, Lenig, Forster, Lipp, & Lanzavecchia, 1999). L-selectin allows naïve T-cell attachment to the vessels of the lymph-nodes and CCR7 is a specific chemokines receptor for those expressed in lymph-nodes (MIP-3β and SLC) (Campbell et al., 1998; Gunn et al., 1998). Circulation of naïve cells between lymph nodes enables them to inspect the lymph node environments of several tissues, raising their chances of encountering specific antigen. Naïve T-cells are maintained by homeostatic proliferation until they experience an APC-dependent novel antigen encounter. Upon such encounter a naïve T-cell acquires an activated phenotype via TCR and CD28 signalling and differentiates into a memory cell. Upon the elimination of the antigen, cells persist in a latent state as memory cell until a second encounter of the specific antigen in which a prompt and more heightened re-expression of the effector function is held. This phenomenon of immunological memory is the foundation of the vaccination.

Memory cells can be further categorized into functionally distinct subsets based on their expression of CCR7 and CD45RO: central memory (TCM), effector memory (TEM) and CD45RA-reverted effector memory (TEMRA). TCMs are antigen-experienced; IL-2 producing cells that express CD45RO and CCR7. These cells are predominantly migrating between blood and lymph nodes (Butcher & Picker, 1996; Gunn et al., 1999). These clones of cells serve as long-lived reservoirs of memory in which upon being stimulated by the same antigen they divide and give rise to long-lived TCM and short-lived TEM cells. TEM cells are C45RO+/CCR7- that relocate to the site of infection and neutralize the pathogen (C. R. Mackay, 1999; Sallusto et al., 1999). Finally, the TEMRA cells are CD45RO-/CCR7- and prone to CD28 loss. This group of cells has cytotoxic activity and is generally associated with NK cells (Sallusto, Geginat, & Lanzavecchia, 2004; Verma et al., 2017).

T-cells recognize and respond to an unlimited number of pathogen-derived peptides presented in the context of MHC on APC via a large variety of receptors expressed on their surface. T-cells have a single antigen specificity per cell. Therefore, a massively diverse number of receptors must be generated, to ensure reactivity to all possible invaders (Janeway CA Jr, 2001). These receptors are not encoded by distinct genes, as the number of genes required will exceed by far the number of genes in the entire human genome (Market & Papavasiliou, 2003). To establish the indispensable level of diversity of the receptor's repertoire, the encoding genes are created by a sophisticated somatic recombination machinery that is specific to lymphocytes. In this process, distant DNA sequences are randomly joined in different combinations to give rise to receptors that can respond to the unlimited number of pathogens.

TCRs are heterodimer proteins that consist of two highly diverse chains; α and β linked by disulfide bonds. They are expressed on the surface of T-cells and form complexes with the invariant CD3 chains. Each TCR chain comprises a variable (V) amino-terminal region, a joining (J) and a constant (C) region.

TCRα locus (chromosome (Chr) 14 both in human and mice) contains 70-80 alternative Vα gene segments each headed by an exon encoding the leader (L) sequence, 61 alternative gene segments for the Joining segment (Jα) plus a single C gene. The TCRβ locus (Chr 7 in human, Chr 6 in mice) contains a cluster of 52 alternative Vβ gene segments, two separate clusters each contains a single D gene segment and J gene segment of six or seven genes plus a single C gene. The C gene in both α and the β genomic loci contains exons encoding the constant, hinge domains and the transmembrane and cytoplasmic regions. Between the V and J segments, random amino acids are inserted (CDR3 region), increasing somatic diversity. The V region with the CDR3 forms the most variable region of the TCR, and it is where the interaction with pathogenic peptide occurs (Janeway CA Jr, 2001). This provides for a large number of probable rearrangement combinations. Although multiple segment exists in the germ-line, only one is expressed for each chain per T-cell.

After their generation in the bone marrow, T-cells migrate to the thymus where the TCR gene rearrangement takes place. Briefly, TCR gene segments are flanked by recombination signal sequences (RSS) (heptamers and nanomers) that are recognized by the RAG enzymes (RAG1 and RAG2) that are fundamental in carrying out cleavage reactions in the recombination process (van Gent et al., 1995). During the somatic recombination, a randomly selected V_α gene segment rearranged to a J_α gene segment to form the variable domain. In the process, random amino acids are added in-between, to create the CDR3. This is followed by transcription and splicing of the VJα exon to Cα generating mRNA that translates into the TCR_α. Similarly, the V_β, D_β, and J_β gene segments rearrange to form the variable domain that transcribes and splices to join C_β.

This generates mRNA that translates into the TCR_β. Also, extraneous level of diversity is introduced during the V(D)J recombination by insertion and deletion of the random nucleotides that form the CDR3 at the junctions between rearranged gene segments (junctional diversity). Finally, since α and β chains ultimately pair to form the α: β TCR heterodimer, the possibilities of different pairing among the chains also increase the diversity (Janeway CA Jr, 2001; Market & Papavasiliou, 2003). The recombination process accompanied by mechanisms of increasing variability in the TCR was estimated to create approximately a minimum of 10^{18} potential antigen-specific TCRs (Janeway CA Jr, 2001).

2.1.2.2 B-cells

B-cells, the second arm of the adaptive immune system, assist in combating pathogens by presenting antigens to T-cells, releasing antibodies, and providing co-stimulation and regulation of T-cells by secreting cytokines. The newly produced B-cell carries approximately 10^5 antibody molecules on its plasma membrane, in which all have the exact unique antigen-binding site (Alberts B, 2002). Unlike TCRs that recognize fragments of antigenic peptides, BCRs identifies and bind to antigens in their native form (Goodnow, Sprent, Fazekas de St Groth, & Vinuesa, 2005). Once a naïve B-cell encounters an antigen, it proliferates and differentiates into an effector plasma cell that continuously release soluble antibodies, which is regarded as the principal function of these cells (Alberts B, 2002).

Antibodies (also called immunoglobulins) are glycosylated bivalent molecules with two antigen-binding sites expressed on the surface of B-cells as antigen receptors (BCRs) or secreted to adhere and neutralize antigens (Hoffman, Lakkis, & Chalasani, 2016).

Based on the number of antigenic determinants of the foreign antigen, antibodies fight pathogens by cross-linking to the antigens forming a large lattice that is next phagocytosed and eliminated by macrophages (Alberts B, 2002). Antibodies are generally described by their Y-shape structure. They are four polypeptide molecules with two light chains (L) and two heavy chains (H) that are attached both by covalent and non-covalent bonds. The N-terminal regions of both L and H chains collectively construct the V region, which is the antigen-binding site (Hoffman et al., 2016). There are five classes (isotypes) of antibodies (IgA, IgD, IgE, IgG, and IgM) and a number of sub-classes. Each of the major isotypes is encoded by its class of heavy chain C-terminus (Fc region) α, δ, ε, γ, and μ, respectively (Alberts B, 2002). Comparable to T-cells, genomic regions encoding antibodies (BCRs) undergo major somatic recombination events, taking place in the bone marrow, in order to create sufficient diversity to combat the wide range of potential pathogens. Moreover, additional mechanisms including non-template nucleotide addition (somatic hypermutation) also take place during a late phase of the immune response in peripheral lymphoid tissues (such as the spleen, lymph nodes and tonsils) to generate a highly diverse receptor repertoire (Hoffman et al., 2016). It was estimated that these processes allow the formation of at least 10^{12} specific antibody binding sites (Alberts B, 2002).

2.2 The Pathogenesis of Autoimmune Disease

The fundamental function of the diverse pleiotropic immune cells is to safeguard the host from infectious agents. Failure in this system leads to one of two pathological forms: first, immune deficiency syndromes in which one or more modules of the immune system are incapable of responding protectively to a pathogen and, secondly autoimmunity in which the immune system fails to identify its self-cells and mistakenly launches an immune response against its own (L. Wang, Wang, & Gershwin, 2015). For the immune system to function correctly, it must be able to distinguish self-antigens from non-self or foreign antigens by maintaining a delicate balance between host defense and self-tolerance. In the state of loss of self-tolerance, the immune system produces self-reactive cells and autoantibodies that react against self-antigens causing their destruction. This results in autoimmune disorders such as Type 1 diabetes (T1D) and celiac disease (CD), which are the focus of this dissertation.

Throughout the early years of the twentieth century, a misconception prevailed, that the normal body is not capable to endangering itself by creating what was described as “forbidden clones”, which are immune cells with the ability to recognize and attack its self-antigens, a concept described by Paul Ehrlich as “horror autotoxicus” (Ehrlich, 1961; Silverstein, 2001). In 1948, Macfarlane Burnet included in his landmark “the clonal selection theory of acquired immunity” his Nobel Prize-winning hypothesis of ‘forbidden clones’ in which he proposed that immunological unresponsiveness to self, which is called ‘tolerance’, is a characteristic adopted during development and works in guarding against “horror autotoxicus” (F. M. Burnet, 1959). Contemporary studies proved the hypothesis that a significant fraction of generated immune cells have receptors capable of identifying and binding to self-antigens; however, via several checkpoints and mechanisms, they are prevented from exerting any destructive action. This phenomenon is a by-product of the purposely-random T-cell and B-cell receptor-generating V(D)J recombination process. Approximately, 20-50% of TCRs and BCRs formed by the V(D)J recombination process recognize and bind, with a potentially high- risk affinity, to self-antigens (Goodnow et al., 2005; Ignatowicz, Kappler, & Marrack, 1996; Laufer, DeKoning, Markowitz, Lo, & Glimcher, 1996; Wardemann et al., 2003; Zerrahn, Held, & Raulet, 1997). Cellular mechanisms have evolved to suppress the activity of these ‘forbidden’ clones and attain self-tolerance. These mechanisms are effective and well regulated, proven by the fact that only 3-8% of the population develop autoimmune diseases (Jacobson, Gange, Rose, & Graham, 1997). Generally, there are four cellular strategies of “checkpoints” to manage clones displaying self-reactive receptors: first, they will be triggered to die (Goodnow et al., 2005); second, they can edit their self-reacting receptor by further V(D)J recombination and/or somatic hypermutation (in B-cells) to display a new less-reactive receptor (Nemazee & Hogquist, 2003); third, anergy mechanisms that involves intrinsic modifications in biochemical reactions and gene expression to reduce the capability of the cell to be triggered by self-reactive receptors (Benschop et al., 2001; Fields & Erikson, 2003; Grossman & Paul, 2000; Healy & Goodnow, 1998; Schwartz, 2003); finally: if the cell escaped the above mechanisms, immunological ignorance takes place in which extrinsic control mechanisms interfere including, limiting the supply of vital growth factors, stimuli pro-inflammatory mediators and other factors (Goodnow et al., 2005).

2.2.1 Tolerance mechanisms in central lymphoid organs

TCRs and BCRs play a dual role in transmitting signals that can be either stimulating to launch an immune response against pathogens or inactivating to inhibit self-reactive clones (Healy & Goodnow, 1998). This positive or negative response of lymphocyte to antigens is controlled by four types of inputs: the antigen concentration, the receptors avidity to the antigen-MHC complex, the timing of antigen encounter and the association of antigen with co-stimuli from the innate system or other lymphocytes (Healy & Goodnow, 1998). Central tolerance in the thymus (for T-cells) and bone marrow (for B-cells) plays a fundamental role in shaping immune system homeostasis. Receptors responding to self-antigens are managed via several checkpoints prohibiting their response and triggering potential autoimmunity including receptor editing and cellular deletion. Nevertheless, deletion appears to be the principal measure as only 5% of maturing thymocytes are exported as mature T-cells (Laufer, Glimcher, & Lo, 1999; Palmer, 2003; van Meerwijk et al., 1997).

Thymocytes at their earliest stages lack the expression of the co-receptors CD4 and CD8 ($CD4^{-}CD8^{-}$) and are termed double negative (DN) cells. These immature DN thymocytes differentiate to express a pre-TCR that constitutes a complex with the co-receptor CD3 and finally express both CD4 and CD8 to constitute a double positive (DP) thymocyte. These DP undergo a positive selection process in which stromal cells of the epithelial layer of the thymic cortex act as APCs by displaying composites of self-peptides and MHC (Derbinski, Schulte, Kyewski, & Klein, 2001; Heath, Moore, Parnell, & Mason, 1998; Klein, Klein, Ruther, & Kyewski, 1998; Klein, Klugmann, Nave, Tuohy, & Kyewski, 2000; Vafiadis et al., 1997; Werdelin, Cordes, & Jensen, 1998). TCRs will be positively selected for recognition and binding to antigen-MHC complex (low avidity is required), and this triggers maturation signals that inhibit the expression of RAG enzymes and thereby inhibiting further editing of the TCR (Palmer, 2003). Moreover, these signals enhance TCR expression and induce the display of homing receptors (Goodnow et al., 2005). Most of the thymocytes that fail to express an MHC-interacting TCR will undergo death by neglect (L. Wang et al., 2015). Nonetheless, a minority will trigger TCR editing process that involves down-regulation of TCRs and further expression of RAG enzymes to generate a potentially less self-engaging α-chain (McMahan & Fink, 1998, 2000).

A positively selected DP cell will next migrate to the medulla, where it will be further tested for its TCRs' reactivity. In the medulla, self-antigens are presented on medullary thymic epithelial cells (mTEC) and dendritic cells that express co-stimulatory molecules, such as CD80 (also known as B7.1) (Freedman, Freeman, Horowitz, Daley, & Nadler, 1987; Freeman et al., 1991; Yokochi, Holly, & Clark, 1982) and CD86 (B7.2) (Azuma et al., 1993; Freeman, Borriello, et al., 1993; Freeman, Gribben, et al., 1993), the ligands for T-cells co-receptor CD28 (Aruffo & Seed, 1987; Gross, St John, & Allison, 1990). Here, actively engaging TCRs to self-peptide-HLA complex triggers apoptosis of the DP cell (negative selection), whereas surviving cells will finally differentiate into single-positive (SP) cells expressing either CD4 or CD8 (Palmer, 2003). It is noteworthy that the positive and negative selection process might not be sequential events and thymocytes can undergo a negative selection at any stage of their development (as DN, DP, and SP) (Baldwin, Trenchak, Altman, & Davis, 1999; Ohashi, Pircher, Burki, Zinkernagel, & Hengartner, 1990; Spain & Berg, 1992).

Discovering the capability of thymic epithelial cells (specifically medullary cells) in expressing a diverse range of ordinarily tissue-specific antigens highlighted their role in central tolerance (Derbinski et al., 2001). This expression is regulated by the transcription factor autoimmune-regulator (AIRE) that causes the transcription of organ-specific genes. Mutations in the *AIRE* gene affect the negative selection in the thymus causing the multi-organ autoimmune disease autoimmune polyendocrinopathy syndrome type 1 (APS1) (Betterle, Greggio, & Volpato, 1998).

The first example of tissue-specific antigens expression in the thymus to be discovered was the expression of insulin in the thymus in low levels correlating with the number of variable tandem repeats (VNTR). These VNTRs are located upstream of the insulin promoter (see section 2.4.2.1.2). My supervisors' Dr. Polychornakos laboratory, had a central role in the discovery of this phenomena (Vafiadis et al., 1997). In the thymus, expression of class III (the longer) VNTR is dominant opposed to class I (shorter) VNTR (Pugliese et al., 1997; Vafiadis et al., 1997). This finding explained the protective outcome of class III VNTRs in T1D. The higher expression of class III VNTRs promotors causes higher expression levels of insulin in the thymus and therefore, facilitate the induction of self-tolerance. Here, self-tolerance negatively selects insulin self-reactive T-cells (in T1D are the fundamental players in the pathogenesis of the disease) (Pugliese et al., 1997; Vafiadis et al., 1997). Validation of this hypothesis was demonstrated by using a mouse models in which knocking out the mouse *INS2* gene induced autoimmune diabetes (Fan et al., 2009). Moreover, with graded thymic insulin levels, a linear correlation between insulin's expression levels in the thymus and the negative selection of insulin-reactive T-cells was found. Chentoufi and Polychronakos showed that mice with low insulin levels in the thymus show measurable peripheral reactivity to insulin compared to mice with normal levels (Chentoufi & Polychronakos, 2002). Moreover, in a diabetic-prone non-obese diabetic (NOD) mice background (section 2. 4. 4), accelerated diabetes was observed (Thebault-Baumont et al., 2003).

B-cell tolerance mechanisms operate in the bone marrow shortly after their generation. If the strength of self-reactivity of the immature B-cell exceeds a certain threshold, the BCR receptor gets internalized and the maturation machinery arrests temporarily (Hartley et al., 1993; Nemazee & Hogquist, 2003). Moreover, acquisition of the homing receptor CD62L is blocked (Hartley et al., 1993) and the expression of the receptor for the B-cell-activating factor (BAFF), a circulating cytokine essential for maintaining the peripheral survival of B-cells, are poorly produced (Goodnow et al., 2005; Hartley et al., 1993; F. Mackay, Schneider, Rennert, & Browning, 2003). Meanwhile, expression of *RAG* enzymes resumes, allowing rearrangement of the secondary light chain locus to form a new BCR (Hertz & Nemazee, 1997). In case the B-cell fails to form a less self-reactive receptor, apoptosis occurs within two days in the bone marrow or soon after reaching the spleen (Hartley et al., 1993).

2.2.2 Tolerance mechanisms in the periphery

Though central tolerance consists of sophisticated mechanisms of editing and deletion to eliminate self-reactive lymphocytes, it is not failsafe. A significant fraction of self-reactive lymphocytes escape central tolerance to the bloodstream, either because they bind with low avidity to self-antigens or the self-antigens do not exist in sufficient abundance in the primary lymphoid organs (Goodnow et al., 2005). Therefore, further tolerance mechanisms exist in the periphery to deal with these lymphocytes including energy, clonal deletion, ignorance (persistence of self-reactive T-cells in a naïve state in the periphery) and immune regulation of the self-reactive lymphocyte (Mueller, 2010; Xing & Hogquist, 2012).

Anergy is considered the dominant peripheral tolerance mechanism for T-cell clones. T-cell activation is mediated by a TCR signal and a co-stimulatory signal induced by CD28 binding to its APC co-stimulatory molecules CD80/86. In the absence or disruption of the second signal (CD28-CD80/86 interaction) a state of long-term hyporesponsiveness is induced known as anergy, in which TCR signaling and IL-2 expression are suppressed (Xing & Hogquist, 2012). One example of anergy T-cell suppression is mediated by CTLA-4 (a structural homolog of CD28) expressed on T-cells. CTLA-4 expression takes place shortly after T-cell activation, and it competes with CD28 for the interaction with CD80/86 with a higher binding avidity, transducing a negative regulation cascade of T-cell (Krummel & Allison, 1996; Walunas et al., 1994). Mutations in *CTLA-4* gene cause CTLA-4 haploinsufficiency and a compromised ligand binding. This causes a complex immune dysregulation syndrome with features of autoimmunity and immunodeficiency (Schubert et al., 2014).

Clonal deletion of self-reactive lymphocytes in the periphery is achieved through apoptotic cell death mediated by the apoptotic signaling pathways of the death receptor Fas (CD95) (Kawabe & Ochi, 1991; Strasser & Pellegrini, 2004; Xing & Hogquist, 2012). Fas is a death-domain-containing receptor, expressed on T-cells and can be activated by its matching ligand FasL (CD178) that is induced on T-cells after its activation (Cohen & Eisenberg, 1991; Xing & Hogquist, 2012). Activation of Fas induces an apoptotic cascade "Caspase-8" leading to the activating-induced-cell-death (AICD). Deficient mice for Fas or its receptor develop progressive lymphadenopathy (significant self-reactivity) (Cohen & Eisenberg, 1991). Human mutations in Fas and FasL cause an autoimmune lymphoproliferative syndrome (ALPS), which is a rare human disease caused by leading to lymphadenopathy and autoantibodies (Bleesing, Nagaraj, & Zhang, 1993).

Another example of T-cell peripheral tolerance is the co-stimulatory mediation of the programmed death 1 (PD1) receptor by its ligand PD-L1/2 (Freeman et al., 2000; Keir et al., 2006; Nishimura, Nose, Hiai, Minato, & Honjo, 1999). Ligation of TCR with an antigen-

MHC complex and the PD-1 ligand to its receptor induce PI3K and AKt pathways that regulate the cell cycle. Moreover, PD1 signaling mediates the differentiation of naïve T-cells into Treg, which are a unique subset of T-cells that play an important role in peripheral tolerance (Xing & Hogquist, 2012). Tregs are identified by their expression of the activation marker CD25 as well as the transcription factor FoxP3 (Sakaguchi, 2004). Differentiation into a Treg cell is initiated upon the recognition of a self-reactive TCR (Itoh et al., 1999; Jordan et al., 2001). Moreover, its development occur only if the antigen is expressed in the thymus (Itoh et al., 1999). Treg cells suppress self-reactive lymphocytes via several mechanisms that are not yet fully understood including direct cell-cell interaction, production of anti-inflammatory cytokines (ex: IL-10) and by modeling the function of APCs (Shevach, 2009; Xing & Hogquist, 2012). Deficiency of functional Tregs causes autoimmunity, and allergy in human (Gambineri, Torgerson, & Ochs, 2003). For example, mutations in the *Foxp3* gene causes immunodysregulation polyendocrinopathy enteropathy X-linked syndrome (IPEX), which is a rare X linked recessive disorder that disrupts immune regulation causing multiple autoimmune disorders including early-onset T1D, severe enteropathy, eczema, anemia, thrombocytopenia, and hypothyroidism (Bennett et al., 2001; Wildin, Smyk-Pearson, & Filipovich, 2002).

2.2.3 Autoimmune Diseases

Autoimmune diseases hit when the immune system focuses its antipathogenic defenses upon self-antigens such as insulin-producing pancreatic β cells in T1D and tissue of the small intestine in CD. Geneticists and immunologists have been joining the effort in decoding the immune system and identifying the genetic and cellular basis of its functional and self-tolerance mechanisms that, when disturbed, cause autoimmunity. Although the central and peripheral tolerance mechanisms are rigorous and effective, minute number of potentially self-reacting lymphocytes escape and leak out into the periphery. However, their existence in the periphery is not always pathogenic. Therefore, autoimmunity may be physiological, in which it is temporary with no clinical symptoms or pathology (L. Wang et al., 2015). Contemporary studies revealed that development of pathological autoimmunity necessitates a genetic predisposition and environmental factors that cause these self-reactive lymphocytes or autoantibodies to be involved in inflammation and tissue destruction and ultimately pathological autoimmunity (L. Wang et al., 2015).

There are about 100 distinct identified autoimmune diseases (L. Wang et al., 2015). Some are organ-specific such as T1D or involve multiple organs reflecting an array of immunological dysfunction such as systemic lupus erythematosus (SLE) (Yu, Gershwin, & Chang, 2014). Autoimmune diseases affect 3-5% of the population with variable incidence, and prevalence rates among different diseases (Eaton, Rose, Kalaydjian, Pedersen, & Mortensen, 2007; Jacobson et al., 1997). The complexity of the geoepidemiology of these diseases increases when considering some factors such as age, gender, ethnicity, and other demographic features. Prevalence of autoimmune disease is high within first-degree relatives of cases and even higher in the case of monozygotic twins (see section 2.4.1 for T1D estimates). Autoimmune diseases can occur at any age; nonetheless, distinct diseases have a specific age of onset. Moreover, generally, this group of diseases preferentially affects women than men (L. Wang et al., 2015).

Autoimmune diseases can be either monogenic such as ALPS1 (Nagamine et al., 1997) and IPEX (Gambineri et al., 2003) or polygenic which is the case for the majority of autoimmune diseases. *MHC* loci encoding for the MHC molecule known as human leucocyte antigens (HLA) is the strongest component for autoimmune diseases (Sollid, Pos, & Wucherpfennig, 2014). Furthermore, autoimmune diseases are triggered by environmental factors that range from infectious agents (the most well-studied factors), nutrition, microbiota and xenobiotics, such as tobacco smoke (see section 2.4. 3 for T1D-studied environmental factors).

2.3 Diabetes Mellitus

The term Diabetes Mellitus (DM) encompasses various groups of diseases marked by chronic hyperglycemia that is caused by insulin deficiency, either alone or in combination with decreased ability to transduce insulin hormone signals (Florez, Hirschhorn, & Altshuler, 2003). Normally, regardless of the glucose levels, insulin is synthesized continuously by the pancreatic beta cells (β-cells), in which it is stored in pancreatic vacuoles. However, when excess glucose is detected in the blood, insulin is released into the bloodstream to be carried to different tissues. When Insulin binds to its receptors, it functions as the chief hormone is regulating glucose uptake from the blood into most cells (skeletal muscle cells and adipocytes being the most important) (Lin & Sun, 2010). Insulin is also the principal hormone in the process of storing glucose as glycogen in the liver and skeletal muscle cells. Any disruption in the biological pathways taking part in this process would imbalance the glucose homeostasis resulting in hyperglycemia causing an array of symptoms such as polyuria, polydipsia, and polyphagia. Failing to manage the disease leads to chronic hyperglycemia that results in numerous complications such as retinopathy, nephropathy, peripheral neuropathy, coronary disease, and peripheral vascular disease (Lin & Sun, 2010).

The International Diabetes Federation (IDF) described diabetes in its atlas (2015) as “a global health emergency of the 21st century”. Indeed, currently, in most countries, diabetes and its complications are major causes of death. In addition, IDF estimated that in 2045, approximately 629 million individuals would be affected by diabetes worldwide (http://www.diabetesatlas.org/). Likewise, the Canadian Diabetes Association/ www.diabetes.ca) estimated that in 2026, approximately 5 million Canadians would be affected by the disease (12.1 % of the Canadian population). Moreover, the cost of treating and managing the disease on the health-care system was about $12.2 billion and is anticipated to rise by an additional $4.7 billion by 2020 (Canadian Diabetes Association, 2016).

2.3.1 Diabetes Mellitus in History

Diabetes was first recognized in 1500 B.C.E by an Egyptian physician who described it in the Ebers Papyrus (Egyptian medical papyrus of herbal knowledge) as ‘passing of too much urine’. The Greek physician Aretaeus who lived around 120 C.E documented the first comprehensive description of the disease. Additionally, he was the first to use the term diabetes mellitus to describe it (Polonsky, 2012). “Diabetes” derives from the Greek: διά- βαινω, διά = through; βαινω; about “the urine” to go across a barrier/hurdle (in this case the kidney barrier). Nonetheless, only in 1776, the English physician Matthew Dobson confirmed the high levels of glucose in patient’s urine by evaporating urine samples of diabetic individuals and then inspecting the remaining sugar-like residue (Dobson, 1776; Polonsky, 2012).

Several significant fundamental discoveries in the field of diabetes led to our current understanding of its underlying causes and enabled the advances in treatment significantly extended the patient’s lifespan. One of these major discoveries was the identification of the pancreatic islet cells by a Paul Langerhans, a German medical student, in 1869. Langerhans (whom the cells were named later after him) described the islet cells in his dissertation, however, could not explain their function (Jolles, 2002). Another fundamental discovery was by the scientists Joseph von Mering and Oskar Minkowski in 1889 from the University of Strasbourg, France, who demonstrated how the excision of the dog’s pancreases causes diabetes (Rosenfeld, 2002; Von Mering J, 1890). Twelve years later, the American pathologist Eugene Opie from John Hopkins University identified the connection between the development of diabetes and the damage of the islets of Langerhans (Opie, 1901; Rosenfeld, 2002).

Another fundamental finding was the discovery of insulin in 1921 by the Nobel Prize winners Frederick Banting with the support of Prof. Macleod and Charles Best from the University of Toronto. Banting and his collegue were able to extract the insulin hormone (called ‘Isletin’ at first) from bovine pancreases and use it on depancreatized dogs. Their work resulted in the development of insulin injections that are the most effective treatment to date. The first successful clinical test of insulin injections on a human subject was in 1922 on Leonard Thompson, a 14 years old diabetic boy who lived for another 13 years after receiving his first insulin injection (Banting, Best, Collip, Campbell, & Fletcher, 1991; Rosenfeld, 2002).

In 1936, Sir Harold Percival made the first characterization of diabetes into its two principal forms, T1D and Type 2 diabetes (T2D) (Himsworth, 2011). Generally, T1D occurs when the pancreas fails to produce enough insulin due to autoimmune destruction and T2D when beta-cells cannot compensate for an inadequate insulin response on target tissues.

2.3.2 Diabetes Mellitus Spectrum

The original subdivision of DM into T1D and T2D is an oversimplification of a wide range of heterogeneous metabolic disorders in which T1D and T2D can be regarded as the two ends of a diabetes spectrum with intermediate subtypes rather than the two diseases being dichotomously distinct (Prasad & Groop, 2015).

2.3.2.1 Type 1 Diabetes

Type 1 diabetes also referred to by insulin-dependent diabetes or juvenile diabetes, is a complex chronic autoimmune disease caused by a targeted autoimmune destruction of pancreatic beta cells by the infiltration self-reactive T-cells into the islets of Langerhans (Polychronakos & Li, 2011). This attack leads to almost a complete loss of insulin secretion, causing a life- long health complications and causing considerable disability and a shorter lifespan making exogenous insulin a necessity for the survival of the patients.

In addition to the absence of secreted endogenous insulin; T1D characterized by the presence of autoantibodies such as islet cell autoantibodies (ICA) (first to be associated with T1D) (Bottazzo, Florin-Christensen, & Doniach, 1974), insulin (IAA), glutamic acid decarboxylase (GAA or GAD) and protein tyrosine phosphatase (IA2 or ICA512) (Polychronakos & Li, 2011; Taplin & Barker, 2008). T1D can develop at any age, but its peak presentation occurs between 10-15 years of age (Leslie & Delli Castelli, 2004). By the time the symptoms are exhibited, the β-cell mass is almost completely destroyed. T1D incidence has been increasing worldwide for several decades making its understanding and therefore, prediction and prevention highly important. T1D is discussed in depth in section 2. 4).

2.3.2.1.1 Latent Autoimmune Diabetes in Adults

Latent autoimmune diabetes in adults (LADA) is a subgroup of diabetes in which, patients have T2D phenotype. However, it is combined with detecting islet antibodies at diagnosis and a slow progression of autoimmune β-cell failure (Stenstrom, Gottsater, Bakhtadze, Berger, & Sundkvist, 2005). LADA affects 10% of patients with phenotypic T2D older than 35 years (Wroblewski, Gottsater, Lindgarde, Fernlund, & Sundkvist, 1998) and much higher (25%) below 35 years (Borg et al., 2003; Rawshani et al., 2014). The type of detected antibody allows predicting the disease prognosis as patients with only GADs or only ICAs takes more than five years to develop β-cell failure. However, patients with multiple islet antibodies develops LADA within five years (Stenstrom et al., 2005). Management of LADA is by exogenous insulin, although, it is not usually required during the first six months after diagnosis (Prasad & Groop, 2015). Any form of diabetes family history is a potent risk factor for LADA (S. Carlsson, Midthjell, & Grill, 2007). Studies showed that LADA patients carry classic T1D-risk HLA genotypes (Hosszufalusi et al., 2003). Moreover, T1D protective genotypes especially DQA1*0102-DQB1*0602 are found in low frequency within LADA patients (Stenstrom et al., 2002).

2.3.2.2 Type 2 Diabetes Mellitus

Type 2 diabetes (T2D) is the highest prevalent type of DM, accounting for 90-95% of cases (American Diabetes, 2012). T2D is initiated by a combination of genetic, environmental, and behavioral risk factors (Y. Wu, Ding, Tanaka, & Zhang, 2014). These lead to hyperglycemia caused by insulin resistance, relative insulin deficiency or impaired insulin action (Y. Wu et al., 2014). Genetics plays a key role in T2M. Indeed, concordance within monozygotic twins is about 96% (Poulsen et al., 2009; Sanghera & Blackett, 2012). Genetic loci associated with T2D were identified by the candidate-gene approach and (mostly) by genome-wide association studies (GWASs). Although 60 loci have been identified so far, these can only explain 10% of the genetic component of the disease (Manolio et al., 2009; McCarthy, 2010; Prokopenko, McCarthy, & Lindgren, 2008). Beside the heritable component, factors such as age, obesity and lack of physical activity increase the risk of T2D (American Diabetes, 2012).

2.3.2.3 Maturity-Onset-Diabetes of the Young

Maturity-Onset-Diabetes of the Young (MODY) is a group of monogenic disorders, genetically characterized by it is autosomal dominantly inherited nature. It is clinically defined as non-insulin dependent diabetes, as patients do not have signs of autoimmunity (American Diabetes, 2012). MODY is a rare form of diabetes affecting 1% of all cases and typically with an early onset (prior to the age of 25) (Pihoker et al., 2013; Shepherd et al., 2016; Shields et al., 2010).

MODY results from heterozygous mutations found in at least 11 different genes (Naylor & Philipson, 2011). The most frequent causes of MODY are mutations in glucokinase (*GCK*) (MODY 2) (Murphy, Ellard, & Hattersley, 2008) and hepatocyte nuclear factor (*HNF) 1A/4A* (MODY3 and MODY1) genes (Shields et al., 2010). Many of MODY cases are misdiagnosed as T1D or T2D. Differentiating patients with MODY from T1D and T2D is critical to determine a patient's treatment and prognosis and to identify the at-risk family members (Naylor & Philipson, 2011).

2.3.2.4 Maternally inherited diabetes and deafness

Maternally inherited diabetes and deafness (MIDD) is a type of diabetes with maternal transmission caused by a mutation in mitochondrial DNA (mtDNA) (A3243G) (Murphy, Turnbull, Walker, & Hattersley, 2008; van den Ouweland et al., 1992). MIDD diagnosis is constructed on finding one or more of the following phenotypes: 1: Maculopathy (pathological conditions of the eyes' macula), 2: Hearing impairment, and 3: Maternal heritability of diabetes. Patients with MIDD also suffer from hyperglycemia (caused by insulin deficiency) (Naing et al., 2014). Close to 1% of patients with diabetes are affected by MIDD with age of onset in children and young adults (Goto, Nonaka, & Horai, 1990).

2.3.2.5 Neonatal diabetes

Neonatal diabetes mellitus (NDM) is a rare disorder occurring in 1:300,000-400,000 live birth as persisting hyperglycemia at birth or within the first few months of life (Flechtner, Vaxillaire, Cave, Froguel, & Polak, 2007). Patients suffer from intrauterine growth retardation (IUGR), and low or undetectable C-peptide levels (Fosel, 1995). Due to the inadequate insulin production as a result of pancreatic dysfunction, exogenous insulin therapy is crucial for the patient's survival.

Neonatal diabetes can be in two forms Transient (TNDM) and Permanent (PNDM). However, the two conditions cannot be distinguished based on clinical features. TNDM occurs in 50% of the patients and at a younger age of onset. Patients recover by 18 months of age, but in half of the patients, it relapses later in life. TNDM is mostly caused by abnormalities within 6q24 imprinted region or point mutation in 6q24 genes (*ZAC/PLAG1*) (Arima et al., 2001) (Flechtner et al., 2007; Polak & Cave, 2007). In PNDM, pancreatic failure occurs in the late fetal or early post-natal period and does not go into remission. PNDM causal mutations are most often found within *KCNJ11* and *ABCC8* genes, encoding the Kir6.2 and SUR1 subunit of the pancreatic KATP channel involved in regulation of insulin secretion (Flechtner et al., 2007; Polak & Cave, 2007). Molecular diagnosis is important, as half of PNDM cases can be treated with oral medication instead of insulin.

2.3.2.6 Gestational Diabetes mellitus

Gestational diabetes mellitus (GDM) is any level of carbohydrate intolerance with onset within gestation (O'Sullivan, 1991). GDM is an impermanent form of diabetes that resolves itself post-partum. However, women affected by it are at higher risk of adverse pregnancy outcomes such as fetal hyperinsulinism, stillbirth, and macrosomia (O'Sullivan, Gellis, Dandrow, & Tenney, 1966). Moreover, females with a history of GDM are at higher risk for T2D after pregnancy, and their children also have a higher risk of developing obesity and T2D early in life (O'Sullivan, 1991). This is likely due to the overlap observed between many of the GDM-associated variants with T2D risk variants (Huopio et al., 2013). Depending on the criteria used and demographic characteristics of the population, GDM has a prevalence ranging from 1 to 14% of all pregnancies (American Diabetes, 2006; Harlev & Wiznitzer, 2010).

2.4 Type 1 Diabetes In Depth

2.4.1 Epidemiology of Type 1 Diabetes

About 10% of diabetic patients suffer from T1D, and it accounts for more than 85% of all young diabetes cases worldwide (American Diabetes, 2012). It mostly starts below the age of 18 years. Adults have low incidence levels, although, about one-fourth of people with T1D are diagnosed as adults (Haller, Atkinson, & Schatz, 2005). Moreover, adult β-cell destruction occurs at a considerably lower rate than in young patients, delaying the demand for insulin therapy after diagnosis (Maahs, West, Lawrence, & Mayer-Davis, 2010).

Prevalence of T1D varies among different populations and ethnicities. It is the highest among populations of European descent with the highest rates reported for Sardinia in Italy and Finland with about 40/100,000 in young children. Intermediate rates were reported among African descent populations and the lowest was reported among East Asians (rate of 1.01 /100,000 in China) (Weng et al., 2018). Moreover, within Europe, there is a geographical distribution in the prevalence of T1D. The prevalence is several-folds higher within northern countries than those in Mediterranean (Borchers, Uibo, & Gershwin, 2010; Polychronakos & Li, 2011). The variation in the diseases prevalence among different populations is likely to be caused by variations in the genetic background and the environment. Unlike most common autoimmune diseases where females have higher risk, T1D affect both genders equally. However, interestingly, regions with high incidence of T1D (populations of European descent) demonstrate a higher male risk, whereas regions with minimal incidence are with higher females risk (Gale & Gillespie, 2001).

T1D has a complex pattern of inheritance, in which the disease susceptibility is determined by an interaction between genetic factors and environmental triggers. Genetic predisposition plays the major role in its etiology. Although, more than 85% of T1D patients lack a positive family history of the disease, the sibling relative risk (also known as familial clustering; λ_s) is one of the highest among common complex disorders. λ_s is defined as the probability of a disease in a sibling of a case, divided by the prevalence in the general population; is estimated to be 15 in T1D (mean prevalence of 6% in sibling compared to 0.4% in the US white population) (Polychronakos & Li, 2011; Steck & Rewers, 2011). This makes the risk of T1D in sibling of patients is 15-fold higher than the risk for T1D in the general population. In case of twins, concordance rate in dizygotic twins is 6%-10% that is similar to non-twin siblings, whereas, up to 50% in monozygotic twins by the age of 40 after a long-term follow up (Redondo, Jeffrey, Fain, Eisenbarth, & Orban, 2008; Steck & Rewers, 2011). This is far from 100%, so environmental factors play a role. However, in young onset T1D most of the environment is shared. This raises the possibility of stochastic causal events. The risk for the second twin pair is significantly less if the first twin develops the disease after the age of 25 years (<5%) with a long-term follows up (Redondo et al., 2008; Steck & Rewers, 2011). Offspring from diabetic fathers are at higher risk of developing T1D, than offspring of diabetic mothers (Steck et al., 2005).

2.4.2 Genetics of Type 1 Diabetes

Genetic studies, seeking to identify risk loci of T1D, started in the 1970s with two primary approaches: linkage studies and candidate gene studies. Linkage studies classically use affected sibling pairs to define regions of the genome that are more frequently shared among affected relatives. The major finding of linkage studies is the revealing of HLA loci in chromosome 6p21 as the key contributor to T1D susceptibility (Risch, 1987). The largest linkage study by the T1D Genetics Consortium (T1DGC) and other linkage studies confirmed the absence of additional loci with a comparable effect size to the HLA effect (Concannon et al., 2009).

Unlike linkage studies, candidate gene studies permit detecting alleles with much lower effect on disease risk given that those alleles are quite common. In candidate gene studies selected markers in genes are genotyped in patients and unaffected control individuals. In the field of T1D those studies revealed additional loci such as insulin (*INS*) (Julier et al., 1991), protein tyrosine phosphatase, non-receptor type 22 (*PTPN22*) (Bottini et al., 2004)*,* cytotoxic T-lymphocyte-associated protein 4 (*CTLA*4) (Ueda et al., 2003) and interleukin 2 receptor alpha (*IL2RA*) in which their functional effects are now well characterized and established (Qu, Montpetit, Ge, Hudson, & Polychronakos, 2007; Vella et al., 2005). Also, genome-wide genotyping of ~6,000 nonsynonymous SNPs (nsSNPs) discovered interferon-induced helicase c domain-containing protein 1 *(IFH1)* as a locus (Smyth et al., 2006). Apart from *INS,* these loci were also identified as risk factors in other autoimmune diseases. Starting in 2007, Genome-wide association studies (GWAs) have identified over 40 loci via a high-throughput SNP genotyping platforms and dense maps of SNPs genome-wide (Fig.1.1) (Hakonarson et al., 2007; Polychronakos & Li, 2011). Very few of these loci have been further fine-mapped to a specific variant or gene.

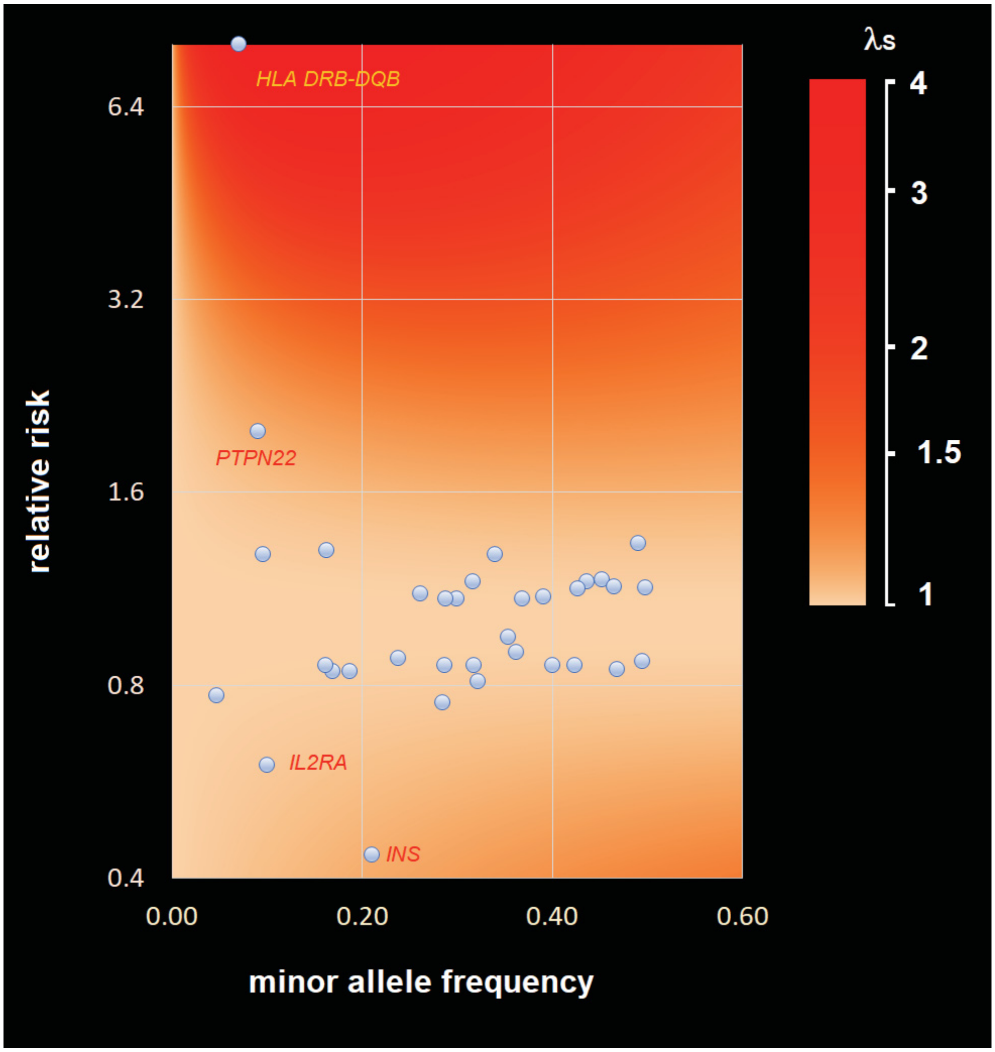

Figure 2-1 T1D susceptibility loci and their contribution to T1D risk.

The two variables that determine the level of importance of a susceptibility locus in a complex phenotype like T1D are the relative risk conferred (Y- axis) and the minor allele frequency (X- axis). The combination of frequency and risk determines the contribution to disease heritability, measured here by the λ_S. (illustrated by the heat map in the background). The four genes with the strongest contribution to the λ_S are labeled (*HLA, PTPN22, INS, IL2RA*). For a low-prevalence disease such as T1D, the relative risk is practically identical to the odds ratio (OR). Adapted from (Polychronakos, 2018).

2.4.2.1 Insight into major T1D loci

2.4.2.1.1 The *MHC* locus

T lymphocytes recognize β-cell antigens by their TCRs in the context of MHC (discussed in section 1.2.1). Human leukocyte antigen (HLA) molecules are a set of homologous cell surface proteins encoded by a family of homologous genes within the MHC genomic region. MHC locus is a 3.6 Mb gene-dense stretch extended in tight linkage disequilibrium (LD) on Chr 6p21 (Polychronakos & Li, 2011). This region encodes 140 protein-coding genes in which almost half have a known immune function. Moreover, the MHC genomic region has evolved to become the most polymorphic mammalian protein-coding region with some genes having more than 200 recognized coding alleles. This high polymorphism assures the recognition of an extensive range of constantly evolving pathogens. HLA locus is by far the strongest associated region of most autoimmune diseases including T1D, in which it makes up for almost half of the genetic risk (Noble et al., 1996; Polychronakos & Li, 2011; Steck & Rewers, 2011). The HLA locus includes three gene clusters. However, the most significant HLA genes in T1D susceptibility are those of class I and class II clusters in tight LD making it challenging to establish which gene is responsible for the T1D association.

Class I HLA proteins (HLA-A, HLA-B, HLA-C) comprise a single chain are expressed on all nucleated cells, and present endogenous antigens to CD8+ CTL T cells. CD8+ T cells eliminate infected cells by mechanisms of direct cellular contact, mostly perforin–granzyme B and FAS receptor–FAS ligand interactions (Hassin, Garber, Meiraz, Schiffenbauer, & Berke, 2011). Whereas, class II HLA (DP, DR, and DQ) constitute of two chains (α and β) and are exclusively expressed on specialized APCs such as DC cells, B-cells, monocytes and the thymus epithelium. Class II molecules present extracellular antigens to CD4+ T cells that facilitate inflammation through secreting cytokines. Antigens are presented in an HLA groove (8-9 amino acids in class I and 15 amino acids in class II) and the confirmations and amino acid context determine the specificity of each allele for various antigen peptides. Class III HLA genes encode TNF-α and –β, heat shock protein 70 (Hsp70) and several members of the complement system (Hauptmann & Bahram, 2004).

In T1D, most of the susceptibility resides in HLA class II DR and DQ loci, mostly in genes encoding the highly polymorphic β-chain genes (*DRB* and *DQB*). Genes encoding the four chains (*DQA, DQB, DRA,* and *DRB*) all lie in a physically compact region and in tight LD making it difficult to determine their relative importance to the T1D association by genetic measures (Undlien, Lie, & Thorsby, 2001). Therefore, *DR-DQ* haplotypes are allocated to determine risk. The highest known risk haplotypes for T1D are DRB*0301DQA1*0501-DQB1*0201 (abbreviated as DR3-DQ2) and DRB*0401-DQA*0301-DQB*0302 (abbreviated as DR4-DQ8) (numbers after the asterisk represent allele numbers) (Erlich et al., 2008). At least one copy of these haplotypes is present in over 90% of young-onset T1D cases compared to ~20% of the general unaffected European-descent population (Erlich et al., 2008). Moreover, the highest risk is conferred by compound heterozygosity for (DR3-DQ2/DR4-DQ8) haplotype, 40% of T1D patients carries it compared to only 2% of the general population (Erlich et al., 2008). Conversely, allele DRB1*1501-DQA1*0102-DQB1*0602 (DR2-DQ6) is a potent protective allele even in the presence of a risk haplotype on the other chromosome or islet autoantibodies (Erlich et al., 2008). This allele is carried by much less than 1% of T1D patients compared to ~15% of Europeans descent (Pugliese et al., 1995; Steck & Rewers, 2011).

Understanding the molecular mechanism underlying the MHC risk of these alleles has been under investigation for decades as it can provide great potential as a therapeutic target. However, our understanding of the possible mechanisms involved remains far from complete. Studies on the risk allele revealed that the absence of Asp at position 57 of the HLA risk protein is a primary cause for T1D pathogenicity both in human and mice (mouse orthologue of DQB (I-A_{g7})) (Corper et al., 2000; Todd, Bell, & McDevitt, 1987). This polymorphism reverses the electric charge of the binding groove reducing the binding affinity of self-antigen molecules leading to autoimmunity. Studies showed that overexpression of the diabetogenic NOD-allele I-Ag7 protects from diabetes in NOD mice, probably by compensating for the reduced affinity (Wherrett, Singer, & McDevitt, 1997). This supports the hypothesis that HLA alleles increase the risk of T1D represents a loss of function (Polychronakos & Li, 2011; Wherrett et al., 1997).

Class I HLA (*MHC-A* and *B* alleles) also has been demonstrated to contribute to T1D risk independently from class II, however, with much weaker effect than Class II (Howson, Walker, Clayton, Todd, & Type 1 Diabetes Genetics, 2009). HLA class I molecules and the CD8+ T-cells, to which they present antigens, are believed to have a significant effect on later stages of the β-cell destruction (Polychronakos & Li, 2011). HLA-A*201 has been shown to bind to peptide epitopes from the pre-proinsulin molecule in addition to other known T1D self-antigens (Skowera et al., 2008).

Unlike *HLA* class I and II, class III loci have not been studied in depth and so far there are no reports showing the regions independent contribution to the risk of T1D (Polychronakos & Li, 2011).

2.4.2.1.2 The *INS* locus

The *INS* locus on Chr 11p15.5 confers the second highest risk to T1D after *MHC*. This region contains VNTRs (variable number of tandem repeats) located about 0.5 kb upstream of *INS* and encodes pre-proinsulin peptide (Rotwein, Yokoyama, Didier, & Chirgwin, 1986). *VNTR* stretch can be either short (Class I) VNTR alleles (26 to 63 repeats) that are the most predisposing to T1D or long (Class III) VNTR alleles (140-210 repeats) that are protective against T1D. Intermediate (Class II) alleles are rare (Barratt et al., 2004). The locus association to T1D risk was fine mapped to two non-coding SNPs within the region and in tight LD with each other and with the VNTR class I (-23HpHI and +1140A/C) (Barratt et al., 2004).

Unlike *INS* expression in the pancreas, thymus expression is influenced by the VNTR alleles. The thymic expression of the protective VNTR allele (class III) is usually more than two folds higher than the predisposing VNTR allele (class I) (Vafiadis et al., 1997). It has been proposed that these polymorphisms can cause alterations in *INS* transcription and therefore a reduction in thymic *INS* expression causing incomplete immune tolerance to INS (Pugliese et al., 1997; Vafiadis et al., 1997). Furthermore, It was shown that engineered mice to be deficient in thymus-specific insulin expression demonstrated higher T-cell reactivity to insulin (Chentoufi & Polychronakos, 2002) and higher diabetes rate (Thebault-Baumont et al., 2003). Mechanisms by which the *INS* VNTR variations control insulin expression in the thymus are still not entirely clear. However, possible mechanisms include interactions with transcription factors such as AIRE or by histone modifications (Koh et al., 2008).

2.4.2.1.3 The *PTPN22* locus

The *PTPN22* locus on Chr 1p13 is the third most major T1D susceptibility locus. *PTPN22* encodes the lymphoid protein tyrosine phosphatase LYP. This protein plays an important part in balancing host defence and self-tolerance by negatively regulating the TCR signal transduction. This takes place by LYP blocking the TCR signaling via dephosphorylating key signaling molecules (R. J. Hill et al., 2002) or by interacting with terminal Src tyrosine kinase (Csk) suppressor (Cloutier & Veillette, 1996). T1D association maps to common nonsynonymous arginine (R) to tryptophan (W) substitution (R620W) that confers a heterozygous risk as strong as the risk of *INS.* Moreover, this allelic alteration mediates risk in several other autoimmune diseases such as rheumatoid arthritis, juvenile rheumatoid arthritis (JRA), systemic lupus erythematosus, Graves' disease, generalized vitiligo, and other human autoimmune diseases. R to W amino acid substitution in PTPN22 hinders the proteins' ability to properly bind to Csk (Gregorieff, Cloutier, & Veillette, 1998). Studies reported contradicting explanations for the effect of the mutation. It was believed that this mutation would cause a loss in the inhibition of TCR signaling and that will lead to an increase in T-cell responsiveness (Zhang et al., 2011). However, studies reported R620W as a gain of function mutation that enhances the inhibitory effect on T-cell signaling by Lyp reducing T-cell activation (Arechiga et al., 2009; Fiorillo et al., 2010; Rieck et al., 2007; Vang et al., 2005; Zheng & Kissler, 2013). During thymic development and the establishment of self-tolerance, such inhibition of TCR signaling can allow autoreactive T-cells to escape negative selection on the periphery causing autoimmunity (Polychronakos & Li, 2011).

2.4.2.1.4 The *CTLA4* Locus

CTLA4 located in Chr 2q33 is another well-established T1D locus. *CTLA4* encodes a trans-membrane co-receptor protein that functions as a negative regulator of T-cell activation. *CTLA4* Ala17Thr polymorphism is T1D associated and affects glycosylation of the mature CTLA4 protein (Anjos, Nguyen, Ounissi-Benkalha, Tessier, & Polychronakos, 2002). Moreover, a G/C variant in the 3' flanking region has been linked to a reduced expression of a soluble variant of CTLA4 (Ueda et al., 2003).

2.4.2.1.5 The *IL-2RA* Locus

The *IL-2RA/CD25* locus mapped on Chr10p15 is associated with a number of autoimmune diseases. *IL2RA* gene encodes the α-subunit of the IL-2 receptor (IL-2R). IL-2 signaling (through IL-2R) is important for both effector and Treg function (Polychronakos & Li, 2011). Fine mapping studies identified two SNPs within an intron (intron 1) of *IL2RA* making difficult to decode the mechanism behind its T1D association (Polychronakos & Li, 2011).

2.4.2.2 Additional T1D loci

Numerous additional loci associated with T1D have been discovered, however, with minute effect. Most of these loci are still not fine mapped. It is unforeseen to identify other loci by GWA studies unless larger sample sizes are used. Moreover, any potential new loci are expected to have quite low effects. This is because the gene involved would not be important in the etiology of the disease or the risk allele would not have a significant effect on the function of the gene (Polychronakos & Li, 2011).

Although genetic predisposition accounts for most of the T1D etiology, genetics can't solely explain all the disease. The increase of T1D incidence in many countries within recent decades points to the significance of the environmental factors, as they cannot be a consequence only of augmented genetic disease susceptibility (Patterson et al., 2009).

2.4.3 Environmental Triggers of T1D

Environmental factors play an essential role in the pathogenesis of T1D both in triggering and enhancing of β-cell destruction. The rapid increase in the incidence of T1D in genetically stable countries can only be explained by environmental factors. However, the contribution of environmental factors is substantial only in genetically predisposed individuals (Rewers & Ludvigsson, 2016). Although studying potential environmental factors has been difficult due to the complexity and diversity of such factors, understanding them could help to prevent or delaying the disease. Several environmental factors have been studied and postulated as the most important exposure factors for T1D such as hygiene, specific infectious agents and some dietary factors but with no clear conclusion to their exact contribution.

2.4.3.1 Dietary factors

In T1D, clinical symptoms occur in childhood usually before the age of three years, pointing to the early induction of β-cell autoimmunity. This implies the importance of early nutrition as a potential essential exogenous contributor to the risk of the disease. A number of studies addressed diet to the risk of T1D, such as vitamin D, benefits of breast-feeding, and pathogenicity of cow's milk, cereals and gluten with no definitive results.

2.4.3.1.1 Vitamin D

Vitamin D can be obtained endogenously when the skin is exposed to sunlight, and ultraviolet B radiation converts 7-dehydrocholesterol to pre-vitamin D, or it can be obtained exogenously from food or supplements. Whether endogenous or exogenous, vitamin D is converted in the liver to its metabolic active form 25-hydroxyvitamin D [25(OH) D]. The significance of vitamin D in preventing adult bone diseases and rickets is well documented. Moreover, studies are expanding to cover the implications of its deficiency in a wide range of medical disorders, including T1D. Particularly that vitamin D has been shown to impact various cell types involved in the immune response (reviewed in (Dankers, Colin, van Hamburg, & Lubberts, 2016). Specific examples of such involvement include vitamin D active form involvement in the maturation and migration of dendritic cell (DC) subsets (Penna & Adorini, 2000; Piemonti et al., 2000) and the expression of vitamin D receptor on various T cell populations, including CD4+ and CD8+ cells, conferring a potential immunoregulatory role and its role in activating T cells by propagating TCR signalling (Veldman, Cantorna, & DeLuca, 2000). Although this role of vitamin D in the immune function points to its possible contribution to the pathogenesis of T1D and other autoimmune diseases, further investigation needed to demonstrate specific mechanisms.

Considerable number of animal-model, biological and human studies examined a potential protective role of vitamin D and the implications of its deficiency in the risk of T1D. However, the findings have been inconsistent with little supporting evidence. Genetic studies found three key genes (*CYP27B1*, *DHCR7*, and *CYPR1*) involved in vitamin D metabolism associated with T1D risk (Cooper et al., 2011).

Although some studies support a protective role of vitamin D in the risk of T1D (Giulietti et al., 2004; Sorensen et al., 2012; Weets et al., 2004; Zipitis & Akobeng, 2008), a number of studies showed contradicting findings (Bizzarri et al., 2010; Dong et al., 2013; Miettinen et al., 2012; Simpson et al., 2011; Walter et al., 2010).

2.4.3.1.2 Breastfeeding and Cows' milk

Breastfeeding effect on the risk of T1D also remains a controversial issue. Although some retrospective studies suggested a protective role (Cardwell et al., 2012), other prospective cohort studies showed no impact (Norris et al., 2003; Virtanen et al., 2006; Ziegler, Schmid, Huber, Hummel, & Bonifacio, 2003) or even shows an increase T1D risk (Holmberg, Wahlberg, Vaarala, Ludvigsson, & Group, 2007; Kimpimaki et al., 2001). The contradictory conclusions of breastfeeding studies are expected to result from differences in breastfeeding practices in different cultures and also because in most studies no differentiation was made between exclusive and non-exclusive breastfeeding (Knip & Simell, 2012).

Studies on the effect of the early introduction of cow's milk (during infancy or later in childhood) on the risk of T1D also gave contradictory results. The mechanism of how cows' milk induces immunopathology was postulated to be due to the development of antibodies to bovine insulin (Vaarala et al., 1999). Several studies showed that early introduction of cow's milk increases the risk of T1D (Kostraba et al., 1993; Verge et al., 1994; Virtanen et al., 1991; Virtanen et al., 1993), whereas others showed no effect (Group, 2002; Wadsworth, Shield, Hunt, & Baum, 1997; Writing Group for the et al., 2018).

2.4.3.2 Infectious agents

The implication of viral infections on the pathogenesis of T1D has long been a subject of intense interest and review. An early observation of a virus-induced T1D in human beings was the association of congenital rubella infection with a very high rate of subsequent T1D (Menser, Forrest, & Bransby, 1978). Subsequently, a variety of studies reported other human viruses to be associated with T1D risk, including but not limited to mumps (Hyoty et al., 1988), enterovirus (Hyoty & Taylor, 2002), cytomegalovirus (Pak, Eun, McArthur, & Yoon, 1988) and retroviruses (M. C. Honeyman et al., 2000; M. C. Honeyman, Stone, & Harrison, 1998). It has been postulated that viruses may act either via direct cytolytic acute β- cell viral infection or by a chronic low- grade viral β- cell infection, leading to an induction of an autoimmune response causing a progressively β-cell destruction (Peng & Hagopian, 2006). Moreover, structural homology studies indicated a potential role of molecular mimicry and epitope spreading, which is the broadening of epitope specificity from a principal epitope to subdominant one, in diabetes-associated autoimmune response (Vanderlugt & Miller, 2002). For instance, molecular homology was reported between the rotavirus protein (VP7) and the T-cell epitopes in the IA-2 molecule and the 65KD isoform of GAD (M. C. Honeyman, Stone, Falk, Nepom, & Harrison, 2010; M. C. Honeyman et al., 1998). Another suggested mechanism in which viruses might trigger islet autoimmunity involves activation of innate immunity that could facilitate specific adaptive immune response towards the islet immune attack (Peng & Hagopian, 2006). To understand the mechanisms connecting viral infections to autoimmunity, most studies have been focusing on identifying the relevant specific infections. So far, the evidence reported for enterovirus is envisaged the most convincing compared to that of other viruses (Yoon, 1995).

The Human Enterovirus (HEV) is a small nonenveloped RNA virus that belongs to the picornavirus family. HEVs are the most common viruses in causing human disease; most are usually mild or asymptomatic infections. However, sporadically the virus could cause more serious conditions such as myocarditis, encephalitis, or paralysis if spread to the myocardium or central nervous system (Knip & Simell, 2012). In relation to T1D, HEV infections are exceptionally interesting as they could infect tissue in contact with the gut-associated lymphoid system and the pancreas (Vaarala, 2002). HEVs; particularly Coxsackie B4 are possibly the best investigated potential T1D environmental factor. However, the evidence connecting it to the risk of T1D remains inconclusive (Yeung, Rawlinson, & Craig, 2011). HEV involvement in T1D risk has been suspected since the late 1960s, as a seasonal variation in T1D following HEV infection was reported (Gamble & Taylor, 1969). Moreover, an increase of neutralizing antibodies against HEV virus serotype *(CVB4)* was found in newly diagnosed T1D patients (Gamble, Taylor, & Cumming, 1973). HEV infection, usually identified by detecting enterovirus IgM and/or IgG, viral RNA and viral capsid protein (Yeung et al., 2011) have been detected in newly diagnosed patients with T1D (Krogvold et al., 2015; Lundberg, Krogvold, Kuric, Dahl-Jorgensen, & Skog, 2016). However, HEV studies have been challenged because control subjects were not matched for HLA alleles (Bergamin & Dib, 2015). Moreover, HEV findings were irreproducible and the role of HEV infection in the risk of T1D has remained controversial.

2.4.4 The non-obese diabetic mouse

Much of the knowledge about the autoimmune β-cell destruction comes from extensive research on two rodent animal models, bio-breeding diabetes-prone (BBDP) rat and the non-obese diabetic (NOD) mice. These two models are inbred stains with remarkable similarities to the human T1D, in which both develop the disease spontaneously at a young age, display polygenic inheritance and involve lymphocytic infiltration of the islets of Langerhans mediating destruction of β-cells. Similar to the human disease both models demonstrate polyuria, glycosuria and weight loss (Makino et al., 1980; Nakhooda, Like, Chappel, Murray, & Marliss, 1977; Pearson, Wong, & Wen, 2016). A comparison between Human, BB rat and NOD mouse autoimmune diabetes is outlined in Table 1. 2.

The BBDP strain was derived in Canada in the 1970s from outbred Wistar rats that spontaneously develop hyperglycemia and ketoacidosis, two clinical characteristics of clinical T1D (Mordes, Bortell, Blankenhorn, Rossini, & Greiner, 2004). The development of the NOD mouse came later in Japan in the 1980s at the Shionogi Research Laboratories from inbreeding the Cataract Shionogi (CTS) strain (Makino et al., 1980). At F6 of inbreeding the CTS strain, some cataract free mice exhibit abnormally high fasting blood glucose. These mice were selectively inbred on the basis of their high levels of fasting blood glucose trait. At F13, the normoglycemic line was developed and separated from the hyperglycemic line. Inbreeding of this line on the basis of normal fasting glucose levels generated at F20 a female characterized with spontaneous development of overt insulin-dependent diabetes mellitus and with insulitis. Breeding the progeny of this female mouse produced the NOD strain (Kikutani & Makino, 1992; Makino et al., 1980). After being originally restricted to distribution in Japan, inbred colonies of NOD mice have become widely distributed and established around the world. Since the original description of the strain susceptibility to spontaneous development of autoimmune diabetes by Makino et al., 1980 (Makino et al., 1980), the NOD model has become preferred over BB rats for T1D research.

T1D in NOD mice is characterized by insulitis that occurs when lymphocytes infiltrate into the pancreatic islets. This begins with the aggregation of lymphocytes at the periphery of the pancreatic islets (peri-insulitis). After starting at one pole, aggregates eventually widespread to cover an entire islet and penetrate the islet core causing the erosion of the β-cell mass. This phenomenon occurs between five and seven weeks of age in female mice and several weeks later in males. However, due to a period of islet development, it partially compensates for the loss of the islets mass during the early weeks (Leiter, 1993). In the β-cell lesions, the majority of infiltrating cells are $CD4^+$ T-cells. However, $CD8^+$ T-cells, NK cells, B cells, DC and macrophages cells are also identified in the lesions (Anderson & Bluestone, 2005; Kikutani & Makino, 1992; Makino et al., 1980). T-cells appear to play the major role in β-cell destruction as they have the capability of transferring the disease from NOD donors with purified $CD4^+$ and $CD8^+$ T cells to genetically susceptible non-diabetic mice (Haskins & Wegmann, 1996; Wong, Visintin, Wen, Flavell, & Janeway, 1996).

Marked reduction in pancreatic insulin occurs at 12 weeks of age in females, and a few weeks later in male mice and by the age of 30 weeks, about 90% of females and 20- 30% of males become diabetic (Kikutani & Makino, 1992). This is evident by moderate glycosuria and by hyperglycaemia (non-fasting plasma glucose higher than 250 mg/dl). Intriguingly, the incidence of T1D is higher when NOD mice are maintained in a fairly germ-free environment but drastically decrease when they are maintained in a conventional “dirty” facility (Singh & Rabinovitch, 1993). The basis of this effect remains unclear, but it has been proposed that microbes in dirty facilities may regulate the immunological status of the immune repertoire away from an autoimmune response in NOD mice (Singh & Rabinovitch, 1993). During the following weeks diabetic mice become hypoinsulinemic and hyperglucagonemic and the severity of the symptoms progress to weight loss, polydipsia, and polyuria (Leiter, 1993). Mice usually survive three-four weeks after the initial detection of glycosuria (Leiter, 1993).

NOD mice are also susceptible to acquiring other autoimmune syndromes, including thyroiditis (Many, Maniratunga, & Denef, 1996), sialitis (Hu, Nakagawa, Purushotham, & Humphreys-Beher, 1992), peripheral polyneuropathy (Salomon et al., 2001). As in human T1D, susceptibility to autoimmune diabetes is under complex polygenic control. Moreover, environmental factors are also exerting a strong effect on T1D penetrance. Also, similar to human T1D, a specific class II major MHC allele has a major role in diabetes susceptibility. This allele in NOD mice is I–Ag7 that resembles the human leukocyte antigen (HLA) DQA*301-DQB*302 allele (Asp at position 57 is replaced by another aa) (Corper et al., 2000). The MHC diabetogenic allele is essential for the disease development, however, is not sufficient alone. Additional 20 loci (known as *Idd* loci) have been mapped in NOD mice that potentially cause immune dysregulation (Polychronakos & Li, 2011). Studying the mechanisms involved in the immune dysregulation of T1D in genetically heterogeneous human populations is more challenging compared to it in inbred mouse strain, which is genetically equivalent to having numerous copies of a single case.

Table 2-1 Comparison between autoimmune diabetes in Human, NOD mice and BB rats. Adopted and modified from (Mordes et al., 2004)

	Human	NOD	BB rat
Age of onset	>6 month up to adulthood	>10 W	7–14 W
Insulitis	DCs, Macrophages, B- Cells, NK- Cells, CD4 & CD8 T- Cells		
Ketoacidosis	Severe	Mild	Severe
Lymphopenia	None	None	Severe
Autoantigens	Insulin, GAD, IA-2, IA-2β, ZnT8, IGRP, IAPP, HSP60, Carboxypeptidase H	Insulin, GAD, IA-2, IA-2β, ZnT8, IGRP, Chromogranin A	Insulin, GAD
TCR repertoire bias	None	None	Anti-TCRVβ13 prevents diabetes
Genetic susceptibility	MHC (most important), >40 non-MHC loci	MHC (most important), >40 non-MHC loci	MHC (most important), >10 non-MHC loci
Gender effect	M and F equally affected before puberty, small M preponderance after puberty	F predominantly affected	M and F equally affected

W: weeks, M: Male, F: Female

2.5 Celiac disease

Celiac disease (CD) in an immune-mediated enteropathy, triggered by the ingestion of gluten (proline and glutamine-rich proteins present in wheat (Gliadin and Glutenin), barley (Hordeins) and rye (Secalins) in genetically predisposed individuals. CD was first diagnosed in 1888; however, it was after the 1940s that the role of gluten was identified (Guandalini & Assiri, 2014; van Berge-Henegouwen & Mulder, 1993). Typical changes and symptoms caused by gluten on the intestinal mucosa were identified after obtaining biopsy specimens from the intestine became feasible.

This permanent sensitivity to gluten has a prevalence of 1% of the general population making it the most prevalent genetically based food intolerance in the world (Guandalini & Assiri, 2014). CD may appear at any age, but it is most common among adults. It predominantly affects the small intestine, causing flattening of its mucosa and therefore, nutrient malabsorption (Guandalini & Setty, 2008). CD has highly variable clinical symptoms with gastrointestinal presentations, as the most common and it comprise chronic diarrhea, failure to thrive, and abdominal distention (Reilly, Fasano, & Green, 2012). Other extra-intestinal manifestations may also occur such as dermatitis herpetiformis, anemia, dental enamel hypoplasia, osteoporosis, arthritis and neurological problems (Guandalini & Assiri, 2014). Indeed, many CD patients may demonstrate no symptoms at all (Rubio-Tapia et al., 2013). Diagnosis of CD is usually conducted by serologic testing of celiac-specific antibodies: serum tissue transglutaminase (tTG), IgA antibody levels, antiendomysial antibodies (EMA) and antigliadin antibodies (AGA) and confirmed by duodenal bulb biopsies, in which intraepithelial lymphocytosis (LIEs) to total villous flattening can be observed (Catassi & Fasano, 2008; Rubio-Tapia et al., 2013).

The treatment of CD is primarily by following a gluten-free diet (GFD) that usually resolves the symptoms in young. Patients diagnosed in adulthood may sometimes be non-responsive affecting the quality of life. Given the incomplete response of some patients to a GFD (glucose-free diet), it is critical to develop new efficient therapies, which is only feasible by understanding the genetic and immunological causes behind the disease.

2.5.1 Epidemiology of CD

The prevalence of CD is approximately 1% of the general population; with higher rates in females (ratio of 2:1). CD has been growing worldwide during the past few decades, with doubling rates approximately every 20 years (Guandalini & Assiri, 2014; Herman et al., 2012; Lohi et al., 2007; van Berge-Henegouwen & Mulder, 1993). This increase has been partially driven by globalization that caused an increased intake of gluten-containing food worldwide (Shanbhogue et al., 2010).

In the United States and Europe, the incidence of CD has been estimated to be 3-13 cases per 1000 (Catassi et al., 1996; I. Hill et al., 2000; I. D. Hill et al., 2005; Lionetti et al., 2012). CD prevalence is higher in individuals with family history of CD (first-degree relatives of CD patients have a higher prevalence of autoimmune diseases, particularly T1D, thyroiditis, IgA deficiency, and some genetic syndromes (Down, Turner, and William syndromes) (Catassi & Fasano, 2008). Due to the atypical features of the disease, 10%-15% of CD cases (1:3 to 1:5 for pediatric and adult population respectively) are misdiagnosed and at risk of long-term complications including infertility and lymphoma (Catassi & Fasano, 2008; Lionetti et al., 2012; Whitacre, 2001).

Until recently, it was believed that the geographical distribution of CD is mostly restricted to Europe and other developed countries (USA, Canada, and Australia);

however, the current availability of sensitive serological markers revealed the true worldwide prevalence of CD. The reason for the increase of CD prevalence is still not fully understood, and it is believed that some environmental factors might be responsible for this significant increase including, the amount and timing of initial gluten exposure and early-life infections (Catassi & Fasano, 2008).

2.5.2 Genetics of CD

CD is known to have a very definite genetic component. It develops in genetically susceptible individuals triggered by environmental factors. Studies on siblings reported a concordance of about 80% in monozygotic twins and >20% in dizygotic twins pointing to the importance of heritable contribution (Greco et al., 2002; Shanbhogue et al., 2010). The heritable components required for the development of CD are not fully understood. However, it is well known that CD is strongly associated with specific HLA class II genes, HLA-DQ2 and HLA-DQ8 both located on Chr 6p21 (Sollid, 2000). These genotypes contribute to about 40% of the CD risk and found in at least 95% of patients (Guandalini & Assiri, 2014). Interestingly, these two haplotypes are also strongly predisposing for T1D.

In addition to HLA genes, other genes involved in innate and adaptive immunity, intestinal barrier regulation and autoimmunity has also been identified as contributors to the CD genetic background. Those include *IL2* and *IL21* genes (van Heel et al., 2007), *CELIAC2* on Chr 5q31-33, *CELIAC3* on Chr 2q33 (containing the T-lymphocyte regulatory genes *CD28*, *CTLA4*, and *ICOS*), and *CELIAC4* (the myosin IXB gene, *MYO9XB*) on Ch 19p13.1 (Catassi & Fasano, 2008; Monsuur et al., 2005; van Heel et al., 2007).

IL-2 and *IL-21* genes are both located in Chr 4q27 and are secreted cytokines by activated T-cells. These cytokines function in triggering the proliferation of different lymphocytes such as B-cells, T-cells and NK cells (van Heel et al., 2007). Interestingly, both IL-2 and IL-21 are implicated in other autoimmune diseases such as T1D and rheumatoid arthritis, suggesting that Chr 4q27 locus is a general autoimmune potential risk locus (Zhernakova et al., 2007).

MYO9B encodes myosin molecule; although unconventional was also found to be associated with other autoimmune diseases including systemic lupus, erythematosus and rheumatoid arthritis suggesting its general risk for autoimmune diseases (Catassi & Fasano, 2008). In regard to CD, it was previously proposed that myosin might have a role in actin remodeling in epithelial enterocytes. Therefore, genetic variations within this gene might cause an impaired intestinal barrier, allowing the passage of gluten peptides (Monsuur et al., 2005).

2.5.3 Environmental triggers of CD

Several environmental factors are suspected to play a role in the pathogenesis of CD including dietary and infectious making genetically predisposed individuals inducing an immune response to gluten even if its introduction was years later. Brest feeding is currently accepted to have a protective effect to CD (Akobeng, Ramanan, Buchan, & Heller, 2006; Ivarsson, Hernell, Stenlund, & Persson, 2002). Rotavirus infections in predisposed individuals is another probable risk factor in CD (Stene et al., 2006). It has been proposed that the destructive nature of the virus to the small intestine permeability can potentially ease the penetration of the immunoreactive gliadin epitopes (Troncone & Auricchio, 2007).

Gluten is the most significant environmental factor in CD. Exposure to gluten within the first three months of age significantly increases the risk of CD in genetically predisposed children (A. Carlsson et al., 2006; Norris et al., 2005). Gluten is inadequately digested protein due to the high levels of proline and glutamine residues within its structure (Guandalini & Setty, 2008). The digestive process starting in the duodenum followed by digestion of peptides and activation of trypsin leaving fragments of peptides (Guandalini & Setty, 2008). *In virto* digestion leaves a large fragment of 33-mer LQLQPFPQPQLPYPQPQLPYPQPQLPYPQPQPF (residues 57–89) (Shan et al., 2002). This 33-mer is interesting due to its high resistance to proteolytic degradation and to the existence within it of three definite T-cell epitopes recognized by DQ2: PFPQPQLPY, PQPQLPYPQ, and PYPQPQLPY (Guandalini & Setty, 2008).

2.5.4 Pathogenesis of the intestine in CD

Both innate and adaptive immunity are contributing to the inflammatory pathogenesis of CD. In the innate immunity, abnormal higher expression of TLR mRNA was observed in CD patients (Szebeni et al., 2007). Whereas, in the adaptive immunity, infiltration of the epithelial tissue is mediated by gluten-specific $CD4^+$ and $CD8^+$ T- cells. In the lamina propria of the intestine, APC activates $CD4^+$- gluten-reactive T-cells restricted by MHC-II DQ2 or DQ8 (Guandalini & Setty, 2008). This is followed by IFN-γ secretion and autoantibodies production such as anti-tissue transglutaminase (TG2) (Di Sabatino et al., 2007). Moreover, it has been suggested that IL-21 have an essential role in the inflammatory mechanism (Fina et al., 2008).

2.6 Somatic mutations

DNA replication is generally achieved with high fidelity. However, this mechanism is not perfect, and errors sporadically occur creating mutations. This constant change in DNA sequence enabled the evolving and adaption of organisms. Mutation of a gene sequence can cause either alteration in the structure of an encoded protein or a partial or a complete loss of its expression.

Mutations can be either germline/meiotic mutations (in germinal tissue) or somatic mutations (in somatic tissue). Germline mutations can be transmitted to some or all progeny, whereas, somatic are not transmitted to progeny. Somatic mutations could occur at any stage during development and if the affected cell is a progenitor of a cell clone, all descended cells will carry the same somatic mutation. Moreover, the earlier the mutation event takes place during development the larger the number of cell clones will be affected. In fully developed organisms, if a somatic mutation is in a post-mitotic cell (no longer dividing), its effect can be insignificant. However, if it occurs in cells with dividing property this also gives rise to a mutant clone's (Griffiths AJF, 2000).

Mutations can be divided into two major classes: Single-nucleotide polymorphisms (SNPs) also known as point mutations and small deletions (indels) or chromosomal rearrangements. Point mutations involve alterations in a single base pair (Missense, Nonsense, or Frameshift), whereas, small deletions involve few base pairs. Chromosomal abnormalities are cytogenetically recognizable, large-scale alterations in chromosome structures and affect several genes. Those can be large deletion or insertion of one or several adjacent genes, inversion, or translocations of large DNA segments. An intermediate size class is recognized as structural variations encompassing copy number variations (CNVs), which comprise unbalanced rearrangements causing an increase or a decrease of the DNA content.

2.6.1 Copy number variations/Aberrations

A copy number variation (CNV) is defined as a segment of at least 50bp that exists in a number of copies other than two, due to copy-loss or copy-gain (MacDonald, Ziman, Yuen, Feuk, & Scherer, 2014; Zarrei, MacDonald, Merico, & Scherer, 2015). When the variation is within the same organism, due to somatic mutation and mosaicism, it is known as copy number aberration (CNA). It has been estimated that up to 12% of the human genome is subject to CNVs (Redon et al., 2006). Changes in copy number can cause gene disruption or alter gene expression causing an increase or a decrease in transcriptional levels. Moreover, additional copies due to copy-gain CNVs provide redundancy, allowing evolving of some copies to acquire a modified function or expression pattern. Nevertheless, most of the CNVs are disadvantageous, leading to a group of pathological conditions known as genomic disorders (Lupski, 1998).

Alteration in copy number requires alteration in chromosome structure in which two formerly separated sequences of DNA are joined. This rearrangement can be either recurrent or non-recurrent. Recurrent CNVs have a common size with recurrent-fixed breakpoints for each event (Gu, Zhang, & Lupski, 2008). The junctions of recurrent CNVs consist of low copy repeats (LCRs) with high homology (>95% and >1Kb in length) (Hastings, Lupski, Rosenberg, & Ira, 2009)(Fig.2-2a). Non-recurrent CNVs at any given locus, have a common overlapped region, in which the smallest is called the smallest region of overlap (SRO). SRO regions comprise the locus associated with the genomic disorder (Gu et al., 2008) (Fig.2-2b). Non-recurrent CNVs can have one of their breakpoints centralized in a single genomic region (non-recurrent CNV with grouping) (Fig.2-2c) (Gu et al., 2008). There are three major mechanisms for CNVs formation: non-allelic homologous recombination (NAHR), non-homologous end- joining (NHEJ) and the Fork Stalling and Template Switching (FoSTeS).

NAHR forms most of the recurrent CNVS between LCR segments. The high level of sequence identity, LCRs can sometimes be misaligned during meiosis or mitosis process resulting crossover and therefore CNV formations in progeny cells. When the two involved LCRs are on the same chromosome and in the same orientation, NAHR process creates deletions and/or duplications (Fig. 2-2d). However, if they are located on the same chromosome but in opposite orientation, inversion CNV is formed (Fig. 2-2e). NAHR can also be between LCRs on different chromosomes causing translocation (Gu et al., 2008).

NHEJ is a mechanism in which human cells repair ‘physiological’ double-strand breaks (DSBs) such as V(D)J recombination to form TCR or BCRs (discussed in section 2.1.2) or ‘pathological’ DSBs (Gu et al., 2008). NHEJ defects account for about 15% of human severe combined immunodeficiency (SCID) and is considered the principal mechanism in attaching translocation between chromosomes in cancer (Lieber, Lu, Gu, & Schwarz, 2008; Schwarz, Ma, Pannicke, & Lieber, 2003). There are four steps in NHEJ (Fig. 2-2f): recognizing DSB segments; molecular bridging of the broken DNA ends; adjustment of the ends to enable their ligation; finally ligation of the ends (Weterings & van Gent, 2004). NHEJ process leaves ‘information scars’ at the joining site that is formed due to the editing step that involves deletion or addition of nucleotides to the ends (Gu et al., 2008; Lieber, 2008).

Complex CNVs were proposed to be formed by the replication Fork Stalling and Template Switching (FoSTeS) Model (Lee, Carvalho, & Lupski, 2007). Here, during the replication process, DNA replication fork stops at a specific position, in which the lagging strand detached from the original template, transfers to another replication fork within the physical proximity where it anneals due to microhomology (limited homology of 2-15 bp) at the 3' end and restarts the DNA synthesis (Lee et al., 2007). In this process, interchanging to a downstream replication fork creates deletions (forward invasion), whereas interchanging to an upstream one creates duplications (backward invasion). Moreover, the new replication fork can be either in direct or inverted position; depending on whether the lagging or the leading strand was invaded and on the direction of the fork advances. FoSTeS can occur in several times in series enhancing the complexity of the rearrangements (Gu et al., 2008).

2.6.2 Frequency of Copy number changes

In Homo sapiens, most copy number changes occur in an inherited fashion. However, a significant fraction of them occur in *de novo* in both germline and somatic cells. The frequency of NAHR mediated copy-loss (α-globin locus) is estimated to be over 10^{-6} in blood cells (Lam & Jeffreys, 2006) compared to 10^{-5} in gametes (Turner et al., 2008). A similar result was found for a copy-gain within the same locus (Lam & Jeffreys, 2007). Thus, the frequency of CNV formation is 100-10,000 times higher than that of point mutations ($\sim 1.2 \times 10^{-8}$ mutation peer base pair) (Conrad et al., 2011; Kong et al., 2012). Moreover, NAHR products are carried in much lower frequency by newborns suggesting their accumulation during life (Flores et al., 2007; Hastings et al., 2009).

In healthy individuals, copy losses and copy gains have similar frequencies, but in sperm cells copy-loses have higher frequency than copy-gains (Hastings et al., 2009; Sebat et al., 2004). Rat and mouse are predicted to have lower frequency of *de novo* CNVs than human represented by their low LCR occurrence (Graubert et al., 2007; Hastings et al., 2009; Tuzun, Bailey, & Eichler, 2004).

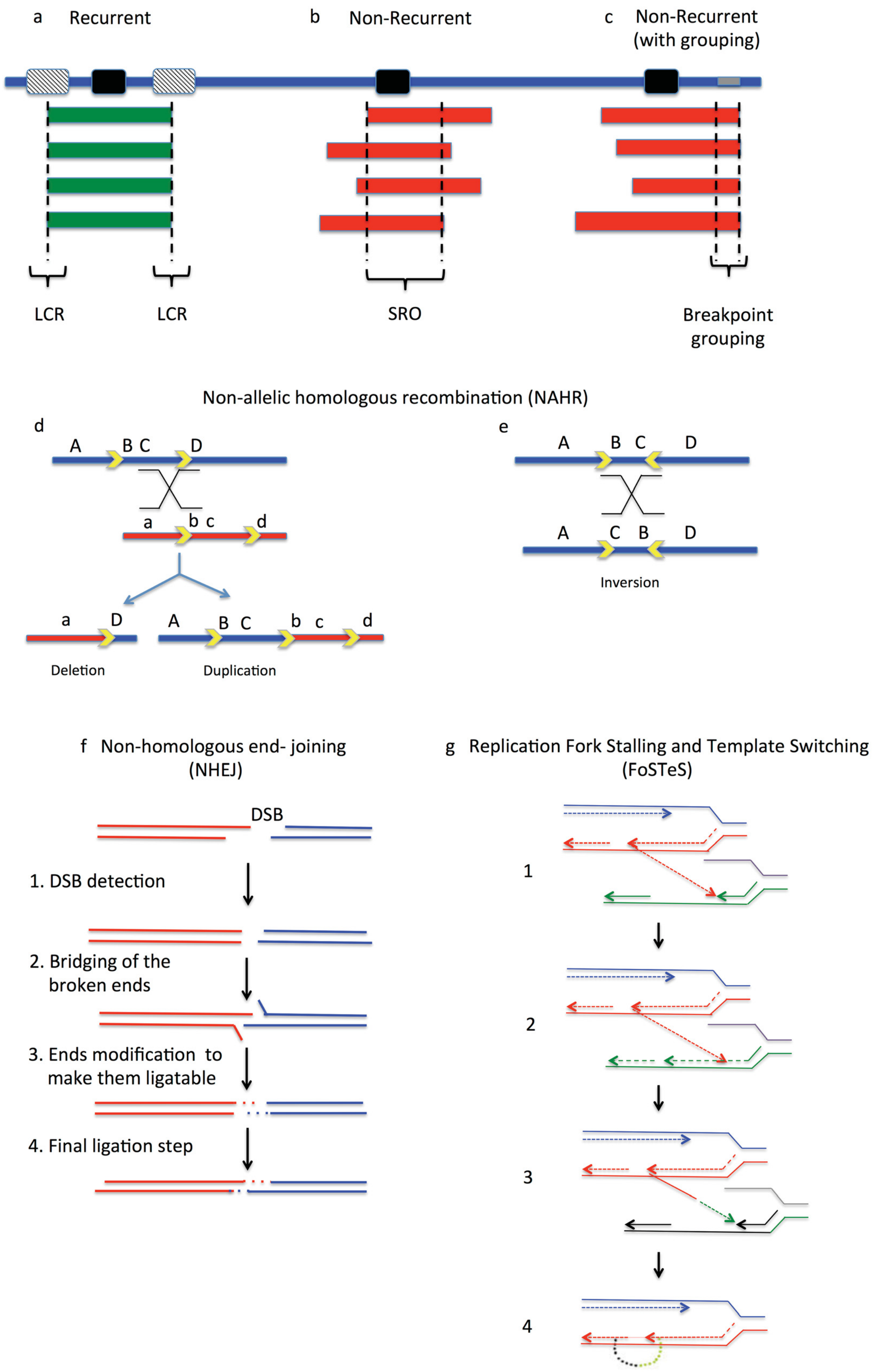

Figure 2-2 Mechanisms of genomic rearrangements.

The different mechanisms of genomic rearrangements: a-c major rearrangement mechanisms: Recurrent, Non-recurrent and non-recurrent with grouping. LSR: Low-copy repeats; SRO: the smallest region of overlap; The black rectangle portrays a gene within the rearranged region; Green bars (in **a**) and red (in **b** and **c**) bars represent potential rearrangements (duplications, deletions or inversions); gray rectangles represent complex architectural elements. **d-e** Non-allelic homologous recombination (NAHR); formed by recombination between LCR segments (yellow arrows); arrowheads indicate the orientation of the LCRs; Capital letters refer to the flanking sequences with homologues on the other strand represented by small letters, diagonal lines represent the recombination events (d. duplication and deletion events and e. inversions). **f.** Non-homologous end-joining (NHEJ) of the A double-stranded DNA break (DSB) regions. Lines (red and blue) represent DNA strands with DSB; dotted lines represent the end modification process before ligation that usually involves addition or deletion of bases leaving information scars of NHEJ. **g.** The replication Fork Stalling and Template Switching (FoSTeS) Model. Replication fork (solid lines, blue, red), lagging strand represented by dotted lines, 1. Separation and annealing to a second fork (solid lines, Green and purple) by microhomology; 2. Extension step of the replication process with of the now 'primed' second fork; 3. After the fork disengages, it can invade a third fork (solid lines, Gray and black). Dotted lines symbolize newly synthesized DNA sequence. This process could occur several times before the last step (4) of recommencement of replication on the original template. Adapted and modified from (Gu et al., 2008) and (Lee et al., 2007).

2.6.3 Discovery of Copy number changes

Currently, there are two primary approaches to discover CNVs, microarrays and next-generation sequencing. Original microarrays studies employed large-insert clones of bacterial artificial chromosomes (BACs) and oligonucleotide arrays (Iafrate et al., 2004; Sebat et al., 2004). Nowadays, comparative genomic hybridization (CGH) to synthetic oligonucleotides and SNP-based arrays are the used microarray assays (Conrad et al., 2010; Redon et al., 2006). Currently, not a single approach has the power to detect the full spectrum of structural variations (Levy et al., 2007; Pang et al., 2010; Pang, Macdonald, Yuen, Hayes, & Scherer, 2014) and the findings are largely dependent on the platform and algorithms used (Pinto et al., 2011; Zarrei et al., 2015). CGH is more potent in detecting copy-gains compared to SNP-base array and NGS but is limited by its low resolution and overestimation of breakpoints. NGS is more sensitive and more accurate in breakpoints resolution (Zarrei et al., 2015).

The Database of Genomic Variants (DGV) created in 2004, is a comprehensive catalogue of human CNVs within controls (defined concerning specific disease research, in which other probable conditions are not eliminated) (Iafrate et al., 2004). DGV also contains studies of somatic CNVs in healthy individuals (usually influenced by the age of the represented population) (Zarrei et al., 2015).

2.7 Project rationale and objectives

2.7.1 Somatic mutations and autoimmunity

Autoimmune diseases are known to depend on both inherited susceptibility and environmental factors. However, these alone may not explain all of the disease causation. As discussed above, in T1D concordance in monozygotic twins is about 30%

and by the age of 60 years it is about 65% (Redondo et al., 2008). Moreover, even in concordant pairs, ages of onset can vary by decades. By the age of onset most twins have been exposed to a similar shared environment, which makes it unlikely that different exposure to putative environmental factors accounts for all of this difference (Knip & Simell, 2012). Similarly, in the inbred NOD (non-obese diabetic) mouse model, males have an incidence of less 50% despite being genetically identical, kept in a standardized germ-free environment and fed the same diet (Makino et al., 1980). These observations suggest an alternative non-heritable part of genetics, i.e. stochastic events. One plausible such stochastic event could consist of post-zygotic genetic alterations in the expanding antigen-specific autoreactive T-cell lineages in autoimmune diseases.

F. M. Burnet first proposed this hypothesis in 1972 (F.M. Burnet, 1972). In a time where understanding of lymphocytes was limited, Burnet proposed that the stochastic nature of autoimmune diseases might be caused by a combination of germline and somatic mutations. These interrupt standard mechanisms for eliminating self-reactive lymphocytes leading to the development of “forbidden clones”. The hypothesis was proposed again by C. Goodnow in 2007 (Goodnow, 2007), who hypothesized a significant contribution of PZMs in the pathogenesis of autoimmune diseases, in a paradigm similar to the pathogenesis of cancer.

As previously discussed, (Section 2.2.1 and 2.2.2), a sequence of checkpoint mechanisms prevents the potential development of self-reactive lymphocytes and only when multiple checkpoints are bypassed, autoimmunity acquire. PZMs are *de novo* non-inherited genetic changes that occur throughout any stage of development. These mutations either copy-number or point mutations can be passed down to a cell lineage during cell division and have a potential role in autoimmunity similar to that in cancer in which, parallel checkpoint mechanisms prevent neoplasia (Goodnow, 2007).

Autoimmune conditions and lymphomas exhibit a latent period and stochastic occurrence. In autoimmunity, the usual assumption has been that this is due to an unknown environmental trigger in which genetically predisposed individuals got exposed to. However, as pointed before, some animal models develop autoimmune diseases in pathogen- and germ-free environment. In cancer, the latent period and stochastic occurrence has been explained to the need for enough time to enable the accruing of somatic mutations in individual clones and bypassing the multiple growth checkpoints (Goodnow, 2007).

On this basis, and the following reasons, Goodnow drew parallels between autoimmunity and lymphoid cancers by pointing to the shared pathogenesis (Goodnow, 2007). First, as mentioned earlier, the rate of somatic mutations has been estimated to be ~10^{-6} per gene per cell division, and replication errors are expected to accumulate during cell divisions (Araten et al., 2005; Araten et al., 2013). This makes it inevitable that a considerable number of cells in every individual carry PZMs. Moreover, somatic mutations commonly and frequently occur in blood cells. A mosaic state has been detected in peripheral whole-blood of healthy individuals (Busque et al., 2012; Forsberg et al., 2012; Genovese et al., 2014; Jacobs et al., 2012; Laurie et al., 2012; Xie et al., 2014). These findings underestimate the rate of these events in the general population, as peripheral whole- blood is a heterogeneous mixture, within which the PZM mosaicism is too low to cause a clinical phenotype or to be detectable by conventional methods

(Jacobs et al., 2012). PZM frequency increases with age, indicating that their rise to detectable levels is due to some proliferation/survival advantage.

Second, some lymphocytes undergo somatic mutation as part of their ordinary maturation course. For example, somatic hypermutation is a specialized mechanism of B- cell maturation (discussed in section 2. 2) and somatic mutation during isotype switching. These mechanisms are error prone, and they trigger oncogenes and deactivate tumor suppressor mechanisms in lymphoma (Goodnow, 2007; Muschen et al., 2000). One example is children with symptoms resemble that of the autoimmune lymphoproliferative syndrome who lack the causal inherited mutation *FAS* gene in their germline (Dowdell et al., 2010; Holzelova et al., 2004). The cause of these symptoms is a somatic *FAS* mutation in a stem cell and therefore, its T-cells and B-cells progeny (Holzelova et al., 2004). Mouse model studies demonstrated the need for the mutation to exist in both T- and B-cells for the disorder to develop, suggest the need for the mutation to occur at an early lymphocytes developmental stage (Goodnow, 2007).

Third, there is epidemiological evidence for an overlap in the pathogenesis of lymphomas and autoimmune disorders. For example, both humans and animal models with inherited *Fas* mutation develop mostly B-lymphomas, although the T-cells are the main affected with lymphoproliferation (Straus et al., 2001). Moreover, somatic *FAS* mutations found in non-Hodgkin's lymphoma patients are mostly in those with a prior history of autoimmune disease (Gronbaek et al., 1998). The risk of lymphoid malignancies is high in individuals with autoimmune diseases such as CD (Cellier et al., 2000), lupus (Bernatsky et al., 2005), rheumatoid arthritis and Sjogren disease (Goodnow, 2007; Zintzaras, Voulgarelis, & Moutsopoulos, 2005). This phenomenon is not observed in other chronic immune reactions, such as allergic disorders (Soderberg, Jonsson, Winqvist, Hagmar, & Feychting, 2006) and inflammatory bowel diseases (Smedby et al., 2006). These evidences suggest some overlaps between proliferation checkpoints that are crucial in preventing lymphomas and tolerance checkpoints that are crucial in preventing autoimmunity.

Examining malignant lymphomas developing following an autoimmune disorder points to evolution from autoreactive cells. In celiac disease, usually, the inflammation remits when gluten-containing food is avoided, except in a group of patients where the disease progress into a gluten-independent gut disorder (refractory sprue). This progression is usually followed by an oligoclonal expansion of T- cells leading to an enteropathy-associated T cell lymphoma (Goodnow, 2007).

2.7.2 Thesis objectives

In the following chapters, we investigate the hypothesis that the occurrence of somatic, post-zygotic mutations (PZM) in autoreactive cells of the immune system is frequent and contributes to the autoimmunity of T1D and CD. We hypothesize that PZMs play a role by causing T- cells to escape self-tolerance checkpoints, causing expansion of auto-reactive lineages that account for the disease's stochastic penetrance. Here we focused on copy-number mutations, whose functional effects are easier to determine.

We proceeded to test our hypothesis in three studies, as reflected in the following manuscript-based chapters. In the first chapter, the hypothesis was tested in NOD mice as an excellent model of human T1D. The first objective was to develop a reliable methodology to test the hypothesis. We used comparative genomic hybridization (CGH) as a method to detect somatic number aberrations (CNAs) and define the detectable level of mosaicism of autoreactive T-cells from pancreatic lymph-nodes of diabetic mice. Our second objective was to explore any recurrent mutations in different diabetic NOD mice. Our third objective was to confirm the CNAs using an independent method. Our fourth objective was to examined potential CNAs in pathogen-reactive lymphocytes as control cells operating in their normal host defense function. Finally, our fifth objective was to predict at which point of developmental stages these CNAs were formed by determining the level of clonality via TCR sequencing. This study is described in chapter 3 (with supplementary in Appendix I) and ready to be submitted for a peer-reviewed publication.

In the second study, we aimed to test the hypothesis in human T1D. Our first objective for this chapter was to develop a methodology to obtain autoreactive lymphocytes from whole blood of newly diagnosed T1D patients. This required developing an *in vitro* protocol to activate the autoreactive cells by insulin as the major antigen in T1D. Our second objective was to look for recurrent CNAs in autoreactive lymphocytes from different patients, as it further supports our hypothesis and points to the CNAs pathogenicity involvement. Our third objective was to test for potential CNAs in pathogen-reactive lymphocytes as negative controls. We examined lymphocytes from the diabetic patients activated by *Tetanus Toxoid* (TT). Our fourth objective was to also look for potential recurrent genes affected in both diabetic NOD mice (from the first study described in chapter 3) and the genes identified with CNAs in this study. Finally, similar to the first study, our fifth objective was to predict the developmental stage of the mutations occurring by determining the level of clonality of these cells. This study is still in progress and is described in chapter 4 (with supplementary in Appendix II).

In the third study, we extended our investigation to test the hypothesis in Celica Disease (CD), as another autoimmune disease. Our first objective in this study was to develop a methodology to obtain autoreactive lymphocytes from whole blood of CD patients. In this study, we obtained whole blood samples from CD patients after they undergo a gluten challenge and using the same approach we used in the second study (chapter 4), we identified recurrent CNAs in these patients. Our second objective was to look for recurrent CNAs in autoreactive lymphocytes from different CD patients. Our third objective was to test for potential CNAs in pathogen-reactive lymphocytes as negative controls. Similar to our approach in chapter 4, we examined lymphocytes from CD patients activated by TT. Our fourth objective was to look for recurrent affected genes with proliferative and/or immune function with T1D identified genes from the first two studies (diabetic NOD mice and T1D patients). This study is still in progress and is described in chapter 5 (with supplementary in Appendix III).

CHAPTER THREE Clonal copy-number mosaicism in autoreactive T-lymphocytes in diabetic NOD mice

Maha Alriyami[1]; Luc Marchand[1]; Quan Li[1]; Xiaoyu Du[1]; Martin Olivier[2]; Constantin Polychronakos[1*]

[1]The Endocrine Genetics Laboratory, Child Health and Human Development Program and Department of Paediatrics, McGill University Health Centre Research Institute, Montreal, Quebec, Canada, H3H 1P3. [2]Departments of Medicine, Microbiology and Immunology, McGill University Health Centre Research Institute, Montreal, Quebec, Canada, H3H 1P3. Correspondence and requests for materials should be addressed to C.P. (email: constantin.polychronakos@mcgill.ca)

Manuscript status: Submitted to Genome research.

Authors Contribution:

Maha Alriyami: Designed and executed the experiments, results analysis and interpretation, writing and preparation of manuscript.

Luc Marchand: Technical expertise and preforming the multiplex ligation-dependent probe amplification and CBS analysis.

Quan Li: Bioinformatics analysis in CBS and MiSeq analysis.

Xiaoyu Du: Technical expertise and executing of the TCR sequencing.

Martin Olivier: Research collaborator, Technical expertise and conducting the *Leishmania major* mice infection and contribution with providing BALB/c mice.

Constantin Polychronakos: Research supervisor and mentor, results interpretation, manuscript editing and corresponding author.

3.1 Preface

The causes underlying Type 1 Diabetes and other autoimmune diseases are not fully known. The contribution of the genetic and environmental elements although established, may not explain all the disease such as the low concordance in identical twins and the incomplete occurrence of the disease in its animal model (NOD mice) in pathogen-free, controlled environments. In the following work, we aimed to investigate the somatic mutations hypothesis in autoimmune diseases by exploring it in T1D by first testing it on NOD mice, the model organism for T1D that spontaneously develops the disease and have many similarities to the human one. Here, I focused on CNAs since their functional significance is relatively easier to deduce. Using a genome-wide scan, we identified recurrent copy-number mutations exclusively in self-reactive lymphocytes. Our findings offer novel avenues for understanding autoimmunity and its future individualized treatment through targeting disease-causing cells. Moreover, we analyzed the affected genes and investigated if any have an immune or cell-proliferation function.

3.2 Abstract

Concordance for type 1 diabetes is far from 100% in monozygotic twins and in the inbred NOD mice, despite genetic identity and shared environment during the years of peak incidence. This points to stochastic determinants. One plausible, never explored, such stochastic event is post-zygotic mutations (PZMs) in the expanding antigen-specific autoreactive T-cell lineages, by analogy to their role in the expanding tumor lineage in cancer. Using high-resolution comparative genomic hybridization (CGH) of DNA from memory CD4+ T-cells from pancreatic lymph nodes of 25 diabetic NOD mice, we found lymphocyte-exclusive mosaic somatic copy-number aberrations (CNAs) with highly non-random independent involvement of the same gene(s) across different mice, some with an immune function and an association with autoimmune diseases such as *Ilf3* and *Dgka*. In lymphocytes expanded during normal host defense (*Leishmania* infection), from 17 control mice, fewer and significantly smaller CNAs were found compared to those in autoreactive cells (P=0.0019). The low T-cell clonality determined by TCR sequencing

suggests a pre-thymic formation of the CNAs. Our data strongly support a causal role for PZMs in autoreactive T-cells in the pathogenesis of T1D. Our observations challenge the classical notions of autoimmune disease and open conceptual avenues toward individualized prevention and therapeutics.

3.3 Introduction

Type 1 diabetes (T1D) is an autoimmune disease that results from the targeted destruction of the insulin-producing beta cells by the infiltration of autoreactive T lymphocytes into the islets of Langerhans (Polychronakos & Li, 2011). The disease is antigen-specific, in which this autoimmune process of infiltration destroys the insulin-producing beta cells only, leaving the alpha and delta cells of islet intact. Although T1D is known to depend on both inherited susceptibility and environmental factors, these alone may not explain all of the disease. Concordance in monozygotic twins is much less than 100% although by the age of onset most twins have been exposed to a similar shared environment, which makes it unlikely that different exposure to putative environmental factors accounts for this difference (Knip et al., 2005). Similarly, in the inbred NOD (non-obese diabetic) mouse model, males have an incidence of less 50% despite being genetically identical, kept in a standardized environment and fed the same diet (Makino et al., 1980). These observations suggest stochastic events. One plausible such stochastic event could consist of post-zygotic genetic changes in the expanding antigen-specific autoreactive T-cell lineages.

The hypothesis suggesting the contribution of postzygotic mutations (PZM) as stochastic events in the pathogenesis of autoimmune diseases was first proposed by F. M. Burnet in 1972 (F.M. Burnet, 1972). Although limited knowledge about lymphocytes was available at the time, Burnet proposed that the stochastic nature of autoimmune diseases might be caused by a combination of germline and somatic mutations that interrupt normal mechanisms for eliminating self-reactive lymphocytes and causing the development of “forbidden clones”. The hypothesis was proposed again by C. Goodnow in 2007 (Goodnow, 2007), who hypothesized a major contribution of PZMs in the pathogenesis of autoimmune diseases, in a paradigm similar to the pathogenesis of cancer.

PZMs are *de novo* non-inherited genetic changes (copy-number or point mutations) that happen during any stage of development and can be passed down to a cell lineage during cell division. In blood cells, this results in a mosaic state that can occasionally be detected in whole peripheral blood of healthy individuals (Forsberg et al., 2012; Jacobs et al., 2012; Laurie et al., 2012). These findings almost certainly underestimate the frequency of these events in the general population, as peripheral whole- blood is a heterogeneous mixture, within which the PZM mosaicism is too low to cause a clinical phenotype or to be detectable by conventional methods (Jacobs et al., 2012). PZM frequency increases with age, indicating that their rise to detectable levels is due to some proliferation/survival advantage. The contribution of copy-number somatic mutations in the pathogenesis of cancer has been established and has enabled therapeutic advances by identifying drug targets essential to disease causation.

In this study, we investigated the PZM hypothesis as part of the cause of diabetes in NOD mice, a model characterized by the spontaneous development of insulitis that closely recapitulates the destruction of the pancreatic beta-cells by autoreactive CD4+ and CD8+ T cells in human T1D (Anderson & Bluestone, 2005; Kikutani & Makino, 1992;

Makino et al., 1980; Pearson et al., 2016; Polychronakos & Li, 2011). Similar to human T1D, NOD diabetes is caused by a combination of polygenic inheritance and environmental factors (Pearson et al., 2016; Polychronakos & Li, 2011). Female mice are predominantly affected (90-100% by 30 weeks of age) compared to males that develop it at an older age with lower frequency. We hypothesize that PZMs play a role by causing T-cells to escape self-tolerance checkpoints, causing expansion of auto-reactive lineages that account for the disease's stochastic penetrance. As a first step, we focused on copy-number mutations, which are easier to detect and have more obvious functional effects.

3.4 Material and Methods

3.4.1 Experimental Model

Wild-type NOD/ShiLtJ (purchased from The Jackson Laboratory, Bar Harbor, ME) and BALB/c (purchased from Jackson Laboratory and Charles River) mice were kept in pathogen-free conditions (maximum of five mice per cage) and were fed a standard chow diet (Tekland irradiated global 18% protein rodent diet, 2918). During the study, animals were housed with lights on from 7:00 am to 7:00 pm, and access to food and water as ad libitum. Mice were monitored for glycosuria every two days. The onset of diabetes was detected by making the animal urinate on a reagent strip, ChemStrip uG/K (cat#: 10647705119, Roche), to detect glucose. Positive animals for glycosuria (>13.8 mmol/l (250 mg/dl) were euthanized, and blood glucose was measured using a glucometer. All animals that fit the inclusion criteria were used (n=25, 22 females and three males, Table. 3. 1); there were no exclusion criteria, and no randomization was applied. Since we had no prior information on which to base power calculations, the number of mice tested was determined by available funds. Diabetic mice were euthanized with CO_2 and dissected to obtain pancreatic lymph nodes (PLN) for the isolation of memory CD4+ T-cells. Tail samples were also obtained for sampling germline. For four mice, cells from other peripheral lymph nodes (Superficial cervical LN, Axillary LN, and Inguinal LN) were also obtained as controls.

To compare with T-cells proliferating in normal host defense, ten NOD (n=10, Two males and eight females) and seven BALB/c mice (n=7, females) (Table. 3. 3) were infected with *Leishmania major* by injecting $5x10^6$ late stationary phase *L. major* promastigotes (50 µl PBS) subcutaneously into the footpad. Three weeks after injection, mice were euthanized, and the popliteal lymph node was dissected.

3.4.2 Isolation of memory T-Lymphocytes

Nodes were placed in 1 ml cold Dulbecco's Saline DPBS (1X) (cat#: 14190-144, Life technologies) and lymphocytes isolated by sheer-force slide dissociation. Next, fluorescence activated cell sorting (*FACS*) was used to isolate memory T-lymphocytes ($CD4^+/CD62L^-/CD44^+$ by FACSAria cell sorter (Becton-Dickinson). In these experiments, cells were stained using: anti-CD4-FITC (cat#: 11-0042-82, eBioscience), anti-CD8α-PE (cat#: 12-0081-82, eBioscience), anti-CD62L-APC (naive-cell marker; cat#: 130-091-805, Miltenyi Biotec) and anti-Human/Mouse $CD44^+$-PreCP-cy5.5 (memory-cell marker; cat#: 45-0441-82, eBioscience). All samples were kept on ice throughout isolation and staining.

3.4.3 DNA extraction and Whole Genome amplification

DNA was extracted from lymphocytes and germline DNA from tail samples. Samples were amplified using GenomePlex complete whole genome amplification

(WGA-2) (cat #: WGA2-50RXN) kit, approved explicitly by Agilent for aCGH (comparative genomic hybridization) to detect copy-number differences. DNA was next purified using PCR Cleanup kit from Sigma (cat #NA1020, Sigma).

3.4.4 Detection of PZMs

We sent 1.5 ug of amplified DNA to Oxford Gene Technologies (OGT) for Comparative Genomic Hybridization analysis (CGH) on the mouse 4X180K *Agilent* array. DNA from memory cells was used as 'test sample' and germline DNA obtained from the tail samples was used as 'reference sample'. To model the sensitivity to detect levels of mosaicism, samples were prepared using germline DNA of NOD as a test and from C57BL6/J as a reference. The NOD samples were mixed with C57BL6/J DNA in different proportions (100% NOD, 50% NOD, and 25% NOD) before amplification, to imitate different levels of mosaicism at inter-strain copy-number variants (CNV). In each case, 100% C57BL6/J was used as a reference.

Copy-number alterations (CNA) were detected by the Agilent dual color, 4x180k mouse CGH array. Test and reference DNA samples were labeled with different fluorescent tags (Cy3 and Cy5, respectively), which were next hybridized to the probes of the 4x180 chip, arrayed genome-wide but with a concentration in and around coding sequences. The fluorescence intensity ratio (Cy3: Cy5) at each probe position reflects copy-number differences between the two DNA samples. CGH quality control (QC)-Derivative log ratio spread (DLRS) values were within Agilent Technologies specifications (Supplementary data*,* Fig. S3. 1).

To evaluate the specificity of the method, two technical controls were tested in which DNA sample from lymphocytes from C57BL6/J mouse was amplified twice by the same kit (WGA-2), and then one of the two amplified samples was used as a test and the other as a reference in CGH (4x180K) analysis. Moreover, DNA was amplified twice from memory CD4$^+$ T-cells obtained from PLN of a diabetic mouse (M9) and twice from germline DNA from a tail-clip sample of the same mouse. These duplicate samples were analyzed separately (M9 and M9B) by CGH (4x180K) using in both samples the amplified memory CD4$^+$ DNA as a test and the amplified germline DNA as a reference.

3.4.5 Bioinformatics analysis

Test and reference signals were calculated for each probe, and internal normalization equalized the systematic difference between the two fluorochromes. The base-2 log of the Cy3/Cy5 ratio (LRR) was used for analysis. For NOD samples, based on the three control samples, probes covering NOD germline deletions were eliminated. Similarly, BALB/c samples probes covering BALB/c germline deletions were eliminated based on a control sample in which BALB/c DNA was used as test and C57BL6/J as a reference. Regions bearing copy number aberrations were identified using two independent algorithms, Agilent Genomic *Workbench 7.0* (Agilent Technologies) implementing the ADM-2 algorithm and DNAcopy software implementing the circular binary segmentation (CBS) algorithm (Venkatraman & Olshen, 2007). In ADM-2 (provided by Agilent technologies, threshold 6.0), the algorithm identifies aberration points that maximize the *t*-test of comparing the averages from the expected value of zero. Once a segment is kept, its median is centered, and the method is repeated on three new segments. This combines the segmentation and calling process (Roy & Motsinger Reif, 2013). We applied Agilent technologies recommended filtering standards of a minimum of 3 consecutive aberrant probes and a minimum absolute average $\log_2$ ratio of LRR

|0.25| and P-value <2.90 x 10-07 (Bonferroni threshold). The mouse genome UCSC mm9 NCBI build 37/July, 2007 was used to match the indexing of the Agilent probes.

In CBS, each chromosome was recursively split into small regions (each containing more than three probes), using a maximal t-statistic test for detecting the change-points: for one segment, a two-sample t-statistic compares the mean of the Log2-ratio in the sub-segment to the mean Log2-ratio of the rest of the segment. The splitting of the DNA stops when no more change-points can be identified. The mouse genome UCSC mm9 NCBI build 37/July, 2007 was used to match the indexing of the Agilent probes. CNAs were kept as true if were called by both algorithms ADM-2 (LRR|0.25|, P-value ≤ 2.90 x 10^{-07}) and CBS (LRR|0.25|, P-value ≤ 1 x 10^{-04}). The lower statistical significance threshold for CBS is justified by the vastly smaller number of hypothesis tested (number of ADM-2-called CNAs).

Blinding between samples obtained from diabetic mice and *L. major* infected animals was not possible because of the different source of material. However, the array data generation and the bioinformatics analysis were done blindly in one batch, using the same parameters. Tissue-specificity of the expression levels of the genes involved was obtained from BioGPS, 2018 (C. Wu, Jin, Tsueng, Afrasiabi, & Su, 2016).

3.4.6 Statistics

The statistical significance of the recurrence of overlapping CNAs in different mice was estimated by permutation testing. The chromosomal coordinates of each CNA were randomly reassigned around the mouse genome, and the number of overlaps noted. This process was repeated for 100,000 iterations. Either the actual length in kb of each CNA or the number of probes covering it were used in this simulation. Both gave similar results, but we retained the results of the probe permutation, a more conservative approach that avoids inflating the statistical significance because of non- homogenous distribution of the probes (favoring coding sequences).

The difference in the number of probes covering CNAs in T-cells from diabetic pancreatic nodes vs. *L. major* infected popliteal nodes was assessed by the Pittman permutation test, which does not require an assumption about the normality of distribution. We compared the number of probes (number of consecutive probes covered) because the gene-centered positioning of the probes, they better reflect the genes covered by them than the actual CNA length.

3.4.7 Multiplex Ligation-dependent Probe Amplification (MLPA)

Some CNAs were selected for confirmation by MLPA based on the availability of unamplified DNA and the presence genes with an interesting immune expression or function. MLPA on the original unamplified DNA samples was used as the gold standard in CNV diagnostics. Primers (Supplementary data, Table S3. 2) were designed for four loci. The amplification was carried out by PCR using 33 cycles, of 95°C for 30 seconds, 60°C for 30 seconds and 72°C for 1 minute. To identify and quantify the amplification products capillary electrophoresis on an ABI310 genome analyzer. GeneMapper software was used to define the peak areas of the PCR products. Data were normalized by dividing each probe's peak area by the average peak area of the control gene in each sample. The normalized peak pattern was divided by the average normalized peak pattern of all the samples in the same experiment.

3.4.8 TCR sequencing

RNA samples were extracted from the $CD4^+$ memory cells isolated from the pancreatic lymph nodes of diabetic mice. For the TCR pre-sequence amplification we used a 5’ RACE approach using the SMARTer®RACE cDNA amplification kit by clontech (Mountain View. CA.USA). This approach uses the known sequence of the C (constant) TCR-α and TCR-β segment for reverse primer (TCRAm (AS5): CAA AGT CGG TGA ACA GGC AGA G, and TCRBm (AS): GCC AAG CAC ACG AGG GTA GC) and an arbitrary added sequence by 5’RACE for the forward primer. PCR products were purified using the QIAquick PCR purification kit by Qiagen and prepared for Miseq sequencing with the *Illumina* Nextera XT library preparation kit according to the manufacturer's manual. Sequencing was done using the MiSeq paired-ends (250 bp) protocol. The reads were aligned to the TCR reference sequence of the international ImMunoGeneTics information system (IMGT). The alignment assigned V and J segments in both the α and β chain. The CDR3 (non-template added random amino acids) was determined starting from the V segment conserved Cysteine (Cys) at position 104 and the conserved Phenylalanine/Tryptophan (Phe/Trp) at positions 118 in the J segment.

3.4.9 Data availability

The CGH data discussed in this publication have been deposited in NCBI's Gene Expression Omnibus (Edgar, Domrachev, & Lash, 2002) and are accessible through GEO Series accession number GSE114660 (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc= GSE114660).

The TCR data discussed in this publication have been deposited in NCBI's Sequence Read Archive (Leinonen, Sugawara, Shumway, & International Nucleotide

Sequence Database, 2011) and are accessible through SRA Series accession number SRP148447 (https://www.ncbi.nlm.nih.gov/sra/SRP148447).

3.4.10 Study approval

In this study, all experiments on animals were approved by the Facility Animal Care Committee (FACC), according to the guidelines established by the Canadian Council on Animal Care and the McGill University Animal Care Committee (AUP#7517).

3.5 Results

In our vivarium, 90-100% of the female NOD mice and about 50% of males become diabetic. Mice displayed glycosuria at a median age of 21.3 weeks for females and 24.5 weeks for males (Supplementary data, Fig. S3. 2).

NOD mice, either male or female, were euthanized within 2-4 days of hyperglycemia onset and memory $CD4^+$ cells were isolated from their pancreatic lymph nodes (PLN) and sorted by flow cytometry on a FACSAria cell sorter. $CD62L^{neg}$ / $CD44^{hi}$ phenotype was used to distinguish memory from naïve cells (Fig. 1 a-b). Sorting memory cells from pancreatic lymph nodes gave an average number of 124,672 $CD4^+$ cells. In six of the mice examined, all T-cells were negative for L-Selectin (CD62L), indicating a strong preponderance of memory cells in the PLN (Fig. 1 c-d).

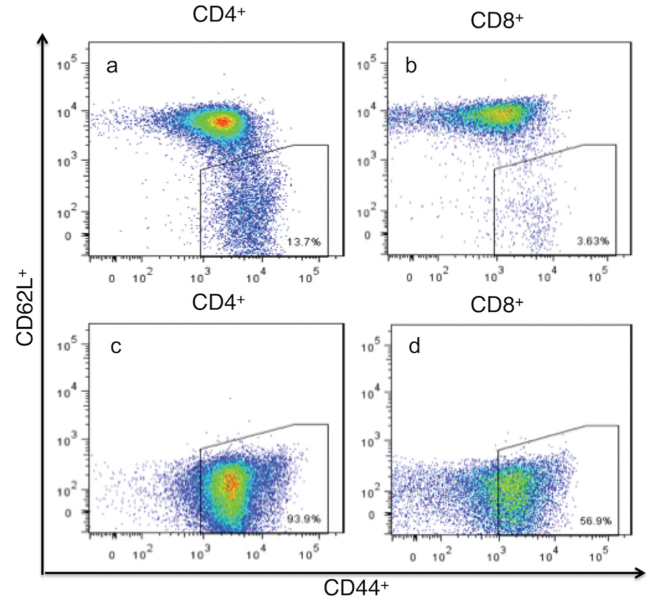

Figure 3-1 Flow-sorting of memory CD4+ and CD8T+ -cells from mouse pancreatic lymph nodes using the established surface-marker phenotype CD62Lneg/CD44hi.

a-b: Normal profile observed in most samples of $CD4^+$ and $CD8T^+$ -cells from mouse pancreatic lymph nodes. **c-d:** Profile of sorted memory cells in six animals in which all cells were $CD62L^{neg}$ with CD44 in the lower part of the range for memory cells.

3.5.1 Positive and negative controls

In comparative genomic hybridization (CGH) where both test and reference DNA are normal, the LRR is zero (log of the ratio 2 copies/ 2 copies = 0), which plotted against the chromosomal coordinates in bp, display a small amount of noise around 0. Series of consecutive probes drastically deviating from background noise indicates a copy-number change. CGH data of all tested samples revealed the expected deletions at the T cell receptor regions (β, γ and α–δ subunits) mapping, respectively, to mouse chromosomes 6, 13 and 14 due to genomic rearrangements within these regions to create TCR diversity. These loci served as internal naturally occurring positive controls for detecting mosaic PZM in T-cells using our approach (Fig. 3. 2).

Technical controls evaluating the specificity of the method demonstrated an absence of amplification artifacts in CNA calls. As expected, no CNAs were called when the same sample was used as test and reference due to the identicality of the two samples (Sample M26; DLRSpead value: 0.17). Moreover, no CNAs were called for the duplicate samples M9 and M9B (DLRSpead value: 0.18 and 0.21 respectively).

To evaluate the sensitivity of CGH 4x180K for mosaic CNAs, three control samples were prepared by mixing NOD tail-clip germline DNA (100%, 50%, and 25%) with C57BJ6/J DNA as test samples and C57BL6/J tail-clip germline DNA (100%) as a reference. Known CNVs between the two strains were detectable and statistically significant even at 25% mosaicism (Fig. 3. 3a) and correlated linearly with the Cy3/Cy5 fluoresces ratio (Fig. 3. 3b, Supplementary data, Dataset. S3. 1). This facilitated a rough estimation of mosaicism levels in unknown samples.

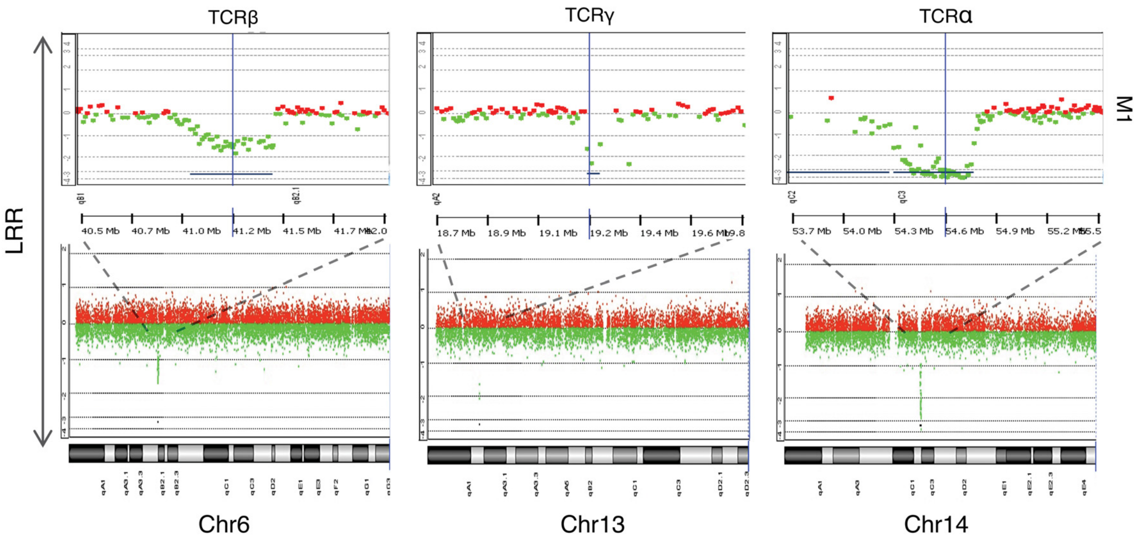

Figure 3-2 CGH array results demonstrating positive controls for T-cell CNAs observed in all samples.

CGH array results demonstrating positive controls for T-cell CNAs observed in all samples (to illustrate M1 is shown here). Copy-loss (regions represented by lines below the graph) at regions of TCR genomic rearrangements of the beta chain on chromosome six, gamma chain on chromosome 13 and alpha chain on chromosome 14 (Purple: LRR>0, Green: LRR<0, DLRSpread value: M1: 0.21).

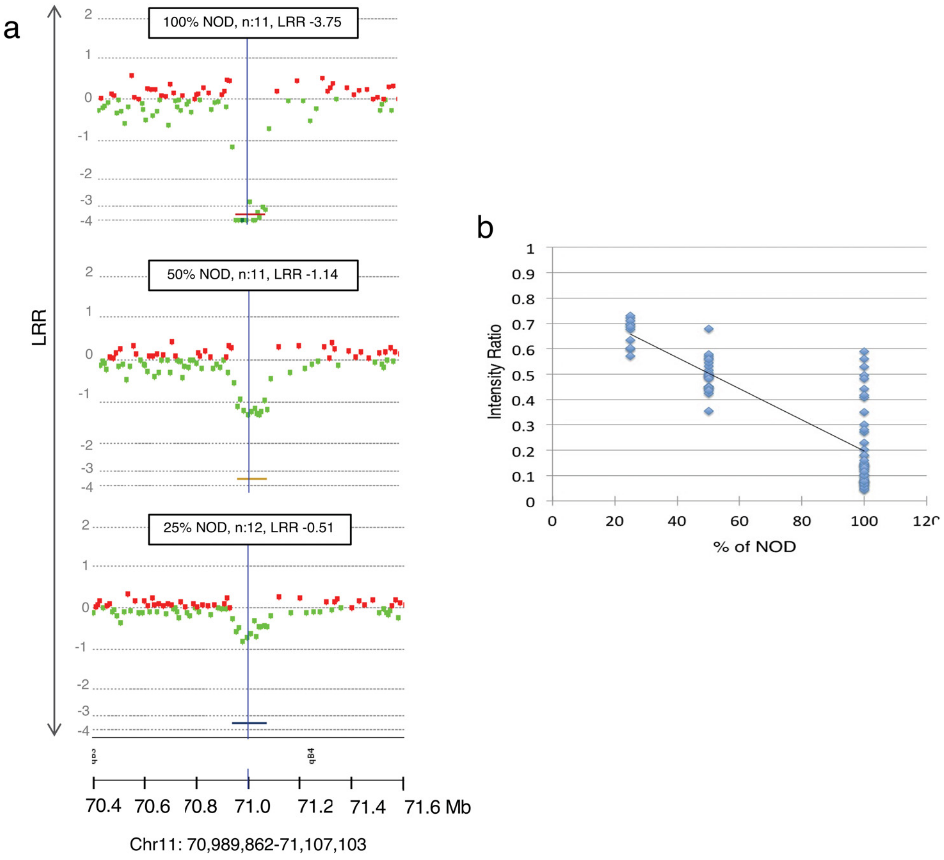

Figure 3-3 Results of mixture experiment indicating the detectable level of mosaicism using our approach.

Demonstration of the level of the detectable level of mosaicism using our approach. n: number of affected probes, Purple: LRR>0, Green: LRR<0. **a.** Example of the CGH array results of the three control samples (100%NOD, 50% NOD, 25% NOD mixed with C57BL6/J against 100% C57BL6/J as reference). A known CNV at chr11: 70,989,862-71,107,103 (region represented by colored lines below the charts, colors are different for different samples) between NOD and C57BL6/J identifiable and highly significant in all mixture ratios even in the 25% sample mimicking this level of mosaicism. **b.** The intensity ratio of known NOD copy-losses is significantly lower than the baseline represented by 1 (DLRSpread values: 100%NOD: 0.23; 50%NOD: 0.20; 25% NOD: 0.15).

3.5.2 Recurrent post zygotic copy number changes in pancreatic lymph nodes of T-cells of different mice

A total of 25 diabetic mice were tested (22 females and three males) (Table.3. 1). Out of the 25 mice, 19 showed a normal sorting profile (Fig. 3. 1 a-b), but in six mice all cells were memory (CD62L^{neg}) (Fig. 3. 1 c-d). The 25 tested mice had a total of 403 somatic CNAs (Supplementary data*,* Dataset. S3. 2, and S3. 3). Four of the mice were also investigated for CNAs in CD4^{+} from the peripheral LN (M16L, M17L, M20L, and M21L). No CNAs were called in samples obtained from the peripheral LN of these mice.

We identified eight recurrent CNAs that occurred independently in different mice (Table. 3. 2, Fig. 3. 4), which is very unlikely to happen by chance alone. After 100,000 iterations of randomizing the genomic coordinates of the probes defining these CNAs, not a single one gave the number of recurrent CNAs observed or more ($p< 10^{-6}$). The same result was found after removing M23 and M25 (two of the mice with memory-only cells in PLNs and with a large number of recurrent CNAs, Table. 3. 1). This non-random recurrence supports causal-functional importance, and in the cancer paradigm, it is considered a strong indicator of pathogenicity.

Two of the recurrent CNAs span Homeobox clusters (*Hoxd* and *Hoxa*). Both are copy losses at chr2: 74,474,401- 74,598,078, spanning the *Hoxd* gene cluster and the other one at chr6: 52,116,749- 52,207,847 spanning *Hoxa* gene cluster, both found independently in CD4+ cells of two separate mice M4 and M12 (Table. 3. 2, Fig. 3. 4 a and 3.4 c). *Hox* genes control proliferation and differentiation of hematopoietic cells and has a crucial role in human T-cell development. Moreover, they have been shown to be the most active cluster during early hematopoiesis (Lawrence, Sauvageau, Humphries,

& Largman, 1996; Magli, Largman, & Lawrence, 1997; Taghon et al., 2002; Taghon et al., 2003). *Hox* genes have been implicated in leukemogenesis (Kawagoe, Humphries, Blair, Sutherland, & Hogge, 1999) and to act as tumor-suppressors (Shah & Sukumar, 2010).

Another recurrent CNA is a copy gain at chr3: 94,767,165- 94,821,010 (Table. 3. 2, Fig. 3. 4b) seen independently in three diabetic mice M23, M25, and M22. This CNA spans *Pi4kb* encoding Phosphatidylinositol 4-kinase beta, highly expressed in hematopoietic cells (C. Wu et al., 2016). It phosphorylates phosphatidylinositol (PI) as the first dedicated step in the production of the second messenger inositol-1, 4,5, -trisphosphate (PIP), an essential molecule in cellular signaling (Heilmeyer, Vereb, Vereb, Kakuk, & Szivak, 2003). Intensively studied members of Phosphatidylinositol kinase family, Phosphoinositide 3-kinases (PI3Ks) are activated by stimulatory receptors on TCRs and B-cell receptors (BCRs) having a central role in their function and proliferation (Buitenhuis & Coffer, 2009; Fruman & Bismuth, 2009; Vanhaesebroeck, Ali, Bilancio, Geering, & Foukas, 2005). The potential overexpression of *Pi4kB* due to the amplification observed in these mice might be contributing to their autoimmunity.

Another recurrent CNA at chr8: 72,706,464- 72,777,429 is a copy gain in two diabetic mice (M3 and M10) (Table. 3. 2, Fig. 3. 4d). A common affected gene is *Armc6,* with coding sequence within the confidence interval of the breakpoint locations, indicating a high likelihood of disruption of the gene by the duplications. *Armc6* is a highly conserved gene with gene ontology that suggests involvement in hematopoietic progenitor cell differentiation (GO:0002244) and in pancreatic cancer (Gress et al., 1996). We hypothesize that the potential overexpression of this gene in the lymphocytes might allow their escape from proliferation checkpoints.

Copy gain at chr11: 68,880,665- 68,909,840 (Table. 3. 2. Fig. 3. 4e), was found in three mice (M22, M23, and M25). This CNA spans two genes, *Tmem107* (transmembrane protein 107) and *Vamp2* (vesicle-associated membrane protein 2). *Tmem107* encodes a transmembrane protein 107, an uncharacterized gene that is highly expressed in T-cells (http://ist.medisapiens.com). Interestingly, another transmembrane encoding gene (*Tmem149*) was also spanned by a recurrent multi-copy amplification at chr7: 31,316,157- 31,433,964 in M25 (Supplementary data, Dataset. S3. 3) spanning several genes including some with high expression in hematopoietic cells such as *Tmem149, Lin37, Cox6b1*, and *Rbm42* (C. Wu et al., 2016). *Tmem149* encodes the transmembrane protein IGF Like Family Receptor 1 that is exclusively expressed in hematopoietic cells (C. Wu et al., 2016) and in mice is primarily expressed on T-cells (Lobito et al., 2011). Similar to *Tmem107,* this gene is also uncharacterized but it is structurally similar to the tumor necrosis factor receptor family (Lobito et al., 2011), and a potential inflammatory role was suggested for its encoded protein (Lobito et al., 2011).

Two CNAs in three of the mice with the unstable genome (M22, M23, and M25), are copy gains at two histone loci at chr13: 21,813,250- 21,921,804 and chr13: 23,648,864- 23,661,397 (Table. 3. 2, Fig. 3. 4g), spanning two clusters of highly homologous genes that encode nuclear proteins collectively referred to as Histone H1, H2, and H3. The histone loci are separated by a normal-copy number stretch encoding other genes. It was previously reported that in human CD4^{+} T cells, TCR activation induces a distinctive promoter histone profile that directs the transcriptional activation of FasL leading to apoptosis (Kaplan, 1989).

A recurrent CNA at chr14: 52,061,318-52,145,237 in mice M5 and M22 is a copy loss that spans two unstudied genes *Gm7247* and *Vmn2r89* (Table. 3. 2, Fig. 3. 4f). These two genes are also spanned by copy losses in mice M6 and M25 that were called by ADM2 but narrowly missed the CBS cut-off (Supplementary data, Fig. S3. 3a).

Finally, the last recurrent CNA is a copy loss at chr5: 23,846,753- 24,135,248 found independently in M16 and M12 (Supplementary data, Fig. S3. 3b). It is mentioned because it includes an important candidate gene, despite the fact that it missed (p=0.0018) the strict significance threshold in one of the two algorithms (CBS) in one of the two mice (M16). This CNA spans several genes that are highly expressed in hematopoietic cells including *Kcnh2*, *Fastk*, *Tmub1,* and *Chpf2* (C. Wu et al., 2016). *Fastk* encodes a protein that belongs to the serine/threonine protein kinase family, and it is a potent activator of lymphocytes apoptosis (Tian, Taupin, Elledge, Robertson, & Anderson, 1995). Moreover, it has been shown that this protein is highly activated during Fas-mediated apoptosis (Izquierdo & Valcarcel, 2007; Tian et al., 1995). The copy loss of this gene we observed in the autoreactive lymphocytes might have mediated autoimmunity by facilitating self-reactive lymphocyte escape from proliferation checkpoints and apoptosis.

Four of the six mice with the memory-only sorting profile (M20, M21, M22, and M24) have a comparable number of CNAs to the other 19 samples (M1-M19). However, M23 and M25 had the most striking results, showing a very large number of CNAs most, of which were recurrent loci between the two mice. ChrX and Y probes clearly showed a male and female genome, ruling out the possibility of sample duplication through a labeling error (Supplementary data, Table. S3. 2). The high number of CNAs in these two mice is reminiscent of CNAs observed in a malignant genome of a leukemic cell and involved many genes, some of them of known immune function. Three interesting examples of these CNAs include: a recurrent CNA in M23 and M25 is a copy gain at chr9: 20,856,727-21,236,076 spanning several genes including *Keap1, S1pr5,* and *Ilf3* with hematopoietic cells expression and an immune-related function (C. Wu et al., 2016) (Fig. 3. 5a, Table. 3. 3). Another large CNA is also at chr10: 79,084,598- 81,041,680. This recurrent CNA spans a large number of genes of which also several have a high or exclusive expression in hematopoietic cells including *Madcam1, Gzmm, Rps1, Mknk2, Dapk3, Matk, S1pr4,* and *Abca7 (C. Wu et al., 2016)* (Table. 3. 3, Fig. 3. 5b). Another one is a recurrent copy gain CNA in these two mice is at chr10: 127,684,108- 128,334,229 also spanning several genes with high or exclusive hematopoietic cell expression and/or an immune function including *Il23A, Pa2g4, Dgka*, *Coq10a* that are expressed in lymphocytes (*Dgka* is exclusively expressed in CD4+ and CD8+ cells) (Table. 3. 3, Fig. 3. 5c).

Since the above recurrent CNAs spans several genes with a high lymphocyte expression and have an immune, and proliferation function in immune cells (Table. 3. 3), we aimed to confirm these CNAs in the original unamplified DNA by multiplex ligation-dependent probe amplification (MLPA) as a technical validation of our approach with a completely different method. MLPA is considered the gold standard method for CNV diagnostics (Feuk, Carson, & Scherer, 2006). We selected three genes within the above three recurrent aberration regions and with an immune- related function to be examined: *Ilf3, Abca7*, and *Dgka*. *Ilf3* on chr9 is highly expressed in lymphocytes and encodes a double-stranded RNA binding protein that is required for T-cell interleukin-2 expression (Jarboui, Wynne, Elia, Hall, & Gautier, 2011). Moreover, it is associated with two immune-related diseases: psoriasis (Tsoi et al., 2012) and rheumatoid arthritis (Okada et al., 2014). *Abca7* on chr10 encodes a transporter protein detected principally in myelo-lymphatic tissues with an expression signature that implies a function in lipid homeostasis in immune cells (Tomioka et al., 2017). *Dgka* is exclusively expressed in CD4+, and CD8+ cells and its encoded protein is involved in cell cycle progression and the function of immune cells (Poli et al., 2017; Prinz et al., 2012) and has been reported to be associated with T1D (Evangelou et al., 2014). We successfully confirmed by MLPA the above three CNAs affecting these genes (*Ilf3, Abca7*, and *Dgka*) (Fig. 3. 5 d-e). Further detailed annotation of the CNAs seen exclusively in these two mice (M23 and M25) was not attempted, because of their large number and the probability that they are a consequence rather than a cause of the rapid proliferation.

Table 3-1 Number of CNAs found in memory CD4+ lymphocytes from PNL of tested mice.

(DLRSpread values; Supplementary data, Fig S3. 1)

Mouse Sample	Sex F/M	Age (weeks)*	Blood Glucose**	#CNAs
M1	F	18.4	11.1	0
M2	F	9	13.7	0
M3	F	18.4	15.8	1
M4	F	23.1	16.3	3
M5	F	19	18.9	1
M6	F	27.3	19.5	0
M7	F	22.6	20.5	1
M8	F	15.1	25.6	0
M9	F	20.3	26.2	0
*M9B****	F	20.3	26.2	0
M10	F	23.7	27	1
M11	F	19	30.5	0
M12	F	14.1	High	4
M13	F	17.3	High	0
M14	F	18.7	High	0
M15	F	23.7	High	0
M16	F	24.3	19.3	1
*M16L*****	F	24.3	19.3	0
M17	F	20.1	High	0
*M17L*****	F	20.1	High	0
M18	M	22.3	High	1
M19	M	24.1	22.2	0
M20	F	21.2	22.5	0
*M20L*****	F	21.2	22.5	0
M21	F	29.1	15.8	0
*M21L*****	F	29.1	15.8	0
M22	F	23.6	19.9	5
M23	F	14	25.1	295
M24	F	21.3	20.7	0
M25	M	18.4	22.7	90

*Age: Age of disease onset in weeks and Blood Glucose in mmol/L
***M9B a duplicate amplification of sample M9
****M16L, M17L, M20L and M21L: samples from the peripheral LNs from the same mice M16, M17, M20 and M21.

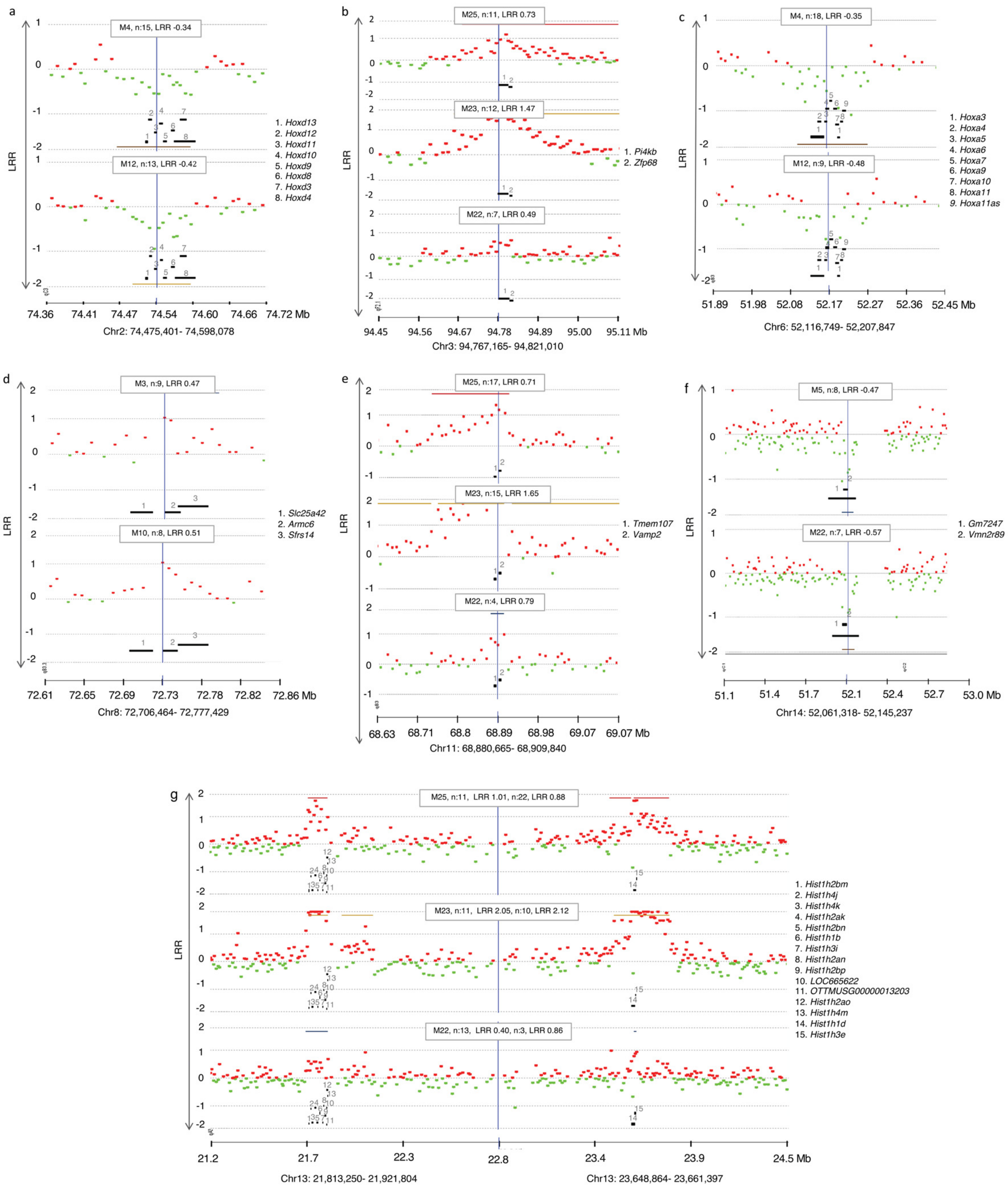

Figure 3-4 CGH array results of recurrent CNAs found in memory cells of diabetic mice.

CGH array results of recurrent CNAs found in memory cells of diabetic mice (n: number of affected probes, Purple: LRR>0, Green: LRR<0, genes location is indicated by numbers). **a** and **c.** Two recurrent copy losses in memory cells from PLN of two diabetic mice, spanning *Hoxa* and *Hoxd* gene family at chr2 and chr6 respectively. **b.** A recurrent copy gain at chr3 of three mice spanning *Pi4kb* expressed in hematopoietic cells. **d.** A recurrent CNA occurred independently in memory cells from PLN of two mice as copy gain at chr8 spanning *Armc6* gene involved in hematopoietic progenitor cell differentiation. **e.** A recurrent copy gain in cells of three mice at chr11 spanning several genes including *Tmem107,* a transmembrane protein highly expressed in hematopoietic cells. **g.** An independent recurrence of copy-gain in three different mice that are spanning two Histone families' loci on Chr13. **f.** Recurrent copy lose at chr14 spanning two undocumented genes (*Gm7247* and *Vmn2r89*). DLRSpread values of samples are in Table. 2.

Table 3-2 List of recurrent CNAs observed among tested diabetic mice excluding overlaps between M23 and M25 (due to their large number) unless shared by at least one other mouse.

A complete list of CNAs in Supplementary datasets 3. 2 and 3. 3.

Sample ID	chr	Locus	Start	End	# Probes	LRR	P-value	Recurrent Genes	DLRS
M4	2	qC3	74,475,401	74,598,078	15	-0.34	8.55E-10	*Hoxa* gene cluster	0.21
M12	2	qC3	74,501,193	74,598,078	13	-0.42	2.33E-12		0.19
M23	3	qF2.1	94,759,757	94,857,185	12	1.47	3.10E-26	*Pi4kb, Zfp687*	0.28
M25	3	qF2.1	94,759,757	94,844,573	11	0.73	1.87E-11		0.23
M5	3	qF2.1	94,767,165	94,821,010	7	0.49	6.82E-10		0.19
M4	6	qB3	52,104,495	52,281,548	18	-0.35	7.06E-12	*Hoxa* gene cluster	0.21
M12	6	qB3	52,116,749	52,207,847	9	-0.48	1.65E-11		0.19
M10	8	qB3.3	72,706,464	72,777,429	8	0.51	3.83E-10	*Slc25a42, Armc6, Sfrs14*	0.18
M3	8	qB3.3	72,718,314	72,795,346	9	0.47	1.18E-10		0.20
M25	11	qB3	69,752,914	68,919,294	17	0.71	7.10E-37	*Tmem107, Vamp2*	0.23
M23	11	qB3	68,766,792	68,909,840	15	1.65	5.46E-118		0.28
M22	11	qB3	68,880,665	68,909,840	4	0.79	2.01E-14		0.19
M22	13	qA3.1	21,798,640	21,921,804	13	0.40	7.92E-12	Histones family	0.19
M23	13	qA3.1	21,813,250	21,921,804	11	2.05	4.45E-127		0.28
M25	13	qA3.1	21,813,250	21,921,804	11	1.01	4.62E-47		0.23
M22	13	qA3.1	23,648,864	23,661,297	3	0.86	1.11E-11	Histones family	0.19
M23	13	qA3.1	23,648,864	23,725,304	10	2.12	7.57E-11		0.28
M25	13	qA3.1	23,847,542	23,847,542	22	0.88	6.56E-69		0.23
M5	14	qC1-qC2	52,061,318	52,152,579	8	-0.47	1.47E-10	*Gm7247, Vmn2r89*	0.19
M22	14	qC1-qC2	52,061,318	52,145,237	7	-0.57	6.92E-13		0.19

Table 3-3 List of genes of interest within the three CNAs confirmed by MLPA in the original unamplified DNA as an independent method.

	Genes	Lymphocyte Expression	Immune/ regulatory related function
chr9: 20,856,727- 21,236,076	*Keap1*	Yes	- Inflammatory regulatory function (Awuh et al., 2015). - Suppresses the nuclear factor Nrf2 causing its degradation (Rockwell, Zhang, Fields, & Klaassen, 2012). - Nrf2 activation have an anti-inflammatory effect, while Nrf2 deletion has pro-inflammatory effects (Awuh et al., 2015; Rockwell et al., 2012).
	S1pr5	High and exclusive in natural NK cells	- SIP controls cell proliferation and apoptosis and regulates T and B-cells migration (Cyster, 2005; Rosen & Goetzl, 2005; Rosen, Sanna, Cahalan, & Gonzalez-Cabrera, 2007). - S1PR5 is necessary for the circulation of NK cells to inflamed tissue (Walzer et al., 2007).
	ilf3	Yes	- Encodes a double-stranded RNA binding protein that is required for T-cell interleukin-2 expression (Jarboui et al., 2011). - Highly expressed in human lymphocytes (C. Wu et al., 2016). - associated with psoriasis (Tsoi et al., 2012) and rheumatoid arthritis (Okada et al., 2014).
chr10: 79,084,598- 81,041,680	*Madcam1*	Highly in spleen and lymph nodes	- Encodes an endothelial cells adhesion molecule, a member of the immunoglobulins. - Ligand to lymphocytes homing receptor (Grayson, Hotchkiss, Karl, Holtzman, & Chaplin, 2003). - Strongly up-regulated in active celiac disease (Di Sabatino et al., 2009).
	Gzmm	High in lymphocytes	- Encoding granzyme M proteins. - Group of enzymes is expressed by NK cells and activated lymphocytes and stored in cytoplasmic granules (Lu et al., 2006).
	Ptbp1	High in lymphocytes	- Encodes a nuclear ribonucleoprotein. – Increase CD5 protein levels upon T-cell activation (Domingues et al., 2016).
	Rps15	Yes	- Encodes the S19P protein belonging to a family of ribosomal proteins. - Recurrently mutated in aggressive chronic lymphocytic leukemia (CLL) (Ljungstrom et al., 2016). - Highly expressed in human lymphocytes (C. Wu et al., 2016).
	Mknk2	Yes	- Encodes a member of the protein kinases super family. - Crucial role of this protein in T-cells function suggested (Gorentla et al., 2013; Zhong, Guo, Zhou, Liu, & Wan, 2008). - Highly expressed in human lymphocytes (C. Wu et al., 2016).
	Dapk3	Yes	- Encodes death-associated protein kinase 3. - Inducing of apoptosis and regulation of cell cycle progression and proliferation. - Tumor suppressor function suggested (Gorentla et al., 2013).
	Matk	Yes	- Crucial in the signal transduction of hematopoietic cells. - Inhibitory function in the regulation of T-cell proliferation (Tan et al., 2011). - Exclusive expressed in lymphocytes (C. Wu et al., 2016).
	S1pr4	High in lymphocytes	- Encodes sphingosine-1-phosphate receptor 4. - Cell signaling of several cell types (C. Wang et al., 2014).
	Abca7	High in lymphocytes	- Encodes a transporter protein detected principally in myelo-lymphatic tissues. - Expression signature implies a function in lipid homeostasis in immune cells (Tomioka et al., 2017).
chr10: 127,684,108- 128,334,229	*Il23a*	Yes	- Encodes a subunit of Il-23 that stimulates the production of interferon-gamma and acts on memory CD_4^+ T cells (Revu et al., 2018). - Higher levels of Il-23 have been associated with autoimmune diseases such as multiple sclerosis and inflammatory bowel disease (Abraham & Cho, 2009; Duerr et al., 2006).
	Pa2g4	Yes	- High in hematopoietic cells, leukemic and lymphoma cells (C. Wu et al., 2016). - Encodes a protein that functions in cell proliferation, transducing growth regulatory signals and inducing differentiation of human cancer cells (Nguyen le et al., 2015; Nguyen le, Zhu, Lee, Ta, & Mitchell, 2016). - Highly expressed in human lymphocytes (C. Wu et al., 2016).
	Dgka	High in lymphocytes	- Involved in cell cycle progression and the function of immune cells (Poli et al., 2017; Prinz et al., 2012). - Associated with T1D (Evangelou et al., 2014).
	Coq10a	High in $CD4^+$ and $CD8^+$	Unstudied gene

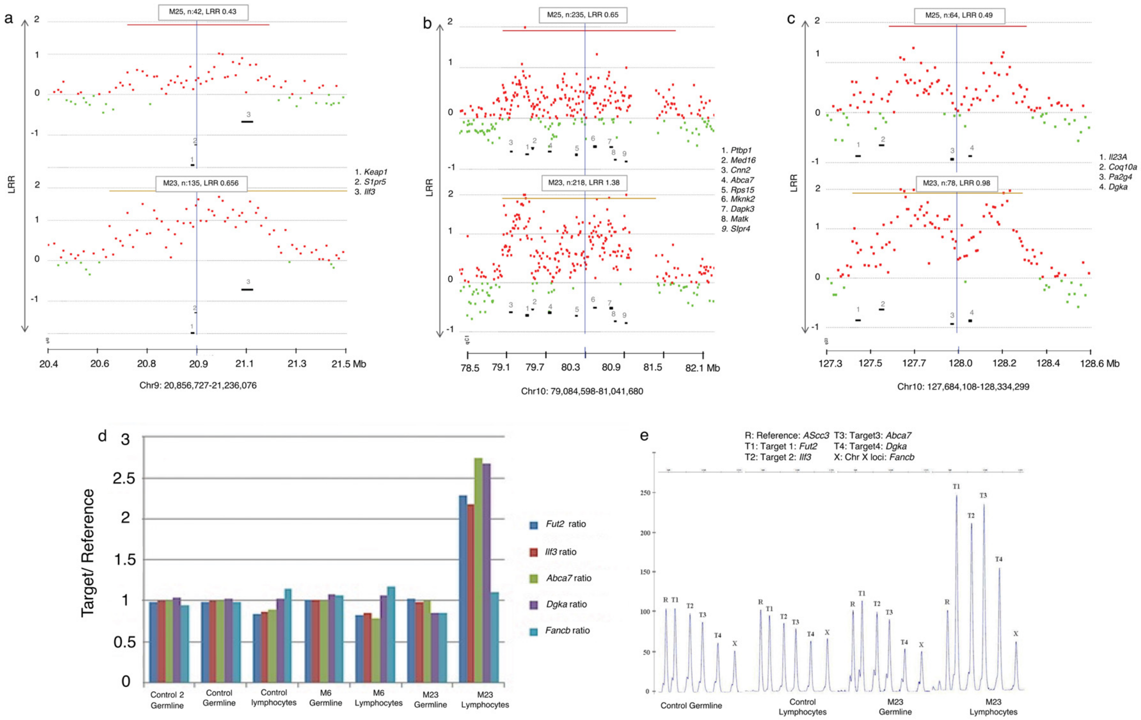

Figure 3-5 Confirming CNAs in original unamplified DNA by MLPA as in independent method.

Confirming CNAs in original unamplified DNA by MLPA as in independent method. Four recurrent loci with copy-gain in (M23 and M5) spanning genes with immune function were tested by MLPA in the original unamplified DNA against a reference probe along with DNA from two other mice that did not have the CNA. (n: number of affected probes, Purple: LRR>0, Green: LRR<0) **a.** Copy gain at chr9 spraining several genes including *Ilf3*. **b.** Copy gain at chr10 spraining several genes including *Abca*. **c.** Copy gain at chr10 spraining several genes including *Dgka*. **d.** The height of the MLPA peak at each locus for each mouse was expressed as a percentage of the reference probe. Only the four loci in the T-cell (but not tail representing the germline) DNA from mouse M23 show increase over 1. **e.** Representative peaks are shown as a percentage of the reference probe. Only mouse M22 shows doubling of the peak in T-cells. DLRSpread M23:0.28, M25:0.23.

3.5.3 T-cells involved in host defense have smaller copy number changes

As a normal host-defense control, DNA from memory CD4$^+$ T cells from the popliteal lymph nodes of ten NOD mice (eight females and two males; 9- 14 weeks) infected with *Leishmania major* (*L. major)* were tested. Out of ten, two had CNAs (one had one and the other one had two CNAs) (Table. 3. 4, *Supplementary data,* Dataset. S3. 4). The same experiment was done on seven non-autoimmunity susceptible BALB/c mice (19 weeks) to determine if the occurrence of CNAs in lymphocytes is promoted by an autoimmune genetic background. Out of the seven mice three had CNAs (1-2 CNAs) (Table. 4, Supplementary data*,* Dataset. S3. 4). The mean size of CNAs in autoreactive cells of diabetic mice (26.02 ± 1.69, mean ± SEM, n=403) was significantly two-fold larger than that in samples from *L. major* infected mice (7.71 ± 2.03, n=7) (Pittman permutation test, P=0.0019).

3.5.4 The CNAs occur in pre-thymic precursors

Sequencing the TCR of the CD4$^+$ memory cells from PLN of ten diabetic mice showed low clonality in both α-chain and β-chain (*Supplementary data,* Dataset. S3. 5), that is too low to explain the high level of mosaicism found in the CNAs, suggesting pre-thymic occurrence in a marrow progenitor. Interestingly, we found that the most common TCR is (CDR3-V-J: CVVGDRGSALGRLHF- TRAV11*01- TRAJ18*01) sequence for the α-chain and (CDR3-V-J-D: CAASSNTDKVVF- TRBV2*01- TRBJ1-1*01- TRBD1*01) sequence for the β-chain are present within all samples with relatively high frequency.

Table 3-4 Number of CNAs found in memory CD4+ T cells from the popliteal lymph nodes of 10 NOD mice and 7 BALB/c mice infected with *L. major*.

Mouse Sample	Sex F/M	Age (w)*	Blood Glucose*	# of CNAs
Leish. NOD 1	M	9	Low	0
Leish. NOD 2	M	9	Low	0
Leish. NOD 3	F	14	Low	0
Leish. NOD 4	F	14	Low	0
Leish. NOD 5	F	14	Low	2
Leish. NOD 6	F	14.2	Low	0
Leish. NOD 7	F	14.2	Low	1
Leish. NOD 8	F	14.2	Low	0
Leish. NOD 9	F	14.2	Low	0
Leish. NOD 10	F	14.2	Low	0
Leish. BALB/c. 1	F	19	Low	0
Leish. BALB/c. 2	F	19	Low	1
Leish. BALB/c. 3	F	19	Low	0
Leish. BALB/c. 4	F	19	Low	0
Leish. BALB/c. 5	F	19	Low	1
Leish. BALB/c. 6	F	19	Low	2
Leish. BALB/c. 7	F	19	Low	0

*Age is age of authorization after three weeks of infection
* Glucose level measured in mmol/L

3.6 Discussion

This study demonstrates a novel discovery of somatic copy-number mutations in immune-related genes in memory cells of diabetic NOD mice, an excellent model for human T1D. These mutations result in gene deletion or amplification that may have functional effects. Some of these genes are highly expressed in T-cells and may well represent an important causal contribution in the autoimmunity of the NOD model and, quite plausibly, of human T1D. Their causal role is supported by the non-random recurrence of eight of these PZMs affecting same genes in different mice. In the paradigm of cancer, independent recurrence of somatic mutations, either point or copy-number, in different patients is considered strong evidence that the mutation is causal. In fact, this is the criterion by which most tumor-suppressor genes have been identified. Somatic mutations are a common occurrence but, being confined to one single cell and its progeny, they are unlikely to cause disease, unless the cell progeny expands exponentially, as is the case in cancer (Jacobs et al., 2012; Lee et al., 2007).

The contribution of somatic mutations in the pathogenesis of cancer has been well established. A PZM in a tumor suppressor gene in a single cell causes a monoclonal expansion during which additional PZMs occur, causing more pathological phenotypes and further release from proliferation controls (Watson, Takahashi, Futreal, & Chin, 2013). The identification of such driver mutations in cancer has enabled therapeutic advances by identifying drug targets essential to disease causation. One example is Gleevec, a selective inhibitor of the BCR-ABL tyrosine kinase, the pathogenic fusion transcript (translocation product) that causes chronic myeloid leukemia (CML) (Hernandez-Boluda & Cervantes, 2002).

In the case of autoimmune diseases, similar to cancer, a disease is caused by a proliferation of clonal lymphocytes from a small number of autoreactive lymphocytes that have escaped natural tolerance to self-antigens. Although autoimmunity involves more functional steps than proliferation and resistance to apoptosis, it does share these two features with cancer. Natural tolerance consists of many checkpoints that are difficult to break. Its failure is likely a multistep process, causing autoimmune diseases to develop over many years. It has been estimated that as many as 50% of all T-cell receptor V(D)J rearrangements will recognize some autoantigen (Ignatowicz et al., 1996). Most of these will be deleted by negative selection in the thymus in which there is an expression of tissue-specific antigens like insulin (Liston et al., 2004; Vafiadis et al., 1997). However, some autoreactive T-cells escape to the periphery and must be dealt with by peripheral tolerance checkpoints that include anergy, activation-induced apoptosis, or inhibition by regulatory T-cells. A large number of molecular players are known to be involved in each of these checkpoints (reviewed by Goodnow et al., (Goodnow et al., 2005)), and many others may be important but still unstudied.

Epidemiological evidence has connected autoimmunity to hematologic malignancy in several scenarios. The risk of lymphoid malignancy is increased in individuals affected by many autoimmune conditions, such as celiac disease, lupus, rheumatoid arthritis and Sjogren disease (Zintzaras, Voulgarelis et al., 2005). Somatic *FAS* mutations in non-Hodgkin's lymphoma are often seen in patients with prior history of autoimmunity (Gronbaek et al., 1998). This suggests overlaps between immune tolerance checkpoints, important in autoimmunity, and proliferation checkpoints, important in lymphoid malignancy.

The plausibility of this model depends on how often such PZMs happen in autoimmunity-relevant hematopoietic lineages. PZMs originated in hematopoietic stem cells, and progenitor cells have been identified in peripheral whole- blood (Busque et al., 2012; Genovese et al., 2014; Xie et al., 2014; Young, Challen, Birmann, & Druley, 2016). SNP-array data show that whole-blood DNA has mosaic, Mb-sized CNAs in about 5% of healthy individuals (Forsberg et al., 2012; Jacobs et al., 2012; Laurie et al., 2012). This detectable mosaicism is due to a proliferative or survival advantage of the copy number mutation (vs. early occurrence in embryogenesis), as it is age-dependent and variable along time, in longitudinal studies (Forsberg et al., 2012). Only a very small fraction of all people carrying them will develop leukemia, leaving a broad gray zone for a role in non-malignant disease related to blood cells. In a related study of SNP-array discrepancies between monozygotic twins, we calculated an average, ~130 point-PZMs per individual, at high enough mosaicism, in whole blood, to flip a SNP genotype call (Li et al., 2014). In logarithmically expanded autoantigen-specific lineages, mosaicism might be much higher and still not detectable without isolating these lineages from the rest of the blood cells. A recent publication identified an exclusive somatic mutation in the expanded CD8$^+$ memory subset in newly diagnosed rheumatoid arthritis (Savola et al., 2017).

Six out of the 25 mice we tested, all cells in pancreatic LNs were memory, and two of these mice showed a very unstable genome with many recurrent CNAs. This instability might be explained by the copy gain in two histone loci (Fig. 3. 4g). Histone overexpression due to copy gain is very likely to have increased the normally tightly regulated expression of these proteins that form the core of the nucleosome and whose correct expression, at the time of DNA replication, is crucial to genomic integrity (Mejlvang et al., 2014). The multiple nearly identical genes encoding these two histones also make the locus susceptible to rearrangements through non-homologous recombination. The remaining CNAs cover a large number of RefSeq genes, most of which are not functionally annotated and have no published literature.

Acutely stimulated T-cells in the context of host defense obtained by infecting NOD mice and BALB/c mice with *L. major* also have CNAs, but they are fewer (7 in 17 mice, vs. 403 in 25 mice) and significantly smaller than those observed in T-cells involved in NOD autoimmunity. Moreover, their occurrence in BALB/c indicates that they are not due to the germline determinants of autoimmunity.

Identification of the genes affected by the CNAs in the autoreactive lymphocytes could serve as a potential diagnostic biomarker or identify novel therapeutic targets (e.g. Gleevec) as their CNAs exist only in disease-causing cells. One example of these is recurrent CNAs that span *Tmem149* (Supplementary data*,* Dataset. S3. 3) and *Tmem107* (Fig. 3. 4e) encoding transmembrane proteins highly expressed in T-cells. Their amplification or deletion should be detectable by flow cytometry in blood cells providing a potential biomarker and therapeutic target.

Sequencing the TCR of ten diabetic mice revealed a percentage of clonal reads too low to explain the observed levels of mosaicism, suggesting that the CNAs are occurring prior to the thymic selection in a bone marrow progenitor and not in the antigen-specific lineage. Additional PZMs, occurring during the autoantigen-activated logarithmic expansion of T-cells likely to happen but their level of mosaicism would have been too low to detect by our approach, as we did not isolate cells by antigen specificity but only by location in inflamed lymph nodes.

Since these post-zygotic mutations do not have to pass selection for fitness of the whole organism, they are likely to have more drastic functional effects than variants that have survived evolution and are inherited in the germline. If so, they could be ideal therapeutic targets, as they exist only in disease-causing cells. The next step is to prove a causal role by gene editing and to extend the studies to human T1D autoimmunity. Other autoimmune diseases should be likewise examined. Detection of point mutations by exome sequencing of the samples is planned, to explore the full PZM spectrum.

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CHAPTER FOUR Somatic mutations in clonally expanded memory T lymphocytes newly diagnosed patients with Type 1 diabetes

Maha Alriyami[1]; Luc Marchand[1]; Xiaoyu Du[1]; Khalid bawazeer[1]; Yao Wang[1]; Constantin Polychronakos[1*]

[1]The Endocrine Genetics Laboratory, Child Health and Human Development Program and Department of Pediatrics, McGill University Health Centre Research Institute, Montreal, Quebec, Canada, H3H 1P3. Correspondence and requests for materials should be addressed to C.P. (email: constantin.polychronakos@mcgill.ca)

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Authors Contribution:

Maha Alriyami: Designed and executed the experiments, results analysis and interpretation, writing and preparation of manuscript.

Luc Marchand: Bioinformatics CBS analysis.

Xiaoyu Du: Technical expertise and executing of the TCR sequencing.

Khalid Bawazeer: Helped with conducting the re-stimulation experiment and in making Figure 4.3 and 4.4.

Yao Wang: Originally developed the T- cell culture proliferation protocol for another project

Constantin Polychronakos: Research supervisor and mentor, result interpretation, manuscript editing and corresponding author.

4.1 Preface

As part of our investigation on the potential contribution of somatic mutations on autoimmunity and after our findings of such CNAs in autoreactive memory cells of diabetic NOD mice, in this study, we shift our focus to human T1D. Here we investigated the existence of similar CNAs in autoreactive lymphocytes from newly diagnosed patients with T1D. Since obtaining fresh lymphocytes from PLNs of patients is not feasible, we obtained autoreactive cells by activating patients' peripheral blood mononuclear cell (PBMCs) *ex vivo*, using proinsulin. To our knowledge, this is the first study investigating the somatic mutation hypothesis in T1D.

4.2 Abstract

In this study, we examine the role of somatic mutations in autoreactive cells involved in type 1 diabetes. Although the contribution of somatic mutations to tumorigenesis is well established, their role in non-malignant conditions is still being explored. Here, we show that 70.6% (12/17) of our study subjects who are newly diagnosed patients with type 1 diabetes harbor somatic mutations in insulin-reactive CD4+ T-cell clones. CNAs (n=9) affecting overlapping genes occurred independently in at least three patients, suggesting that these genetic events underlie pathogenicity. Moreover, we identified genes (*Casz1* and *E2f1*) that we previously identified in diabetic NOD mice and have a T-cell proliferation and differentiation regulatory function. The level of clonality of the tested lymphocytes shows that these somatic mutations can occur both pre- and post- to the thymic selection. Lymphocytes involved in host defense and performing their normal function by reacting to the tetanus toxoid also harbored somatic mutations. However, they were significantly smaller in size (p=0.0018). Our data provide further evidence of the role of somatic mutation in Type 1 diabetes and, potentially, other autoimmune diseases.

4.3 Introduction

Type 1 Diabetes (T1D) is an autoimmune disease caused by the targeted destruction of the pancreatic β cells by the autoreactive T-lymphocytes infiltrating the islets of Langerhans (Polychronakos & Li, 2011). This result in insulin deficiency making a lifetime of insulin replacement crucial for patients' survival and, therefore, a hallmark of the disease. T1D was generally considered a disease affecting children as its peak presentation occurs between 10-12 years of age. However, this belief has changed over the past decade since the disease can manifest at any age (Atkinson, Eisenbarth, & Michels, 2014; Leslie, 2010). The autoimmune process of T1D is antigen-specific in which only pancreatic β cells are destroyed leaving α and δ cells of the islet intact.

It is well established that genetic predisposition has a significant role in T1D. The sibling relative risk (λS) for the disease is estimated to be 15, making it the highest among common complex diseases (Davies et al., 1994; Polychronakos & Li, 2011). Candidate gene approach, as well as genome-wide association studies, resulted in identifying over 40 genetic risk loci, most of confer minute effects (Polychronakos & Li, 2011).

The inherited susceptibility in T1D cannot explain all of the disease. In monozygotic twins, the concordance is much less than 100%, and even in concordant pairs, age of onset can vary by decades. The environment contribution in autoimmune diseases although fundamental, may not explain such observations as most monozygotic twins are subject to similar environmental influences in the first few decades of life (Knip et al., 2005). Likewise, in the inbred NOD (non-obese diabetic) mouse model of spontaneous autoimmune diabetes, not more than half of males will develop the disease, despite genetic identity and standardized environment. We have previously provided evidence that somatic stochastic post-zygotic genetic changes (PZMs) in the expanding antigen-specific autoreactive T-cell lineages are an additional explanation for the non-heritable part of T1D in NOD mice (Chapter 3).

Somatic mutations frequently occur during cell division. In human, throughout mitosis, errors-termed somatic mutations- occur every 10^{-7}-10^{-8} base pairs making between 10-100 replication errors in every daughter cell (Araten et al., 2005; Kuick et al., 1992; Lily, 2004). As a protective mechanism, human has evolved repair mechanisms that reduces error rate significantly compared to that in lower organisms were such mistakes have an evolutionary importance (Drake, 1999; Lily, 2004).

Given the vast number of cells produced through life, it is inevitable that a substantial number of cells in every individual will PZMs. These are all in a mosaic state, confined to the progeny of the one cell that underwent the mutation. Since the vast majority of PZMs involve only a tiny fraction of all cells, their level of mosaicism is too low to cause a disease or to be detected by current methods. A well-established exception to this is cancer.

The causal role of somatic mutations has been for at least the last 50 years the prevailing paradigm in cancer research. The foundation of this theory is that cancer is derived from the expansion of a single cell following a PZM that deactivates its proliferation control. This results in an inadequately controlled proliferation allowing a second mitotic error that further increases cell proliferation, and therefore, the accumulation of more subsequent PZM mutations (Egley, Gutliph, & Bowes, 1985; Soto & Sonnenschein, 2004). From this compelling hypothesis, at least 100 oncogenes and 30 tumor suppressor genes have been identified (Soto & Sonnenschein, 2004).

Autoimmune diseases are caused by the logarithmic proliferation of clones from a small number of autoreactive cells (vs. a single cell in cancer). The existing parallel between autoimmune diseases and lymphomas suggest that autoimmunity could be partially caused by somatic mutations in the autoreactive lymphocytes, generated during the logarithmic expansion of these cells or at the pre-thymic stages at the level of marrow progenitors. The mosaicism of these PZMs could be too low to be detected in whole blood but can be high enough among the small fraction of cells with an autoreactive TCR to promote autoimmunity by inactivating a self-tolerance checkpoint. Moreover, as the lineage proliferation is enhanced, further accumulation of such mutations could take place, inactivating more tolerance checkpoints. The plausibility of this model depends on how often such PZMs happen in hematopoietic cell lineages. Recent evidence strongly supports an enabling frequency, in which examining SNP-array data from solid-cancer studies revealed that about 5% of individuals (both patients and controls) have mosaic, Mb-sized copy number alterations (CNA) in peripheral blood (Forsberg et al., 2012; Jacobs et al., 2012; Laurie et al., 2012).

CNAs are created by the same mutational mechanisms as CNVs (Forsberg et al., 2012; Jacobson et al., 1997). The difference is that CNAs modify the individual's inherited DNA while CNVs are differences between germlines of different individuals. Studies have showed that only a tiny fraction of all people carrying CNAs would get leukemia (Forsberg et al., 2012; Jacobs et al., 2012; Laurie et al., 2012), leaving a broad gray zone for a role in non-malignant diseases related to blood cells. These findings represent the tip of the iceberg, as they examine whole blood. In this study, we present lineage-specific levels of mosaicism that would normally be too low to be detected in whole blood, with statistical evidence of a causal role.

4.4 Martials and Methods

4.4.1 Patient recruitment

The McGill Research Ethics Board approved patient recruitment strategy (protocol number: 1230- PED entitled “A cell-lineage based approach to the immune dysregulation in type 1 diabetes”). Study subjects were recruited in the Diabetes Clinic at the Montreal Children’s hospital. Study subjects who have met our inclusion criteria (clinical diagnosis of T1D within the last three months) were informed about the project and written informed consent forms were obtained from all patients and their guardians. All patients were diagnosed under the age of 19 with ethnic background of mixed European descent (Table 4. 1). Patients have been treated with insulin since diagnosis, and none has stopped treatment for any reason during that time. About 30 ml of blood was obtained for the early-diagnosed patients (within three months of diagnosis). As controls, we also tested eight patients in the same age range, tested for growth hormone deficiency and found to be normal. Cells from these patients did not show a good proliferative response to rh- PI (Supplementary data, Table S4. 1).

4.4.2 Genotyping of *INS* and *PTPN22*

DNA was extracted from whole blood 200 ul samples obtained from each patient using QIAamp DNA Minikit (cat#: 51304, Qiagen). The genotyping for the *PTPN22* 1858C/T (rs2476601) was done by amplifying the targeted fragment using specific primers (Supplementary data, Table S4. 2) (sense and antisense were 5’ – CTCAAGGCTCACACATCAG – 3’ and 5’ – GAATATAAGAATTTCCTTTGGA – 3’, respectively). For the Insulin *INS*−23 A/T (rs689) polymorphisms (sense and antisense primers were 5’ – ATCAGAAGAGGCCATCAAGC – 3’ and 5’ –

GCGGGTCTTGGGTGTGTAG – 3’ respectively) (Supplementary data, Table S4. 2). Both reactions were amplified in a 25 ul reaction containing 16.95 ul of dH2O (Thermofischer), 1 um of forward and reverse primers (Invitrogen), 1.5 mM MgCL2 (Invitrogen), .2 mM dNTP, 2.5 ul 10x PCR Rxn buffer (Invitrogen), 1.3 units Taq DNA Polymerase (GeneDireX), and 2 ul of template DNA (50-100 ng). For *PTPN22*, the thermal cycle programmed for 90sec at 95°C as initial denaturation, followed by 35 cycles of 20sec at 94°C for denaturation, 20sec at 55.5°C as annealing, 20sec at 72 °C for the extension. For *INS*, the thermal cycle programmed for 90sec at 95°C as initial denaturation, followed by 35 cycles of 20sec at 94°C for denaturation, 20sec at 56°C as annealing, 30sec at 72 °C for the extension. Amplified DNA fragments were sent to Genome Quebec Innovation Centre (Montreal) for Sanger Sequencing.

4.4.3 Lymphocyte isolation and proliferation

In humans we are confined to peripheral blood samples, therefore, to identify autoreactive cells, we used *ex vivo* expansion of T-cells to proinsulin (PI), the major T1D autoantigen. Peripheral blood mononuclear cells (PBMCs) were isolated from buffy coats using Ficoll-hypaque^{TM} PLUS (Cat #:17-1440-02, GE Healthcare) density gradient centrifugation. Cells were stained with CFSE (carboxyfluorescein diacetate succinimidyl ester) (Cat #: C34554, Invitrogen) and plated at 3 million cells/well in flat-bottom 24-well plates. Cells were activated by ten µg/mL of recombinant human Proinsulin (rh-PI) (1336-PN, R&D systems) and 5U/ml rhIl-2 (cat #: PHC0026, ThermoFisher Scientific) in vitro for 12 days in serum-free media, CTS OpTmizer T-cell Expansion SFM (A10221-01, Life Technologies). 1000 ml of media was supplemented with 26 mL/L of OpTmizer CTS T-Cell Expansion Supplement and ten mL/L of 200 mM L- Glutamine solution for a final concentration of two mM. Moreover, media was also supplemented with 250 ng/mL of Fungizone (Cat #: 15290-018, ThermoFisher Scientific) and 5 mg/mL of Gentamicin (Cat #: 15750-060, ThermoFisher Scientific). Culturing was in standard conditions of 37°C, 5% CO2 in a humidified incubator. rhIL-2 was added every three days, and half the dose of rh-PI was added in day six of culture. Lymphocytes from the same patients were also activated by 2 μg/mL Tetanus toxoid (TT) (Cat#: 582231-25UG, Calbiochem) as a positive control for the method and cultured with rhIL-2 or in media alone as a negative control. Lymphocyte proliferation in response to responding to rh-PI and TT was determined by sorting for CFSE dilution, after staining for anti-CD3 (monoclonal antibody, APC, OKT3, cat#: 17-0037-42, eBioscience) using the FACSAria sorter. $CD3^+CFSE^{high}$ (non-proliferating) and $CD3^+CFSE^{low}$ (proliferating) were sorted. Staining was performed according to the manufacturer. All samples were kept on ice throughout isolation and staining.

4.4.4 Technical validation of rh-PI stimulation assay

To confirm the antigen-specificity of $CFSE^{low}$ cells sorted from total PBMC cultures were re-stimulated with rh-PI. PBMCs were isolated from the blood of two recent-diagnosed patients with T1D (P10 and P18). Ten million cells were cryopreserved to be used as feeders in the re-stimulation. The rest of the cells were plated in flat-bottom 24-well plates as described above. PBMCs were labeled with CFSE and cultured for 12 days in the presence of rh-PI, TT or left unstimulated. On day 12, $CD4^+$ and $CD8^+$ cells were labeled with anti-Human CD_4 (monoclonal antibody, PE-Cyanine7, cat #: HCD0412, eBioscience) and anti-Human CD8a (monoclonal antibody, PerCP-Cyanine5.5, cat #: 45-0088-42, eBioscience) respectively and sorted using the FACSAria sorter. Sorted $CD4^+$

and CD8$^+$ were re-stimulated separately in flat-bottom 48 well plates in the presence of irradiated autologous PBMCs pre-pulsed for two hours with antigens (rh-PI or TT) or with feeder cells with no antigen. Cells were cultured in T cell to PBMC ratio of 1:3. The culture was supplemented with 2.5 U/mL of rhIL-2 every three days and analyzed by flow cytometry eight days post-re-stimulation. Fixable viability dye efluor 780 (cat #: 65-0865-14, eBioscience) and anti-human PE-Ki67 (BD Bioscience) as a marker of proliferation were used in the sorting process. All samples (except for the Irradiated feeders) were tested in duplicate.

4.4.5 DNA extraction and Whole Genome amplification

DNA was extracted from lymphocytes. Samples were amplified using GenomePlex complete whole genome amplification (WGA-2) (cat #: WGA2-50RXN) kit, specifically approved by Agilent for comparative genomic hybridization (CGH) to detect copy-number differences. DNA was next purified using PCR Cleanup kit from Sigma (cat #: NA1020, Sigma).

4.4.6 Detection of PZMs

We sent 1.5 ug of amplified DNA to Oxford Gene Technologies (OGT), or Vancouver Prostate Center for Agilent dual color CGH analysis on the human 1x1M Agilent array. DNA from CD3+CFSElow (proliferating) cells were used as ‘test sample’, and CD3+CFSE^{high} (non-proliferating) representing germline DNA was used as ‘reference sample’. In Agilent dual color, 1x1M human CGH array, reference, and test DNA samples were labeled with different fluorescent tags (Cy3 and Cy5, respectively), which were next hybridized to the probes of the 1x1M chip, distributed genome-wide but with a concentration in, and around coding sequences. The fluorescence intensity ratio

(Cy3:Cy5) at each probe position reflects copy-number differences between the two DNA samples. CGH quality control (QC)- Derivative log ratio spread (DLRS) values were within Agilent Technologies specifications (Supplementary data; Fig. S4. 1).

4.4.7 Bioinformatics analysis

Test and reference signals were calculated for each probe, and internal normalization equalized the systematic difference between the two fluorochromes. The base-2 log of the Cy3/Cy5 ratio (LRR) was used for analysis. The lowest 3% of probes in terms of fluorescence intensity were eliminated. Regions bearing copy number aberrations were identified using two independent algorithms, Agilent Genomic *Agilent CytoGenomics* software v4.0 (Agilent Technologies) implementing the ADM-2 algorithm and DNAcopy software implementing the circular binary segmentation (CBS) algorithm (Venkatraman & Olshen, 2007). In ADM-2 (provided by Agilent technologies, threshold 6.0), the algorithm identifies aberration points that maximize the *t*-test of comparing the averages from the expected value of zero. Once a segment is kept, its median is centered, and the method is repeated on three new segments. This combines the segmentation and calling process (Roy & Motsinger Reif, 2013). We applied Agilent-Technologies recommended filtering standards of a minimum of 3 consecutive aberrant probes and a minimum absolute average $\log_2$ ratio of LRR |0.25| and P-value $<5\text{x}10^{-8}$ (Bonferroni threshold). The Human GRCh37/hg19 assembly, Feb. 2009 was used, to match the indexing of the Agilent probes.

In CBS, each chromosome was recursively split into small regions (each containing more than three probes), using a maximal t-statistic test for detecting the change-points: for one segment, a two-sample t-statistic compares the mean of the Log2-

ratio in the sub-segment to the mean Log2-ratio of the rest of the segment. The splitting of the DNA stops when no more change-points can be identified. The Human GRCh37/hg19 assembly, Feb. 2009 was used, to match the indexing of the Agilent probes. CNAs were kept as true if were called by both algorithms ADM-2 (LRR|0.25|, P-value $\leq 1x10^{-10}$) and CBS (LRR|0.25|, P-value $\leq 5 \times 10^{-08}$). The lower statistical significance threshold for CBS is justified by the vastly smaller number of hypotheses tested (number of ADM-2-called CNAs).

Blinding between rh-PI activated cells was not possible because of the different source of material. However, the array data generation and the bioinformatics analysis were done blindly in one batch, using the same parameters. Tissue-specificity of the expression levels of the genes involved was obtained from BioGPS, 2018 (C. Wu et al., 2016).

4.4.8 Statistics

The difference in the number of probes covering CNAs in T-cells from cell activated by rh-PI vs. those activated by TT was assessed by the unequal-variance, Two-sided Welch *t*-test. We compared the number of probes (number of consecutive probes covered) because the gene-centered positioning of the probes, they better reflect the genes covered by them than the actual length.

4.4.9 TCR sequencing

RNA samples were extracted from the $CD_3^+CFSE_{low}$ (proliferating) rh-PI cells. For the TCR pre-sequence amplification we used a template-switch 5' RACE approach using the SMARTer®RACE cDNA amplification kit by clontech (Mountain View. CA.USA). This approach uses the known sequence of the C (constant) segment TRA-AS-6 and TRB-

AS-5 for reverse primer, and TRB-AS-5:) and an arbitrary added sequence by 5'RACE for the forward primer (primers listed in supplementary data, Table S4. 2). PCR products were purified using the QIAquick PCR purification kit by Qiagen and prepared for Miseq sequencing with the *Illumina* Nextera XT library preparation kit according to the manufacturer's manual. Sequencing was done using the MiSeq paired-end (250 bp) protocol. The reads were aligned to the TCR reference sequence of the international ImMunoGeneTics information system (IMGT). The alignment assigned V and J segments in both the α and β chain. The CDR3 (non-template added random amino acids) was determined starting from the V segment conserved Cysteine (Cys) at position 104 and the conserved Phenylalanine/Tryptophan (Phe/Trp) at positions 118 in the J segment.

4.4.10 Data availability

The CGH data discussed in this publication will be deposited in NCBI's Gene Expression Omnibus (Edgar et al., 2002) to be publicly accessible upon publishing.

The TCR data discussed in this publication will be deposited in NCBI's Sequence Read Archive (Leinonen et al., 2011) to be publicly accessible upon publishing.

4.5 Results

Autoreactive CD_3^+ T- lymphocytes from 17 newly diagnosed children (n= 17, 11 females and six males) between the age of 5 and 19 years old, were examined (Table. 4.1). Isolated PBMCs from each patient were proliferated by rh-PI and sorted based on CFSE dilution (Fig. 4. 1). Lymphocytes activated by PI and TT showed proliferation ($CD3^+CFSE^{low}$ cells) (Fig. 4.1 a-b, Table. 4.1). On the other hand, cells cultured in the media with no antigen or with media and IL-2 showed no or minimal proliferation (Fig. 4.1 c-d, Table. 4.1).

4.5.1 Positive controls

To investigate the existence of somatic mutations in autoreactive cells, comparative genomic hybridization (CGH), was used to identify potential CNAs in rh-PI reactive cells ($CD3^{+}CFSE^{low}$ cells, used as the test sample) and not in germline DNA represented by DNA obtained from clones that had not proliferated to the *in vitro* activation ($CD3^{+}CFSE^{high}$ cells, used as reference). CGH data of all tested samples revealed the expected copy number change at the T cell receptor regions (α and γ subunits) mapping, respectively, to human chromosomes 14 and seven due to genomic rearrangements within these regions to create TCR diversity. These loci served as internal naturally occurring positive controls for detecting mosaic PZM in T-cells using our approach (Fig. 4. 2).

Table 4-1 List of patients included in the T1D human study.

Proliferation percentage with or without antigen are shown for each patient. The # CNA column lists the number of CNAs observed in CD3+ T-cell clones that responded to rh-PI activation but not in the germline (CD3+ T-cell clones that did not show proliferative response).

Patient ID	Sex F/M	Age	*INS*	*PTPN22*	Media%	IL-2%	TT%	PI%	# CNAs	DLRS
P1	F	>5, <19	A/A	C/C	0.1	0.4	42.1	10.8	15	0.2
P2	F	7	A/A	C/C	0.6	/	6.9	1.5	0	0.18
P3	F	9	A/A	C/C	2.2	/	45.8	4.2	0	0.17
P4	F	>5, <19	A/A	C/C	0.1	0.1	9.1	3.9	861	0.22
P5	F	5	A/A	C/C	4.1	6.3	22.3	13.3	2	0.18
P6	F	5	A/A	C/C	0.5	0.6	10.5	1.4	347	0.23
P7	F	10	A/A	C/C	1.4	0.9	9.6	13.5	19	0.19
P8	F	16	A/A	C/C	0.9	1.6	5.2	7.1	1	0.18
P9	F	>5, <19	A/T	C/C	0.1	0	3.3	0	9	0.17
P10	F	14	A/A	C/C	0.3	0	8.5	6.7	10	0.16
P11	F	>5, <19	A/T	C/C	3.4	4.2	12.7	18.6	2	0.16
P12	M	>5, <19	A/A	C/C	3.1	3.2	31	8.7	2	0.09
P13	M	>5, <19	A/A	C/C	0.7	0	34.3	28.4	2	0.22
P14	M	8	A/A	C/T	0	2.1	25	4.3	0	0.18
P15	M	>5, <19	A/T	C/C	0.4	1.4	65.7	27.3	13	0.18
P16	M	10	A/A	C/C	0.3	0	8.5	6.7	0	0.16
P17	M	8	A/A	C/C	0	0.4	4.8	0.9	0	0.1
P18*	M	17	A/T	C/C	0.5	0.4	6.4	20.6	/	/

*P18 a sample used for the re-stimulation experiment and was not tested by CGH.

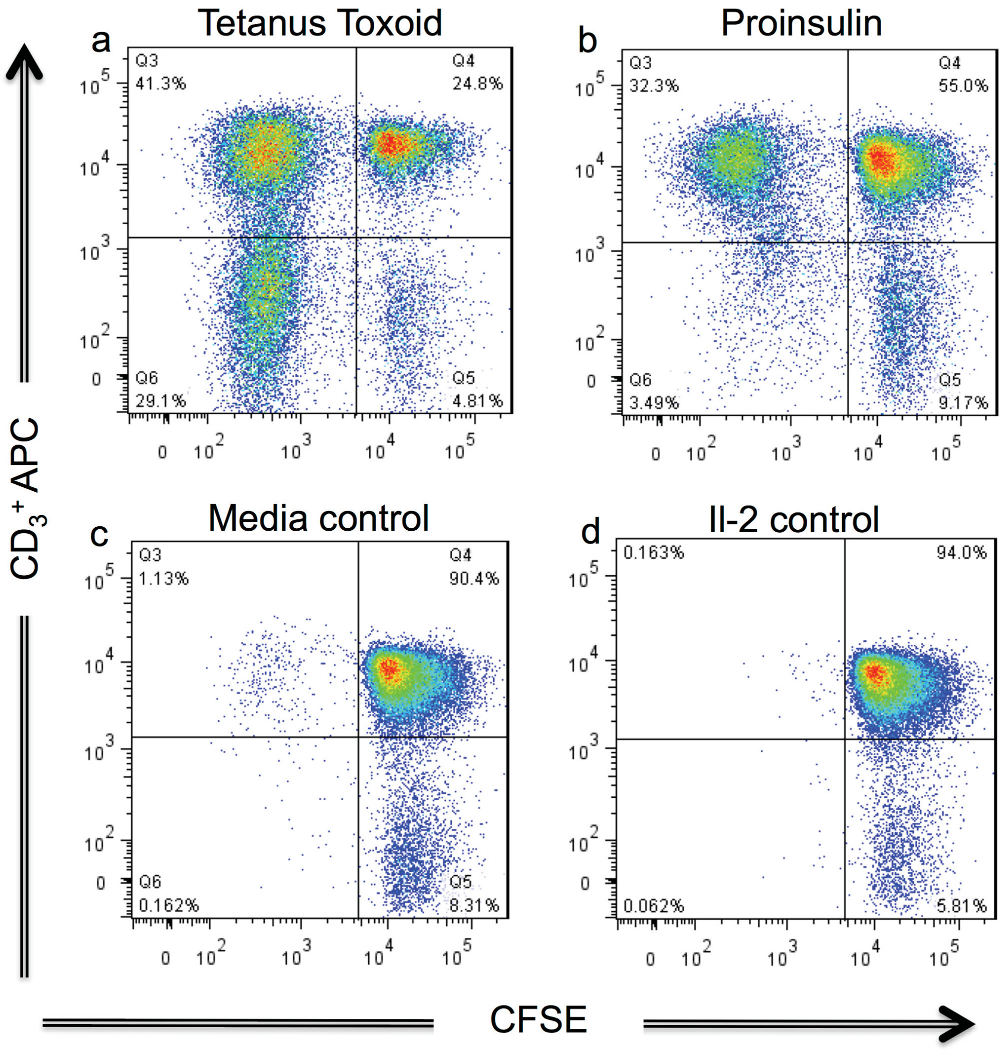


Figure 4-1 Activation of T-cells *ex vivo* with rh-PI as an antigen for 12 days.

Cells were sorted based on the dilution of CFSE as a result of proliferation. Media alone and Il-2 alone (negative controls) and TT (positive control) are also shown.

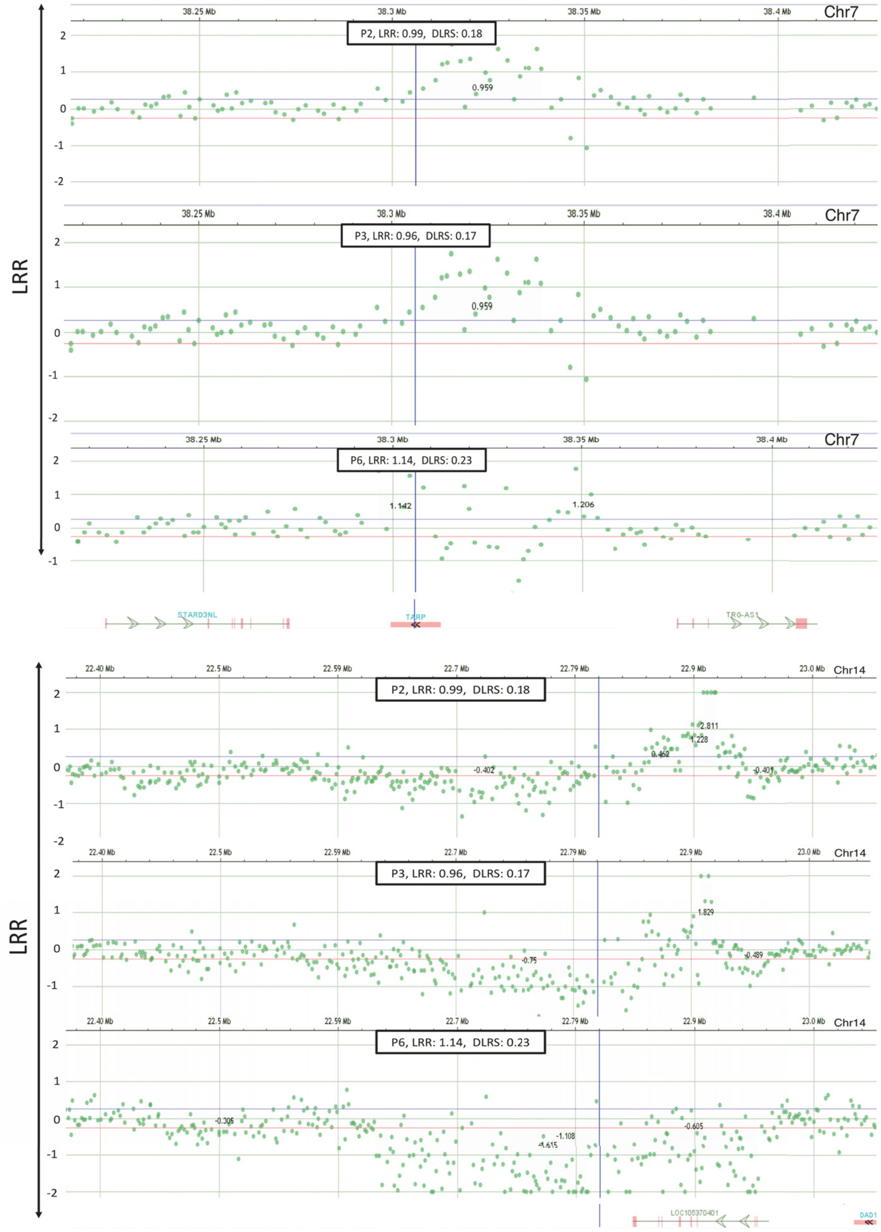


Figure 4-2 CGH array results demonstrating internal positive controls for T-cell CNAs in cells activated by PI.

CGH array results demonstrating positive controls for T-cell CNAs observed in all samples (to illustrate three samples are shown here): Copy-loss and gains (represented by colored lines below the chart) at regions of TCR genomic rearrangements of the gamma chain on chromosome 7 and alpha chain on chromosome 14 (DLRSpread values: P.2: 0.18, P3: 0.17, P6: 0.23).

4.5.2 Technical validation of the method

To confirm the specificity of the rh-PI- reactive lymphocytes response, lymphocytes from two samples (P10 and P18) of newly-diagnosed patients with T1D were isolated and stained with CFSE and cultured for 12 days with rh-PI and TT as described above. Proliferated lymphocytes to rh-PI and TT activation ($CD4^+CFSE^{low}$) were sorted and cultured with a second antigen (rh-PI, TT or with no antigen) for five days then stained with viability dye and the proliferation marker Ki67. FACS analysis showed that in both tested samples, cells sorted from rh-PI stimulated PBMCs showed the highest proliferation when the second activation was done with rh-PI (second respond to antigen exposure). Similarly, TT stimulated PBMCs had the highest proliferation for cell treated with TT as a second antigen (Table. 4. 2 and Fig 4. 2). Whereas, when proliferated cells were exposed to a different antigen in the second activation other than the one used in the first activation step, cell viability was drastically reduced and low or no response was observed (Table. 4. 2 and Fig 4. 3).

To determine the percentage of CD_4^+ and CD_8^+ proliferation during our *in vitro* protocol, after 12 days of culture with rh-PI, cells from sample P11 were stained with anti-CD_4^+ and anti-CD_8^+ antibodies. As expected from an activation with an exogenous peptide, FACS analysis showed that after 12 days of culture most proliferation was attributed to CD4+ cells (60.6% of the total, with proliferation of 30.2%). In the CD_8^+ cells (22.9% of the total), proliferation was only 6.75% (Fig 4. 4).

Table 4-2 Technical confirmation of the specificity of the *In vitro* response

Confirming the specificity of the lymphocyte's activation response in samples from two patients (P10 and P18). All samples (except for the Irradiated feeders) were tested in duplicate.

P10	Irradiated feeders		cells sorted from PI stimulated PBMCs				cells sorted from TT stimulated PBMCs				
			CD4$^+$CFSE^{low}		CD4$^+$CFSE^{High}		P10	CD4$^+$CFSE^{low}		CD4$^+$CFSE^{High}	
2nd Antigen	Viability %	Proliferation %	Viability %	Proliferation %	Viability %	Proliferation %	2nd Antigen	Viability %	Proliferation %	Viability %	Proliferation %
PI	0.15	0	22.2	82.15	0.48	3.33	PI	0.915	13.745	0.49	19.59
TT	0.16	0	2.05	21.5	0.435	0.745	TT	18.05	81.5	0.285	3.4
None	6.48	0	2.35	24.65	0.725	0	None	0.365	16.1	0.16	5

P18	Irradiated feeders		cells sorted from PI stimulated PBMCs				cells sorted from TT stimulated PBMCs				
			CD4$^+$CFSE^{low}		CD4$^+$CFSE^{High}		P18	CD4$^+$CFSE^{low}		CD4$^+$CFSE^{High}	
2nd Antigen	Viability %	Proliferation %	Viability %	Proliferation %	Viability %	Proliferation %	2nd Antigen	Viability %	Proliferation %	Viability %	Proliferation %
PI	0.16	6.25	11.65	72.3	0.13	8.35	PI	0.46	31.2	0.105	4.54
TT	0.068	0	0.665	23.1	0.16	1.51	TT	10.55	76.9	0.15	4.26
None	2.17	0	0.365	15.25	0.11	0	None	0.175	26.3	0.12	2.94

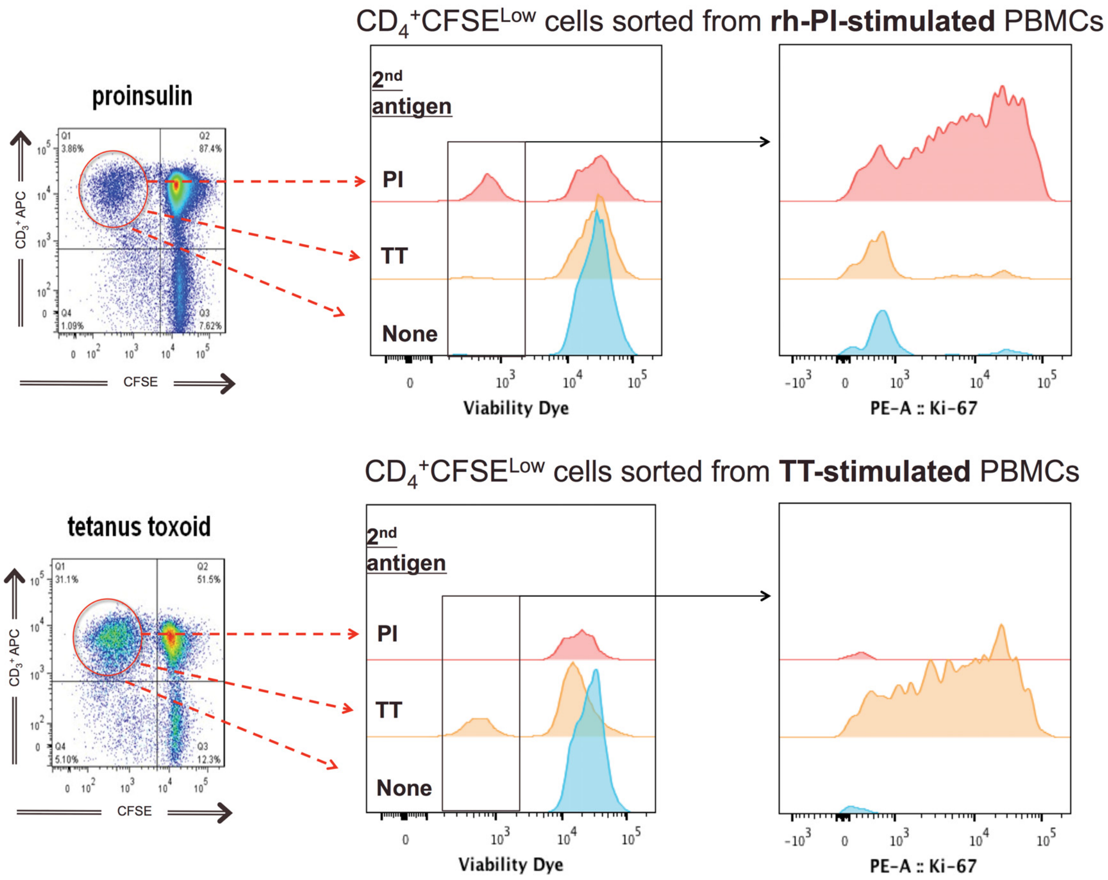


Figure 4-3 Technical validation of the specificity of the proliferation protocol.

Lymphocytes were reactivated with a second antigen and proliferation evaluated by expression of KI-67, a proliferation marker. Activation with the same antigen resulted in the highest proliferation and cell survival, while an antigen different than the one initially used, was associated with limited proliferation and increased cell death.

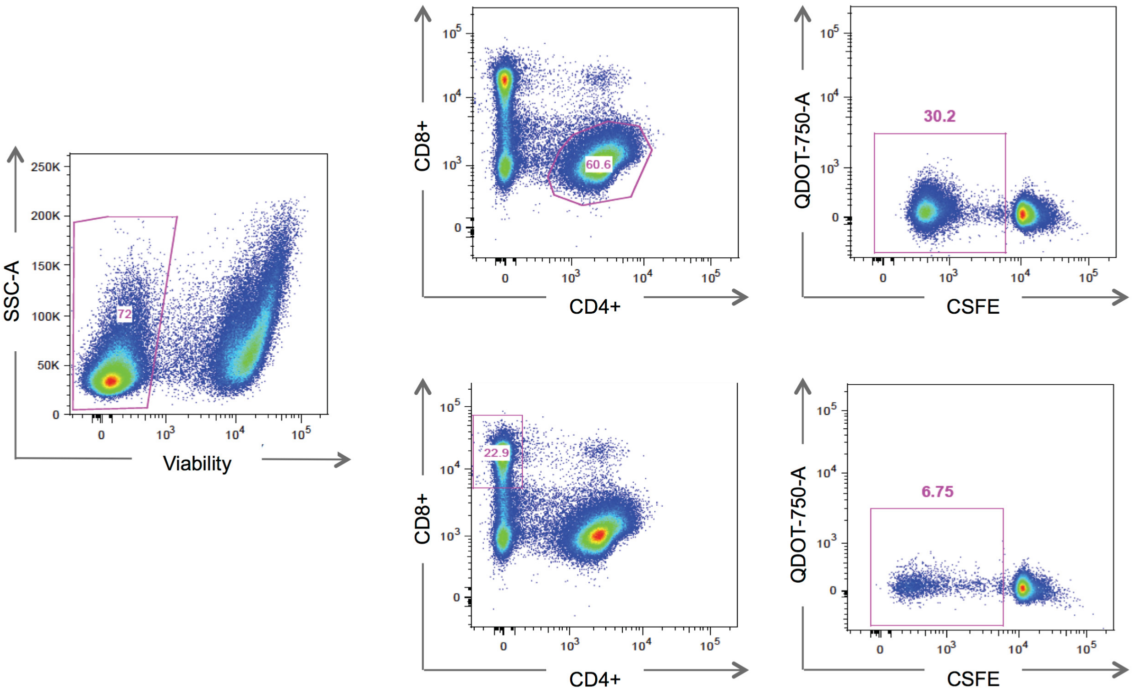


Figure 4-4 Proliferation percentage of CD4+ vs. CD8+ in our *in vitro* antigen stimulation.

After 12 days of culture with rh-PI, most proliferation was attributed to CD4+ cells (60.6% of the total, with proliferation of 30.2%). Whereas, in the CD$_8^+$ cells the proliferation was as much lower (2.9% of the total, with proliferation of only 6.75%).

4.5.3 Recurrent post zygotic copy number changes in rh-PI reactive lymphocytes of different patients

A total of 17 newly diagnosed patients with T1D were tested (11 females and six males) (Table 4.1) by Agilent 1x1M CGH array, using DNA from cells that responded to rh-PI activation as the test sample and DNA from cells that did not respond to the activation as reference (representing germline DNA). 11 out of the 17 tested patients have CNAs, 11 with CNAs ranging between one and 19 per patient and two patients with a very large number of CNAs (Supplementary data, Dataset S4. 1). The high number of CNAs in these two patients is reminiscent of CNAs observed in a malignant genome of a leukemic cell and involve many genes, some of them of known immune function. Detailed annotation of the CNAs seeing exclusively in these two patients (P4 and P6) was not attempted, because of their large number and the probability that they are a consequence rather than a cause of the rapid proliferation. Some of these CNAs overlap reported human germline CNVs. All are rare, and none is associated with an immune phenotype. Importantly, we identified CNAs affecting the same gene(s) in different patients. CNAs discussed below are recurrent in at least three patients (Table 4. 3).

One recurrent CNA seen independently in three patients (P10, P6 and P4) is at chr7: 50,343,122- 50,346,310 (Table, 4.3, Fig 4.5 a). This CNA observed as copy loss in two patients and copy gain in the third, affects *IKZF1,* a gene that encodes a transcription factor associated with chromatin remodeling. The encoded protein IKaros has a restricted expression to hematopoietic cells with high expression in CD4+ and CD8+ cells (C. Wu et al., 2016). Moreover, it works as a regulator of lymphocyte differentiation and maintenance of expression of cytokines in mature lymphocytes (Umetsu & Winandy, 2009; Winandy, Wu, Wang, & Georgopoulos, 1999). A null mutation (IKaros$^{-/-}$) in mice results in a complete penetrance of leukemia, elevated CD4^{+} to CD8^{+} T-cell ratios, and T-cell maturation abnormalities (Winandy et al., 1999). Milder phenotypes exhibited by mice heterozygous for the mutation (Georgopoulos, 2002). Moreover, in human, deletion of *IKZF1* was reported in acute lymphoblastic leukemia (Pui, Relling, & Downing, 2004). Moreover, its overexpression has also been associated with B-cell malignancies (Martinelli et al., 2009). Interestingly, *IKZF1* also maps to a locus associated with T1D (Swafford et al., 2011) (https://www.immunobase.org/disease/T1D/) and is the third Ikaros family member associated with the diseases along with (*IKZF3*) on chromosome 17q21.2 regulating *BCL-2* (Barrett et al., 2009) and Eos (*IKZF4*) on chromosome 12q13.2 regulating *FOXP3* (Todd et al., 2007). Ikaros interactions with signaling proteins including Notch (Merkenschlager, 2010) and STAT (Yap, Yeoh, Tay, Brenner, & Venkatesh, 2005) suggest that it affects T-cell development and activation leading to T1D or leukemia susceptible T-cell repertoire (Swafford et al., 2011).

A second recurrent CNA is a copy loss at chr7: 101,888,196- 101,896,854 seen independently in three patients (P4, P6, and P7) (Table, 4.3, Fig 4.5 b). This locus is within *CUX1* encoding a member of the homeodomain family of DNA binding proteins. The function of this gene is unknown, but functions of gene expression regulation, morphogenesis, differentiation, and cell cycle progression has been suggested. Moreover, it can function as a tumor suppressor in which a reduction of its expression promotes tumor development (Ramdzan & Nepveu, 2014).

Another recurrent CNA seen independently in three patients (P4, P6, and P7) is at chr8: 61,588,520- 61,593,702 (Table, 4.3, Fig 4.5 c). This copy-loss affects *CHD7*, a gene encoding a chromatin-remodeling protein. Mutations in *CHD7* cause CHARGE syndrome, a congenital disorder affecting several organs causing growth retardation. This disorder is usually accompanied by Immunodeficiency and T lymphopenia that are caused by the *CHD7* mutations (Z. Z. Liu et al., 2018). This suggests a T- cells proliferation control function for the gene.

Another recurrent CNA identified independently in three patients (P4, P6, and P7) is a copy loss at chr9: 2,043,102- 2,049,904 in *SMARCA2* (Table, 4.3, Fig 4.5 d). *SMARCA2* encodes a member of the SWI/SNF family of proteins. SWI/SNF is an evolutionarily conserved, large (~2 MDa) multi-subunit protein with ATPase activity and controls the transcription process by changing the chromatin structure around certain genes. SWI/SNF subunits regulate cellular processes including cell cycle progression, programmed cell death, differentiation, genomic instability and DNA repair and, in mice, they critically regulate hematopoiesis (Krasteva, Crabtree, & Lessard, 2017; Narlikar, Sundaramoorthy, & Owen-Hughes, 2013). Moreover, they play a role in tumor suppression, and mutations causing loss of function of several of its subunits has been identified at high frequency in several cancers (Biegel, Busse, & Weissman, 2014). *SMARCA2* copy loss observed in our samples from rh-PI reactive T-cells might be contributing to the proliferation process of these clones with autoreactive characteristics.

A recurrent CNA seen independently in three patients (P4, P7, and P9) is a copy loss in chr10: 22,607,561- 22,612,702 (Table, 4.3, Fig 4.5 e). This CNA spans the *COMMD3-BMI1* locus. This locus is a read-through naturally occurring transcription between neighboring genes *COMMD3* and *BMI1* producing a fusion transcript that shares sequence identity with each individual gene product. The fusion protein is a conserved protein with a high expression in haematopiotic cells (C. Wu et al., 2016). Moreover, both genes *COMMD3* and *BMI1* have independent high expression in hematopoietic cells (C. Wu et al., 2016). The function of the fusion protein is still unknown.

Another recurrent CNA seen independently in three patients (P4, P6, and P7) is a copy loss in chr15: 29,861,670- 29,867,088 (Table, 4.3, Fig 4.5 f). This CNA affects *FAM189A1,* an un unstudied gene.

Another recurrent CNA seen independently in patients P4, P6, and P7 is a copy loss in chr15: 101,789,504- 101,793,149 (Table, 4.3, Fig 4.5 g). This CNA affects *CHSY1* that encodes a member of the chondroitin N-acetylgalactosaminyltransferase family that is involved in many biological mechanisms including cell proliferation and morphogenesis. Lower expression of this gene plays a role in some types of cancer. Moreover, in memory CD4+ cells Chsy1 is linked to alterations in DNA methylation. This protein also activates Notch2 signaling in myeloma cells and may play an essential role in cell–cell interactions (Hashimoto et al., 2013).

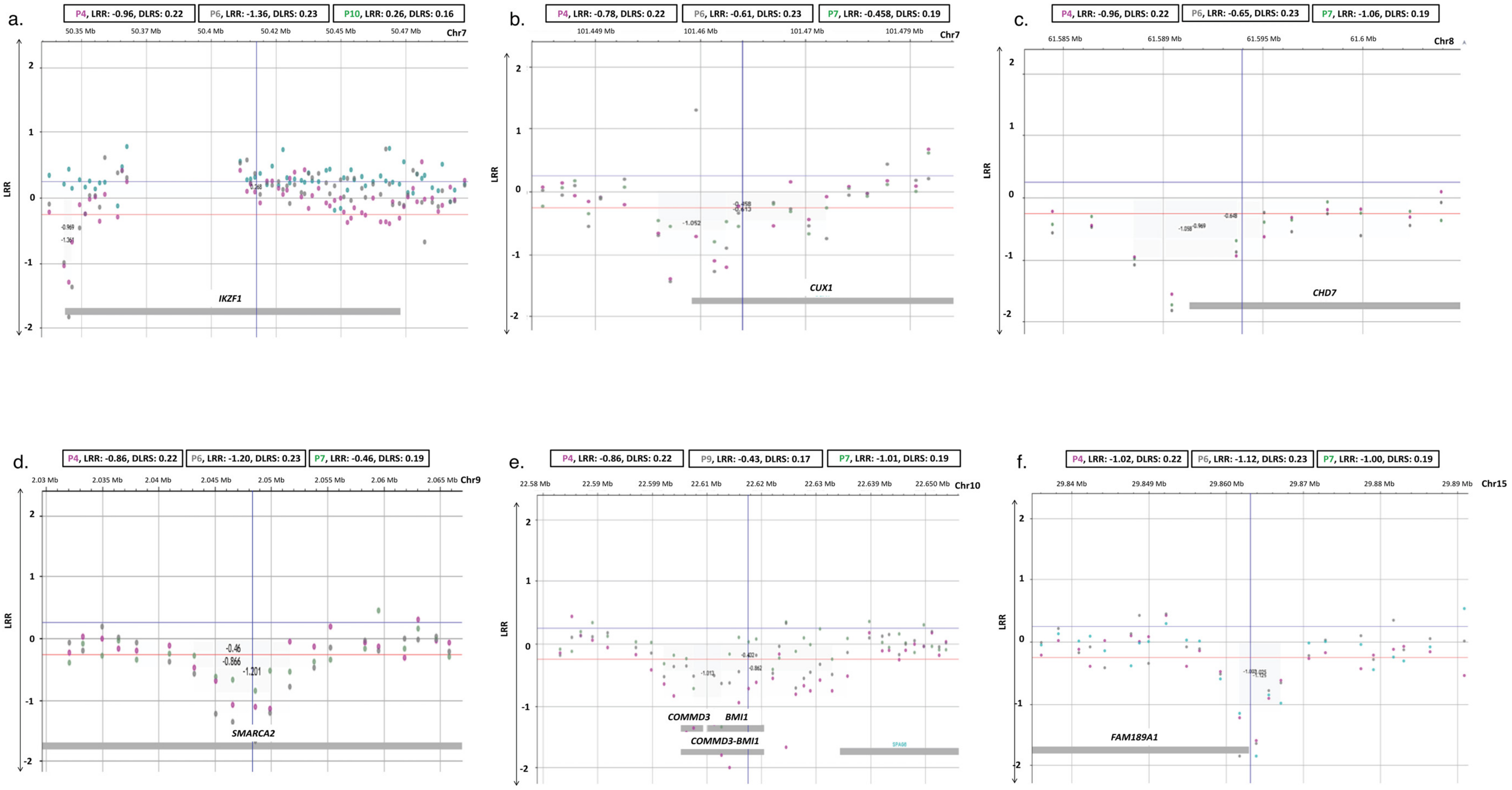
Another recurrent CNA seen independently in three patients (P6, P7, and P9) is a copy loss on chr18: 76,746,058- 76,758,150 (Table, 4.3, Fig 4.5 h). This CNA spans *SALL3* encoding a zinc-finger protein that belongs to a family of evolutionarily conserved genes. It has been suggested that silencing *SALL3* results in acceleration of DNA methylation and that this gene plays a role in some cancers (Shikauchi et al., 2009).

Finally, the last recurrent CNA in a minimum of three patients (P4, P6, and P7) is a copy loss at chr19: 14,195,682- 14,204,159, affecting three genes *C19orf67, SAMD1, PRKACA* (Fig 4.5 i). Copy-number changes at this locus, encompassing the three genes were also found in our first study (Chapter 3) in autoreactive lymphocytes obtained from pancreatic lymph nodes of two NOD mice. *C19orf67* and *SAMD1* are two unstudied genes. *PRKACA* encodes one of protein kinase A catalytic subunits. The primary structure is highly conserved from human to mice, zebrafish, and yeast. Moreover, more than 90 organisms have orthologs to this gene (Turnham & Scott, 2016). In patients with fibrolamellar hepatocellular carcinoma (FL-HCC), *PRKACA* has been found to be part of a translocation and a fusion of two genomic regions- *DNAJB1,* that encodes a heat shock protein 40, and *PRKACA* (Cheung et al., 2015; Cornella et al., 2015; J. N. Honeyman et al., 2014; Xu et al., 2015).

No correlation was found between the number of CNAs and the genotype of *INS* (R=0.147, p-value: 0.93) and *PTPN22* (R=-0.0899, p-value: 0.97).

Table 4-3 List of recurrent CNAs observed among a minimum of three tested newly diagnosed diabetic patients.

Sample ID	chr	Locus	Start	End	# Probes	LRR	P-value	Recurrent Genes	DLRS
P10	7	p12.2 - p12.1	50,333,095	50,501,756	61	0.26	4.78E-23	*IKZF1*	0.16
P6	7	p12.2	50,343,122	50,346,310	3	-1.36	1.03E-20		0.23
P4	7	p12.2	50,343,122	50,346,310	3	-0.96	3.88E-13		0.22
P6	7	q22.1	101,455,968	101,472,053	10	-0.61	1.16E-15	*CUX1*	0.23
P7	7	q22.1	101,455,968	101,472,053	9	-0.46	9.67E-11		0.19
P4	7	q22.1	101,888,196	101,896,854	8	-0.78	1.63E-19		0.22
P6	8	q12.1 - q12.2	61,584,412	61,602,381	10	-0.64	1.25E-19	*CHD7*	0.23
P7	8	q12.1	61,588,520	61,593,702	3	-1.05	1.15E-15		0.19
P4	8	q12.1	61,588,520	61,595,100	4	-0.96	8.05E-18		0.22
P7	9	p24.3	2,037,997	2,055,305	10	-0.46	5.46E-12	*SMARCA2*	0.19
P4	9	p24.3	2,043,102	2,049,904	5	-0.86	9.69E-18		0.22
P6	9	p24.3	2,045,009	2,051,680	5	-1.20	3.91E-28		0.23
P9	10	p12.2	22,602,135	22,632,965	18	-0.43	3.10E-17	*COMMD3-BMI1, COMMD3, BMI1*	0.17
P4	10	p12.2	22,602,135	22,635,726	19	-0.86	1.27E-57		0.22
P7	10	p12.2	22,607,561	22,612,702	3	-1.01	5.37E-15		0.19
P7	15	q13.1	29,859,183	29,867,088	5	-1.00	4.73E-22	*FAM189A1*	0.19
P6	15	q13.1	29,861,670	29,867,088	4	-1.12	2.07E-20		0.23
P4	15	q13.1	29,861,670	29,867,088	4	-1.02	3.75E-17		0.22
P6	15	q26.3	101,786,076	101,797,325	7	-0.73	4.77E-18	*CHSY1*	0.23
P7	15	q26.3	101,786,076	101,797,325	7	-0.58	2.62E-13		0.19
P4	15	q26.3	101,789,504	101,793,149	3	-1.14	1.23E-17		0.22
P9	18	q23	76,724,307	76,770,904	24	-0.27	2.16E-10	*SALL3*	0.17
P6	18	q23	76,736,376	76,758,150	11	-0.78	4.85E-29		0.23
P7	18	q23	76,746,058	76,758,150	7	-0.74	2.05E-19		0.19
P4	19	p13.12	14,182,246	14,232,289	25	-0.41	5.09E-21	*C19orf67, SAMD1, PRKACA*	0.22
P6	19	p13.12	14,191,532	14,232,289	21	-0.48	1.06E-21		0.23
P7	19	p13.12	14,195,682	14,204,159	6	-0.63	5.73E-14		0.19


a.
P4, LRR: -0.96, DLRS: 0.22
P6, LRR: -1.36, DLRS: 0.23
P10, LRR: 0.26, DLRS: 0.16
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50.37 Mb
50.4 Mb
50.42 Mb
50.45 Mb
50.47 Mb
Chr7
LRR
2
1
0
-1
-2
IKZF1
b.
P4, LRR: -0.78, DLRS: 0.22
P6, LRR: -0.61, DLRS: 0.23
P7, LRR: -0.458, DLRS: 0.19
101.449 Mb
101.46 Mb
101.47 Mb
101.479 Mb
Chr7
LRR
2
1
0
-1
-2
-1.052
CUX1
c.
P4, LRR: -0.96, DLRS: 0.22
P6, LRR: -0.65, DLRS: 0.23
P7, LRR: -1.06, DLRS: 0.19
61.585 Mb
61.589 Mb
61.595 Mb
61.6 Mb
Chr8
LRR
2
1
0
-1
-2
CHD7
d.
P4, LRR: -0.86, DLRS: 0.22
P6, LRR: -1.20, DLRS: 0.23
P7, LRR: -0.46, DLRS: 0.19
2.03 Mb
2.035 Mb
2.04 Mb
2.045 Mb
2.05 Mb
2.055 Mb
2.06 Mb
2.065 Mb
Chr9
LRR
2
1
0
-1
-2
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-0.866
-1.201
SMARCA2
e.
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Chr10
LRR
2
1
0
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-2
COMMD3
BMI1
COMMD3-BMI1
SPAG6
f.
P4, LRR: -1.02, DLRS: 0.22
P6, LRR: -1.12, DLRS: 0.23
P7, LRR: -1.00, DLRS: 0.19
29.84 Mb
29.849 Mb
29.860 Mb
29.87 Mb
29.88 Mb
29.89 Mb
Chr15
LRR
2
1
0
-1
-2
FAM189A1

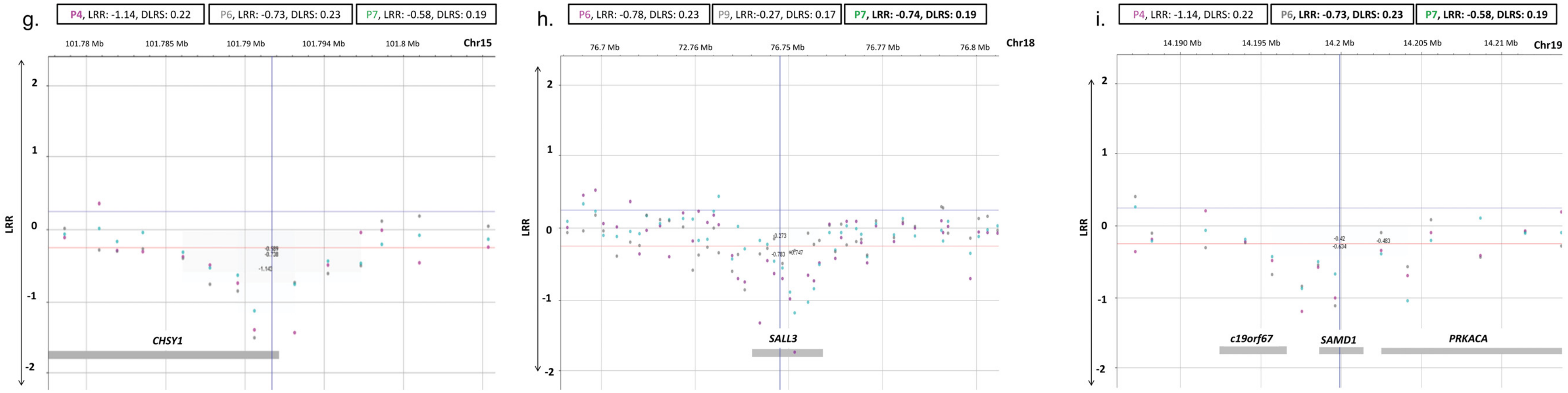

Figure 4-5 Recurrent CNAs observed in rh-PI reactive lymphocytes of at least three newly diagnosed T1D patients.

Copy number changes are represented by different colors for different patients. a. A recurrent copy loss in rh-PI reactive lymphocytes of three newly diagnosed patients with T1D within *IKZF1*, a gene associated with T1D. b. A recurrent copy loss affecting *CUX1*, a gene a potential function as a tumor suppressor. c. A recurrent copy loss within *CHD7* gene, a gene with a potential immune function. d. A recurrent copy loss in *SMARCA2*, encoding SWI/SNF a conserved protein with a tumor suppression function. e. A recurrent copy number loss spanning two genes *COMMD3* and *BMI1* that encodes an unstudied read-through transcript that have a high expression in haematopoietic cells. f. a recurrent copy loss affecting *FAM189A1* an unstudied gene. g. A copy loss affecting *CHSY1,* a gene involved in cell proliferation and DNA methylation. h. a recurrent copy loss spanning *SALL3,* a conserved gene involved in DNA methylation. i. A recurrent CNA spanning genes *SAMD1* and affecting *C19orf67* and *PRKACA. PRKACA* is a conserved gene associated with fibrolamellar hepatocellular carcinoma.

4.5.4 Human T-cells involved in host defense have smaller copy number changes

As a normal host-defense control, lymphocytes isolated from 14 of the newly diagnosed patients with T1D (10 were also tested for PI activation, eight females and six males, 5 -19 years old) were activated *in vitro* by Tetanus toxoid for 12 days (Table. 4.4, Supplementary data, dataset S4. 2). DNA from CD3$^+$ were tested by CGH. Excluding samples PI-6 and TT-13 (lymphocytes obtained from the same patient), and PI-10 and TT-14 (lymphocytes obtained from the same patient) due to the oddly large number of CNAs in these samples, the mean size of CNAs in rh-P reactive cells (21.13 ± 2.46, mean ± SEM, n=75) is two-fold larger than that in TT reactive cells (12.83 ± 0.74, n=458) (Welch *t.* test, p=0.0018). Moreover, comparing sizes of only samples from eight patients with both rh-P and TT reactive cells, the mean size of CNAs in rh-P reactive cells (19.98 ± 2.97, mean ± SEM, n=47) is almost two-fold larger than that in TT reactive cells (12.77 ± 1.13, n=283) (Welch *t.* test, P=0.027).

4.5.5 Some of the CNAs occur in pre-thymic precursors

Sequencing the TCR of the rh-P reactive cells (PXL) from the newly diagnosed patients with T1D showed both low and high clonalities ranging between 0.81% and 26.23% (for the Beta chain) indicating that at least some of the CNAs are of pre-thymic occurrence in a marrow progenitor conferring proliferation or survival advantage to multiple TCR lineages. In cases where the TCR clonality was high enough to explain the mosaicism level, the CNA, likely occurred in the specific lineage expanding to PI (Table. 4. 5). Sequencing the TCR of the rh-P non- reactive cells (PXH) as expected showed much lower clonalities than what is observed in rh-P reactive cells (PXL) ranging from

0.05% and 1.88% (for the Beta chain) indicating the different clones constituting this group of cells (Table. 4. 6). One exception seen in P6H alpha chain having a relatively high clonality compared to the rest of the PXH samples (6.25%). The rh-P reactive cells from the same patient P6L also showed the highest clonality (26.23%). Interestingly, this sample is one of the two patients with the large number of CNAs (TCR was not successfully sequenced for the second patient).

We also sequenced the TCRs for the control TT- reactive cells (TTXL) and TT-non-reactive cells (TTXH). Similar to the test samples TTXL showed higher clonalities compared to TTXH cells (Table. 4. 6 and 4. 7).

4.5.6 Common affected genes between diabetic human rh-P reactive lymphocytes T1D and diabetic mouse autoreactive lymphocytes

In our study, we identified 161 genes that were previously found to be involved in somatic copy number aberrations in autoreactive lymphocytes isolated from the pancreatic lymph nodes of newly diabetic NOD mice (Chapter 3) (Supplementary data. Dataset S4. 3). Some of these genes have an immune function or a cell proliferation response. *C19orf67*, *SAMD1*, *PRKACA,* discussed above, are within the same recurrent genomic interval, independently occurred in the lymphocytes of three patients (P4, P6, and P7) and in two different NOD mice (Chapter 3). *CASZ1* was identified in two patients (P1 and P6) and one NOD mouse; it encodes a regulatory protein that regulates T- helper cell differentiation and inflammation processes (Bhaskaran et al., 2018).

E2f1 is another affected gene identified in the lymphocytes of one patient (P4) and two diabetic NOD mice (with the abnormal memory only cells, Chapter 3). This gene encodes an essential regulator of different T-cell process including proliferation, differentiation, and apoptosis by controlling transcription process of certain genes that typically regulate the G1 to S phase of the cell cycle. Deficient NOD mice for *E2f1* and *E2f1* homozygous mutant NOD mice show an early and higher onset of T1D and demonstrate defect in T-cell development causing excessive numbers of mature T cells due to defects in apoptosis of thymocytes and peripheral T-cells (Salam et al., 2004). Moreover, these mice also showed a significant and profound reduction of T-reg cells (Salam et al., 2004).

Another interesting gene is *PHRF1*, found in the lymphocytes of a diabetic patient and a diabetic mouse. This gene encodes a tumor suppressor and is associated with the autoimmune disease systemic Lupus (Ettahar et al., 2013; Kawasaki et al., 2012).

Table 4-4 **List of control samples, lymphocytes from newly diagnosed patients with T1D activated with Tetanus toxoid.**

sample ID	Sex F/M	Age	*INS*	*PTPN22*	Media%	IL-2%	TT%	PI%	# CNAs	DLRS	PI ID*
TT1	F	>5, <19	T/A	C/C	3.4	4.2	12.7	18.6	91	0.23	P11
TT2	F	19	T/T	C/C	0.4	/	20	0.4	1	0.17	/
TT3	M	>5, <19	T/T	C/C	0.7	0	34.3	28.4	2	0.18	P13
TT4	M	8	A/A	C/T	0	2.1	25	4.3	4	0.24	P14
TT5	F	5	A/A	C/C	4.1	6.3	22.3	13.3	135	0.17	/
TT6	M	10	A/A	C/C	0.3	0	8.5	6.7	1	0.17	P16
TT7	F	10	A/A	C/C	1.4	0.9	9.6	13.5	6	0.21	P7
TT8	F	16	A/A	C/C	0.9	1.6	5.2	7.1	2	0.23	P8
TT9	M	10	A/A	C/C	/	/	30.7	/	171	0.2	/
TT10	F	14	A/A	C/C	0.3	0	8.5	6.7	0	0.16	P10
TT11	M	19	A/A	C/T	/	/	65	/	1	0.19	/
TT12	M	>5, <19	A/T	C/C	0.4	1.4	65.7	27.3	44	0.2	P15
TT13	F	5	A/A	C/C	0.5	0.6	10.5	1.4	3929	0.23	P6
TT14	F	>5, <19	A/A	C/C	0.1	0.1	9.1	3.9	1254	0.23	P4

* PI ID: In case cells from the same patient were activated both by rh-I and TT

Table 4-5 TCR sequences and clonalities of the α and β chains of rh- PI reactive cells.

	α-chain				**β-chain**				
Sample	**%**	**CD3**	**V**	**J**	**%**	**CD3**	**V**	**J**	**D**
P2L	**1.13**	CIRLPYFGNEKLTF	TRAV26-2*01	TRAJ48*01	**1.37**	CASSLSMGLGYTF	TRBV27*01	TRBJ1-2*01	TRBD1*01
P2L	**0.94**	CANAGGTSYGKLTF	TRAV36/DV7*04	TRAJ52*01	**0.81**	CASSYEQGARNSPLHF	TRBV6-5*01	TRBJ1-6*02	TRBD1*01
P3L	**/**	/	/	/	**14.28**	CATSGNTYTGELFF	TRBV24-1*01	TRBJ2-2*01	TRBD1*01, TRBD2*02, TRBD2*01
P3L	**/**	/	/	/	**3.34**	CASSYSYGSDTIYF	TRBV6-5*01	TRBJ1-3*01	TRBD2*02, TRBD2*01
P5L	**2.92**	CALSEAKTGANNLFF	TRAV19*00	TRAJ36*00	**3.4**	CASSLARGGTGLSEQYF	TRBV12-4*00	TRBJ2-7*00	TRBD1*00
P5L	**2.80**	CAVLTLQGAQKLVF	TRAV36DV7*00	TRAJ54*00	**3.26**	CASSPTGGGNQPQHF	TRBV18*00	TRBJ1-5*00	TRBD1*00
P6L	**11.10**	CILRDGCEGSNYKLTF	TRAV26-2*00	TRAJ53*00	**26.23**	CASHGGGYNEQFF	TRBV2*00	TRBJ2-1*00	TRBD1*00, TRBD2*00
P6L	**11.10**	CAYRRGGSNYKLTF	TRAV38-2DV8*00	TRAJ53*00	**9.62**	CASSTSGAISYEQYF	TRBV18*00	TRBJ2-7*00	TRBD2*00
P8L	**7.93**	CAAPPGQFYF	TRAV13-1*0	TRAJ49*00	**3.62**	CASTPGGTSGGSQETQYF	TRBV5-4*00	TRBJ2-5*00	TRBD2*00
P8L	**5.24**	CALSGGSYIPTF	TRAV6*00	TRAJ6*00	**2.55**	CASRMTGGSYNEQFF	TRBV12-3*00	TRBJ2-1*00	TRBD1*00
P10L	**11.92**	CAVRRGGGGNKLTF	TRAV21*00	TRAJ10*00	**2.53**	CASSLLANYGYTF	TRBV4-3*00, TRBV4-2*00	TRBJ1-2*00	
P10L	**3.44**	CAVMDSSYKLIF	TRAV1-2*00	TRAJ12*00	**1.9**	CASSSIFRGLGYTF	TRBV7-8*00	TRBJ1-2*00	TRBD1*00
P11L	**3.76**	CAVIGYSSASKIIF	TRAV12-2*00	TRAJ3*00	**9.98**	CASRQRGREYTGELFF	TRBV12-4*00,T RBV12-3*00	TRBJ2-2*00	TRBD1*00, TRBD2*00
P11L	**2.13**	CIVRVPHNAGNMLTF	TRAV26-1*00	TRAJ39*00	**3.19**	CASSPPLSLHEQFF	TRBV18*00	TRBJ2-1*00	TRBD2*00
P14L	**7.50**	CAANPSTGGGNKLTF	TRAV13-1*02	TRAJ10*01	**8.1**	CAISAVAGNTDTQYF	TRBV10-3*01	TRBJ2-3*01	TRBD2*02, TRBD2*01
P14L	**3.49**	CALGTGTYKYIF	TRAV6*02	TRAJ40*01	**6.69**	CASSWDGSTDTQYF	TRBV5-1*01	TRBJ2-3*01	TRBD1*01, TRBD2*02, TRBD2*01
P15L	**6.26**	CAANRMDYGGSQGNLIF	TRAV29DV5*00	TRAJ42*00	**17.67**	CASSRGLAGLTYNEQFF	TRBV7-8*00	TRBJ2-1*00	TRBD2*00
P15L	**5.02**	CAGAPASGTYKYIF	TRAV27*00	TRAJ40*00	**6.29**	CSVGPPGDFYNEQFF	TRBV29-1*00	TRBJ2-1*00	TRBD1*00, TRBD2*00
P16L	**8.42**	CAVSVNFGNEKLTF	TRAV8-6*00	TRAJ48*00	**18.61**	CASSPGVGREQYF	TRBV7-9*00	TRBJ2-7*00	TRBD1*00, TRBD2*00
P16L	**6.07**	CAMRDSSYKLIF	TRAV14DV4*00	TRAJ12*00	**4.95**	CASSLAGGGGYGYTF	TRBV12-3*00	TRBJ1-2*00	TRBD2*00, TRBD1*00

Table 4-6 TCR sequences and clonalities of α and β chains of rh-PI non-reactive cells.

	α-chain				β-chain				
Sample	**%**	**CD3**	**V**	**J**	**%**	**CD3**	**V**	**J**	**D**
P2H	**1.03**	CAVGASGSYGKLTF	TRAV8-3*01	TRAJ52*01	**0.57**	CASSLANYGYTF	TRBV5-1*01	TRBJ1-2*01	TRBD1*01, TRBD2*02, TRBD2*01
P2H	**0.90**	CALSRTTGNQFYF	TRAV9-2*01	TRAJ49*01	**0.50**	CAISGDISWDGYTF	TRBV10-3*01	TRBJ1-2*01	TRBD1*01
P3H	/	/	/	/	**1.88**	CASSTNNEQFF	TRBV5-1*01	TRBJ2-1*01	TRBD1*01
P3H	/	/	/	/	**1.51**	CASRRDYNEQFF	TRBV12-4*01	TRBJ2-1*01	TRBD2*02
P5H	**0.05**	CAPKNQGGKLIF	TRAV21*00	TRAJ23*00	**0.05**	CASLGAGESYNEQFF	TRBV6-2*00, TRBV6-3*00	TRBJ2-1*00	TRBD1*00
P5H	**0.05**	CAVNDSTLTF	TRAV1-1*00	TRAJ11*00	**0.05**	CASSLGQVSSGNTIYF	TRBV5-1*0	TRBJ1-3*00	TRBD1*00
P6H	**6.25**	CALSGSRAGGTSYGKLTF	TRAV9-2*00	TRAJ52*00	**0.29**	CASSLASDESYEQYF	TRBV7-2*00	TRBJ2-7*00	
P6H	**6.25**	CAVSDGPIGGGADGLTF	TRAV8-4*00, TRAV8-2*00	TRAJ45*00	**0.21**	CASHGGGYNEQFF	TRBV2*00	TRBJ2-1*00	TRBD1*00, TRBD2*00
P8 H	**1.15**	CAYRSAGGNEKLTF	TRAV38-2DV8*00	TRAJ48*00	**0.43**	CASSLGVNEQFF	TRBV7-9*00	TRBJ2-1*00	
P8 H	**0.62**	CAATGFQKLVF	TRAV13-2*00	TRAJ8*00	**0.35**	CASSLAVRETQYF	TRBV7-6*00	TRBJ2-5*00	
P10H	**0.24**	CAVRDSNYQLIW	TRAV1-2*00	TRAJ33*00	**0.15**	CATSRDLPDEQYF	TRBV15*00	TRBJ2-7*00	
P10H	**0.12**	CAVMDSNYQLIW	TRAV1-2*00	TRAJ33*00	**0.07**	CASSPNGFPRGSYEQYF	TRBV6-2*00, TRBV6-3*00	TRBJ2-7*00	
P14H	**0.39**	CAVRDSNYQLIW	TRAV1-2*01	TRAJ33*01	**0.06**	CASSLLPGAGELFF	TRBV7-2*01	TRBJ2-2*01	TRBD2*01
P14H	**0.27**	CAVMDSNYQLIW	TRAV1-2*01	TRAJ33*01	**0.05**	CASSLMWGPMNTEAFF	TRBV12-4*01	TRBJ1-1*01	TRBD1*01, TRBD2*02, TRBD2*01
P15H	**0.41**	CAANRMDYGGSQGNLIF	TRAV29DV5*00	TRAJ42*00	**1.02**	CASSRGLAGLTYNEQFF	TRBV7-8*00	TRBJ2-1*00	TRBD2*00
P15H	**0.24**	CAGAPASGTYKYIF	TRAV27*00	TRAJ40*00	**0.42**	CSVGPPGDFYNEQFF	TRBV29-1*00	TRBJ2-1*00	TRBD1*00, TRBD2*00
P16H	**0.89**	CAVSLMYSGGGADGLTF	TRAV21*00	TRAJ45*00	**0.90**	CAISDNFGNTIYF	TRBV10-3*00	TRBJ1-3*00	
P16H	**0.59**	CAMRETTSGTYKYIF	TRAV14DV4*00	TRAJ40*00	**0.50**	CASSLGRRLNTEAFF	TRBV11-2*00	TRBJ1-1*00	

Table 4-7 TCR sequences and clonalities of α and β chains of TT- reactive lymphocytes obtained from T1D patients.

	α-chain				**β-chain**				
Sample	**%**	**CD3**	**V**	**J**	**%**	**CD3**	**V**	**J**	**D**
TT1L	**5.24**	CILRDDAGGTSYGKLTF	TRAV26-2*00	TRAJ52*00	**4.74**	CASRQRGREYTGELFF	TRBV12-4*00	TRBJ2-2*00	TRBD1*00, TRBD2*00
TT1L	**4.33**	CAVSDTAYKYIF	TRAV8-4*00	TRAJ40*00	**3.4**	CATSGGAFFRPQHF	TRBV15*00	TRBJ1-5*00	TRBD2*00, TRBD1*00
TT3L	**7.44**	CAENKRFSGGYNKLIF	TRAV13-2*01	TRAJ4*01	**8.31**	CAENKRFSGGYNKLIF	TRBV12-5*01	TRBJ2-2*01	TRBD2*02, TRBD2*01
TT3L	**2.53**	CAGVYGGSNYKLTF	TRAV27*01	TRAJ53*01	**5.23**	CASSPRTGEGYGQFF	TRBV5-4*01	TRBJ2-1*01	TRBD1*01
TT4L	**41.22**	CAPGDTGRRALTF	TRAV38-2/DV8*01	TRAJ5*01	**10.36**	CSARDWETQYF	TRBV20-1*01	TRBJ2-5*01	TRBD2*02
TT4L	**8.80**	CAVQGGSEKLVF	TRAV21*02	TRAJ57*01	**7.09**	CASSLPGASNSPLHF	TRBV5-5*02	TRBJ1-6*02	TRBD2*02
TT5L	**3.57**	CAASDSWGKLQF	TRAV13-1*00	TRAJ24*00	**3.4**	CASSLARGGTGLSEQYF	TRBV12-4*00	TRBJ2-7*00	TRBD1*00
TT5L	**3.51**	CAASIGASGGSYIPTF	TRAV23DV6*00	TRAJ6*00	**3.26**	CASSPTGGGNQPQHF	TRBV18*00	TRBJ1-5*00	TRBD1*00
TT6L	**10.63**	CAMSRPSGYSTLTF	TRAV12-3*00	TRAJ11*00	**7.29**	CASSFSPDTQYF	TRBV12-3*00	TRBJ2-3*00	
TT6L	**5.33**	CAVDTGRRALTF	TRAV12-2*00	TRAJ5*00	**5.32**	CASSLAGGGGYGYTF	TRBV12-3*00	TRBJ1-2*00	TRBD2*00, TRBD1*00
TT8L	**4.03**	CAAIKAAGNKLTF	TRAV13-1*00	TRAJ17*00	**3.8**	CASSRTGTSGYEQYF	TRBV7-9*00	TRBJ2-7*00	TRBD2*00
TT8L	**1.59**	CALNTNAGKSTF	TRAV9-2*00	TRAJ27*00	**3.05**	CASSFYQGLAFF	TRBV7-2*0	TRBJ1-1*00	TRBD1*00
TT9L	**3.97**	CASSFSPGELFF	TRAV9-1*01	TRAJ4*01	**5.82**	CASSAYGDTQYF	TRBV7-2*01	TRBJ2-3*01	TRBD1*01, TRBD2*02, TRBD2*01
TT9L	**3.22**	CAVDTGRRALTF	TRAV12-2*01	TRAJ5*01	**4.8**	CASSFSPGELFF	TRBV12-3*01	TRBJ2-2*01	TRBD1*01, TRBD2*02, TRBD2*01
TT12L	**9.24**	CALSDPRGSTLGRLYF	TRAV9-2*00	TRAJ18*00	**16.1**	CASSSGLVYEQYV	TRBV7-9*00	TRBJ2-7*00	TRBD2*00
TT12L	**8.56**	CAVQARNQGGKLIF	TRAV20*00	TRAJ23*00	**8.82**	CASSPDRKLAALGVYNEQFF	TRBV7-8*00	TRBJ2-1*00	TRBD2*00

Table 4-8 TCR sequences and clonalities of α and β chains of TT-non-reactive cells.

	α-chain				**β-chain**				
Sample	**%**	**CD3**	**V**	**J**	**%**	**CD3**	**V**	**J**	**D**
TT1H	**1.03**	CAVRDSNYQLIW	TRAV1-2*00	TRAJ33*00	**0.12**	CASRQRGREYTGELFF	TRBV12-4*00, TRBV12-3*00	TRBJ2-2*00	TRBD1*00, TRBD2*00
TT1H	**0.60**	CAVMDSNYQLIW	TRAV1-2*00	TRAJ33*00	**0.09**	CASSLTGDHNEQFF	TRBV6-2*00, TRBV6-3*00	TRBJ2-1*00	TRBD1*00
T4H	**0.76**	CAVMDSNYQLIW	TRAV1-2*01	TRAJ33*01	**0.10**	CASNKQGTVSAETQYF	TRBV5-1*01	TRBJ2-5*01	TRBD1*01
T4H	**0.52**	CAVRDSNYQLIW	TRAV1-2*01	TRAJ33*01	**0.10**	CASSRTGQAGNTIYF	TRBV5-1*01	TRBJ1-3*01	TRBD1*01
T5H	**0.11**	CAVRDMGSSASKIIF	TRAV1-1*00	TRAJ3*00	**0.06**	CASDRNTEAFF	TRBV7-9*00	TRBJ1-1*00	
T5H	**0.10**	CVVSDRGSTLGRLYF	TRAV10*00	TRAJ18*00	**0.05**	CASSVLLDRGRHEQYF	TRBV4-1*00	TRBJ2-7*00	TRBD1*00
TT6H	**1.05**	CAVSLMYSGGGADGLTF	TRAV21*00	TRAJ45*00	**0.81**	CAISDNFGNTIYF	TRBV10-3*00	TRBJ1-3*00	
TT6H	**0.74**	CAMRETTSGTYKYIF	TRAV14DV4*00	TRAJ40*00	**0.63**	CASSLGRRLNTEAFF	TRBV11-2*00	TRBJ1-1*00	
TT8H	**1.46**	CAYRSAGGNEKLTF	TRAV38-2DV8*00	TRAJ48*00	**0.55**	CASSLGVNEQFF	TRBV7-9*00	TRBJ2-1*00	
TT8H	**0.99**	CAATGFQKLVF	TRAV13-2*00	TRAJ8*00	**0.42**	CASSLAVRETQYF	TRBV7-6*00	TRBJ2-5*00	
T9H	**0.33**	CAVRDSNYQLIW	TRAV1-2*01	TRAJ33*01	**0.57**	CASSKIPGQGFYEQYF	TRBV7-9*03	TRBJ2-7*01	TRBD1*01
T9H	**0.20**	CAVMDSNYQLIW	TRAV1-2*01	TRAJ33*01	**0.16**	CASSQVFRSGPTDTQYF	TRBV4-3*01	TRBJ2-3*01	TRBD1*01
TT12H	**0.57**	CALSDPRGSTLGRLYF	TRAV9-2*00	TRAJ18*00	**0.72**	CASSSGLVYEQYV	TRBV7-9*00	TRBJ2-7*00	TRBD2*00
TT12H	**0.53**	CAVQARNQGGKLIF	TRAV20*00	TRAJ23*00	**0.37**	CASSPDRKLAALGVYNEQFF	TRBV7-8*00	TRBJ2-1*00	TRBD2*00

4.6 Discussion

In this study, we present a novel finding of somatic mutations in genes of rh-PI reactive CD4+ T cells of patients newly diagnosed T1D. Somatic mutations have been previously reported in whole blood of healthy individuals and increase with age (Busque et al., 2012; Forsberg et al., 2012). Although they increase the risk of hematological cancers (Genovese et al., 2014; Jacobs et al., 2012; Jaiswal et al., 2014; Laurie et al., 2012; Xie et al., 2014) they are commonly found in healthy individuals. A recent report has shown the exciting of somatic mutations affecting genes of both immune and proliferation function in newly diagnosed, untreated patients with rheumatoid arthritis (RA) (Savola et al., 2017). Moreover, we previously demonstrated that somatic mutations are originating in memory CD4+ T cells from PLNs of diabetic mice (Chapter 3).

To extend our investigation to human T1D, we obtained examined autoreactive cells from the peripheral blood of 17 newly diagnosed patients with T1D. To obtain antigen-specific memory cells we activated *in vitro* PBMCs by the primary antigen of the disease, proinsulin, and isolated CD_4+ responding cells based on their CFSE dilution for genomic testing. The non-responding cells were also isolated and used as germline reference. To our knowledge, this is the first study demonstrating the emergence of somatic mutations in insulin-reactive cells of patients with T1D as a non-malignant autoimmune disease.

We identified recurrent copy number aberrations affecting the same genes independently in different patients such as *IKZF1* that is expressed in CD_4+ cells and known to be associated with T1D. Moreover, we also identified recurrent genes that we previously identified as recurrent in our mouse study (Chapter 3) that are known regulators of immune cells proliferation process (such as *CASZ1* and *E2f1*).

Interestingly, we identified four genes (*CDYL, CLIP2, IRF1, and MAST1*) that were previously reported to be affected by somatic mutations in immune cells of RA patients (Savola et al., 2017). *IRF1* is particularly interesting as it is expressed in hematopoietic cell lineages and is a known tumor suppressor and a transcriptional regulator of genes involved in both innate and acquired immune responses controlling process including cell proliferation, apoptosis, and the immune response.

As expected, somatic CNAs were also found in activated CD_4+ from the same patients by TT as negative controls since these lymphocytes are performing their normal function. However, they are two-fold significantly smaller (p= 0.0018) than CNAs found in Insulin reactive cells. We expect that most CNAs in TT responding cells are a result of the promote proliferation taking place to respond to the virus xenoantigen. Unlike what we previously found in mice (Chapter 3), TT responding cells showed a higher number of CNAs compared to what was found in memory cells of NOD mice infected with *L. major* parasite. We speculate that this because the response to TT in human is a second immune response due to the previous exposure to the antigen by vaccination. This is vigorous antigen-driven proliferation compared to that after a first antigen encounter, therefore, could cause a higher accumulation of random CNAs.

To determine the stage of the CNAs development, we sequenced the reactive cells and showed that at least some of the CNAs occurred pre-thymic and we speculate that there are probably many more post-thymic that we cannot see because of the very low level of mosaicism).

In this study, we extended our investigation to human T1D to test the novel putative somatic mutation hypothesis as shared pathogenetic mechanism between autoimmunity and cancer. Our findings demonstrate the existence of non-random recurrent PZM in auto-reactive T lymphocyte lineages in patients of T1D. Further investigation is warranted to confirm and understand the biological consequences of these CNAs.

We expect that these somatic mutations have more drastic functional effects than germline-inherited variants since they occur at a cellular level and are not subject to evolutionary pressure. Moreover, identification of the genes involved could serve as potential therapeutic targets as they exist only in disease-causing cells.

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CHAPTER FIVE Somatic mutations in clonally expanded memory T lymphocytes newly diagnosed patients with Celiac disease

Maha Alriyami[1]; Luc Marchand[1]; Jonathan Wyse[2]; Brent Richards[3], Constantin Polychronakos[1*]

[1]The Endocrine Genetics Laboratory, Child Health and Human Development Program and Department of Pediatrics, McGill University Health Centre Research Institute, Montreal, Quebec, Canada, H3H 1P3. [2]Jewish General Hospital, McGill Department of Medicine, Division of Gastroenterology. [3]Departments of Medicine, Human Genetics, Epidemiology and Biostatistics. Correspondence and requests for materials should be addressed to C.P. (email: constantin.polychronakos@mcgill.ca)

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Authors Contribution:

Maha Alriyami: Designed and executed the experiments, results analysis and interpretation, writing and preparation of manuscript.

Luc Marchand: Bioinformatics CBS analysis.

Jonathan Wyse: Patients recruitment.

Brent Richards: Research collaborator, patient recruitment and ethics.

Constantin Polychronakos: Research supervisor and mentor, result interpretation, manuscript editing and corresponding author.

5.1 Preface

Our findings, in both diabetic mice and newly diagnosed T1D patients (described in the previous studies, chapter 3 and 4) strongly support the somatic mutation hypothesis of autoimmunity. The obvious question that arises is whether the somatic mutation hypothesis applies to autoimmunity in general and is not specific to T1D. Towards an answer to this question, we investigated the hypothesis in another autoimmune disorder, celiac disease (CD). Similar to T1D, celiac is a complex disorder believed to be caused by a combination of genetic and environmental exposure to dietary gluten. We selected this disease for two important reasons. First, the antigenic stimulus (gluten peptides), has been well characterized (as in T1D) allowing the *ex vivo* expansion of autoreactive cells from peripheral blood (Tye-Din et al., 2010). Second, a risk of developing lymphoid malignancy has been well established in CD. This is associated with the oligoclonal expansion of T-cells in the intraepithelial layer of the intestine and followed by enteropathy-associated T cell lymphoma (Goodnow, 2007). In this study, we test the hypothesis on samples of CD patients obtained after a gluten challenge. We also aimed to investigate whether the same genes might be involved in the causal CNAs between CD and T1D patients.

5.2 Abstract

The role of somatic mutations in the tumorigenesis and lymphomas is well established. However, studies examining their role in non-malignant diseases are few. In previous studies, we provided evidence for the existence of somatic copy number aberrations in autoreactive lymphocytes in diabetic NOD mice and early diagnosed patients with Type 1 Diabetes. Here, we extended our investigation to autoreactive lymphocytes from celiac patients as another autoimmune disease. Here, we activated lymphocytes obtained from celiac patients who underwent a gluten challenge with gluten peptides and sorted the reactive cells by CFSE dilution. The acquired autoreactive lymphocytes were examined for somatic copy number variations. We identified CNAs in 7 out of 10 patients with three recurrent CNAs affecting three genes: *CHD7, C8orf33, and LOC339685*. Moreover, we were able to identify genes that we previously identified to be affected by CNAs in T1D (Human and NOD mice). Some are known to be associated

with celiac diseases such as *UBE2E3* and *NFIA*. Our data provide further evidence of for the putative mechanistic overlap between autoimmunity and Cancer offering novel avenues for decrypting autoimmunity and its future individualized treatment through targeting disease-causing cells.

5.3 Introduction

Celiac disease (CD) is an autoimmune disease, categorized by an aberrant immune response triggered by dietary gluten in genetically susceptible subjects. This results in intestinal injury accompanied by highly variable symptoms including abdominal discomfort, chronic diarrhea, anemia and several vitamin deficiencies caused by the malabsorption due to intestinal damage leading to further complications. CD is usually resolved by eliminating gluten from the diet (Gluten-free diet, GFD).

The current prevalence of CD is about 1% in the majority of Western populations and is on the rise partly due to the improvement and the current accuracy of serological antibody testing with ~95% specificity (Sulkanen et al., 1998). Other reasons for the CD prevalence increase is unknown. The majority of individuals with this permanent intolerance to gluten are carries of HLA-DQ2 (~95%) and the remainder ~5% are usually carriers of HLA- DQ8 (Marsh, 1992; Sollid et al., 1989; Spurkland et al., 1997; Tighe et al., 1992). These are the same two haplotypes that are also associated with high risk for T1D.

One of the long-term complications of CD is the increased risk of cancer, particularly non-Hodgkin’s lymphoma (30%-40%) (Grainge, West, Solaymani-Dodaran, Card, & Logan, 2012; West, Logan, Smith, Hubbard, & Card, 2004). This risk persists despite complying with a strict GFD pointing to a potential contribution of somatic mutations.

Somatic mutations are non-inherited *de novo* mutations that occur in a single cell at any stage during development and are passed to all descended cells creating mosaicism. In cancer pathogenesis, the role of somatic mutations has been well established; such a mutation causes an uncontrolled proliferation in single cell clone, resulting in the disease. However, they are common in hematopoietic cell lineages (clonal hematopoiesis) of healthy individuals (Busque et al., 2012; Genovese et al., 2014; Jaiswal et al., 2014; Xie et al., 2014). The pathogenic role of somatic mutation in non-malignant T-cells has been seldom explored. We have previously investigated their existence in autoreactive lymphocytes involved in the autoimmunity of T1D (mouse paper and Chapters 3 and 4). Moreover, they have been reported in autoreactive cells of newly diagnosed rheumatoid arthritis patients (Savola et al., 2017).

In this study, we investigated the somatic mutation hypothesis in non-malignant individuals diagnosed with the autoimmune disorder CD. Here, we discovered in gluten-peptide activated peripheral-blood T-cells, somatic CNAs, similar to what we found in diabetes and, importantly, some that affect the same specific genes.

5.4 Martials and Methods

5.4.1 Patient's recruitment

The McGill Research Ethics Board approved patient recruitment strategy (protocol number: A09-M86-14B entitled "The identification of driver mutations in celiac disease"). Study subjects were recruited from the network of McGill University affiliated hospitals including the Jewish General Hospital, Montreal General Hospital, and the Royal Victoria

Hospital. Study subjects who have met our inclusion criteria (positive for the highly sensitive transglutaminase (tTG) antibody test and confirmed by bowel epithelium biopsy) were informed about the project and written informed consent forms were obtained from all participants. Participants underwent a gluten challenge for three days, in which they eat four slices of gluten-containing bread per day (2 for breakfast and 2 for lunch, a total of 9g of gluten/day). After the gluten challenge, 30ml of blood is drawn from the patients for the study.

5.4.2 Lymphocyte isolation and proliferation

In humans, we are confined to peripheral blood samples. Therefore, to identify autoreactive cells to gluten, the major CD autoantigen, we needed to expand them *ex vivo*. Peripheral blood mononuclear cells (PBMCs) were isolated from buffy coats of CD patients using Ficoll-hypaque^{TM} PLUS (Cat #:17-1440-02, GE Healthcare) density gradient centrifugation. Cells were stained by CFSE (carboxyfluorescein diacetate succinimidyl ester) (Cat #: C34554, Invitrogen) and plated at 3,000,000 cells/well in flat-bottom 24-well plates. Cells were activated by 50 ug/mL of one of seven gluten custom-designed peptides obtained from Proimmune (Pep 1-7, Supplementary data, Table S5. 1; >95% purity) and 5U/ml rhIL-2 (Cat # PHC0026, ThermoFisher Scientific) in vitro for 12 days in serum-free media, CTS OpTmizer T-cell Expansion SFM (A10221-01, Life Technologies). These peptides were chosen because they are the most immunogenic in CD (Tye-Din et al., 2010). 1000 ml of media was supplemented with 26 mL/L of OpTmizer CTS T-Cell Expansion Supplement and ten mL/L of 200 mM L- Glutamine solution for a final concentration of 2 mM. Media was also supplemented with 250 ng/mL of Fungizone (Cat #: 15290-018, ThermoFisher Scientific) and 5 mg/mL of Gentamicin (Cat #: 15750-

060, ThermoFisher Scientific). Culturing was in standard conditions of 37°C, 5% CO2 in a humidified incubator. rhIL-2 was added every three days, and half the dose of peptide was added in day six of culture. Lymphocytes from the same patients were also activated by 2ug/mL tetanus toxoid (TT) (Cat#: 582231-25UG, Calbiochem) as a positive control for the method and cultured with rhIL-2 or in media alone as a negative control. Lymphocyte proliferation in response to peptides and TT was detected by CFSE dilution, and proliferating cells were sorted by staining for anti- Human CD_3 (monoclonal antibody, APC, OKT3, cat#: 17-0037-42, eBioscience) in a FACSAria sorter. $CD3^+CFSE^{high}$ (non-proliferating) and $CD_3^+CFSE^{low}$ (proliferating) were sorted. Staining was performed according to the manufacturer's instructions. All samples were kept on ice throughout isolation and staining.

5.4.3 DNA extraction and Whole Genome amplification

DNA was extracted from lymphocytes and amplified using GenomePlex complete whole genome amplification (WGA-2) (cat #: WGA2-50RXN) kit, approved explicitly by Agilent for Comparative genomic hybridization (CGH) to detect copy-number differences. Amplification products were next purified using PCR Cleanup kit from Sigma (cat #: NA1020, Sigma).

5.4.4 Detection of PZMs

We sent three µg of amplified DNA to the McGill University/Genome Quebec Innovation Center or Vancouver prostate center, for Agilent dual color CGH analysis on the human 1x1M Agilent array. DNA from $CD3^+CFSE^{low}$ (proliferating) cells were used as 'test sample', and $CD3+CFSE^{high}$ (non-proliferating) representing germline DNA was used as 'reference sample.' In Agilent dual color, 1x1M human CGH array, reference and test DNA samples were labeled with different fluorescent tags (Cy3 and Cy5, respectively), which were next hybridized to the probes of the 1x1M chip, designed with one million probes for genome-wide coverage but with a concentration in and around coding sequences. The fluorescence intensity ratio (Cy3: Cy5) at each probe position reflects copy-number differences between the two DNA samples.

5.4.5 Bioinformatics analysis

Test and reference signals were calculated for each probe, and internal normalization equalized the systematic difference between the two fluorochromes. The base-2 log of the Cy3/Cy5 ratio (LRR) was used for analysis. Regions bearing copy number aberrations were identified using two independent algorithms, Agilent Genomic *Agilent CytoGenomics* software v4.0 (Agilent Technologies) implementing the ADM-2 algorithm and DNAcopy software implementing the circular binary segmentation (CBS) algorithm (Venkatraman & Olshen, 2007). In ADM-2 (provided by Agilent technologies, threshold 6.0), the algorithm identifies aberration points that maximize the *t*-test of comparing the averages from the expected value of zero. Once a segment is kept, its median is centered, and the method is repeated on three new segments. This combines the segmentation and calling process (Roy & Motsinger Reif, 2013). We applied Agilent technologies recommended filtering standards of a minimum of three consecutive aberrant probes and a minimum absolute average $\log_2$ ratio of LRR |0.25| and P-value $<5x10^{-8}$ (Bonferroni threshold). The Human GRCh37/hg19 assembly, Feb. 2009 was used, to match the indexing of the Agilent probes.

In CBS, each chromosome was recursively split into small regions (each containing more than three probes), using a maximal t-statistic test for detecting the change-points: for one segment, a two-sample t-statistic compares the mean of the Log_2-ratio in the sub-segment to the mean Log_2-ratio of the rest of the segment. The splitting of the DNA stops when no more change-points can be identified. The Human GRCh37/hg19 assembly, Feb. 2009 was used, to match the indexing of the Agilent probes. CNAs were kept as true if were called by both algorithms ADM-2 (LRR|0.25|, P-value $<5x10^{-8}$) and CBS (LRR|0.2|, P-value $1x10^{-5}$). The lower statistical significance threshold for CBS is justified by the vastly smaller number of hypothesis tested (number of ADM-2-called CNAs).

Blinding between GP activated cells and TT activated cells was not possible because of the different source of material. However, the array data generation and the bioinformatics analysis were done blindly in one batch, using the same parameters. Tissue-specificity of the expression levels of the genes involved was obtained from BioGPS, 2018 (C. Wu et al., 2016).

5.4.6 Statistics

The difference in the number of probes covering CNAs in T-cells from cell activated by GP vs. those activated by TT was assessed by the unequal-variance, Two-sided T-test, after log-transforming the values to assure normal distribution. We compared the number of probes (number of consecutive probes covered) because the gene-centered positioning of the probes, they better reflect the genes covered by them than the actual length.

5.4.7 Data availability

The CGH data discussed in this publication will be deposited in NCBI's Gene Expression Omnibus (Edgar et al., 2002) to be publicly accessible upon publishing.

The TCR data discussed in this publication will be deposited in NCBI's Sequence Read Archive (Leinonen et al., 2011) to be publicly accessible upon publishing.

5.5 Results

Autoreactive CD_3^+ T- lymphocytes from 10 adult CD patients (n=10, Five females and five Males), were examined (Table. 5. 1). Isolated PBMCs from each patient were proliferated by gluten peptide (GP) and sorted based on CFSE dilution (Fig. 5. 1). Lymphocytes activated by GP and TT showed proliferation ($CD3^+CFSE^{low}$ cells) (Fig. 5.1 c-i, Table. 5.1). On the other hand, cells cultured in the media with no antigen or with media and IL-2 showed no or minimal proliferation (Fig. 5.1 a and b, Table. 5.1).

5.5.1 Positive and negative controls

To investigate the existence of somatic mutations in GP reactive cells, we used the same method used in chapter 3 and 4 in which comparative genomic hybridization (CGH), was used to identify potential CNAs in GP reactive cells ($CD3^+CFSE^{low}$ cells, used as the test sample) and not in germline DNA represented by DNA obtained from clones that had not proliferated to the *in vitro* activation ($CD3^+CFSE^{high}$ cells, used as reference). CGH data of all tested samples revealed the expected copy number change at the T cell receptor regions (α and γ subunits) mapping, respectively, to human chromosomes 14 and 7 due to genomic rearrangements within these regions to create TCR diversity. These loci served as internal naturally occurring positive controls for detecting mosaic PZM in T-cells using our approach (Fig. 5. 2).

Table 5-1 List of patients included in the Celiac study.

Proliferation percentage with or without antigen are shown for each patient. The # CNA column lists the number of CNAs observed in CD3+ T-cell clones that responded to GP activation but not found in the germline DNA (represented by DNA from CD3+ T-cell clones that did not show proliferative response).

Patient ID	Sex F/M	Age	Media%	IL-2%	TT%	GP2/3%	# CNAs	DLRS
GP 1	M	NA	0.2	0	8.7	GP2: 10.9	4	0.2
GP 2	M	49	2.4	3.1	12.6	GP2: 3.4	0	0.19
GP 3	F	19	0.1	0.2	52.7	GP3: 25.4	0	0.18
GP 4	M	56	0.8	0.5	8.5	GP3: 7.8	17	0.22
GP 5	F	NA	0.2	0.3	9.3	GP3: 4.1	0	0.17
GP 6	M	45	2	0	0.3	GP3: 3.3	2	0.19
GP 7	M	56	0.2	2.2	18.4	GP3: 7.8	5	0.17
GP 8	F	34	0.5	1.4	3	GP2: 3.2	662	0.17
GP 9	F	35	0	0.2	54.6	GP2: 4.5	6	0.21
GP10	F	19	3.5	2.8	25.3	GP2: 9.3	1	0.21

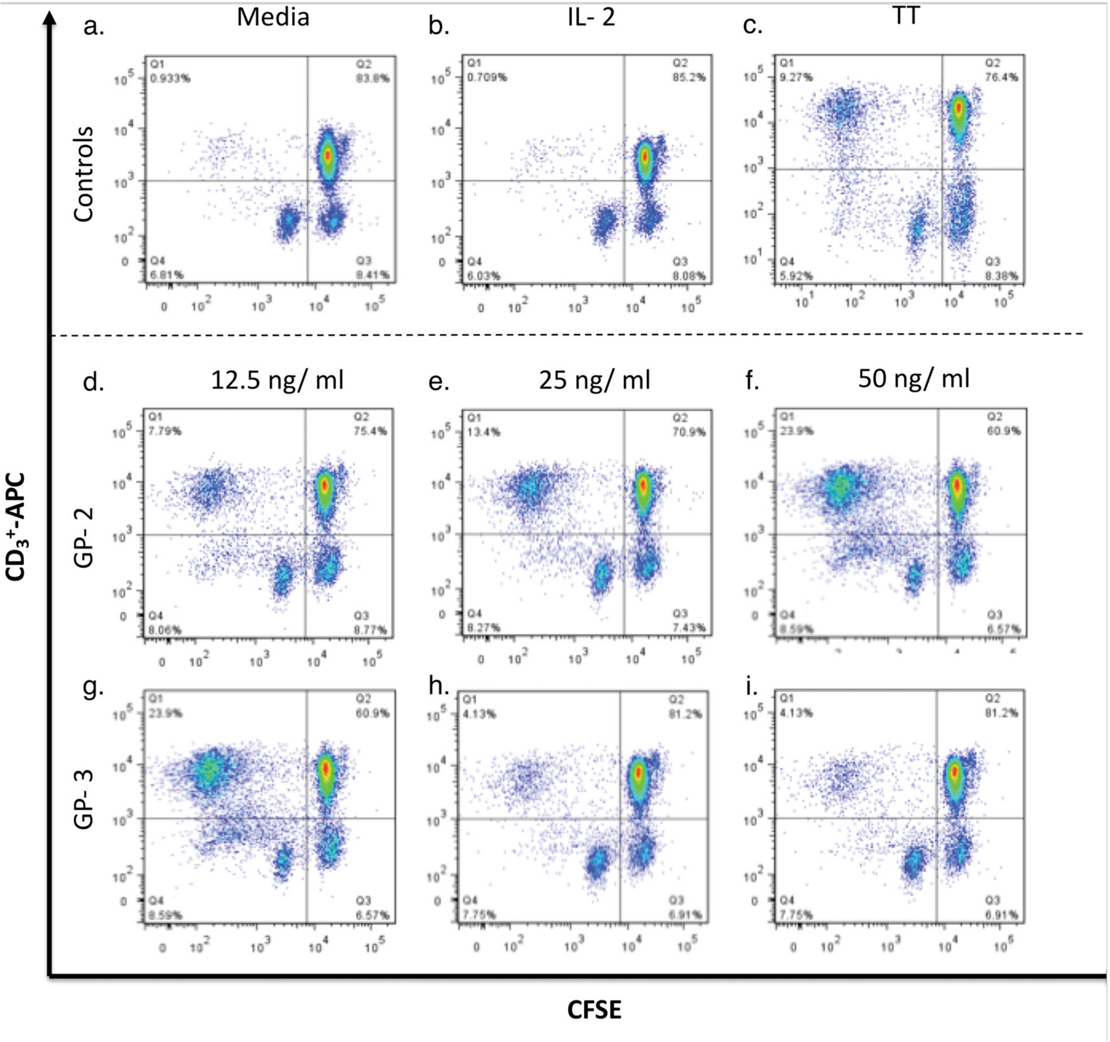

Figure 5-1 Activation of T-cells *ex vivo* with GP as an antigen for 12 days.

Cells were sorted based on the dilution of CFSE as a result of proliferation. Media alone and Il-2 alone (negative controls) and TT (positive control) are also shown.

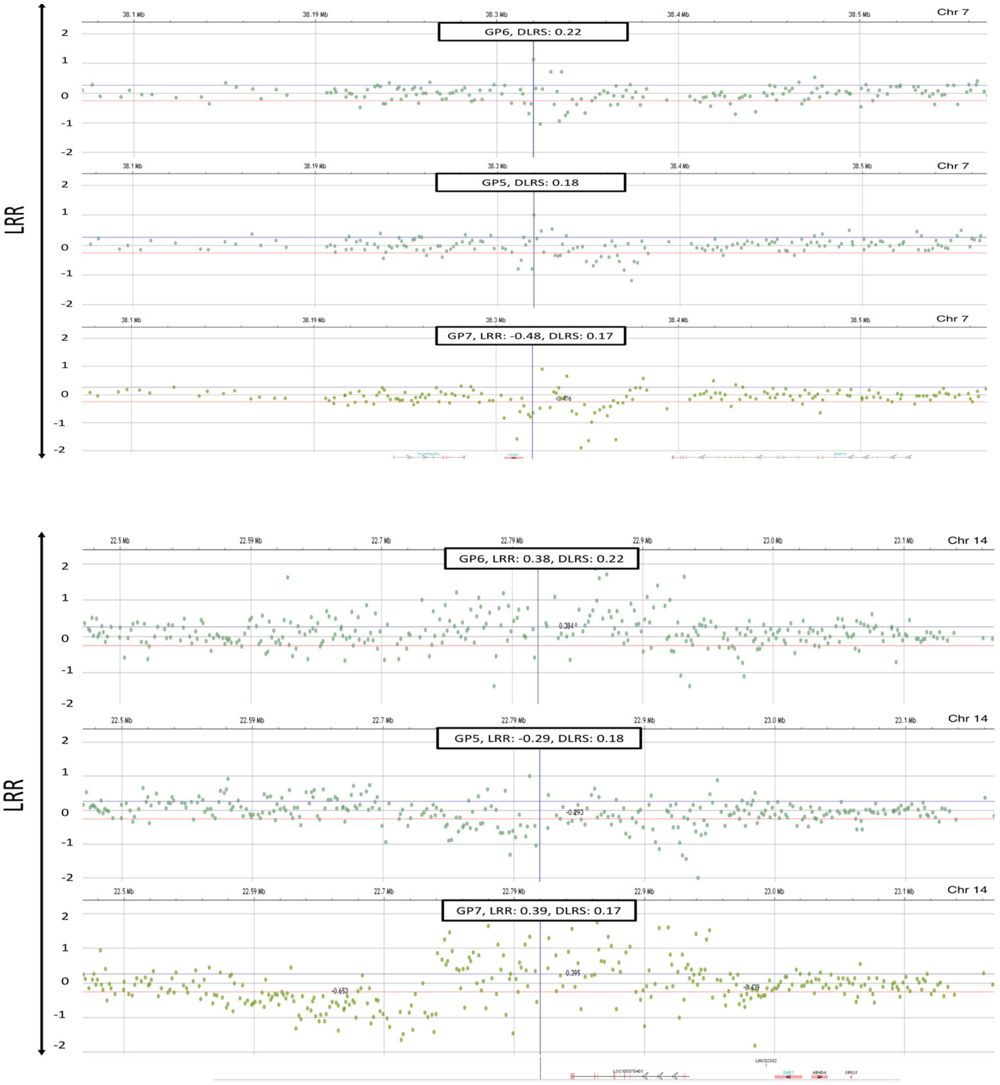

Figure 5-2 CGH array results demonstrating internal positive controls for T-cell CNAs in cells activated by GP.

CGH array results demonstrating positive controls for T-cell CNAs observed in all samples (to illustrate three samples are shown here): Copy-loss and gains (represented by colored lines below the chart) at regions of TCR genomic rearrangements of the gamma chain on chromosome 7 and alpha chain on chromosome 14 (DLRSpread values: GP5: 0.17, GP6: 0.22, GP7: 0.19).

5.5.2 Recurrent post zygotic copy number changes in PG reactive lymphocytes of different patients

A total of 10 gluten-challenged patients with CD were tested (Table 5.1) by the Agilent 1x1M CGH, using DNA from cells that responded to GP activation as the test sample and DNA from responding cells as a reference (representing germline DNA). Seven out of the ten tested patients carry CNAs in their GP reactive cells ranging between one and 17 CNAs and one with a substantial number (662 CNAs) (Supplementary data, Dataset S5. 1). We identified three recurrent CNAs two in two patients and one in three patients (Table 5. 2).

The first independently recurrent CNA in two celiac patients (PG8 and PG9) is at chr8: 61,586,383-61,596,459 (Table 5.2, Fig 5.3a) overlapping with *CHD7*. *CHD7* encodes for a chromatin-remodeling-DNA binding protein with a critical role in early T-cell development (Z. Z. Liu et al., 2018). Interestingly, we have previously identified CNAs affecting *CHD7* in autoreactive lymphocytes of three newly diagnosed patients with T1D (Chapter 4).

The second independently recurrent CNA in two celiac patients (PG8 and PG9) is at chr8: 146,274,776-146,280,020 (Table 5.2, Fig 5.3b) spanning *C8orf33*, an un-studied gene.

The third independently recurrent CNA in three celiac patients (PG1, GP5 and PG9) is at chr22: 47,768,694- 47,777,489 (Table 5.2, Fig 5.3c) spanning *LOC339685* also an un-studied gene.

Table 5-2 List of recurrent CNAs observed among newly diagnosed celiac patients

Sample ID	chr	Locus	Start	End	# Probes	LRR	P-value	Recurrent Genes	DLRS
GP8	8	q12.1	61,586,383	61,596,459	6	0.68	8.20E-11	*CHD7*	0.17
GP9	8	q12.1	61,586,383	61,596,459	6	-1.12	1.01E-25		0.21
GP8	8	q24.3	146,271,091	146,294,098	8	0.59	4.99E-12	*C8orf33*	0.17
GP9	8	q24.3	146,274,776	146,280,020	4	-1.15	1.18E-19		0.21
GP1	22	q13.31	47,768,694	47,777,489	5	-0.71	3.9E-11	*LOC339685*	0.2
GP5	22	q13.31	47,770,715	47,777,489	4	0.77	3.58E-11		0.17
GP9	22	q13.31	47,772,729	47,777,489	3	-1.29	6.21E-17		0.21

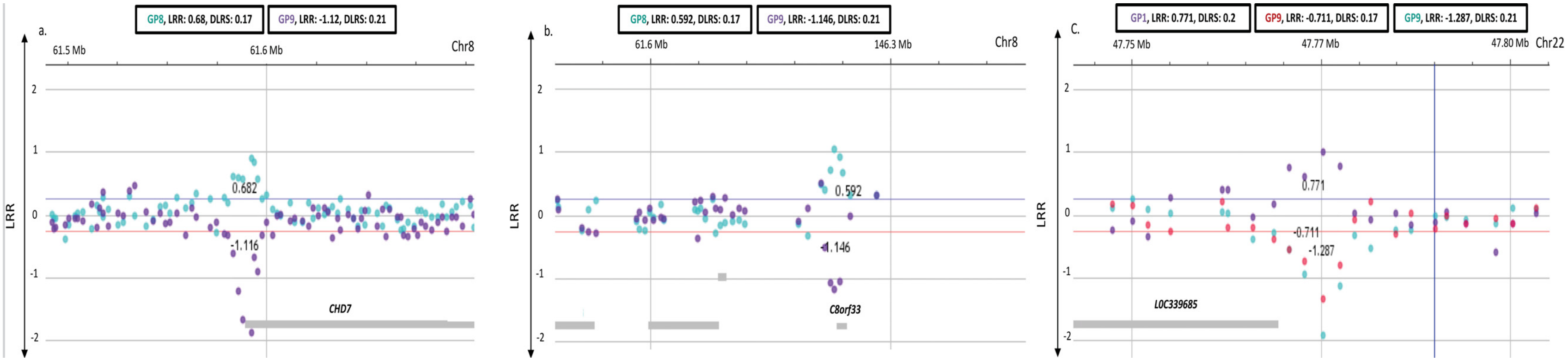

Figure 5-3 Recurrent CNAs observed in autoreactive lymphocytes of newly diagnosed celiac patients

Copy number changes are represented by different colors for different patients. a. A recurrent copy change in GP reactive lymphocytes of two newly diagnosed celiac patients affecting *CHD7*. b. A recurrent copy change recurrent in two different patients affecting *C8orf33,* an unstudied gene. c. A recurrent copy change in three celiac patients affecting the unidentified gene *L0C339685.*

5.5.3 Human T-cells involved in host defense in celiac patients carry copy number changes

As an ordinary host defense control, lymphocytes obtained from seven of the tested newly diagnosed patients with celiac disease were activated *in vitro* by Tetanus toxoid for 12 days (Table 5. 3, Supplementary data, dataset S5. 2). DNA from $CD3^+$ were tested by CGH. No difference was observed in the number of CNAs between cells activated by GP (69.6± 65.84, mean ± SEM, n=10) and TT (29.14± 28.64, n=7) (*t.* test, p=0.63). Moreover, no significant difference in the CNA size of cells activated by GP (6.81± 0.21, n=10) from TT (7.39± 0.32, n=7) (*t.* test, p=0.14) was seen.

5.5.4 Common affected genes in celiac autoreactive lymphocytes and T1D human and mouse autoreactive lymphocytes

In this study, we identified 65 genes that we previously identified to be affected by CNAs in early diabetic NOD mice (Chapter 3, Supplementary data. S5. 3) and 495 genes previously identified to be affected by CNAs in early diagnosed patients with T1D (Chapter 4, Supplementary dataset. S5. 3). Moreover, there are 36 genes that are shared among gluten-challenged patients with celiac, diabetic NOD mice and early diagnosed patients with T1D (Table. 5.4).

One gene with high expression in hematopoietic cells, identified in a CD patient, T1D patient, and a diabetic NOD mouse is *ATMIN.* It encodes a cofactor (ATMIN) to the signaling kinase (ATM) that functions in resolving DNA damage (Schmidt et al., 2014). *ATMIN* is essential for T- cell and B-cell proliferation and activation. Loss of *ATMIN* causes DNA damage that drives spontaneous peripheral T cells high activation, proliferation as well as high secretion of proinflammatory cytokines and chemokines, creating a favorably inflammatory environment (Prochazkova et al., 2015). Moreover, ATMIN plays a role in maintaining the genomic integrity of B-cells and in the suppression of B-cell lymphoma (Loizou et al., 2011).

Another exciting gene is *UBE2E3,* located on chr 2q31.1, that was identified to be affected in a patient newly diagnosed with T1D (chapter 4) and a patient with celiac disease. *UBE2E3* has been associated with celiac disease (Dubois et al., 2010) and encodes one of three members of ubiquitination enzymes (E1, ubiquitin-activating; E2, ubiquitin-conjugating; and E3 ubiquitin-ligases enzymes) that targets abnormal or short-lived proteins to modify them for degradation. *UBE2E3* encodes class E2 of ubiquitination enzymes. The encoded protein is highly conserved in eukaryotes with 100% identity with mouse and rat counterparts. *UBE2E3* is involved in class I MHC mediated antigen processing and presentation. Moreover, besides celiac *UBE2E3* is associated with two other autoimmune diseases Ankylosing Spondylitis and Sjogren syndrome (International Genetics of Ankylosing Spondylitis et al., 2013; Lessard et al., 2013).

Another interesting gene found in two T1D patients and one celiac patient is *HMGB1* located on chr 13q12.3 and encoding a non-histone nuclear protein that is highly expressed in hematopoietic cells. This gene is associated with T1D (Evangelou et al., 2014) and is involved in the cellular process such as inflammation, cell differentiation, and migration of tumor cells (H. Wang et al., 1999).

NFIA is another gene identified in a patient with CD and a patient with T1D that encodes a transcription factor that is associated with celiac disease (Dubois et al., 2010).

NFKB1 located on chr 1p31.3 is exclusively expressed in hematopoietic cells was identified in a patient with T1D and a patient with celiac. The encoded transcription inhibitor that is regulated by some intra- and extra-cellular stimuli such as cytokines and viral products. This gene maps to a locus associated with a number of autoimmune and inflammatory disorders such as inflammatory bowel disease (Jostins et al., 2012), primary biliary cirrhosis (J. Z. Liu et al., 2012), ulcerative colitis (Jostins et al., 2012), and systemic scleroderma (Mayes et al., 2014). Moreover, inhibition of NFkB1 causes inappropriate immune cell development and delayed cell growth (Hayden, West, & Ghosh, 2006).

Table 5-3 List of control samples, lymphocytes from newly diagnosed patients with celiac activated with Tetanus toxoid.

sample ID	Sex F/M	Age	Media%	IL-2%	TT%	# CNAs	DLRS	PI ID*
c. TT1	F	19	0.1	0.2	52.7	1	0.19	GP3
c. TT2	M	56	0.8	0.5	8.5	0	0.16	GP4
c. TT3	F	NA	0.2	0.3	9.3	201	0.18	GP5
c. TT4	M	56	0.2	2.2	18.4	0	0.17	GP7
c. TT5	F	34	0.5	1.4	3	0	0.2	GP8
c. TT6	F	35	0	0.2	54.6	1	0.21	GP9
c. TT7	F	19	3.5	2.8	25.3	1	0.22	GP10

Table 5-4 List of genes carrying somatic CNAs identified in Celiac patients, T1D patients and diabetic NOD mice.

Genes	Expression	Immune/ regulatory related function	Identified in
ATMIN	High in Hematopoietic cells	- Required to suppress T cell activation (Prochazkova et al., 2015). - Play a role in maintaining genomic integrity and suppression of B- cell lymphoma (Loizou et al., 2011).	1 Celiac, 1 T1D, 1 NOD
CNNM3	High in Hematopoietic cells	- Membrane protein functions in magnesium homeostasis. - Disruption in its function promotes oncogenesis (Hardy et al., 2015).	1 Celiac, 1 T1D, 1 NOD
GATAD2A	High and exclusive in Hematopoietic cells	- Encodes for a subunit of NuRD complex (a transcriptional regulator complex). - NuRD complex is involved in tumor growth inhibition, differentiation of cells and regulation of transcription (Smits, Jansen, Poser, Hyman, & Vermeulen, 2013; Torchy, Hamiche, & Klaholz, 2015).	1 Celiac, 2 T1D, 1 NOD
GMFG	High and exclusive in Hematopoietic cells	- Encodes for a component of T- cell pseudopodia. - Regulates migration and adherence of human T- cells (Lippert & Wilkins, 2012).	1 Celiac, 1 T1D, 1 NOD
PTCH1	High in CD4+ and CD8+ cells	- Encodes a receptor for Hedgehog (Hh) signaling. - Exclusive T-cell extrinsic factor essential for T cells development (Uhmann et al., 2011).	1 Celiac, 2 T1D, 1 NOD
SF1	High in Hematopoietic cells	- Encodes a nuclear pre-mRNA splicing factor.	1 Celiac, 1 T1D, 2 NOD mice
UBE2E3	Hematopoietic	- Associated with celiac disease (Dubois et al., 2010) - Encodes for class E2 of ubiquitination enzymes. - Involved in class I MHC mediated antigen processing and presentation.	1 Celiac and 1T1D
HMGB1	High in Hematopoietic cells	- Encoding a non-histone nuclear protein. - Associated with T1D (Evangelou et al., 2014). - Involved in inflammation, cells differentiation and migration of tumor cells (H. Wang et al., 1999).	1 Celiac and 2 T1D
NFkB1	Hematopoietic	- Encode a transcription inhibitor that is regulated by cytokines, viral products. - Inhibition of NFkB1 causes inappropriate immune cells development and delayed cell growth (Hayden et al., 2006). - Associated with celiac disease (Dubois et al., 2010), inflammatory bowel disease (Jostins et al., 2012), primary biliary cirrhosis (J. Z. Liu et al., 2012), ulcerative colitis (Jostins et al., 2012), and systemic scleroderma (Mayes et al., 2014).	1 Celiac and 1 T1D
PHIP	High in Hematopoietic cells	- Can be translated into three proteins through alternate splicing (PHIP1, PHIP, and NDRP). - Binds to Insulin receptor and regulates its transportation into cells. - Associated with the autoimmune disease Sjögren's syndrome (Lessard et al., 2013).	1 Celiac and 2 T1D

5.6 Discussion

Numerous aspects of autoimmune disease triggers are incompletely understood. Until recently, somatic mutations have been overlooked as a cause of non-malignant diseases because unless they happen in a large number of cells, they are not expected to have a clinical phenotypic effect. Autoimmunity could be caused by somatic mutations occurring in auto-reactive immune cells modifying them to escape proliferation checkpoints.

This study presents preliminary results of somatic mutation in CD4+ autoreactive cells of patients newly diagnosed with Celiac disease after undergoing a gluten challenge. Somatic mutations have been found to occur in hematopoietic cells of healthy individuals and their rate increases with age and increase the risk of hematological cancers (Busque et al., 2012; Forsberg et al., 2012; Genovese et al., 2014; Jacobs et al., 2012; Jaiswal et al., 2014; Laurie et al., 2012; Xie et al., 2014). However, most carriers of such mutations do not develop leukemia or lymphoma. In autoimmune diseases, somatic mutations were reported in CD8+ cells of RA patients (Savola et al., 2017). Moreover, we previously identified somatic copy number changes in CD4+ cells of diabetic NOD mice (Chapter 3) and in insulin-reactive CD4+ cells of newly diagnosed patients with T1D (Chapter 4). To extend our investigation to another autoimmune disease, we investigate the existence of copy number somatic mutations in CD4+ gluten-peptide reactive cells, obtained from celiac patients after a gluten challenge.

We identified somatic CNAs in immune and proliferation genes in CD4+ T cells of 10 celiac patients, including one patient with a large number of CNAs (662 CNAs). Moreover, we identified several recurrent affected genes among celiac patients. Some of these recurrent genes were previously identified in CD4+ cells of T1D patients (Chapter 4).

Notably, somatic mutations were also detected in *Tetanus Toxoid* reactive cells from the same patients, and unlike our finding in T1D NOD mice and T1D patients (chapters 3 and 4) the size of CNAs are not significantly different from that in autoreactive cells. Identifying CNAs in *Tetanus Toxoid* reactive cells is not unexpected as somatic mutations occur in hematopoietic cells of healthy individuals and should not have an adverse effect since these cells do not target self-antigens. Nonetheless, their occurrence in autoreactive cells affecting genes with roles in proliferation and immune function allowing them to escape regulatory checkpoints might be an autoimmunity trigger.

In this study, we identified genes that we previously found to be affected somatic mutations in both diabetic NOD mice and human T1D such as *ATMIN* and *PTCH1* with high expression in lymphocytes and have a developmental or a proliferative function in T-cells. Identifying these recurrent genes in autoreactive lymphocytes of patients with different autoimmune diseases points to a potential contribution of the somatic mutations in the pathogenesis of autoimmunity.

To our knowledge, this is the first report demonstrating the occurrence of somatic mutations in autoreactive CD4+ T- cells in celiac patients. Further studies needed to understand the effect of these mutations on the protein function and demonstrate its role in the pathogenesis of celiac disease. Moreover, expanding the investigation to include identifying CNAs CD8+ T-cells as there is an increasing body of evidence supporting the involvement of both types T-cells in the pathogenesis of celiac disease (Han et al., 2013).

Furthermore, extending the investigation to include point mutations will further support the association of the affected genes in the lymphocytes with the pathogenicity of the disease.

Our study provides further evidence for the putative mechanistic overlap between autoimmunity and cancer. We show the occurrence of somatic mutations in expanded CD4+ T cells, in which some might contribute significantly to the pathogenicity of the disease as driver mutations.

It is important to note two properties of these mutations that make them particularly attractive in the context of precision diagnostics and therapeutics. First, not being subject to purifying selection, they can have much stronger biological effects than germline ones. Second, since these mutations are limited to the pathogenic lymphocytes, these cells can be targeted for treatment without interfering with the fitness of other lymphocytes or other cells in general.

5.7 Acknowledgments

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CHAPTER SIX Discussion and final conclusions

6.1 Towards a mechanistic model for autoimmune diseases

The studies presented in this thesis describes a new phenomenon of memory-cell exclusive somatic copy-number mutation in patients with autoimmune diseases (T1D and CD). Our findings support the hypothesis of somatic mutations as a common etiology factor in the pathogenesis of autoimmune diseases similar to lymphoid cancers. Somatic mutations occur commonly, but when restricted to a single cell and its progeny it is unlikely to cause a disease unless it results in an exponential clonal expansion.

Lymphocytes; due to their clonal expansion and high proliferation rates; have a high mutation rate. These mutations can cause dysregulation resulting in lymphatic cancer or as I propose in my studies here could result in abnormal reactivity to self-antigens, by allowing their escape from natural tolerance process.

Natural tolerance consists of multiple layers that are difficult to bypass with a large number of molecular contributors involved at each checkpoint. The failure of the tolerance is likely to be a multistep process causing a latent period preceding the development of autoimmunity (Goodnow, 2007). The proposed model here starts with individuals carrying a predisposing genetic germline background for autoimmunity that gets triggered by an environmental factor leading to the initial proliferation of the autoreactive lymphocytes that will be inhibited by the next tolerance checkpoint. Therefore, the majority of individuals with a predisposing genetic background to autoimmunity and sharing the same or similar environment will not develop autoimmunity as shown by twin studies (Redondo et al., 2008). However, if one of these autoreactive lymphocyte clones develops PZM allowing its escape from the next self-tolerance checkpoint and its further proliferation, this will allow further proliferation that could potentially increase the chance of further occurrence of somatic mutations enabling them to ultimately bypass all the checkpoints and finally attack the self-antigen.

6.2 Overlaps between autoimmunity and cancer

The fact that PZMs frequently occur in hematopoietic lineages of healthy individuals, without ever causing lymphoid malignancy, supports the plausibility of this hypothesis (Busque et al., 2012; Forsberg et al., 2012; Genovese et al., 2014; Jacobs et al., 2012; Laurie et al., 2012; Xie et al., 2014; Young et al., 2016). The mutation rate in lymphoid precursors has been estimated to be about 10^{-6} per cell division, making replication errors likely to accumulate (Araten et al., 2005; Araten et al., 2013). The mosaicism in lymphocytes is more detectable than other cell types due to their proliferative and survival advantage compared to other cell-types where the level of mosaicism is usually too low to be detectable or to cause a disease. A well-established exception is cancer, in which proliferative control is inactivated following a PZM in a single cell. As the progeny of this cell proliferates, a second mitotic hit occurs increasing the proliferation rate and therefore, the occurrence of more subsequent PZMs (Watson et al., 2013). Nonetheless, not all individuals with PZMs will not develop hematological cancers, leaving a broad gray zone for the possibility of non-malignant diseases involving immune cells.

In this study, I have presented results supporting the parallel between cancer and autoimmunity. In autoimmunity, a disease is driven by autoreactive clones (estimated to be up to 50% of all TCR V(D) rearrangements) (Ignatowicz et al., 1996), (vs. a single cell in cancer) that undergoes logarithmic expansion after escape proliferation checkpoints to reach disease-causing numbers. If a PZM in these autoreactive cell clones triggered their expansion, their very low mosaicism level would make their detection challenging in whole-blood, but they will still be in high enough numbers at the site of inflammation to cause a disease. In order to study them, these antigen-specific blood clones must be isolated.

Testing this hypothesis required obtaining T-cells that are highly enriched in autoreactive lymphocytes both in mice and human (chapter 3 and 4). In NOD mice (Chapter 3), we isolated the lymphocytes by dissecting the pancreatic lymph-nodes from newly diabetic mice. For the human studies (T1D; Chapter 4 and CD; Chapter 5), since we do not have access to the inflammation sites, we developed an *in vitro* approach to obtain the autoreactive cells from peripheral blood. Here, T-cells from PBMCs of newly diagnosed T1D or gluten-challenged CD patients were activated by the main antigen of the disease for two weeks in culture, and the proliferated cells were sorted via dye dilution.

In the three studies presented here, I have identified recurrent copy-number mutations affecting genes highly expressed in T-cells and with a proliferative or an immune-related function. The causal role of these mutations is supported by their non-random recurrence in different diabetic mice or patients of T1D or CD. Interestingly, I've also identified such recurrent genes with a proliferative and immune function in patients of the two different autoimmune diseases: T1D and CD such as (*UBE2E3* and *NFIA)*. It would be of interest to evaluate the contribution of these genes in the causality in autoimmunity. In the well-established paradigm of cancer, after numerous rounds of cell division and mitotic errors, cancer cell lineages lose controlled function of genes essential for genome stability (due to driver mutations) resulting in a large number of random aberrations and point mutations (passenger mutations). Unlike passenger mutations, drivers reoccur in the same genes in different tumors (Pon & Marra, 2015). The recurrent genes identified in our studies resemble driver mutations in cancer. Although some might have occurred *in vitro* during culture, it is doubtful that such mutations will result in mosaicism that is high enough to be identified.

Identifying CNAs in lymphocytes responding to pathogens (TT reactive cells) is not unexpected since these somatic mutations are normally found in healthy individuals. We expected these mutations to have an adverse effect if they occur in lymphocytes with self-reactive TCRs altering genes involved in immune or proliferation functions.

The occurrence of the “driver” PZMs only in disease-causing cells, allows them to escape natural selection for fitness of the whole organism. Therefore, they are expected to have more drastic functional effects than variants that have survived evolution and are inherited in the germline. In the cancer paradigm, the identification of such driver mutations has enabled therapeutic advances by identifying drug targets essential to disease causation. One example is Gleevec, a drug that selectively targets inhibitor of the BCR-ABL tyrosine kinase, the pathogenic fusion transcript (translocation product) expressed only in abnormal cells causing chronic myeloid leukemia (CML) (Hernandez-Boluda & Cervantes, 2002). If we prove that the observed CNAs in autoreactive lymphocytes have a causal role, they could be ideal and better therapeutic targets compared to germline variants in an individual-personalized way.

6.3 Future directions

My data support a potential role of somatic mutations in autoreactive lymphocytes in the pathogenesis of autoimmunity in two different diseases T1D and Celiac disease.

Nonetheless, further investigation is necessary to fully understand the role of these mutations in autoimmunity. Some of the limitations of my study are: I have only focused on the identification of CNAs (gain and loss); CNAs observed in human T1D, and CD patients are yet to be confirmed by an independent method. Finally, the function of some of the recurrent genes within different patients or between T1D and CD is still uninvestigated; also, the underlying mechanisms that resulting in these somatic mutations and how the affected recurrent genes result in autoimmunity requires exploration. These outstanding questions could be attended by the experiments proposed below.

6.3.1 Confirming the CNAs found in human T1D and Celiac lymphocytes by an independent method

Genes affected by recurrent "driver" CNAs selected for having a cellular localization in immune cells and/or having an immune function will be confirmed by MLPA or Digital PCR (dPCR) on unamplified DNA. MLPA is a multiplex PCR method used as a gold standard for CNV diagnostics and allows identifying abnormal copy-numbers of up to 50 unique genomic sequences simultaneously. Another advantage MLPA has over other techniques (such as Southern blot analysis and FISH analysis) is its ability to identify very small aberrations (of 50-70 nucleotides) (Schouten et al., 2002).

Digital PCR (dPCR) is a quantitative PCR technique in which the sample is segregated into a high number of wells prior to the parallel amplification step. Some of these reaction wells contain the target molecule (positive) while others do not (negative). During amplification, dye-labeled probes are used to identify sequence-specific targets, and the fraction of positive wells is used to quantify an absolute count of the target copy-number in the sample (Huggett & Whale, 2013).

6.3.2 Map the breakpoints in CNAs involving “driver” genes

CGH results are not precise enough to interpret the functional effects of a CNA. For example, the effect of copy-number duplications depends on whether the entire gene and its regulatory sequences are within the affected CNA segment, in which it will cause overexpression of the gene. However, in the case of inverted duplications, or when both breakpoints are intragenic, the structure of the gene and its function are most likely to be altered, and its function will be lost. Since the resolution of 1x1M CGH array is limited to 2.1kb (median probe spacing), finer mapping of the breakpoints is required to predict the functional consequences of the CNA. To pinpoint the breakpoints, I will use targeted capture followed by next-generation sequencing. This approach was previously described by Talkowski et al., (Talkowski et al., 2011). I will design a SureSelect Agilent custom “bait” library of oligonucleotides covering the sequence of the CGH estimated breakpoint regions.

6.3.3 Determine the chronology of the CNAs occurrence

To understand the role of the mosaic CNAs, and to further support their causal role, it is crucial to determine when the altered clones were first created. I will test T1D Ab+ subjects at the time of first positivity; at six months; and at a year later. For those who develop T1D, will be tested at six months and at a year after clinical T1D and finally at five years point for both groups. Although, at the five years point, the number of T-cells will be more likely much smaller, our protocol works successfully with only 10ng of genomic DNA. This experiment will allow identifying driver mutations that undergo the first copy-number change, highlighting their causal role. Moreover, it will allow determining the chronology of the altered clones’ occurrence. Understanding the sequence of events in a patient will allow for a more meaningfully guided personalized medical intervention. The Type 1 Diabetes TrialNet; an international collaboration that tests first-degree relatives of cases for antibodies; has a large number of frozen PBMC samples, and my supervisor has obtained approval in principle to use them, on condition of obtaining peer-reviewed funding for doing them (CIHR and NIH applications pending).

6.3.4 Exploring for somatic point mutations in lymphocytes of patients with T1D and Celiac disease

In the studies presented in this thesis, I only focused on large duplications and deletions. However, other forms of copy-number changes such as inversions, translocations, and point mutations, would be essential to detect. In the cancer paradigm, carrying both somatic point mutation and a somatic CNA leading to an inactivation of the gene function is regarded as strong evidence for pathogenicity involvement. To extend our investigation to include other forms of mutations, I will use whole exome sequencing (WES). Sequencing the libraries will be on the Illumina HiSeq at three samples per lane and to assure high variant-calling sensitivity, coverage will be of 100x, with ~95% of exons covered at ≥20x.

6.3.5 Increase the number of Celiac patients and extend the investigation to other autoimmune diseases

Our data in T1D and celiac suggest that somatic mutations occur in causal cells of autoimmune diseases. However, our celiac results are preliminary. To continue our investigation in the celiac study, I will recruit more patients to undergo the gluten challenge to test the hypothesis of somatic mutations in their autoreactive lymphocytes using the same protocol discussed in chapter 5. I will also test their clonality by TCR sequencing as described in our T1D human study (chapter 4). I am also aiming to extend our investigation to other autoimmune diseases.

6.3.6 Functional studies

In this work, I identified several genes affected by CNAs. Functional studies on recurrent genes are essential to understand the mechanisms by which the observed CNAs could bridge the genetic predisposition with the autoimmunity. To test the functional effect of these mutations, I will use CRISPR–Cas9 genome-targeting system to engineer the copy-number changes in T-lymphocytes and then test their response to autoantigens. In a recent study, this system was successfully used in a rapid and efficient insertion of DNA sequences in primary human T-cells genomes without the need for viral vectors, and without interfering with the cells viability and function (Roth et al., 2018).

6.4 Conclusion summary

The original research studies presented in this dissertation focused on exploring the potential role of somatic mutations in autoreactive lymphocyte clones in the pathogenicity of autoimmunity. I investigated this in two autoimmune diseases (T1D: NOD and patients, and CD: patients). I developed methods to test the hypothesis for copy number aberrations. Also, I identified recurrent genes with proliferation and/or immune function among diabetic NOD mice and patients. Interestingly, I also found overlapping genes between the two autoimmune disease (T1D and CD). Our data backs a causal role for PZMs in T-cells in the pathogenicity of autoimmunity and challenges the classical notions of autoimmune diseases and open conceptual avenues toward individualized prevention and therapeutics.

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APPENDICES

APPENDIX A: Supplementary information for chapter 3- Clonal copy-number mosaicism in autoreactive T-lymphocytes in diabetic NOD mice

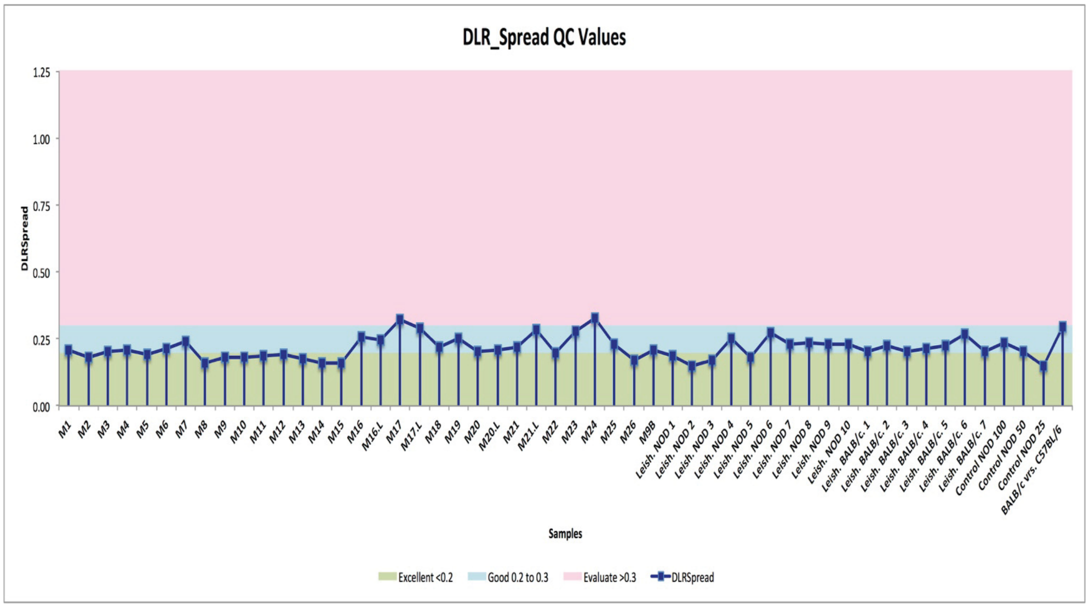

Figure S3. 1 Derivative log ratio spread (DLRS)-Quality control values for tested samples using Comparative Genomic Hybridization analysis (CGH) on the mouse 4x180K Agilent array. DLRSpead values are within Agilent technologies specifications.

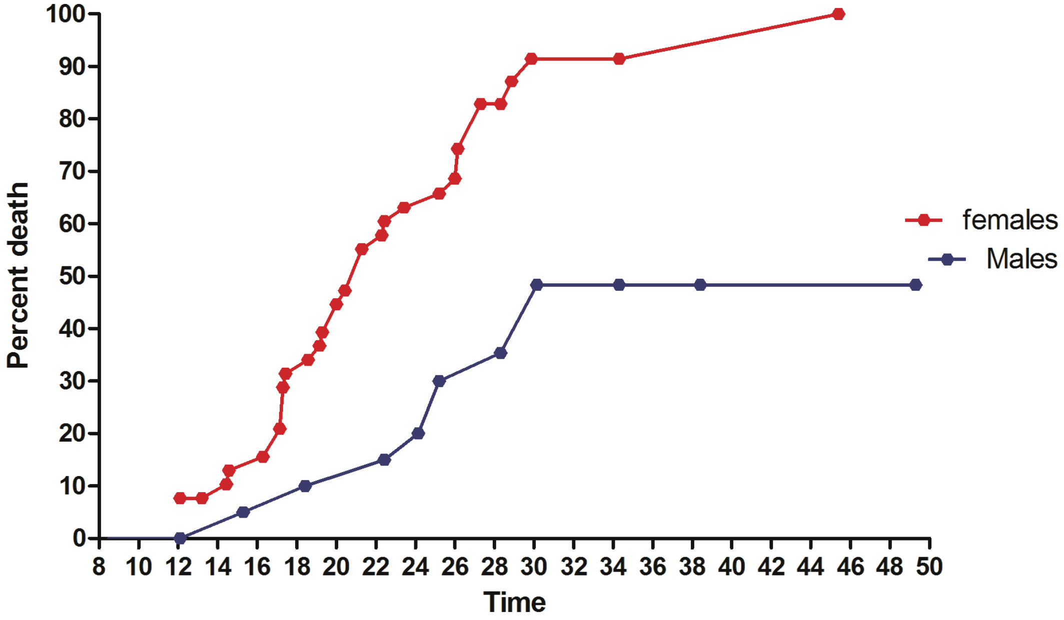

Figure S3. 2 Survival curve of NOD mice showing the percentage of deaths per week for Female and Male mice.

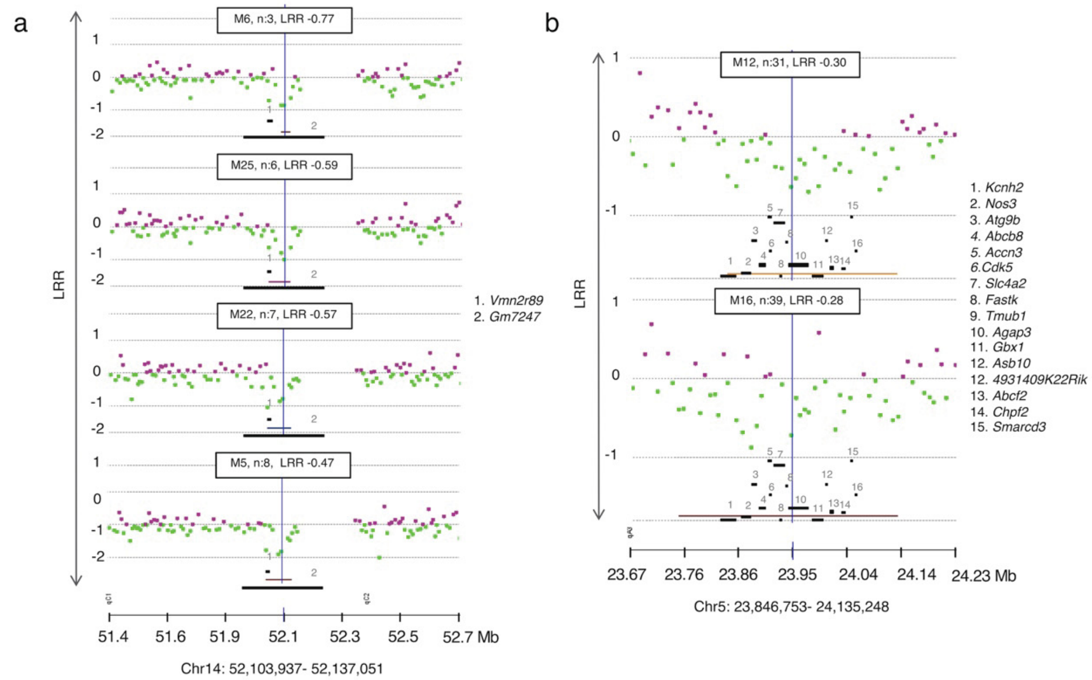

Figure S3. 3 Additional interesting recurrent CNAs in two mice or more.

a. CNA is in chr14 (chr14: 52,061,318-52,145,237) in the memory cells of M5 and M22 is a copy loss that spans *Gm7247* and *Vmn2r89.* These two genes are also spanned by copy losses CNAs in mice M6 and M25 called by ADM2, however, missed the CBS cut off. **b.** An interesting recurrent CNA is a copy loss in chromosome 5 (chr5: 23,846,753- 24,135,248) found independently in two different diabetic mice M16 and M12 in which both were called by ADM2, however, missed the CBS cut off for one of the mice (M16).

Table. S3. 1 The average of all probes of mice M23 and M25 in each chromosome clearly shows the sex differences between them. Fluorescent signals for test and reference intensity is in normalized arbitrary units.

M23			M25		
Chr	**Test**	**Reference**	**Chr**	**Test**	**Reference**
19	**1,363**	**1,358**	**19**	**1,392**	**1,405**
X	**1,342**	**1,339**	**X**	**760**	**742**
Y	**128**	**133**	**Y**	**691**	**723**

Table. S3. 2 Primer and Probes used for MLPA.

LPO: Left probe oligonucleotide; LHS: Left hybridizing sequence; RPO: Right hybridizing sequence, RPO: Right Probe oligonucleotide. Len: number of nucleotides.

Dataset S3. 1 List of known and statistically significant CNVs called by both ADM-2 and CBS algorithms in three control samples prepared by mixing NOD tail-clip germline DNA (100%, 50% and 25%) with C57BJ6/J DNA as test samples and C57BL6/J tail-clip germline DNA (100%) as reference.

(ADM2: mean LRR |0.25| and P-value <2.90 x 10^{-07} and CBS: mean LRR |0.25| and P-value <1 x 10^{-04}) (At the end of this dissertation).

Dataset S3. 2 List of CNAs in memory CD4+ lymphocytes of PLN in 19 tested diabetic mice with normal sorting profile (ADM2: mean LRR |0.25| and P-value <2.90 x 10-07 and CBS: mean LRR |0.25| and P-value <1 x 10-04).

Since we have no prior information in which to base power calculations the number of mice tested was determined by available funds (At the end of this dissertation).

Dataset S3. 3 List of CNAs in the CD4+ lymphocytes from PNL of the six animals in which all cells were memory, CD62Lneg, CD44+ (M20-M25). M23 and M25 had the largest number of CNAs indicating an unstable genome.

Dataset S3. 4 List of CNAs in memory lymphocytes from the popliteal lymph nodes of NOD and BALB/c mice infected with *L. major*.

Dataset S3. 5 The percentage of the top three CD4+ T-cell clones per mouse in lymphocytes from PLNs of 10 NOD mice. Clones were determined on the basis of the highly random, non-template aa sequence in the CDR3 region. The sequence in red is shared by all mice.

(Table S3.2 and datasets S3.1- S3.5 are at the end of the dissertation)

APPENDIX B: Supplementary information for chapter 4- Somatic mutations in clonally expanded memory T lymphocytes newly diagnosed patients with Type 1 diabetes

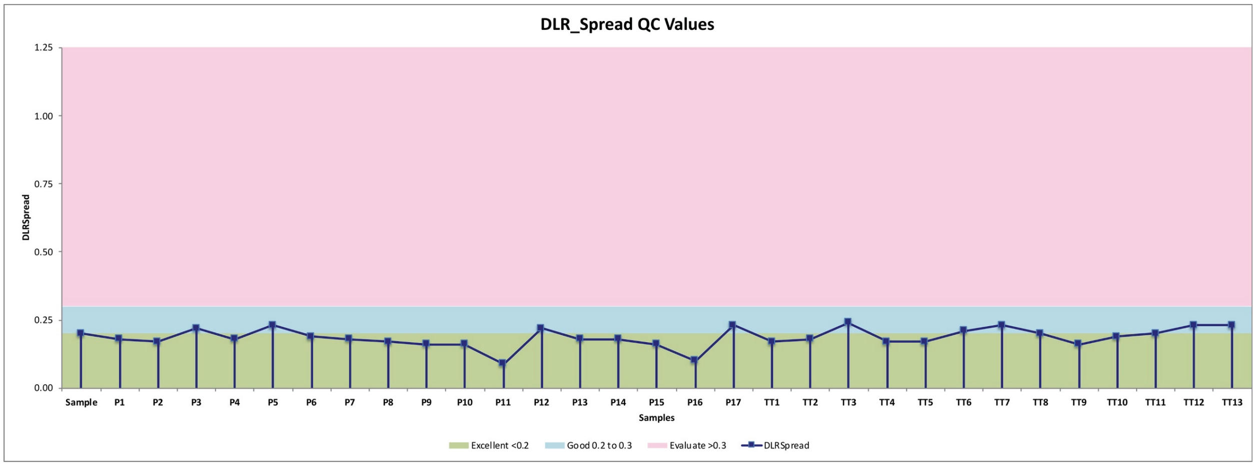

Figure S4. 1 Derivative log ratio spread (DLRS)-Quality control values for tested samples using Comparative Genomic Hybridization analysis (CGH) on the human 1x1M Agilent array. DLRSpead values are within Agilent technologies specifications.

Table. S4. 1 Proliferation percentage in different in vitro conditions are shown for each patient with growth hormone deficiency.

Patient	Media control	IL-2 control	TT	Rh-PI
CTL001	0.2 %	9.3 %	/	11.6 %
CTL002	0.2 %	2.6 %	/	3.9 %
CTL003	5.3 %	8.1 %	20.4 %	7.4 %
CTL004	5.7 %	2.8 %	15.5 %	7.0 %
CTL005	0 %	0 %	0.3 %	0 %
CTL006	0.1 %	0.1 %	0.2 %	2.2 %
CTL007	0 %	0 %	/	0 %
CTL008	0 %	0 %	0 %	0.1 %

Table. S4. 2 List of primers used in the study.

PTPN22 (rs2476601)-F	5’ – CTCAAGGCTCACACATCAG – 3’
PTPN22 (rs2476601)-R	5’ – GAATATAAGAATTTCCTTTGGA – 3’
INS–23 A/T (rs689)-F	5’ – ATCAGAAGAGGCCATCAAGC – 3’
INS–23 A/T (rs689)-R	5’ – GCGGGTCTTGGGTGTGTAG – 3’
TRA-AS-6	TGG TAC ACG GCA GGG TCA GGG TTC T
TRB-AS-5	GTG TGG CCT TTT GGG TGT GGG AGA T

Dataset S4. 1 List of CNAs in rh-PI- reactive lymphocytes of 17 tested diabetic patients (ADM-2 (LRR|0.25|, P- value ≤1x10-10) and CBS (LRR|0.25|, P-value ≤5 x 10-08)). Since we have no prior information in which to base power calculations the number of patients tested was determined by available funds.

Dataset S4. 2 List of CNAs in TT- reactive lymphocytes of 14 tested diabetic patients (ADM-2 (LRR|0.25|, P- value ≤1x10-10) and CBS (LRR|0.25|, P-value ≤5 x 10-08)).

Dataset S4. 3 List of common affected genes by CNAs in Human rh-PI reactive lymphocytes from newly diagnosed T1D patients and memory cells from PLNs of newly diabetic NOD mice (Chapter 3).

(Datasets S4. 1- S4. 3 are at the end of the dissertation)

APPENDIX C: Supplementary information for chapter 5- Somatic mutations in clonally expanded memory T lymphocytes newly diagnosed patients with Celiac disease

Table S5. 1 Gluten peptides tested for in vivo expansion of autoreactive lymphocytes in newly diagnosed patients with celiac disease.

Pep 1	PQQPQQPQQPFPQPEQPFPWQP
Pep 1	PQQPQQPQQPFPQPEQPFPWQP
Pep 2	QPEQPFPQPEQPFPWQP
Pep 3	QPFPQPEQPFPW
Pep 4	QLQPFPQPELPYPQPQ
Pep 5	GQQPFPQPEQPFPLQG
Pep 6	GQQPFPQPEQPTPYQG
Pep 7	GQQPFPQPEQPFPQSG

Dataset S5. 1 List of CNAs in rh-PI- reactive lymphocytes of 10 tested CD patients (ADM-2 (LRR|0.25|, P- value ≤1x10-10) and CBS (LRR|0.25|, P-value ≤5 x 10-08)). Since we have no prior information in which to base power calculations the number of patients tested was determined by availability of funds.

Dataset S5. 2 List of CNAs in TT- reactive lymphocytes of seven tested CD patients (ADM-2 (LRR|0.25|, P- value ≤1x10-10) and CBS (LRR|0.25|, P-value ≤5 x 10-08)).

Dataset S5. 3 List of common affected genes by CNAs in Human CD patients and memory cells from PLNs of newly diabetic NOD mice (Chapter 3) and rh-PI reactive lymphocytes from newly diagnosed T1D patients (Chapter 4).

(Datasets S5. 1- S5. 3 are at the end of the dissertation)

Table S3. 2. Primer and Probes used for MLPA, LPO: Left probe oligonucleotide; LHS: Left hybridizing sequence; RPO: Right hybridizing sequence, RPO: Right Probe oligonucleotide. Len: number of nucleotides

Gene	LPO	LHS	RHS	RPO	LHS len	RHS len	Hs len	Total len
IFNG	GGGTTCCCTAAGGGTTGGA	TCCAGCCTCAGGAAGCGGAAAAGGAGTCG	CTGCTGATTCGGGGTGGGGAAGAGATTGT	TCTAGATTGGATCTTGCTGGCAC	29	29	58	100
CanX	GGGTTCCCTAAGGGTTGGA	GTCCTAGGAGAGGGCCTGGTGTACCTTAG	GTGGGAGCTCAAAACCTCAAGATGTCACC	TCTAGATTGGATCTTGCTGGCAC	29	29	58	100
Ascc3	GGGTTCCCTAAGGGTTGGA	TGACGGACTCTGTTGGTTACATGGAGACA	AAGGCTATCAGACAGACGTTTGGTCCCTT	TCTAGATTGGATCTTGCTGGCAC	29	29	58	100
Sod3	GGGTTCCCTAAGGGTTGGA	GATGCTGCCGAGATGCATGCAATCTGCAGGG	TACAACCATCAGCCACGCTGCCACCGGATCA	TCTAGATTGGATCTTGCTGGCAC	31	31	62	104
Sepsecs	GGGTTCCCTAAGGGTTGGA	CTGTGCCTCTTGGGAACGTGCAAACTGTGAG	TGGCCATACTTTTCGAGGCTTCATGTCCCAT	TCTAGATTGGATCTTGCTGGCAC	31	31	62	104
Fancb (ChrX)	GGGTTCCCTAAGGGTTGGA	GGAGAACAGATAATAGGGCCATGACATTTTTAGGGAGAAGG	GCCAAAATCCGTCAGTCCAAGCGCAAAGTTCAGAGAGAAAG	TCTAGATTGGATCTTGCTGGCAC	41	41	82	124

Dataset S3. 1. List of known and statistically significant CNVs called by both ADM-2 and CBS algorithms in three control samples prepared by mixing NOD tail-clip germline DNA (100%, 50% and 25%) with C57BJ6/J DNA as test samples and C57BL6/J tail-clip germline DNA (100%) as reference (ADM2: mean LRR l0.25l and P-value <2.90 x 10-07 and CBS: mean LRR l0.25l and P-value <1 x 10-04).

NO.	ID	chrom	chrom	chr region	loc.start	loc.end	num.mark	Amplification	Deletions	mean LRR	pval
252741110768_1_2	100% NOD	chr1	1	qD	90115633	90193738	10	0	-1.031619	-1.031619	6.05E-43
252741110768_1_3	50% NOD+50% Black6	chr1	1	qD	90115633	90193738	10	0	-0.556285	-0.556285	4.46E-17
252741110768_1_3	50% NOD+50% Black6	chr1	1	qE1.1	101783952	101807547	4	0	-0.772888	-0.772888	1.30E-12
252741110768_1_3	50% NOD+50% Black6	chr1	1	qE2.3	118535504	118606734	3	0	-0.926571	-0.926571	3.61E-13
252741110768_1_2	100% NOD	chr1	1	qF	141582304	141678786	9	0	-2.596859	-2.596859	1.19E-125
252741110768_1_3	50% NOD+50% Black6	chr1	1	qF	141582304	141678786	9	0	-0.973764	-0.973764	1.61E-38
252741110768_1_2	100% NOD	chr1	1	qH3	173457380	173490445	3	2.238914	0	2.238914	3.37E-40
252741110768_1_3	50% NOD+50% Black6	chr1	1	qH3	173457380	173490445	3	1.710151	0	1.710151	1.93E-30
252741110768_1_4	25% NOD+75% Black6	chr1	1	qH3	173457380	173490445	3	1.144675	0	1.144675	5.68E-18
252741110768_1_2	100% NOD	chr2	2	qG3	148796924	148870304	4	0	-2.75037	-2.75037	3.55E-48
252741110768_1_3	50% NOD+50% Black6	chr2	2	qG3	148796924	148870304	4	0	-0.82428	-0.82428	1.10E-12
252741110768_1_2	100% NOD	chr3	3	qA3	24180913	24239424	3	0	-4.029461	-4.029461	5.89E-57
252741110768_1_3	50% NOD+50% Black6	chr3	3	qA3	24180913	24239424	3	0	-1.237438	-1.237438	2.86E-20
252741110768_1_2	100% NOD	chr3	3	qC	47498870	49545797	71	0	-0.285795	-0.285795	5.04E-24
252741110768_1_2	100% NOD	chr3	3	qG1	118759992	118812959	6	3.701974	0	3.701974	1.58E-104
252741110768_1_3	50% NOD+50% Black6	chr3	3	qG1	118759992	118812959	6	3.601638	0	3.601638	9.75E-99
252741110768_1_4	25% NOD+75% Black6	chr3	3	qG1	118759992	118812959	6	3.166193	0	3.166193	1.14E-86
252741110768_1_2	100% NOD	chr4	4	qD1	111726014	113574763	126	0	-2.170005	-2.170005	0
252741110768_1_3	50% NOD+50% Black6	chr4	4	qD1	111726014	113676203	131	0	-0.826859	-0.826859	0
252741110768_1_4	25% NOD+75% Black6	chr4	4	qD1	111726014	113658273	130	0	-0.397682	-0.397682	9.85E-104
252741110768_1_2	100% NOD	chr4	4	qD1	111742887	111771968	4	0	-3.434703	-3.434703	3.95E-11
252741110768_1_2	100% NOD	chr4	4	qD1	112510205	112564300	6	0	-3.857255	-3.857255	9.46E-23
252741110768_1_2	100% NOD	chr4	4	qE1 - qE2	144993951	147187553	27	0.889329	0	0.889329	3.01E-81
252741110768_1_3	50% NOD+50% Black6	chr4	4	qE1 - qE2	144993951	147187553	27	0.575092	0	0.575092	1.90E-43
252741110768_1_4	25% NOD+75% Black6	chr4	4	qE1 - qE2	144993951	147187553	27	0.404852	0	0.404852	6.69E-24
252741110768_1_2	100% NOD	chr5	5	qB3	46653879	46747143	3	0	-4.157685	-4.157685	1.36E-55
252741110768_1_3	50% NOD+50% Black6	chr5	5	qB3	46653879	46747143	3	0	-0.984052	-0.984052	2.60E-14
252741110768_1_2	100% NOD	chr6	6	qC1	68059687	69589968	56	0	-0.706377	-0.706377	7.52E-96
252741110768_1_3	50% NOD+50% Black6	chr6	6	qC1	68059687	70647130	107	0	-0.263901	-0.263901	6.07E-38
252741110768_1_2	100% NOD	chr6	6	qC1	69297101	69397879	3	0.455852	0	0.455852	1.07E-17
252741110768_1_2	100% NOD	chr6	6	qC1	70401733	70417677	3	0	-0.977632	-0.977632	2.20E-12
252741110768_1_2	100% NOD	chr6	6	qC1	70457367	70647130	11	0	-2.091203	-2.091203	2.17E-107
252741110768_1_2	100% NOD	chr6	6	qC1	70457367	70482914	3	0	-4.190757	-4.190757	2.32E-16
252741110768_1_3	50% NOD+50% Black6	chr6	6	qC1	70457367	70647130	11	0	-0.805908	-0.805908	2.23E-16
252741110768_1_2	100% NOD	chr6	6	qC1	70556115	70624032	3	0	-3.530168	-3.530168	1.47E-10
252741110768_1_2	100% NOD	chr6	6	qF3	128726561	128763313	4	0	-1.540001	-1.540001	5.54E-28
252741110768_1_3	50% NOD+50% Black6	chr6	6	qF3	128726561	128763313	4	0	-0.693035	-0.693035	8.32E-11
252741110768_1_2	100% NOD	chr6	6	qF3	130204536	130317661	6	1.028672	0	1.028672	1.09E-29
252741110768_1_3	50% NOD+50% Black6	chr6	6	qF3	130204536	130317661	6	0.674244	0	0.674244	3.58E-14
252741110768_1_2	100% NOD	chr7	7	qA3	24552339	24704561	9	0.666264	0	0.666264	3.32E-17
252741110768_1_3	50% NOD+50% Black6	chr7	7	qA3	24552339	24580772	4	0.693907	0	0.693907	5.94E-11
252741110768_1_2	100% NOD	chr7	7	qB2 - qB3	39015743	46797041	20	0	-0.701094	-0.701094	3.82E-39
252741110768_1_3	50% NOD+50% Black6	chr7	7	qB2 - qB3	39015743	46797041	20	0	-0.33459	-0.33459	5.48E-13
252741110768_1_2	100% NOD	chr7	7	qB4	54811136	54883844	4	1.304188	0	1.304188	2.20E-25
252741110768_1_3	50% NOD+50% Black6	chr7	7	qB4	54844755	54883844	3	1.144045	0	1.144045	1.14E-17
252741110768_1_4	25% NOD+75% Black6	chr7	7	qB4	54844755	54883844	3	0.754618	0	0.754618	9.33E-10
252741110768_1_3	50% NOD+50% Black6	chr7	7	qB4	54920080	55758120	41	0	-0.259294	-0.259294	1.58E-15
252741110768_1_2	100% NOD	chr7	7	qB4	55409198	55715246	20	0	-0.568817	-0.568817	3.96E-25
252741110768_1_3	50% NOD+50% Black6	chr7	7	qE3	111393528	111473425	5	0	-0.80525	-0.80525	1.05E-13
252741110768_1_2	100% NOD	chr7	7	qE3	111430424	111459364	3	0	-3.447686	-3.447686	3.92E-49
252741110768_1_2	100% NOD	chr7	7	qF4	145407110	145523440	12	0	-0.428757	-0.428757	1.96E-10
252741110768_1_3	50% NOD+50% Black6	chr10	10	qA3	21904748	22072759	10	0.951189	0	0.951189	2.73E-41
252741110768_1_2	100% NOD	chr10	10	qA3	21998927	22072759	9	1.457405	0	1.457405	1.07E-69
252741110768_1_4	25% NOD+75% Black6	chr10	10	qA3	21998927	22072759	9	0.676491	0	0.676491	1.81E-21
252741110768_1_2	100% NOD	chr10	10	qD2	117724452	117752882	3	0	-3.583002	-3.583002	2.44E-53
252741110768_1_3	50% NOD+50% Black6	chr10	10	qD2	117724452	117752882	3	0	-1.012358	-1.012358	4.05E-15
252741110768_1_2	100% NOD	chr11	11	qA3.1	20264570	20318317	4	0	-1.499111	-1.499111	1.15E-30
252741110768_1_3	50% NOD+50% Black6	chr11	11	qA3.1	20264570	20318317	4	0	-0.675589	-0.675589	2.56E-10
252741110768_1_3	50% NOD+50% Black6	chr11	11	qA4	31049571	31227838	5	0	-0.687125	-0.687125	1.20E-12
252741110768_1_4	25% NOD+75% Black6	chr11	11	qB4	70976924	71107103	12	0	-0.516537	-0.516537	9.96E-18
252741110768_1_2	100% NOD	chr11	11	qB4	70989862	71107103	11	0	-3.751361	-3.751361	1.63E-197
252741110768_1_3	50% NOD+50% Black6	chr11	11	qB4	70989862	71107103	11	0	-1.146648	-1.146648	3.28E-61
252741110768_1_2	100% NOD	chr11	11	qB5	74184906	74199333	3	1.02059	0	1.02059	4.64E-14
252741110768_1_3	50% NOD+50% Black6	chr11	11	qB5	74184906	74199333	3	0.771882	0	0.771882	3.46E-10
252741110768_1_2	100% NOD	chr12	12	qD3	89456049	89496285	3	1.227517	0	1.227517	3.81E-18
252741110768_1_3	50% NOD+50% Black6	chr12	12	qD3	89456049	89496285	3	0.885945	0	0.885945	3.02E-12
252741110768_1_2	100% NOD	chr12	12	qE	105063971	105192170	4	0	-2.624555	-2.624555	5.86E-58
252741110768_1_3	50% NOD+50% Black6	chr12	12	qE	105063971	105192170	4	0	-1.113361	-1.113361	2.60E-22
252741110768_1_2	100% NOD	chr13	13	qA3.3	40292873	40316799	3	0	-1.173607	-1.173607	1.70E-17
252741110768_1_2	100% NOD	chr13	13	qB3	61743712	62011180	5	0	-3.131776	-3.131776	1.27E-78
252741110768_1_3	50% NOD+50% Black6	chr13	13	qB3	61743712	62048006	7	0	-0.965814	-0.965814	1.35E-28
252741110768_1_3	50% NOD+50% Black6	chr13	13	qD1	101110785	101177268	5	0.633096	0	0.633096	2.38E-11
252741110768_1_2	100% NOD	chr13	13	qD1	101132822	101183591	5	0.960619	0	0.960619	8.27E-20
252741110768_1_2	100% NOD	chr13	13	qD2.3	118804387	118962896	5	0	-1.024423	-1.024423	1.97E-21
252741110768_1_2	100% NOD	chr14	14	qC1	44380406	44579789	7	0	-1.642304	-1.642304	8.88E-53

252741110768_1_3	50% NOD+50% Black6	chr14	14	qC1	44380406	44579789	7	0	-0.774986	-0.774986	2.69E-21
252741110768_1_2	100% NOD	chr14	14	qC2	52460107	52489945	3	0	-2.133337	-2.133337	6.18E-36
252741110768_1_3	50% NOD+50% Black6	chr14	14	qC2	52460107	52489945	3	0	-0.808357	-0.808357	1.19E-10
252741110768_1_2	100% NOD	chr14	14	qD2	69876584	70083135	22	0	-0.513151	-0.513151	1.71E-24
252741110768_1_2	100% NOD	chr15	15	qE1	77244685	77364452	5	0	-3.837598	-3.837598	5.31E-91
252741110768_1_3	50% NOD+50% Black6	chr15	15	qE1	77244685	77364452	5	0	-1.027284	-1.027284	9.13E-24
252741110768_1_2	100% NOD	chr15	15	qE3	90874048	90963018	6	0	-1.086988	-1.086988	6.28E-23
252741110768_1_3	50% NOD+50% Black6	chr15	15	qF1	100172426	100205602	4	0	-0.875662	-0.875662	1.62E-15
252741110768_1_2	100% NOD	chr15	15	qF1	100182640	100205602	3	0	-3.757847	-3.757847	3.97E-54
252741110768_1_2	100% NOD	chr16	16	qB3	35483725	35550180	7	0.974941	0	0.974941	7.61E-28
252741110768_1_3	50% NOD+50% Black6	chr16	16	qB3	35483725	35550180	7	0.627193	0	0.627193	3.31E-15
252741110768_1_2	100% NOD	chr16	16	qB3	36245661	36319122	6	0	-2.460501	-2.460501	3.08E-74
252741110768_1_3	50% NOD+50% Black6	chr16	16	qB3	36245661	36319122	6	0	-1.041032	-1.041032	1.50E-29
252741110768_1_4	25% NOD+75% Black6	chr16	16	qB3	36245661	36319122	6	0	-0.554228	-0.554228	6.97E-11
252741110768_1_2	100% NOD	chr16	16	qB4	44835805	44872692	4	0	-1.985869	-1.985869	1.60E-41
252741110768_1_3	50% NOD+50% Black6	chr16	16	qB4	44835805	44872692	4	0	-0.824597	-0.824597	3.45E-14
252741110768_1_2	100% NOD	chr17	17	qB1	36890283	36959863	9	0	-0.823091	-0.823091	1.47E-19
252741110768_1_2	100% NOD	chr18	18	qE3	75696173	75751889	7	0	-0.848804	-0.848804	2.28E-21
252741110768_1_3	50% NOD+50% Black6	chr18	18	qE3	75696173	75751889	7	0	-0.501785	-0.501785	2.20E-10
252741110768_1_2	100% NOD	chr19	19	qA	12253807	12308192	6	0	-3.350553	-3.350553	1.61E-100
252741110768_1_3	50% NOD+50% Black6	chr19	19	qA	12253807	12308192	6	0	-1.187877	-1.187877	2.51E-36
252741110768_1_2	100% NOD	chrX	X	qD	100008370	100023414	3	0.854986	0	0.854986	5.88E-10

Dataset S3. 2. List of CNAs in memory CD4+ lymphocytes of PLN in 19 tested diabetic mice with normal sorting profile (ADM2: mean LRR I0.25I and P-value <2.90 x 10-07 and CBS: mean LRR I0.25I and P-value <1 x 10-04). Since we have no prior information in which to base power calculations the number of mice tested was determined by available funds.

ID	ID	chrom	chrom	chr region	loc.start	loc.end	num.mark	Amplification	Deletions	mean LRR	pval
252741111071_1_1	M3	chr8	8	qB3.3	72,718,314	72,795,346	9	0.474046	0	0.474046	1.18E-10
252741110805_1_1	M4	chr2	2	qC3	74,475,401	74,598,078	15	0	-0.3411	-0.3411	8.55E-10
252741110805_1_1	M4	chr6	6	qB3	52,104,495	52,281,548	18	0	-0.35059	-0.35059	7.06E-12
252741110805_1_1	M4	chr10	10	qC1	79,084,598	81,041,680	203	0	-0.253642	-0.253642	2.32E-62
252741110818_1_3	M5	chr14	14	qC1 - qC2	52,061,318	52,152,579	8	0	-0.468412	-0.468412	1.47E-10
252741110818_1_4	M7	chr12	12	qF1	110,259,036	110,803,088	28	0	-0.286577	-0.286577	3.71E-10
252741111071_1_4	M10	chr8	8	qB3.3	72,706,464	72,777,429	8	0.509067	0	0.509067	3.83E-10
252741111093_1_2	M12	chr2	2	qC3	74,501,193	74,598,078	13	0	-0.421032	-0.421032	2.33E-12
252741111093_1_2	M12	chr4	4	qE2	148,271,563	148,338,029	6	0	-0.531873	-0.531873	6.58E-10
252741111093_1_2	M12	chr5	5	qA3	23,846,753	24,135,248	31	0	-0.29753	-0.29753	3.21E-15
252741111093_1_2	M12	chr6	6	qB3	52,116,749	52,207,847	9	0	-0.482734	-0.482734	1.65E-11
252741111496_1_3	M16	chr5	5	qA3	23,764,189	24,135,248	39	0	-0.279024	-0.279024	1.09E-10
252741111496_1_3	M16	chr7	7	qB1	31,309,621	31,448,527	18	0	-0.360452	-0.360452	9.43E-10
252741110818_1_1	M18	chrY	Y	qA1	1,846,529	2,506,368	7	0	-0.696958	-0.696958	6.49E-15

Table S3. 3. List of CNAs in the CD4+ lymphocytes from PNL of the six animals in which all cells were memory, CD62Lneg, CD44+ (M20-M25). M23 and M25 had the largest number of CNAs indicating an unstable genome.

ID	ID	chrom	chrom	chr region	loc.start	loc.end	num.mark	Amplification	Deletions	mean LRR	pval
252741110806_1_1	M22	chr3	3	qF2.1	94767165	94821010	7	0.485703	0	0.485703	6.82E-10
252741110806_1_1	M22	chr11	11	qB3	68880665	68909840	4	0.790815	0	0.790815	2.01E-14
252741110806_1_1	M22	chr13	13	qA3.1	21798640	21921804	13	0.395523	0	0.395523	7.92E-12
252741110806_1_1	M22	chr13	13	qA3.1	23648864	23661397	3	0.860912	0	0.860912	1.11E-11
252741110806_1_1	M22	chr14	14	qC1 - qC2	52061318	52145237	7	0	-0.567054	-0.567054	6.92E-13
252741110767_1_2	M23	chr1	1	qB	36503701	36617344	12	1.348272	0	1.348272	1.50E-65
252741110767_1_2	M23	chr1	1	qC2	64163925	64184658	3	0.996945	0	0.996945	1.46E-10
252741110767_1_2	M23	chr1	1	qC3 - qC4	75145560	75336820	21	0.502374	0	0.502374	2.10E-17
252741110767_1_2	M23	chr1	1	qD	88220343	88486976	23	0.666803	0	0.666803	8.11E-32
252741110767_1_2	M23	chr1	1	qD	93127340	93347023	23	0.985482	0	0.985482	8.50E-65
252741110767_1_2	M23	chr1	1	qD	95194949	95466157	32	0.691444	0	0.691444	1.34E-46
252741110767_1_2	M23	chr1	1	qE4	133405674	133461744	6	0.814173	0	0.814173	1.65E-13
252741110767_1_2	M23	chr1	1	qE4	135961313	136028652	8	0.958129	0	0.958129	2.14E-23
252741110767_1_2	M23	chr1	1	qG3	156935025	156998380	9	0.892209	0	0.892209	7.97E-23
252741110767_1_2	M23	chr1	1	qH2.3	167515575	167634731	13	0.585428	0	0.585428	6.41E-15
252741110767_1_2	M23	chr1	1	qH3	171879998	172067400	18	0.41261	0	0.41261	8.28E-11
252741110767_1_2	M23	chr1	1	qH3	173156460	173313303	16	0.754672	0	0.754672	1.45E-28
252741110767_1_2	M23	chr1	1	qH6	193146204	193769254	56	0.405128	0	0.405128	1.22E-28
252741110767_1_2	M23	chr2	2	qA1	3326658	3460492	14	0.595535	0	0.595535	2.03E-16
252741110767_1_2	M23	chr2	2	qB	29706837	30335662	64	0.599361	0	0.599361	6.25E-69
252741110767_1_2	M23	chr2	2	qB	30231835	30304849	8	1.289378	0	1.289378	5.85E-13
252741110767_1_2	M23	chr2	2	qB	32275427	32382803	10	1.004846	0	1.004846	7.96E-10
252741110767_1_2	M23	chr2	2	qB	34605928	34652887	5	1.032654	0	1.032654	1.70E-17
252741110767_1_2	M23	chr2	2	qC1.1	52918437	53167467	24	0.37251	0	0.37251	1.35E-11
252741110767_1_2	M23	chr2	2	qC3	75395873	75544907	12	0.490615	0	0.490615	2.76E-10
252741110767_1_2	M23	chr2	2	qD	84479654	84612390	13	0.730203	0	0.730203	3.45E-22
252741110767_1_2	M23	chr2	2	qE1	92209084	92288997	9	0.717189	0	0.717189	1.97E-15
252741110767_1_2	M23	chr2	2	qE2	103298789	103417743	8	0.770814	0	0.770814	8.52E-16
252741110767_1_2	M23	chr2	2	qE3	105670148	105755474	9	0.583789	0	0.583789	8.12E-11
252741110767_1_2	M23	chr2	2	qE5	119365664	119455924	12	1.111103	0	1.111103	3.45E-45
252741110767_1_2	M23	chr2	2	qE5	121096018	121281283	21	1.064143	0	1.064143	3.39E-71
252741110767_1_2	M23	chr2	2	qF1	127004358	127124309	12	0.643761	0	0.643761	1.92E-16
252741110767_1_2	M23	chr2	2	qF1	127904068	127975791	7	0.701258	0	0.701258	6.28E-12
252741110767_1_2	M23	chr2	2	qF1	130991074	131126299	14	0.881717	0	0.881717	9.79E-34
252741110767_1_2	M23	chr2	2	qH1	152657878	152699043	4	0.839291	0	0.839291	4.48E-10
252741110767_1_2	M23	chr2	2	qH1	154271883	154387627	13	0.490308	0	0.490308	5.46E-11
252741110767_1_2	M23	chr2	2	qH1	154396040	154442189	5	1.886955	0	1.886955	2.03E-46
252741110767_1_2	M23	chr2	2	qH3	164527709	164708702	20	0.976282	0	0.976282	1.50E-57
252741110767_1_2	M23	chr2	2	qH3	164600494	164641540	5	1.78452	0	1.78452	2.09E-11
252741110767_1_2	M23	chr2	2	qH4	179746352	180189103	45	0.573341	0	0.573341	9.08E-45
252741110767_1_2	M23	chr3	3	qA2	19064447	19123792	8	0.952194	0	0.952194	3.94E-23
252741110767_1_2	M23	chr3	3	qA3	27026426	27078912	6	0.71889	0	0.71889	5.33E-10
252741110767_1_2	M23	chr3	3	qA3	32578869	32623867	4	0.917167	0	0.917167	6.45E-11
252741110767_1_2	M23	chr3	3	qF1	87875723	88320684	47	0.40236	0	0.40236	3.95E-24
252741110767_1_2	M23	chr3	3	qF1	88856521	88964570	12	0.659978	0	0.659978	3.45E-17
252741110767_1_2	M23	chr3	3	qF1	89199720	89234878	5	1.421394	0	1.421394	1.87E-31
252741110767_1_2	M23	chr3	3	qF1	90072599	90314045	27	0.798966	0	0.798966	3.10E-52
252741110767_1_2	M23	chr3	3	qF2.1	94667476	96399306	174	0.635965	0	0.635965	3.87E-206
252741110767_1_2	M23	chr3	3	qF2.1	94759757	94857185	12	1.468373	0	1.468373	3.10E-26
252741110767_1_2	M23	chr3	3	qF2.1	95679706	95744139	9	1.291426	0	1.291426	3.50E-13
252741110767_1_2	M23	chr3	3	qF2.1	96012726	96069190	6	1.727496	0	1.727496	1.19E-22
252741110767_1_2	M23	chr3	3	qF2.2	100648887	100779147	13	0.524805	0	0.524805	2.45E-12
252741110767_1_2	M23	chr3	3	qG3	135060963	135090752	5	0.838265	0	0.838265	3.87E-12
252741110767_1_2	M23	chr4	4	qA5	41303485	41454957	17	0.557374	0	0.557374	2.39E-17
252741110767_1_2	M23	chr4	4	qA5	42960366	43071029	12	1.076454	0	1.076454	1.53E-42
252741110767_1_2	M23	chr4	4	qB1	44956141	45056026	11	0.591038	0	0.591038	4.12E-13
252741110767_1_2	M23	chr4	4	qB1	46466992	46553140	9	0.636181	0	0.636181	1.61E-12
252741110767_1_2	M23	chr4	4	qC7	108672012	108798956	14	1.245611	0	1.245611	2.79E-65
252741110767_1_2	M23	chr4	4	qD1	114615652	114709283	11	0.56203	0	0.56203	5.04E-12
252741110767_1_2	M23	chr4	4	qD1	116364137	116466983	13	0.788577	0	0.788577	1.16E-17
252741110767_1_2	M23	chr4	4	qD2.1	117813491	117876094	7	1.159713	0	1.159713	5.26E-23
252741110767_1_2	M23	chr4	4	qD2.1	118759284	119076632	31	0.726074	0	0.726074	1.53E-32
252741110767_1_2	M23	chr4	4	qD2.2	120450783	120526655	10	0.731512	0	0.731512	6.27E-12
252741110767_1_2	M23	chr4	4	qD2.2	126350864	126471171	14	0.596134	0	0.596134	3.54E-10
252741110767_1_2	M23	chr4	4	qD2.2	129019114	129299035	30	0.85803	0	0.85803	1.72E-46
252741110767_1_2	M23	chr4	4	qD3	134322506	135004897	55	0.426465	0	0.426465	1.19E-14
252741110767_1_2	M23	chr4	4	qD3	137777067	137884856	14	0.637974	0	0.637974	1.43E-18
252741110767_1_2	M23	chr4	4	qD3	139149848	139235816	10	0.629434	0	0.629434	1.83E-13
252741110767_1_2	M23	chr4	4	qE2	147826917	147965105	15	0.82774	0	0.82774	5.76E-32
252741110767_1_2	M23	chr4	4	qE2	151205425	151264151	7	0.890396	0	0.890396	3.89E-18
252741110767_1_2	M23	chr5	5	qA3	20367300	20548127	18	0.771356	0	0.771356	3.15E-33
252741110767_1_2	M23	chr5	5	qB1	31016567	31826213	75	0.278044	0	0.278044	1.11E-18
252741110767_1_2	M23	chr5	5	qB1 - qB2	33624527	34986581	132	0.290132	0	0.290132	2.13E-34
252741110767_1_2	M23	chr5	5	qB3	36797005	36921007	13	0.55001	0	0.55001	6.72E-13
252741110767_1_2	M23	chr5	5	qC3.2 - qC3.3	73616435	73907085	31	0.496776	0	0.496776	2.72E-24
252741110767_1_2	M23	chr5	5	qC3.3	74443234	74548549	10	0.809964	0	0.809964	4.22E-21

252741110767_1_2	M23	chr5	5	qE2	92464792	92504843	6	0.785666	0	0.785666	1.06E-12
252741110767_1_2	M23	chr5	5	qF	110070043	110714343	37	0.352535	0	0.352535	2.43E-15
252741110767_1_2	M23	chr5	5	qF	111232124	111314204	9	0.604873	0	0.604873	1.74E-11
252741110767_1_2	M23	chr5	5	qF	121027814	121131582	13	0.787634	0	0.787634	1.67E-25
252741110767_1_2	M23	chr5	5	qF	123236577	123344478	11	1.395915	0	1.395915	1.30E-63
252741110767_1_2	M23	chr5	5	qF	123354661	123596940	26	0.453754	0	0.453754	1.47E-17
252741110767_1_2	M23	chr5	5	qG1.1	125874080	125936115	7	1.284969	0	1.284969	5.09E-34
252741110767_1_2	M23	chr5	5	qG1.3	130300469	130700471	41	0.826984	0	0.826984	3.00E-83
252741110767_1_2	M23	chr5	5	qG2	135415016	135686905	27	0.581034	0	0.581034	2.19E-28
252741110767_1_2	M23	chr5	5	qG2	138042701	138141235	13	1.608518	0	1.608518	2.83E-97
252741110767_1_2	M23	chr5	5	qG2	138546341	139081347	44	0.307421	0	0.307421	4.82E-14
252741110767_1_2	M23	chr5	5	qG2	139635330	139723622	10	1.05389	0	1.05389	2.19E-34
252741110767_1_2	M23	chr5	5	qG2	141082172	141353671	28	0.627569	0	0.627569	8.45E-34
252741110767_1_2	M23	chr5	5	qG2	144496662	144722096	17	0.925954	0	0.925954	1.71E-44
252741110767_1_2	M23	chr6	6	qA1	13585562	13643575	7	0.699923	0	0.699923	6.87E-12
252741110767_1_2	M23	chr6	6	qA3.3	30200359	30534427	32	0.303157	0	0.303157	2.04E-10
252741110767_1_2	M23	chr6	6	qB1	34225544	34454018	23	0.472285	0	0.472285	1.18E-16
252741110767_1_2	M23	chr6	6	qB1	38386583	38584989	22	0.494649	0	0.494649	1.20E-17
252741110767_1_2	M23	chr6	6	qB2.3	47512880	47934978	28	0.542964	0	0.542964	4.65E-26
252741110767_1_2	M23	chr6	6	qB2.3	48502537	48650197	17	0.589359	0	0.589359	9.81E-19
252741110767_1_2	M23	chr6	6	qC1	70689731	72381338	155	0.271546	0	0.271546	2.71E-35
252741110767_1_2	M23	chr6	6	qC3	82931597	83395998	52	0.519268	0	0.519268	7.04E-43
252741110767_1_2	M23	chr6	6	qD1	86344235	86697888	36	0.39675	0	0.39675	1.76E-18
252741110767_1_2	M23	chr6	6	qE3	112981299	113423565	48	0.578158	0	0.578158	9.04E-49
252741110767_1_2	M23	chr6	6	qF2 - qF3	124592833	125194662	64	0.415472	0	0.415472	5.38E-34
252741110767_1_2	M23	chr6	6	qG2	142323903	142368319	5	0.861301	0	0.861301	1.02E-12
252741110767_1_2	M23	chr7	7	qA1	3552752	3659662	11	1.110033	0	1.110033	1.62E-41
252741110767_1_2	M23	chr7	7	qA1	4674882	4976931	30	1.030548	0	1.030548	9.77E-95
252741110767_1_2	M23	chr7	7	qA1	4705310	4825141	13	1.522806	0	1.522806	4.61E-11
252741110767_1_2	M23	chr7	7	qA1	13467306	13618490	16	1.133597	0	1.133597	4.43E-39
252741110767_1_2	M23	chr7	7	qA2	16629583	16712046	9	0.91871	0	0.91871	6.18E-14
252741110767_1_2	M23	chr7	7	qA3	19675357	20314658	68	0.847873	0	0.847873	3.11E-74
252741110767_1_2	M23	chr7	7	qA3	26007497	26063247	6	1.860421	0	1.860421	2.06E-47
252741110767_1_2	M23	chr7	7	qA3	27969029	28361263	39	0.878451	0	0.878451	4.71E-48
252741110767_1_2	M23	chr7	7	qA3	29183335	29213130	4	1.667379	0	1.667379	1.10E-25
252741110767_1_2	M23	chr7	7	qA3	29506048	29595005	9	1.659063	0	1.659063	7.59E-54
252741110767_1_2	M23	chr7	7	qB1	31019945	31433496	48	0.98104	0	0.98104	3.74E-78
252741110767_1_2	M23	chr7	7	qB1	31019945	31108349	10	1.806096	0	1.806096	1.40E-21
252741110767_1_2	M23	chr7	7	qB4	52042937	53163167	116	0.875818	0	0.875818	9.96E-260
252741110767_1_2	M23	chr7	7	qB4	52183033	52265135	10	1.736073	0	1.736073	6.93E-23
252741110767_1_2	M23	chr7	7	qB4	52936676	53060518	15	1.359883	0	1.359883	3.83E-12
252741110767_1_2	M23	chr7	7	qC	73803225	73929540	15	0.493781	0	0.493781	1.45E-12
252741110767_1_2	M23	chr7	7	qD1	80681415	80752765	5	0.920225	0	0.920225	2.88E-14
252741110767_1_2	M23	chr7	7	qD3	87381901	87716158	34	0.423294	0	0.423294	9.96E-20
252741110767_1_2	M23	chr7	7	qE2	106213265	106325843	12	0.493983	0	0.493983	2.10E-10
252741110767_1_2	M23	chr7	7	qE3	107656860	107754926	11	0.734819	0	0.734819	2.79E-19
252741110767_1_2	M23	chr7	7	qF1	117182461	117264581	10	0.809901	0	0.809901	4.25E-21
252741110767_1_2	M23	chr7	7	qF1	118191694	118262423	9	0.944354	0	0.944354	2.16E-25
252741110767_1_2	M23	chr7	7	qF1	123592438	123684496	9	0.571377	0	0.571377	4.90E-10
252741110767_1_2	M23	chr7	7	qF2	125200914	125392689	18	0.400465	0	0.400465	2.79E-10
252741110767_1_2	M23	chr7	7	qF2	128079949	128192678	12	0.540522	0	0.540522	4.07E-12
252741110767_1_2	M23	chr7	7	qF3	134335755	134729212	39	0.805719	0	0.805719	9.85E-76
252741110767_1_2	M23	chr7	7	qF4	144596191	144618068	3	0.974956	0	0.974956	3.55E-10
252741110767_1_2	M23	chr7	7	qF5	148276792	148640164	39	0.409722	0	0.409722	1.04E-20
252741110767_1_2	M23	chr8	8	qA1.1	4142160	4297584	15	0.660111	0	0.660111	1.66E-18
252741110767_1_2	M23	chr8	8	qA2	23870456	23937263	9	0.804477	0	0.804477	2.27E-16
252741110767_1_2	M23	chr8	8	qA2	26717138	26929223	25	0.445239	0	0.445239	1.49E-13
252741110767_1_2	M23	chr8	8	qB2	59941610	60061654	12	0.608891	0	0.608891	4.95E-13
252741110767_1_2	M23	chr8	8	qB3.1	67202364	67259766	7	0.760992	0	0.760992	2.32E-12
252741110767_1_2	M23	chr8	8	qB3.3	72158714	75102925	264	0.376996	0	0.376996	1.05E-110
252741110767_1_2	M23	chr8	8	qB3.3	72158714	72355110	17	0.948517	0	0.948517	3.81E-18
252741110767_1_2	M23	chr8	8	qB3.3	73196715	73383491	21	1.076989	0	1.076989	5.30E-32
252741110767_1_2	M23	chr8	8	qB3.3	73891011	74013507	12	0.60384	0	0.60384	1.31E-11
252741110767_1_2	M23	chr8	8	qC1	77520154	77624527	10	0.820321	0	0.820321	1.35E-21
252741110767_1_2	M23	chr8	8	qC2 - qC3	86113629	86786228	63	1.164913	0	1.164913	8.89E-249
252741110767_1_2	M23	chr8	8	qC2 - qC3	86202947	86465905	20	0.528312	0	0.528312	1.27E-25
252741110767_1_2	M23	chr8	8	qC3	91156122	91287339	14	0.759596	0	0.759596	1.53E-25
252741110767_1_2	M23	chr8	8	qC5	93408702	93654918	26	0.406599	0	0.406599	1.86E-14
252741110767_1_2	M23	chr8	8	qC5	97104559	97166458	7	0.939078	0	0.939078	1.20E-12
252741110767_1_2	M23	chr8	8	qD3	112085034	112227210	14	0.622482	0	0.622482	9.04E-18
252741110767_1_2	M23	chr8	8	qE1	119465366	119534493	8	0.677589	0	0.677589	1.31E-12
252741110767_1_2	M23	chr8	8	qE1	125551124	125625493	9	0.84481	0	0.84481	1.06E-20
252741110767_1_2	M23	chr9	9	qA3	20330908	20527974	21	0.564638	0	0.564638	1.70E-21
252741110767_1_2	M23	chr9	9	qA3	20808916	22149371	135	0.65663	0	0.65663	3.45E-171
252741110767_1_2	M23	chr9	9	qA3	21006076	21226381	25	1.158039	0	1.158039	2.70E-20
252741110767_1_2	M23	chr9	9	qA4	30984794	31091424	12	0.914508	0	0.914508	2.92E-31
252741110767_1_2	M23	chr9	9	qA4	37000996	37068897	8	0.690213	0	0.690213	5.10E-13
252741110767_1_2	M23	chr9	9	qA5.1 - qA5.2	43844831	44106807	30	0.536577	0	0.536577	5.74E-27
252741110767_1_2	M23	chr9	9	qA5.2	44118120	44193914	9	1.794228	0	1.794228	9.16E-84
252741110767_1_2	M23	chr9	9	qB	56784437	56997922	21	0.658772	0	0.658772	1.44E-28
252741110767_1_2	M23	chr9	9	qB	59467622	59485687	3	0.907199	0	0.907199	7.23E-10
252741110767_1_2	M23	chr9	9	qE3.3 - qE4	100431078	100523531	9	0.623918	0	0.623918	4.14E-12
252741110767_1_2	M23	chr9	9	qF1	106728067	106854862	14	0.572608	0	0.572608	2.57E-15
252741110767_1_2	M23	chr9	9	qF1 - qF2	107462867	108548541	110	0.415274	0	0.415274	2.80E-57
252741110767_1_2	M23	chr9	9	qF2	109775895	109833275	6	0.945905	0	0.945905	1.32E-17
252741110767_1_2	M23	chr9	9	qF4	121574085	121806168	26	0.64944	0	0.64944	5.64E-34
252741110767_1_2	M23	chr10	10	qB4	61997029	62129155	13	0.538326	0	0.538326	6.87E-13
252741110767_1_2	M23	chr10	10	qC1	75210713	75523409	32	0.979638	0	0.979638	7.21E-91
252741110767_1_2	M23	chr10	10	qC1	79304826	81481292	192	0.776421	0	0.776421	0
252741110767_1_2	M23	chr10	10	qC1	79448762	79688301	26	1.381452	0	1.381452	1.66E-29
252741110767_1_2	M23	chr10	10	qC1	84566714	84654929	11	0.867971	0	0.867971	3.74E-26
252741110767_1_2	M23	chr10	10	qC1	86041367	86246908	14	0.604833	0	0.604833	7.04E-17
252741110767_1_2	M23	chr10	10	qD3	127511153	128313675	78	0.986931	0	0.986931	2.50E-221

252741110767_1_2	M23	chr11	11	qA1	4057583	4148688	11	0.649239	0	0.649239	1.88E-15
252741110767_1_2	M23	chr11	11	qA1	6194658	6426112	26	0.683904	0	0.683904	1.85E-37
252741110767_1_2	M23	chr11	11	qA3.2	23012594	23194141	12	0.60183	0	0.60183	1.34E-14
252741110767_1_2	M23	chr11	11	qA4	32342053	32547392	23	0.438277	0	0.438277	8.27E-15
252741110767_1_2	M23	chr11	11	qA5	40519273	40577298	6	1.203143	0	1.203143	3.79E-27
252741110767_1_2	M23	chr11	11	qB1.3	50048571	50176586	14	0.732166	0	0.732166	7.24E-24
252741110767_1_2	M23	chr11	11	qB1.3	54616283	54870653	27	0.488558	0	0.488558	9.22E-21
252741110767_1_2	M23	chr11	11	qB1.3 - qB2	58633072	61376495	247	0.295877	0	0.295877	1.76E-64
252741110767_1_2	M23	chr11	11	qB1.3	58667480	58772598	11	1.125513	0	1.125513	4.63E-24
252741110767_1_2	M23	chr11	11	qB2	60121835	60235296	13	0.889882	0	0.889882	2.93E-15
252741110767_1_2	M23	chr11	11	qB2	60989454	61062117	10	1.04742	0	1.04742	9.92E-18
252741110767_1_2	M23	chr11	11	qB3	63710411	63768021	7	0.749216	0	0.749216	1.80E-12
252741110767_1_2	M23	chr11	11	qB3	68766792	68909840	15	1.652251	0	1.652251	5.46E-118
252741110767_1_2	M23	chr11	11	qB4	70796008	70850932	7	1.38962	0	1.38962	5.32E-27
252741110767_1_2	M23	chr11	11	qB4	72781596	73035193	28	0.488619	0	0.488619	1.82E-21
252741110767_1_2	M23	chr11	11	qB5	75159849	75371093	21	1.164331	0	1.164331	6.93E-85
252741110767_1_2	M23	chr11	11	qB5	78298988	78523376	25	0.617886	0	0.617886	7.93E-30
252741110767_1_2	M23	chr11	11	qB5	79773834	79823293	7	0.548992	0	0.548992	2.73E-10
252741110767_1_2	M23	chr11	11	qC	82923607	83141110	17	0.568095	0	0.568095	5.96E-18
252741110767_1_2	M23	chr11	11	qC	86744860	87555571	84	0.461455	0	0.461455	8.98E-54
252741110767_1_2	M23	chr11	11	qC	86810572	86933115	14	1.039202	0	1.039202	1.47E-15
252741110767_1_2	M23	chr11	11	qD	94058422	94131827	8	0.696125	0	0.696125	3.26E-13
252741110767_1_2	M23	chr11	11	qD	95154099	95250832	12	1.063923	0	1.063923	1.33E-41
252741110767_1_2	M23	chr11	11	qD	96636809	97083470	44	1.135474	0	1.135474	5.25E-166
252741110767_1_2	M23	chr11	11	qD	96649609	96841593	19	1.669092	0	1.669092	1.46E-17
252741110767_1_2	M23	chr11	11	qD	100779807	101033294	28	0.601035	0	0.601035	1.72E-31
252741110767_1_2	M23	chr11	11	qD	101284408	101465864	21	0.451122	0	0.451122	2.20E-14
252741110767_1_2	M23	chr11	11	qE1	102782644	103139856	35	0.817628	0	0.817628	5.13E-70
252741110767_1_2	M23	chr11	11	qE1	105897499	106081504	20	1.220727	0	1.220727	1.02E-87
252741110767_1_2	M23	chr11	11	qE2	114992045	116368193	144	0.513592	0	0.513592	2.97E-112
252741110767_1_2	M23	chr11	11	qE2	115032358	115050127	3	1.465178	0	1.465178	8.95E-10
252741110767_1_2	M23	chr11	11	qE2	116241080	116292548	8	1.154676	0	1.154676	1.96E-11
252741110767_1_2	M23	chr11	11	qE2	118291801	118369612	9	0.584108	0	0.584108	7.93E-11
252741110767_1_2	M23	chr11	11	qE2	118886773	118966536	9	0.984185	0	0.984185	2.06E-27
252741110767_1_2	M23	chr11	11	qE2	119799402	120635173	83	1.098087	0	1.098087	5.39E-292
252741110767_1_2	M23	chr11	11	qE2	119799402	119936549	16	0.681308	0	0.681308	5.82E-10
252741110767_1_2	M23	chr11	11	qE2	120085078	120204360	11	1.619338	0	1.619338	1.39E-10
252741110767_1_2	M23	chr12	12	qA1.3	21335507	25381974	40	0.49145	0	0.49145	3.63E-30
252741110767_1_2	M23	chr12	12	qB1	40735723	41221744	44	0.32414	0	0.32414	2.06E-15
252741110767_1_2	M23	chr12	12	qC1	60126848	60178960	7	0.751938	0	0.751938	1.88E-13
252741110767_1_2	M23	chr12	12	qC3	72046117	72152544	13	0.858863	0	0.858863	5.87E-30
252741110767_1_2	M23	chr12	12	qC3	74957038	75083433	12	0.520715	0	0.520715	2.27E-11
252741110767_1_2	M23	chr12	12	qC3	76677031	76813649	17	1.232771	0	1.232771	1.26E-76
252741110767_1_2	M23	chr12	12	qC3	77340196	77498327	17	0.576145	0	0.576145	2.07E-18
252741110767_1_2	M23	chr12	12	qC3	79820057	79945050	14	0.480617	0	0.480617	2.60E-11
252741110767_1_2	M23	chr12	12	qD1	85663406	85839161	16	0.634979	0	0.634979	8.82E-21
252741110767_1_2	M23	chr12	12	qD2	87109694	87213302	10	0.674711	0	0.674711	3.32E-15
252741110767_1_2	M23	chr12	12	qD2	88679622	88794219	13	0.574863	0	0.574863	1.89E-14
252741110767_1_2	M23	chr12	12	qE	101415698	101451885	5	0.822929	0	0.822929	9.22E-12
252741110767_1_2	M23	chr12	12	qF1	112759383	113145492	36	0.635016	0	0.635016	2.54E-44
252741110767_1_2	M23	chr12	12	qF1	114199229	114421426	22	0.621425	0	0.621425	9.18E-27
252741110767_1_2	M23	chr13	13	qA1	5830955	5935750	8	0.679761	0	0.679761	1.11E-12
252741110767_1_2	M23	chr13	13	qA1	8871211	9121585	19	0.483899	0	0.483899	6.70E-15
252741110767_1_2	M23	chr13	13	qA3.1	21813250	21921804	11	2.054245	0	2.054245	4.45E-127
252741110767_1_2	M23	chr13	13	qA3.1	22001321	22177580	18	0.447332	0	0.447332	2.12E-12
252741110767_1_2	M23	chr13	13	qA3.1	23648864	23725304	10	2.124522	0	2.124522	7.57E-11
252741110767_1_2	M23	chr13	13	qA5	48596353	48710553	13	0.651418	0	0.651418	4.86E-18
252741110767_1_2	M23	chr13	13	qB1	55461278	55635040	19	0.802631	0	0.802631	1.09E-37
252741110767_1_2	M23	chr13	13	qB3	63537169	64388163	65	0.262048	0	0.262048	6.07E-15
252741110767_1_2	M23	chr13	13	qD1	100068624	100194789	15	0.486137	0	0.486137	3.12E-12
252741110767_1_2	M23	chr14	14	qA3	21678192	21906281	25	0.529385	0	0.529385	2.09E-22
252741110767_1_2	M23	chr14	14	qC1	45789074	45977510	22	0.618687	0	0.618687	1.52E-26
252741110767_1_2	M23	chr14	14	qC1	47360060	47465025	12	0.728865	0	0.728865	1.48E-20
252741110767_1_2	M23	chr14	14	qC1	51491923	51650719	18	0.414076	0	0.414076	1.39E-10
252741110767_1_2	M23	chr14	14	qC2	52650660	52891234	24	0.475702	0	0.475702	8.67E-18
252741110767_1_2	M23	chr14	14	qC3	56150381	56228251	10	0.893538	0	0.893538	2.87E-25
252741110767_1_2	M23	chr14	14	qC3	57183021	57520968	35	0.527435	0	0.527435	2.18E-30
252741110767_1_2	M23	chr14	14	qD1	63691413	63826197	15	0.52235	0	0.52235	7.52E-14
252741110767_1_2	M23	chr14	14	qD1	68103247	68386202	19	0.443565	0	0.443565	8.37E-13
252741110767_1_2	M23	chr14	14	qE4	119330641	119406329	9	0.794597	0	0.794597	1.58E-18
252741110767_1_2	M23	chr14	14	qE4	120644586	120945177	29	0.342638	0	0.342638	8.12E-12
252741110767_1_2	M23	chr15	15	qA1	11315563	11394029	6	0.671542	0	0.671542	9.63E-10
252741110767_1_2	M23	chr15	15	qD3	72906373	72976751	8	0.732917	0	0.732917	1.88E-14
252741110767_1_2	M23	chr15	15	qD3	76134040	76604261	51	0.451516	0	0.451516	3.30E-32
252741110767_1_2	M23	chr15	15	qE1	77645924	77775814	12	0.500562	0	0.500562	1.23E-10
252741110767_1_2	M23	chr15	15	qE1	78743259	78923034	20	1.507451	0	1.507451	1.03E-133
252741110767_1_2	M23	chr15	15	qE1	79515033	79588749	8	1.176055	0	1.176055	2.90E-34
252741110767_1_2	M23	chr15	15	qE1	80971938	82190009	117	0.512592	0	0.512592	2.26E-91
252741110767_1_2	M23	chr15	15	qE1	81958797	82170027	20	0.980861	0	0.980861	1.29E-14
252741110767_1_2	M23	chr15	15	qE3	88578704	88700383	14	0.670929	0	0.670929	2.41E-20
252741110767_1_2	M23	chr15	15	qF1	98333856	99302697	94	0.402561	0	0.402561	2.08E-46
252741110767_1_2	M23	chr15	15	qF3	102185293	102452714	28	1.041129	0	1.041129	3.28E-90
252741110767_1_2	M23	chr15	15	qF3	103041789	103136644	10	1.237549	0	1.237549	4.43E-46
252741110767_1_2	M23	chr16	16	qA1	4915472	5055147	15	0.812686	0	0.812686	6.94E-31
252741110767_1_2	M23	chr16	16	qA1	11050440	11226723	20	0.458692	0	0.458692	3.44E-14
252741110767_1_2	M23	chr16	16	qA3	18790688	18873617	9	0.812353	0	0.812353	2.79E-19
252741110767_1_2	M23	chr16	16	qB1	22371811	22943160	52	0.378201	0	0.378201	1.14E-23
252741110767_1_2	M23	chr16	16	qC3.3	91590666	91710817	14	1.258447	0	1.258447	1.37E-66
252741110767_1_2	M23	chr16	16	qC4	96260776	96341157	10	0.670648	0	0.670648	4.82E-15
252741110767_1_2	M23	chr17	17	qA1	13056204	13200129	16	0.788724	0	0.788724	5.08E-31
252741110767_1_2	M23	chr17	17	qA3.3	24299219	25229050	97	0.805873	0	0.805873	9.54E-185
252741110767_1_2	M23	chr17	17	qA3.3	24591547	24666064	8	1.464851	0	1.464851	5.81E-12
252741110767_1_2	M23	chr17	17	qA3.3	24999351	25149304	19	1.732203	0	1.732203	1.60E-49

252741110767_1_2	M23	chr17	17	qA3.3	25857341	26079251	24	0.719588	0	0.719588	3.10E-38
252741110767_1_2	M23	chr17	17	qA3.3	26680821	27153971	48	0.471152	0	0.471152	4.55E-33
252741110767_1_2	M23	chr17	17	qA3.3	27067800	27128740	7	1.178527	0	1.178527	4.16E-12
252741110767_1_2	M23	chr17	17	qA3.3	29623271	29715140	13	0.611765	0	0.611765	3.99E-16
252741110767_1_2	M23	chr17	17	qB1	33135013	33225520	10	1.138779	0	1.138779	1.76E-14
252741110767_1_2	M23	chr17	17	qB1	34744070	34780986	5	1.809123	0	1.809123	1.19E-27
252741110767_1_2	M23	chr17	17	qB1	35977610	36052013	10	1.26019	0	1.26019	1.35E-19
252741110767_1_2	M23	chr17	17	qB3	44209493	44261201	6	0.748921	0	0.748921	1.06E-11
252741110767_1_2	M23	chr17	17	qC	46687464	47051542	38	0.783581	0	0.783581	5.82E-70
252741110767_1_2	M23	chr17	17	qD	57084694	57194349	13	1.395756	0	1.395756	5.84E-15
252741110767_1_2	M23	chr17	17	qE4	85260908	85435450	15	0.64735	0	0.64735	2.03E-19
252741110767_1_2	M23	chr17	17	qE4	87992703	88544090	43	0.327822	0	0.327822	2.38E-15
252741110767_1_2	M23	chr18	18	qB1	34796474	35107434	33	0.935444	0	0.935444	4.53E-86
252741110767_1_2	M23	chr18	18	qB2	36615954	36975321	37	0.423877	0	0.423877	2.34E-21
252741110767_1_2	M23	chr18	18	qB3	42363672	42751398	36	0.426264	0	0.426264	4.80E-21
252741110767_1_2	M23	chr18	18	qE4	84790105	85056799	20	0.411935	0	0.411935	8.74E-12
252741110767_1_2	M23	chr19	19	qA	3756960	4206236	49	0.841796	0	0.841796	4.87E-22
252741110767_1_2	M23	chr19	19	qA	4766119	4911304	15	1.437627	0	1.437627	4.38E-43
252741110767_1_2	M23	chr19	19	qA	6335953	6412025	9	1.063338	0	1.063338	3.28E-11
252741110767_1_2	M23	chr19	19	qA	7042155	7109861	9	1.754091	0	1.754091	1.16E-44
252741110767_1_2	M23	chr19	19	qA	8807896	9020081	24	1.301632	0	1.301632	2.77E-120
252741110767_1_2	M23	chr19	19	qA	12793239	12904231	11	0.576141	0	0.576141	1.51E-12
252741110767_1_2	M23	chr19	19	qA	14633402	14688105	6	0.811321	0	0.811321	1.99E-13
252741110767_1_2	M23	chr19	19	qB	21699493	21817157	10	0.652552	0	0.652552	2.44E-14
252741110767_1_2	M23	chr19	19	qC1	29066264	29526925	42	0.405943	0	0.405943	3.70E-22
252741110767_1_2	M23	chr19	19	qC1	34582338	34628345	6	0.693968	0	0.693968	2.74E-10
252741110767_1_2	M23	chr19	19	qC3	40584551	40922464	35	0.540193	0	0.540193	8.86E-32
252741110767_1_2	M23	chr19	19	qC3	41881924	42220697	36	0.864235	0	0.864235	2.70E-80
252741110767_1_2	M23	chr19	19	qC3	43548618	43758890	19	0.796157	0	0.796157	4.07E-37
252741110767_1_2	M23	chr19	19	qC3	44289208	44471807	17	0.694466	0	0.694466	6.77E-26
252741110767_1_2	M23	chr19	19	qC3	46265222	46419727	20	0.273173	0	0.273173	3.44E-11
252741110767_1_2	M23	chr19	19	qD2	53927153	54009843	8	0.617648	0	0.617648	9.02E-11
252741110767_1_2	M23	chrX	X	qA1.1	7099553	7819962	74	0.586091	0	0.586091	5.01E-76
252741110767_1_2	M23	chrX	X	qA1.3	20244096	20565345	32	0.538994	0	0.538994	7.10E-29
252741110767_1_2	M23	chrX	X	qA4	45479538	45634154	18	0.70244	0	0.70244	6.85E-28
252741110767_1_2	M23	chrX	X	qD	98543000	98718279	19	0.684113	0	0.684113	6.37E-28
252741110767_1_2	M23	chrX	X	qD	103152099	103468529	35	0.296138	0	0.296138	8.00E-11
252741110767_1_2	M23	chrX	X	qF3	148673200	148808852	14	0.504401	0	0.504401	2.78E-12
252741110767_1_2	M25	chr1	1	qD	95194949	95492549	35	0.347178	0	0.347178	5.73E-19
252741110767_1_1	M25	chr1	1	qE4	135961313	135998646	5	0.752028	0	0.752028	2.31E-13
252741110767_1_1	M25	chr2	2	qA3	24786220	25512737	69	0.374732	0	0.374732	3.48E-41
252741110767_1_1	M25	chr2	2	qE5	118651509	118751803	11	0.519973	0	0.519973	6.85E-12
252741110767_1_1	M25	chr2	2	qE5	121103503	121273261	19	0.460723	0	0.460723	2.73E-18
252741110767_1_1	M25	chr2	2	qF1	131041518	131086201	5	0.82118	0	0.82118	1.13E-13
252741110767_1_1	M25	chr2	2	qH1	154387568	154442189	6	0.932707	0	0.932707	6.53E-21
252741110767_1_1	M25	chr2	2	qH3	164543040	164701609	17	0.473466	0	0.473466	1.43E-21
252741110767_1_1	M25	chr3	3	qF1	89199720	89234878	5	0.811406	0	0.811406	2.90E-15
252741110767_1_1	M25	chr3	3	qF2.1	94690236	96419630	174	0.266702	0	0.266702	4.51E-52
252741110767_1_1	M25	chr3	3	qF2.1	94759757	94844573	11	0.730184	0	0.730184	1.87E-11
252741110767_1_1	M25	chr3	3	qF2.1	96012726	96069190	6	0.861104	0	0.861104	1.88E-10
252741110767_1_1	M25	chr4	4	qC7	108610059	108850077	26	0.424869	0	0.424869	5.58E-21
252741110767_1_1	M25	chr4	4	qD2.1	118775893	119049312	26	0.343194	0	0.343194	2.52E-14
252741110767_1_1	M25	chr4	4	qD3	135709886	135886915	19	0.522634	0	0.522634	8.63E-22
252741110767_1_1	M25	chr5	5	qC3.3	74493276	74512562	3	0.877472	0	0.877472	3.14E-11
252741110767_1_1	M25	chr5	5	qF	123251244	123313445	7	0.837482	0	0.837482	7.36E-22
252741110767_1_1	M25	chr5	5	qF	124783126	125070939	26	0.349385	0	0.349385	8.83E-15
252741110767_1_1	M25	chr5	5	qG2	138053731	138141235	12	1.083076	0	1.083076	9.59E-57
252741110767_1_1	M25	chr6	6	qC3	85292696	85416197	12	0.44694	0	0.44694	1.36E-11
252741110767_1_1	M25	chr6	6	qE3	112981299	113329710	40	0.319527	0	0.319527	1.70E-18
252741110767_1_1	M25	chr7	7	qA1	3552752	3649707	10	0.549329	0	0.549329	3.85E-14
252741110767_1_1	M25	chr7	7	qA1	4688857	4825141	14	0.77575	0	0.77575	4.02E-36
252741110767_1_1	M25	chr7	7	qA1	13422605	13626353	21	0.449899	0	0.449899	3.55E-19
252741110767_1_1	M25	chr7	7	qA3	19653533	20314658	71	0.442348	0	0.442348	9.22E-58
252741110767_1_1	M25	chr7	7	qA3	26007497	26072479	7	1.067399	0	1.067399	1.00E-33
252741110767_1_1	M25	chr7	7	qA3	26480622	26536738	6	0.788066	0	0.788066	6.17E-17
252741110767_1_1	M25	chr7	7	qA3	27953239	28370374	41	0.326483	0	0.326483	1.15E-19
252741110767_1_1	M25	chr7	7	qA3	29136478	29603148	48	0.372867	0	0.372867	5.10E-29
252741110767_1_1	M25	chr7	7	qB1	31019945	31134228	13	0.772858	0	0.772858	1.90E-33
252741110767_1_1	M25	chr7	7	qB1	31316157	31433496	16	0.546094	0	0.546094	2.68E-21
252741110767_1_1	M25	chr7	7	qF5	150455411	150832863	41	0.272703	0	0.272703	3.07E-14
252741110767_1_1	M25	chr8	8	qB3.3	72158714	72363938	18	0.522415	0	0.522415	1.90E-12
252741110767_1_1	M25	chr8	8	qB3.3	73179890	73370169	20	0.476536	0	0.476536	6.01E-11
252741110767_1_1	M25	chr8	8	qC2 - qC3	86062345	86786228	68	0.530784	0	0.530784	2.48E-79
252741110767_1_1	M25	chr9	9	qA3	20856727	21236076	42	0.436822	0	0.436822	2.80E-20
252741110767_1_1	M25	chr9	9	qA5.2	44106748	44185261	9	0.947828	0	0.947828	9.80E-35
252741110767_1_1	M25	chr9	9	qB	56793679	56960044	17	0.398761	0	0.398761	7.65E-16
252741110767_1_1	M25	chr10	10	qC1	75198171	75532642	34	0.375817	0	0.375817	2.35E-21
252741110767_1_1	M25	chr10	10	qC1	79310794	81758681	209	0.323691	0	0.323691	9.61E-90
252741110767_1_1	M25	chr10	10	qC1	79448762	79688301	26	0.647209	0	0.647209	9.72E-13
252741110767_1_1	M25	chr10	10	qD3	127684108	128334299	64	0.489463	0	0.489463	5.30E-64
252741110767_1_1	M25	chr11	11	qA1	4030407	4111741	11	0.422531	0	0.422531	8.29E-10
252741110767_1_1	M25	chr11	11	qB1.3	50088411	50193323	12	0.480122	0	0.480122	4.13E-13
252741110767_1_1	M25	chr11	11	qB1.3	58667480	58766426	10	0.567086	0	0.567086	5.94E-15
252741110767_1_1	M25	chr11	11	qB3	68752914	68919294	17	0.712561	0	0.712561	7.10E-37
252741110767_1_1	M25	chr11	11	qB3	69545863	69805761	26	0.385655	0	0.385655	1.31E-17
252741110767_1_1	M25	chr11	11	qB4	70752304	70923577	17	0.504363	0	0.504363	2.25E-19
252741110767_1_1	M25	chr11	11	qB5	75108007	75388896	28	0.487474	0	0.487474	6.07E-29
252741110767_1_1	M25	chr11	11	qD	95154099	95250832	12	0.516232	0	0.516232	7.03E-15
252741110767_1_1	M25	chr11	11	qD	96655766	96861085	20	0.859464	0	0.859464	8.57E-61
252741110767_1_1	M25	chr11	11	qD	100779807	100988268	23	0.322307	0	0.322307	1.46E-11
252741110767_1_1	M25	chr11	11	qE1	102782644	103030339	25	0.418876	0	0.418876	1.08E-19
252741110767_1_1	M25	chr11	11	qE1	105897499	106081504	20	0.643669	0	0.643669	1.47E-35
252741110767_1_1	M25	chr11	11	qE2	117504217	117577026	10	0.309699	0	0.309699	3.75E-10

252741110767_1_1	M25	chr11	11	qE2	118905794	118946210	5	0.779586	0	0.779586	3.79E-14
252741110767_1_1	M25	chr11	11	qE2	119787886	120619902	83	0.513909	0	0.513909	3.75E-90
252741110767_1_1	M25	chr12	12	qC3	72073255	72121590	5	0.627395	0	0.627395	7.96E-10
252741110767_1_1	M25	chr12	12	qD2	87163978	87202530	5	0.637874	0	0.637874	4.24E-10
252741110767_1_1	M25	chr13	13	qA3.1	21813250	21921804	11	1.017711	0	1.017711	4.62E-47
252741110767_1_1	M25	chr13	13	qA3.1	23648864	23847542	22	0.878153	0	0.878153	6.56E-69
252741110767_1_1	M25	chr14	14	qC1	45829177	45992834	18	0.422397	0	0.422397	6.19E-15
252741110767_1_1	M25	chr14	14	qC3	56160682	56213555	8	0.677966	0	0.677966	7.74E-17
252741110767_1_1	M25	chr15	15	qD3	76456657	76537831	10	0.458094	0	0.458094	2.30E-10
252741110767_1_1	M25	chr15	15	qE1	79515033	79572112	6	0.695293	0	0.695293	1.16E-13
252741110767_1_1	M25	chr15	15	qE1	81437837	82221284	78	0.262508	0	0.262508	9.78E-24
252741110767_1_1	M25	chr15	15	qF1	98711137	98893849	15	0.389171	0	0.389171	4.44E-11
252741110767_1_1	M25	chr15	15	qF3	102224632	102368167	15	0.686838	0	0.686838	1.17E-30
252741110767_1_1	M25	chr15	15	qF3	103051412	103126464	8	0.706089	0	0.706089	1.10E-17
252741110767_1_1	M25	chr16	16	qC3.3	91598617	91720599	14	0.608914	0	0.608914	5.28E-23
252741110767_1_1	M25	chr17	17	qA3.3	24582588	24725770	15	0.597691	0	0.597691	1.10E-23
252741110767_1_1	M25	chr17	17	qA3.3	24959233	25149304	23	0.767469	0	0.767469	8.31E-57
252741110767_1_1	M25	chr17	17	qA3.3	25847070	26063433	23	0.355385	0	0.355385	1.12E-13
252741110767_1_1	M25	chr17	17	qA3.3	27067800	27139396	8	0.504093	0	0.504093	4.30E-10
252741110767_1_1	M25	chr17	17	qB1	34744070	34780986	5	0.997096	0	0.997096	4.12E-16
252741110767_1_1	M25	chr17	17	qC	46825132	46916057	12	0.546354	0	0.546354	1.89E-16
252741110767_1_1	M25	chr17	17	qD	56022622	57194349	122	0.38729	0	0.38729	1.05E-75
252741110767_1_1	M25	chr18	18	qB1	34761157	35134214	39	0.359778	0	0.359778	2.01E-22
252741110767_1_1	M25	chr19	19	qA	3756960	4974372	127	0.343912	0	0.343912	1.20E-62
252741110767_1_1	M25	chr19	19	qA	5990950	6412025	44	0.361202	0	0.361202	3.09E-25
252741110767_1_1	M25	chr19	19	qA	7042155	7109861	9	0.930153	0	0.930153	1.99E-33
252741110767_1_1	M25	chr19	19	qA	8819802	9038759	25	0.595698	0	0.595698	6.27E-38
252741110767_1_1	M25	chr19	19	qC3	41909502	42198945	31	0.424159	0	0.424159	1.42E-24
252741110767_1_1	M25	chr19	19	qC3	46152863	46893200	84	0.264225	0	0.264225	9.69E-26
252741110767_1_1	M25	chrX	X	qA1.1	7129853	7763099	66	0.426523	0	0.426523	2.02E-50
252741110767_1_1	M25	chrX	X	qA1.3	20232130	20565345	33	0.369671	0	0.369671	1.63E-19
252741110767_1_1	M25	chrX	X	qA4	45452473	45717707	27	0.46607	0	0.46607	1.05E-25
252741110767_1_1	M25	chrX	X	qD	98508150	98791186	29	0.447145	0	0.447145	3.09E-25
252741110767_1_1	M25	chrX	X	qF1	133256795	133358924	10	0.479552	0	0.479552	3.41E-11
252741110767_1_1	M25	chrX	X	qF3	148743603	148788786	5	0.796943	0	0.796943	8.68E-15

Dataset S3. 4. List of CNAs in memory lymphocytes from the popliteal lymph nodes of NOD and BALB/c mice infected with L. major.

NO.	NO.	ID	chrom	chrom	chr region	loc.start	loc.end	num.mark	Amplification	Deletions	mean LRR	pval
252741111474_1_2	6479	Leish. BALB/c. 2	chr6	6	qB3	52,116,749	52,217,998	10	0	-0.595246	-0.595246	2.89E-14
252741111475_1_1	6488	Leish. BALB/c. 5	chr8	8	qE1	121,550,538	121,579,434	3	0.776536	0	0.776536	6.03E-10
252741111475_1_4	6725	Leish. BALB/c. 6	chr2	2	qC3	74,516,368	74,598,078	11	0	-0.550485	-0.550485	1.12E-10
252741111475_1_4	6730	Leish. BALB/c. 6	chr8	8	qC3	87,143,254	87,559,938	47	0	-0.28501	-0.28501	1.32E-11
252741111069_1_3	6090	Leish. NOD 5	chr5	5	qG1.1	125,559,251	125,638,710	10	0	-0.377774	-0.377774	9.29E-11
252741111069_1_3	6099	Leish. NOD 5	chr19	19	qA	3,742,078	3,881,787	16	0.359714	0	0.359714	3.82E-10
252741111476_1_2	6739	Leish. NOD 7	chr6	6	qB3	52,104,495	52,207,847	11	0	-0.475518	-0.475518	3.06E-10

Dataset S3. 5. The percentage of the top three CD4+ T-cell clones per mouse in lymphocytes from PLNs of 10 NOD mice. Clones were determined on the basis of the highly random, non-template aa sequence in the CDR3 region. The sequence in red is shared by all mice.

	α Chain				β Chain				
Mouse	CDR3	V	J	% reads	CDR3	V	J	D	% reads
A	CALSESSFSKLVF	TRAV6D-7*02	TRAJ50*01	2.56	CAWSPGGSAETLYF	TRBV31*01	TRBJ2-3*01	TRBD2*01	2.21
	CAASGSTNTGKLTF	TRAV7-4*01	TRAJ27*01	2.32	CASSRDRDREVFF	TRBV17*01	TRBJ1-1*01	TRBD1*01, TRBD2*01	1.15
	CVVGDRGSALGRLHF	TRAV11D*01, TRAV11*01	TRAJ18*01	0.4	CAASSNTDKVVF	TRBV2*01	TRBJ1-1*01	TRBD1*01	0.04
B	CVVGDRGSALGRLHF	TRAV11D*01, TRAV11*01	TRAJ18*01	0.71	CAWSPGGSAETLYF	TRBV31*01	TRBJ2-3*01	TRBD1*01	0.68
	CAAGGSALGRLHF	TRAV10D*01, TRAV10D*02	TRAJ18*01	0.59	CASSRDRDREVFF	TRBV17*01	TRBJ1-1*01	TRBD1*01, TRBD2*01	0.61
	CAVSNNNNAPRF	TRAV3-4*01	TRAJ43*01	0.4	CAASSNTDKVVF	TRBV2*01	TRBJ1-1*01	TRBD1*01	0.02
C	CAASRNYKYVF	TRAV14D-3/DV8*03	TRAJ40*01	0.96	CAASGGNNRIFF	TRBV2*01	TRBJ1-1*02, TRBJ1-1*01	TRBD1*01, TRBD2*01	0.59
	CVVGDRGSALGRLHF	TRAV11D*01, TRAV11*01	TRAJ18*01	0.94	CASSDWGSSYEQYF	TRBV13-3*01	TRBJ2-7*01	TRBD2*01	0.53
	CAVRPSDTNAYKVIF	TRAV3-4*01	TRAJ30*01	0.65	CAASSNTDKVVF	TRBV2*01	TRBJ1-1*01	TRBD1*01	0.02
D	CAASGNTNTGKLTF	TRAV7-4*01	TRAJ27*01	5.29	CASSQRLGGIAEQFF	TRBV5*01	TRBJ2-1*01	TRBD2*01	2.07
	CVVGDRGSALGRLHF	TRAV11D*01, TRAV11*01	TRAJ18*01	2.12	CASSFQGAGQFF	TRBV15*01	TRBJ2-1*01	TRBD1*01	1.89
	CAASWNMGYKLTF	TRAV10*01	TRAJ9*01	1.82	CAASSNTDKVVF	TRBV2*01	TRBJ1-1*01	TRBD1*01	0.35
E	CVVGDRGSALGRLHF	TRAV11D*01, TRAV11*01	TRAJ18*01	1.1	CASSLTGGEQYF	TRBV15*01	TRBJ2-7*01	TRBD1*01	0.32
	CALEGAGGADRLTF	TRAV17*01	TRAJ45*01	0.3	CASGDANSPLYF	TRBV13-2*01	TRBJ2-5*01	TRBD1*01, TRBD2*01	0.26
	CAMANNNAGAKLTF	TRAV13D-4*01, TRAV13N-4*01	TRAJ39*01	0.29	CAASSNTDKVVF	TRBV2*01	TRBJ1-1*01	TRBD1*01	0.19
F	CVVGDRGSALGRLHF	TRAV11D*01, TRAV11*01	TRAJ18*01	1.46	CAASSNTDKVVF	TRBV2*01	TRBJ1-1*01	TRBD1*01	0.4
	CAANTGGADRLTF	TRAV14D-1*02	TRAJ45*01	0.66	CALEGPGGSALGRLHF	TRBV12-1*01, TRBV12-1*02	TRBJ1-5*03	TRBD2*01	0.4
	CAAETGNTRKLIF	TRAV4D-3*01	TRAJ57*01	0.47	CASSLGDQDTQYF	TRBV14*01	TRBJ2-5*01	TRBD1*01, TRBD2*01	0.35
G	CAVSASMGYKLTF	TRAV9D-3*01	TRAJ9*01	0.3	CASSLAGLDAEQFF	TRBV15*01	TRBJ2-1*01	TRBD1*01, TRBD2*01	0.63
	CAASATSSGQKLVF	TRAV14D-3/DV8*05	TRAJ16*01	0.28	CASSDIQGAETLYF	TRBV13-3*01	TRBJ2-3*01	TRBD1*01	0.32
	CAMARNNYAQGLTF	TRAV13D-1*01	TRAJ26*01	0.26	CAASSNTDKVVF	TRBV2*01	TRBJ1-1*01	TRBD1*01	0.13
H	CVVGDRGSALGRLHF	TRAV11D*01, TRAV11*01	TRAJ18*01	1.46	CASRRQDQAPLF	TRBV15*01	TRBJ1-5*01	TRBD1*01	1.02
	CAMERGGGSGNKLIF	TRAV13D-1*01	TRAJ32*02	0.32	CASRTGTGGPGQLYF	TRBV15*01	TRBJ2-2*01	TRBD2*01	0.25
	CAASKGGNYKYVF	TRAV14D-3/DV8*03	TRAJ40*01	0.24	CAASSNTDKVVF	TRBV2*01	TRBJ1-1*01	TRBD1*01	0.09
I	CALSENTGANTGKLTF	TRAV6D-7*02	TRAJ52*01	4.19	CASSLGQGDTEVFF	TRBV4*01	TRBJ1-1*01	TRBD1*01	3.93
	CALSPPQGGRALIF	TRAV6-5*01, TRAV6-5*02	TRAJ15*01	4.19	CASSYWGNQDTQYF	TRBV13-3*01	TRBJ2-5*01	TRBD2*01	2.42
	CVVGDRGSALGRLHF	TRAV11D*01, TRAV11*01	TRAJ18*01	1.35	CAASSNTDKVVF	TRBV2*01	TRBJ1-1*01	TRBD1*01	0.01
J	CVVGDRGSALGRLHF	TRAV11D*01, TRAV11*01	TRAJ18*01	1.81	CASRYRGRNTEVFF	TRBV14*01	TRBJ1-1*01	TRBD1*01	0.67
	CAVSEGGYKVVF	TRAV3D-3*01	TRAJ12*01	1.46	CASSRRRDTGQLYF	TRBV13-3*01	TRBJ2-2*01	TRBD1*01	0.46
	CAATGANTGKLTF	TRAV14-1*02	TRAJ52*01	0.67	CAASSNTDKVVF	TRBV2*01	TRBJ1-1*01	TRBD1*01	0.12

Dataset S4. 1. List of CNAs in rh-PI- reactive lymphocytes of 17 tested diabetic patients (ADM-2 (LRRl0.25l, P- value ≤1x10-10) and CBS (LRRl0.25l, P-value ≤5 x 10-08)). Since we have no prior information in which to base power calculations the number of patients tested was determined by available funds.

ID	NO.	ID	chrom	chrom	chr region	loc.start	loc.end	num.mark	Amplification	Deletions	mean LRR	pval
252152938940	1	PI-5	chr2	2	q33.2	204717721	204771475	22	0	-0.274407	-0.274407	3.56E-10
252152938940	8	PI-5	chr17	17	q23.1	57893432	57924260	32	0	-0.293052	-0.293052	1.62E-15
252152938964	1	PI-15	chr1	1	p34.1	45259064	45265455	4	0.773546	0	0.773546	4.89E-10
252152938964	2	PI-15	chr1	1	p22.3	87254644	87266450	7	0.515395	0	0.515395	1.96E-10
252152938964	3	PI-15	chr2	2	p11.2	85096508	85133999	18	0.417834	0	0.417834	5.33E-13
252152938964	6	PI-15	chr3	3	q26.2	169483860	169491968	5	0.619405	0	0.619405	5.11E-10
252152938964	7	PI-15	chr5	5	p14.1	28610977	28640741	12	0.377318	0	0.377318	1.38E-11
252152938964	9	PI-15	chr6	6	p22.3	24352516	24380835	14	0.410374	0	0.410374	1.64E-11
252152938964	10	PI-15	chr6	6	p12.1	55960088	55974350	10	0.435461	0	0.435461	9.12E-11
252152938964	11	PI-15	chr7	7	p14.2	35669247	35754079	38	0.283619	0	0.283619	1.58E-12
252152938964	12	PI-15	chr8	8	p12	29892640	30027230	57	0.288328	0	0.288328	5.40E-14
252152938964	14	PI-15	chr9	9	q31.3	113438155	113467599	13	0.407032	0	0.407032	3.42E-12
252152938964	16	PI-15	chr12	12	q13.11	47601458	47628330	14	0.427401	0	0.427401	5.68E-13
252152938964	17	PI-15	chr13	13	q14.13	45991680	46006480	11	0.569649	0	0.569649	8.86E-16
252152938964	21	PI-15	chr21	21	q21.1	19620375	19629293	8	0.642474	0	0.642474	4.20E-17
252152938972	2	PI-11	chr12	12	p13.31	7777178	7787402	5	0	-0.743347	-0.743347	1.63E-14
252152938972	3	PI-11	chr12	12	q21.33	92509286	92566506	29	0.272849	0	0.272849	5.53E-11
252152938949	1	PI-6	chr1	1	p36.33	1161233	1170786	5	0	-0.90182	-0.90182	1.16E-18
252152938949	4	PI-6	chr1	1	p36.22	10697093	10702119	3	0	-1.32924	-1.32924	2.62E-21
252152938949	5	PI-6	chr1	1	p36.22	10748432	10759946	6	0	-0.79265	-0.79265	1.34E-15
252152938949	7	PI-6	chr1	1	p36.13	17761695	17769964	5	0	-0.85993	-0.85993	2.88E-16
252152938949	8	PI-6	chr1	1	p36.13	17860247	17873219	7	0	-0.65479	-0.65479	8.57E-14
252152938949	9	PI-6	chr1	1	p36.12	22464571	22473398	6	0	-1.06342	-1.06342	3.29E-27
252152938949	10	PI-6	chr1	1	p36.12	22887170	22897061	5	0	-0.81258	-0.81258	3.65E-15
252152938949	11	PI-6	chr1	1	p36.12	23488109	23496713	6	0	-0.8392	-0.8392	1.13E-16
252152938949	12	PI-6	chr1	1	p36.11	25939557	25947827	4	0	-0.86055	-0.86055	2.83E-14
252152938949	14	PI-6	chr1	1	p36.11	27143675	27156287	7	0	-0.84826	-0.84826	3.26E-20
252152938949	15	PI-6	chr1	1	p35.3	28990653	28997655	4	0	-0.74607	-0.74607	2.61E-11
252152938949	17	PI-6	chr1	1	p35.2	32222873	32233683	6	0	-0.82317	-0.82317	6.07E-17
252152938949	19	PI-6	chr1	1	p35.1	33426685	33431071	3	0	-0.9655	-0.9655	1.87E-13
252152938949	20	PI-6	chr1	1	p35.1	33720488	33724397	3	0	-1.69775	-1.69775	2.57E-27
252152938949	21	PI-6	chr1	1	p35.1	33808437	33817799	6	0	-0.65558	-0.65558	1.49E-12
252152938949	22	PI-6	chr1	1	p34.3	35437744	35447506	7	0	-0.8146	-0.8146	1.76E-20
252152938949	24	PI-6	chr1	1	p34.2	42119806	42133042	7	0	-0.73118	-0.73118	2.78E-17
252152938949	25	PI-6	chr1	1	p34.1	44441473	44449888	4	0	-0.85045	-0.85045	5.06E-12
252152938949	26	PI-6	chr1	1	p13.3	109100537	109105616	4	0	-0.99708	-0.99708	1.04E-18
252152938949	27	PI-6	chr1	1	p12	120160783	120169523	6	0	-0.86205	-0.86205	1.74E-19
252152938949	28	PI-6	chr1	1	q21.3	151427909	151433411	4	0	-1.0532	-1.0532	2.94E-19
252152938949	30	PI-6	chr1	1	q24.1	166937636	166948513	6	0	-0.84415	-0.84415	1.86E-17
252152938949	31	PI-6	chr1	1	q25.1	173445728	173449185	3	0	-1.19801	-1.19801	1.02E-18
252152938949	32	PI-6	chr1	1	q41	215252377	215258703	5	0	-1.04673	-1.04673	9.35E-20
252152938949	33	PI-6	chr1	1	q42.12	224620789	224626236	4	0	-0.78274	-0.78274	3.69E-12
252152938949	34	PI-6	chr1	1	q42.13	228191488	228200101	5	0	-0.89324	-0.89324	1.35E-15
252152938949	35	PI-6	chr1	1	q42.13	228340877	228349826	4	0	-0.89141	-0.89141	2.26E-14
252152938949	36	PI-6	chr1	1	q42.13	229759370	229765103	4	0	-1.12635	-1.12635	5.27E-22
252152938949	37	PI-6	chr1	1	q42.13	230559321	230564552	4	0	-1.24362	-1.24362	8.15E-23
252152938949	38	PI-6	chr1	1	q42.3	234740153	234749721	7	0	-0.78556	-0.78556	6.85E-18
252152938949	41	PI-6	chr2	2	p23.3	24711131	24715739	3	0	-1.13177	-1.13177	2.12E-17
252152938949	42	PI-6	chr2	2	p23.3	25888918	25901567	6	0	-0.65292	-0.65292	7.40E-13
252152938949	44	PI-6	chr2	2	p23.3	26905516	26918014	9	0	-0.59341	-0.59341	1.59E-15
252152938949	47	PI-6	chr2	2	p13.2	72371485	72378767	5	0	-0.90617	-0.90617	7.37E-18
252152938949	48	PI-6	chr2	2	p13.1	74210382	74216010	3	0	-1.19362	-1.19362	3.48E-18
252152938949	49	PI-6	chr2	2	p11.2	85196363	85200883	3	0	-0.9374	-0.9374	1.72E-12
252152938949	50	PI-6	chr2	2	q11.1	96005413	96013437	5	0	-0.8577	-0.8577	3.65E-16
252152938949	51	PI-6	chr2	2	q11.2	99344766	99349698	4	0	-1.42013	-1.42013	3.79E-29
252152938949	52	PI-6	chr2	2	q11.2	100722048	100724330	3	0	-1.19238	-1.19238	4.99E-18
252152938949	53	PI-6	chr2	2	q11.2	102311073	102318092	5	0	-0.77905	-0.77905	3.63E-13
252152938949	54	PI-6	chr2	2	q12.1	105470985	105477210	3	0	-1.41705	-1.41705	4.62E-21
252152938949	55	PI-6	chr2	2	q12.1	105943329	105948437	4	0	-0.77226	-0.77226	2.03E-11
252152938949	56	PI-6	chr2	2	q13	113235630	113243627	6	0	-0.82803	-0.82803	2.58E-16
252152938949	58	PI-6	chr2	2	q14.2	121745463	121753112	4	0	-0.92642	-0.92642	1.20E-13
252152938949	59	PI-6	chr2	2	q24.2	162191668	162195040	3	0	-0.83781	-0.83781	1.57E-10
252152938949	60	PI-6	chr2	2	q31.1	176971881	176975944	4	0	-1.36187	-1.36187	4.04E-21
252152938949	61	PI-6	chr2	2	q31.3	181837913	181855210	8	0	-0.6647	-0.6647	9.32E-17
252152938949	62	PI-6	chr2	2	q33.1	198169927	198177264	5	0	-0.82456	-0.82456	5.70E-14
252152938949	63	PI-6	chr2	2	q33.3	208387038	208403314	10	0	-0.78019	-0.78019	1.91E-27
252152938949	64	PI-6	chr2	2	q34	214010725	214020099	5	0	-1.08737	-1.08737	6.09E-24
252152938949	66	PI-6	chr2	2	q37.1	234259365	234268284	7	0	-0.92531	-0.92531	5.13E-21
252152938949	67	PI-6	chr2	2	q37.2	237122073	237126402	4	0	-1.03589	-1.03589	2.26E-16
252152938949	68	PI-6	chr2	2	q37.3	238874812	238881786	5	0	-0.67543	-0.67543	2.68E-11
252152938949	69	PI-6	chr2	2	q37.3	240320894	240324140	3	0	-1.42546	-1.42546	3.40E-17
252152938949	71	PI-6	chr3	3	p25.2	12039153	12050170	7	0	-0.9624	-0.9624	5.30E-27
252152938949	72	PI-6	chr3	3	p25.1	13320807	13328079	3	0	-1.14395	-1.14395	1.39E-16
252152938949	73	PI-6	chr3	3	p25.1	14850631	14858235	4	0	-0.84342	-0.84342	9.53E-13
252152938949	74	PI-6	chr3	3	p22.1	43325893	43331904	5	0	-1.22565	-1.22565	2.44E-29
252152938949	75	PI-6	chr3	3	p21.31	45264355	45269773	5	0	-0.91958	-0.91958	2.81E-18
252152938949	78	PI-6	chr3	3	p21.1	53072344	53081754	6	0	-0.88359	-0.88359	1.23E-20
252152938949	79	PI-6	chr3	3	p21.1	53523729	53534833	5	0	-0.76538	-0.76538	2.54E-14
252152938949	80	PI-6	chr3	3	p14.2	62856559	62863997	4	0	-0.75626	-0.75626	7.89E-12
252152938949	81	PI-6	chr3	3	p14.1	63846162	63852530	4	0	-1.0951	-1.0951	5.68E-19
252152938949	82	PI-6	chr3	3	p13	71769739	71809842	20	0	-0.53831	-0.53831	2.20E-25
252152938949	83	PI-6	chr3	3	p13	72931718	72941872	7	0	-0.74536	-0.74536	4.27E-18
252152938949	84	PI-6	chr3	3	q21.1	123162474	123165735	3	0	-0.83877	-0.83877	1.47E-10
252152938949	86	PI-6	chr3	3	q21.2	124770896	124777685	4	0	-0.84693	-0.84693	2.48E-13
252152938949	87	PI-6	chr3	3	q21.3	127346735	127351298	3	0	-1.24069	-1.24069	3.47E-19
252152938949	89	PI-6	chr3	3	q26.32	176912261	176917249	3	0	-0.93206	-0.93206	8.92E-13
252152938949	90	PI-6	chr3	3	q27.2	185537809	185550224	7	0	-0.56187	-0.56187	3.90E-10
252152938949	92	PI-6	chr4	4	p16.3	1236812	1249453	6	0	-0.72942	-0.72942	6.95E-15

252152938949	96	PI-6	chr4	4	p16.2	5890426	5897005	4	0	-1.02287	-1.02287	4.05E-15
252152938949	99	PI-6	chr4	4	p15.2	21940389	21958331	10	0	-0.51154	-0.51154	3.47E-13
252152938949	100	PI-6	chr4	4	p15.2	26315674	26327728	7	0	-0.6334	-0.6334	1.55E-12
252152938949	102	PI-6	chr4	4	q23	100866951	100875041	5	0	-0.86639	-0.86639	1.50E-15
252152938949	103	PI-6	chr4	4	q31.1	140027321	140043262	9	0	-0.66818	-0.66818	5.01E-18
252152938949	107	PI-6	chr5	5	p15.33	2746963	2754445	4	0	-1.07602	-1.07602	3.47E-19
252152938949	108	PI-6	chr5	5	p15.31	6446105	6455232	5	0	-0.712	-0.712	4.81E-12
252152938949	109	PI-6	chr5	5	p15.31	6707258	6717780	5	0	-0.99364	-0.99364	3.12E-20
252152938949	110	PI-6	chr5	5	p15.2	11900407	11907663	6	0	-1.07376	-1.07376	1.59E-27
252152938949	111	PI-6	chr5	5	p15.2	14137939	14151055	9	0	-0.67352	-0.67352	1.27E-18
252152938949	112	PI-6	chr5	5	p15.2	14484401	14497064	6	0	-0.92566	-0.92566	5.17E-22
252152938949	113	PI-6	chr5	5	p15.2	14869647	14876170	5	0	-0.82639	-0.82639	3.91E-14
252152938949	114	PI-6	chr5	5	p13.1	38555754	38560170	3	0	-0.98874	-0.98874	2.92E-14
252152938949	115	PI-6	chr5	5	q12.1	60625904	60634164	3	0	-0.8025	-0.8025	5.79E-10
252152938949	116	PI-6	chr5	5	q13.2	72736905	72745282	5	0	-0.86335	-0.86335	3.22E-17
252152938949	117	PI-6	chr5	5	q13.3	76329022	76344673	8	0	-0.51426	-0.51426	4.53E-11
252152938949	118	PI-6	chr5	5	q14.1	81027222	81061693	18	0	-0.35936	-0.35936	8.54E-12
252152938949	119	PI-6	chr5	5	q31.1	132300208	132338025	13	0.487412	0	0.487412	1.02E-14
252152938949	120	PI-6	chr5	5	q33.2	153565287	153582637	9	0	-0.61604	-0.61604	4.78E-16
252152938949	121	PI-6	chr5	5	q34	167951830	167958053	4	0	-1.15429	-1.15429	5.12E-22
252152938949	122	PI-6	chr5	5	q35.3	176979363	176982223	4	0	-1.0735	-1.0735	8.06E-17
252152938949	125	PI-6	chr5	5	q35.3	179632572	179640279	5	0	-0.98282	-0.98282	2.80E-20
252152938949	126	PI-6	chr6	6	p25.1	4774780	4779865	3	0	-0.94516	-0.94516	1.17E-12
252152938949	127	PI-6	chr6	6	p24.3	7904608	7916169	6	0	-0.57449	-0.57449	2.13E-10
252152938949	128	PI-6	chr6	6	p24.1	12008097	12013632	4	0	-1.25767	-1.25767	1.23E-22
252152938949	129	PI-6	chr6	6	p22.3	17984614	17990306	4	0	-1.18026	-1.18026	1.15E-22
252152938949	131	PI-6	chr6	6	q14.1	79784507	79789852	4	0	-1.21358	-1.21358	2.32E-24
252152938949	132	PI-6	chr6	6	q21	105625169	105630421	4	0	-1.28331	-1.28331	1.27E-26
252152938949	133	PI-6	chr6	6	q21	114177937	114181892	3	0	-0.83601	-0.83601	1.71E-10
252152938949	134	PI-6	chr6	6	q22.31	124123115	124127580	3	0	-0.89846	-0.89846	3.46E-12
252152938949	135	PI-6	chr6	6	q23.1	130337779	130343379	3	0	-1.22599	-1.22599	3.12E-18
252152938949	136	PI-6	chr6	6	q24.1	139451101	139461526	4	0	-0.91579	-0.91579	1.28E-15
252152938949	137	PI-6	chr6	6	q24.2	143378370	143384299	4	0	-1.42879	-1.42879	7.44E-30
252152938949	138	PI-6	chr6	6	q24.3	147521494	147527219	3	0	-0.8675	-0.8675	1.14E-11
252152938949	139	PI-6	chr6	6	q25.3	157093875	157108055	8	0	-0.66076	-0.66076	1.53E-16
252152938949	140	PI-6	chr6	6	q25.3	158243414	158250063	5	0	-0.88318	-0.88318	9.18E-17
252152938949	143	PI-6	chr6	6	q27	170121435	170127040	4	0	-1.16442	-1.16442	3.85E-23
252152938949	144	PI-6	chr7	7	p22.3	1268386	1273991	4	0	-1.14864	-1.14864	3.87E-20
252152938949	146	PI-6	chr7	7	p22.3	2612635	2623881	7	0	-1.17821	-1.17821	5.98E-37
252152938949	149	PI-6	chr7	7	p22.1	4718668	4727460	5	0	-0.74798	-0.74798	2.16E-12
252152938949	150	PI-6	chr7	7	p22.1	6648279	6698360	23	0	-0.65131	-0.65131	1.22E-37
252152938949	151	PI-6	chr7	7	p15.2	27166945	27171520	4	0	-0.94727	-0.94727	4.13E-17
252152938949	152	PI-6	chr7	7	p15.1	28216387	28222380	4	0	-0.95922	-0.95922	8.29E-17
252152938949	153	PI-6	chr7	7	p14.3	30319389	30326807	6	0	-0.69842	-0.69842	5.98E-14
252152938949	154	PI-6	chr7	7	p14.3	32930034	32935481	4	0	-0.88939	-0.88939	1.05E-12
252152938949	155	PI-6	chr7	7	p14.2	35069089	35080318	5	0	-0.80812	-0.80812	1.41E-15
252152938949	158	PI-6	chr7	7	p14.1	42273529	42279753	4	0	-0.80492	-0.80492	1.38E-12
252152938949	159	PI-6	chr7	7	p12.2	50343122	50346310	3	0	-1.36061	-1.36061	1.03E-20
252152938949	160	PI-6	chr7	7	q21.11	77644551	77650842	4	0	-1.11974	-1.11974	1.63E-21
252152938949	161	PI-6	chr7	7	q22.1	98742296	98745745	3	0	-0.82404	-0.82404	1.11E-10
252152938949	163	PI-6	chr7	7	q22.1	101455968	101472053	10	0	-0.61256	-0.61256	1.16E-15
252152938949	164	PI-6	chr7	7	q22.1	101888196	101896854	8	0	-1.1692	-1.1692	4.50E-37
252152938949	166	PI-6	chr7	7	q32.1	128760927	128769917	6	0	-0.85279	-0.85279	1.35E-19
252152938949	167	PI-6	chr7	7	q32.3	130781493	130796469	8	0	-0.57407	-0.57407	3.24E-13
252152938949	169	PI-6	chr7	7	q34	142337376	142492085	40	0	-0.62925	-0.62925	4.15E-61
252152938949	171	PI-6	chr7	7	q36.1	149124837	149173798	26	0	-0.47898	-0.47898	2.21E-26
252152938949	172	PI-6	chr7	7	q36.1	150087179	150106229	11	0	-0.71345	-0.71345	1.58E-25
252152938949	175	PI-6	chr7	7	q36.1	152128912	152134515	3	0	-0.88524	-0.88524	1.22E-11
252152938949	176	PI-6	chr7	7	q36.2	154791894	154801863	5	0	-0.64921	-0.64921	1.06E-10
252152938949	177	PI-6	chr7	7	q36.3	156795837	156809249	8	0	-0.89513	-0.89513	2.55E-22
252152938949	178	PI-6	chr7	7	q36.3	158185930	158194433	6	0	-0.70138	-0.70138	7.80E-14
252152938949	179	PI-6	chr8	8	p23.3	631326	655907	12	0	-0.54204	-0.54204	3.83E-16
252152938949	180	PI-6	chr8	8	p23.3	1708621	1715613	4	0	-1.22735	-1.22735	3.84E-25
252152938949	181	PI-6	chr8	8	p23.3	1786757	1808966	13	0	-0.40167	-0.40167	6.80E-11
252152938949	182	PI-6	chr8	8	p23.1	12608291	12628718	12	0	-0.43266	-0.43266	3.14E-11
252152938949	184	PI-6	chr8	8	p11.21	41905520	41912212	4	0	-1.00049	-1.00049	2.63E-18
252152938949	185	PI-6	chr8	8	p11.21	42745197	42757937	8	0	-0.72684	-0.72684	1.62E-19
252152938949	186	PI-6	chr8	8	q12.1	56012260	56017767	5	0	-1.11299	-1.11299	5.24E-18
252152938949	187	PI-6	chr8	8	q12.1 - q12.2	61584412	61602381	10	0	-0.64795	-0.64795	1.25E-19
252152938949	188	PI-6	chr8	8	q21.11	74653564	74662906	5	0	-0.90433	-0.90433	5.30E-17
252152938949	189	PI-6	chr8	8	q21.13	80676557	80687357	7	0	-0.88184	-0.88184	7.76E-22
252152938949	192	PI-6	chr8	8	q24.11	117949790	117968293	10	0	-0.5132	-0.5132	4.98E-13
252152938949	193	PI-6	chr8	8	q24.23	136463887	136474632	5	0	-0.93161	-0.93161	2.58E-19
252152938949	194	PI-6	chr8	8	q24.3	141642302	141647348	3	0	-1.26832	-1.26832	1.19E-19
252152938949	196	PI-6	chr8	8	q24.3	144437412	144446966	5	0	-0.89565	-0.89565	2.97E-18
252152938949	199	PI-6	chr9	9	p24.3	2045009	2051680	5	0	-1.20062	-1.20062	3.91E-28
252152938949	200	PI-6	chr9	9	p22.3	14307028	14321607	7	0	-0.61901	-0.61901	1.31E-12
252152938949	201	PI-6	chr9	9	p13.3	34953435	34961045	6	0	-0.79991	-0.79991	4.46E-18
252152938949	202	PI-6	chr9	9	p13.3	35788888	35795407	4	0	-0.97497	-0.97497	9.72E-18
252152938949	203	PI-6	chr9	9	q21.11	71623658	71635398	9	0	-0.68099	-0.68099	4.29E-19
252152938949	204	PI-6	chr9	9	q21.11	71939165	71942782	3	0	-1.55601	-1.55601	4.61E-26
252152938949	205	PI-6	chr9	9	q21.11	72127040	72133993	6	0	-0.75214	-0.75214	1.32E-16
252152938949	206	PI-6	chr9	9	q22.2	92287505	92299807	6	0	-0.76347	-0.76347	3.02E-13
252152938949	208	PI-6	chr9	9	q22.31	96208809	96227148	9	0	-0.58517	-0.58517	4.77E-15
252152938949	209	PI-6	chr9	9	q22.31	96335537	96345000	6	0	-0.80873	-0.80873	5.05E-16
252152938949	210	PI-6	chr9	9	q22.32	96712247	96724936	7	0	-0.65598	-0.65598	3.56E-13
252152938949	211	PI-6	chr9	9	q22.32	97761873	97770187	6	0	-0.84253	-0.84253	7.54E-19
252152938949	212	PI-6	chr9	9	q22.32	98046555	98061710	6	0	-0.65304	-0.65304	1.08E-12
252152938949	213	PI-6	chr9	9	q22.32	98274246	98284265	7	0	-0.59423	-0.59423	8.80E-12
252152938949	214	PI-6	chr9	9	q22.33	99379157	99382944	3	0	-1.06069	-1.06069	3.61E-15
252152938949	216	PI-6	chr9	9	q22.33	101863999	101873345	6	0	-0.5586	-0.5586	5.42E-10
252152938949	218	PI-6	chr9	9	q31.3	112079831	112084853	3	0	-1.00283	-1.00283	1.21E-14
252152938949	219	PI-6	chr9	9	q31.3	112255821	112263808	4	0	-0.70852	-0.70852	3.41E-10
252152938949	220	PI-6	chr9	9	q32	115242307	115252623	6	0	-1.0407	-1.0407	1.48E-26
252152938949	221	PI-6	chr9	9	q32	116632755	116642488	6	0	-0.82784	-0.82784	7.97E-19
252152938949	222	PI-6	chr9	9	q33.1	118912806	118920303	5	0	-1.26915	-1.26915	2.23E-29

252152938949	223	PI-6	chr9	9	q33.2	124447465	124474865	17	0	-0.51818	-0.51818	2.26E-19
252152938949	224	PI-6	chr9	9	q33.3	127016299	127023652	4	0	-1.00654	-1.00654	3.43E-16
252152938949	225	PI-6	chr9	9	q33.3	128498626	128513769	7	0	-0.67236	-0.67236	1.30E-14
252152938949	226	PI-6	chr9	9	q33.3	129086622	129095085	5	0	-1.18247	-1.18247	6.78E-24
252152938949	227	PI-6	chr9	9	q34.11	131449302	131455424	4	0	-1.00314	-1.00314	1.33E-17
252152938949	229	PI-6	chr9	9	q34.12	133705609	133717829	8	0	-0.67737	-0.67737	2.83E-17
252152938949	230	PI-6	chr9	9	q34.13	134149769	134157410	4	0	-1.02239	-1.02239	1.90E-16
252152938949	234	PI-6	chr9	9	q34.3	138366743	138380766	7	0	-0.76442	-0.76442	1.00E-18
252152938949	235	PI-6	chr9	9	q34.3	138600326	138607836	4	0	-0.97989	-0.97989	6.58E-17
252152938949	237	PI-6	chr9	9	q34.3	140506624	140519724	7	0	-0.80216	-0.80216	3.68E-17
252152938949	239	PI-6	chr10	10	p13	13567770	13574704	4	0	-0.93293	-0.93293	3.87E-16
252152938949	240	PI-6	chr10	10	p13	14629230	14653381	10	0	-0.47711	-0.47711	1.61E-11
252152938949	241	PI-6	chr10	10	p13	15407939	15418293	7	0	-0.69618	-0.69618	9.15E-15
252152938949	243	PI-6	chr10	10	p12.2	23000716	23006417	4	0	-1.03742	-1.03742	1.93E-19
252152938949	244	PI-6	chr10	10	p12.1	25009566	25014502	3	0	-1.14835	-1.14835	8.65E-16
252152938949	245	PI-6	chr10	10	p12.1	26854436	26858737	4	0	-1.06155	-1.06155	3.76E-18
252152938949	246	PI-6	chr10	10	p11.21	35620587	35632866	5	0	-0.87546	-0.87546	1.81E-17
252152938949	247	PI-6	chr10	10	p11.21	35922572	35934470	6	0	-0.7907	-0.7907	1.75E-15
252152938949	248	PI-6	chr10	10	q11.21	43744089	43767920	13	0	-0.44092	-0.44092	1.68E-11
252152938949	250	PI-6	chr10	10	q11.23	50322806	50327075	3	0	-0.96211	-0.96211	1.30E-12
252152938949	251	PI-6	chr10	10	q22.3	79390905	79405358	9	0	-0.67885	-0.67885	5.81E-17
252152938949	253	PI-6	chr10	10	q23.2	88852158	88855782	3	0	-0.9582	-0.9582	3.81E-13
252152938949	254	PI-6	chr10	10	q23.31	92616024	92618536	3	0	-1.02706	-1.02706	7.39E-14
252152938949	255	PI-6	chr10	10	q23.32	92919743	92927117	4	0	-0.8378	-0.8378	1.06E-12
252152938949	256	PI-6	chr10	10	q24.1	98588727	98596596	11	0	-0.91079	-0.91079	7.15E-37
252152938949	257	PI-6	chr10	10	q24.2	99468124	99477896	5	0	-0.77978	-0.77978	8.51E-15
252152938949	258	PI-6	chr10	10	q25.2	114703492	114716831	8	0	-0.63717	-0.63717	1.83E-14
252152938949	260	PI-6	chr10	10	q26.3	134199027	134214828	6	0	-0.96184	-0.96184	6.04E-18
252152938949	263	PI-6	chr11	11	p15.4	6647796	6657347	6	0	-0.88898	-0.88898	3.80E-19
252152938949	266	PI-6	chr11	11	q12.2	61342766	61354478	6	0	-0.84799	-0.84799	4.78E-16
252152938949	267	PI-6	chr11	11	q13.1	63528548	63540745	5	0	-0.87428	-0.87428	2.00E-16
252152938949	269	PI-6	chr11	11	q13.1	64542025	64546879	4	0	-0.93217	-0.93217	2.26E-16
252152938949	271	PI-6	chr11	11	q13.1	65806073	65814470	5	0	-0.96655	-0.96655	8.96E-21
252152938949	272	PI-6	chr11	11	q13.2	66494511	66498204	3	0	-1.51995	-1.51995	2.18E-25
252152938949	273	PI-6	chr11	11	q13.2	67023840	67067067	20	0	-0.4252	-0.4252	1.35E-14
252152938949	275	PI-6	chr11	11	q14.1	78126482	78138065	7	0	-0.74545	-0.74545	1.96E-16
252152938949	276	PI-6	chr11	11	q21	93273959	93279938	4	0	-1.00722	-1.00722	4.19E-18
252152938949	278	PI-6	chr11	11	q24.3	129144896	129151574	3	0	-1.20545	-1.20545	9.49E-19
252152938949	280	PI-6	chr12	12	p13.33	2157578	2167648	7	0	-0.62057	-0.62057	5.75E-11
252152938949	281	PI-6	chr12	12	p13.31	7026930	7043222	9	0	-0.68636	-0.68636	1.90E-19
252152938949	282	PI-6	chr12	12	p13.31	7778761	7787402	4	0	-1.23879	-1.23879	1.40E-25
252152938949	283	PI-6	chr12	12	p12.3	19282053	19285386	3	0	-1.30205	-1.30205	2.16E-21
252152938949	284	PI-6	chr12	12	q12	42979841	42997790	10	0	-0.43063	-0.43063	6.50E-10
252152938949	285	PI-6	chr12	12	q12	46120090	46127415	4	0	-0.98252	-0.98252	1.29E-17
252152938949	287	PI-6	chr12	12	q13.13	52344104	52348294	3	0	-1.11619	-1.11619	1.57E-17
252152938949	288	PI-6	chr12	12	q13.13	52404481	52409678	3	0	-1.20229	-1.20229	6.34E-18
252152938949	290	PI-6	chr12	12	q13.3	57398905	57403889	4	0	-0.93065	-0.93065	5.55E-17
252152938949	291	PI-6	chr12	12	q23.1	96579046	96593111	8	0	-0.59004	-0.59004	7.77E-14
252152938949	292	PI-6	chr12	12	q23.1	100372561	100380585	5	0	-1.02194	-1.02194	1.45E-22
252152938949	294	PI-6	chr12	12	q24.11	111470217	111476055	4	0	-1.2412	-1.2412	1.43E-16
252152938949	295	PI-6	chr12	12	q24.13	113513912	113519840	4	0	-0.86624	-0.86624	1.01E-13
252152938949	296	PI-6	chr12	12	q24.21	116711535	116720310	5	0	-0.96513	-0.96513	4.18E-21
252152938949	298	PI-6	chr12	12	q24.31	120700734	120705288	4	0	-1.02669	-1.02669	1.01E-16
252152938949	299	PI-6	chr12	12	q24.31	121900223	121906630	3	0	-1.37592	-1.37592	6.31E-20
252152938949	300	PI-6	chr12	12	q24.31	122904008	122909814	4	0	-1.39416	-1.39416	1.34E-27
252152938949	301	PI-6	chr12	12	q24.31	123630015	123639185	5	0	-0.95022	-0.95022	1.20E-19
252152938949	303	PI-6	chr12	12	q24.33	129304311	129310507	3	0	-1.07523	-1.07523	1.95E-15
252152938949	308	PI-6	chr13	13	q12.11	21275506	21289313	9	0	-0.61398	-0.61398	1.83E-15
252152938949	309	PI-6	chr13	13	q12.13	27333018	27335796	3	0	-1.47911	-1.47911	4.90E-23
252152938949	311	PI-6	chr13	13	q12.3	31035934	31042977	4	0	-1.11738	-1.11738	1.82E-22
252152938949	312	PI-6	chr13	13	q13.1	33589780	33595426	4	0	-1.06752	-1.06752	1.43E-18
252152938949	313	PI-6	chr13	13	q14.3	51793637	51799234	4	0	-0.68987	-0.68987	4.85E-10
252152938949	314	PI-6	chr13	13	q31.1	79172416	79177090	3	0	-0.79947	-0.79947	9.92E-10
252152938949	315	PI-6	chr13	13	q32.1	96738891	96745339	5	0	-1.02742	-1.02742	1.49E-20
252152938949	317	PI-6	chr13	13	q32.2	99221868	99234070	8	0	-0.84755	-0.84755	2.55E-25
252152938949	319	PI-6	chr13	13	q32.3	100635594	100638825	3	0	-1.3195	-1.3195	1.26E-20
252152938949	320	PI-6	chr13	13	q34	114232364	114244350	9	0	-0.72855	-0.72855	5.72E-22
252152938949	321	PI-6	chr14	14	q11.2	21563163	21569461	4	0	-1.03206	-1.03206	1.02E-19
252152938949	326	PI-6	chr14	14	q23.2	62276772	62281091	3	0	-1.19958	-1.19958	1.91E-18
252152938949	327	PI-6	chr14	14	q24.2	70719730	70724229	4	0	-1.44086	-1.44086	6.33E-28
252152938949	330	PI-6	chr14	14	q32.11	89882072	89889042	5	0	-1.21339	-1.21339	4.20E-28
252152938949	331	PI-6	chr14	14	q32.11	91280043	91286449	4	0	-1.20531	-1.20531	3.90E-22
252152938949	332	PI-6	chr14	14	q32.11	91517216	91531647	8	0	-0.53627	-0.53627	3.47E-11
252152938949	333	PI-6	chr14	14	q32.12	93183557	93186424	3	0	-0.9572	-0.9572	3.85E-13
252152938949	334	PI-6	chr14	14	q32.13	95782873	95788362	4	0	-1.02435	-1.02435	4.21E-18
252152938949	335	PI-6	chr14	14	q32.2	100065783	100078930	9	0	-0.7622	-0.7622	6.44E-21
252152938949	337	PI-6	chr14	14	q32.31	102222967	102230992	5	0	-0.86774	-0.86774	2.11E-14
252152938949	338	PI-6	chr14	14	q32.32	103240021	103249292	7	0	-1.05214	-1.05214	1.47E-29
252152938949	340	PI-6	chr14	14	q32.33	104597055	104611076	9	0	-0.63832	-0.63832	1.99E-14
252152938949	344	PI-6	chr15	15	q13.1	29861670	29867088	4	0	-1.1251	-1.1251	2.07E-20
252152938949	345	PI-6	chr15	15	q13.1	30106957	30116999	5	0	-0.74786	-0.74786	1.13E-13
252152938949	346	PI-6	chr15	15	q13.1	30259899	30263524	3	0	-1.34355	-1.34355	2.83E-21
252152938949	347	PI-6	chr15	15	q15.1	40604398	40625153	10	0	-0.46853	-0.46853	2.43E-11
252152938949	348	PI-6	chr15	15	q15.1	40728112	40737800	7	0	-0.76761	-0.76761	2.44E-15
252152938949	349	PI-6	chr15	15	q22.2	59728028	59733211	4	0	-0.94164	-0.94164	3.41E-16
252152938949	350	PI-6	chr15	15	q22.31	65064409	65076694	14	0	-0.69527	-0.69527	3.55E-27
252152938949	351	PI-6	chr15	15	q22.31	65709151	65718974	6	0	-0.72327	-0.72327	2.91E-13
252152938949	353	PI-6	chr15	15	q24.1	74040230	74052632	6	0	-0.76962	-0.76962	2.29E-16
252152938949	354	PI-6	chr15	15	q24.2	76350018	76354556	3	0	-1.39055	-1.39055	2.33E-23
252152938949	355	PI-6	chr15	15	q24.3	77918690	77935178	10	0	-0.53316	-0.53316	1.25E-12
252152938949	356	PI-6	chr15	15	q25.1	80982431	80995109	7	0	-0.7593	-0.7593	6.57E-19
252152938949	357	PI-6	chr15	15	q26.1	90187477	90195804	9	0	-0.75659	-0.75659	3.00E-20
252152938949	358	PI-6	chr15	15	q26.1	90544433	90548236	3	0	-1.16352	-1.16352	2.94E-16
252152938949	359	PI-6	chr15	15	q26.1	91411246	91417920	5	0	-0.76791	-0.76791	8.55E-13
252152938949	360	PI-6	chr15	15	q26.2	96870693	96878995	10	0	-0.95903	-0.95903	2.47E-34
252152938949	362	PI-6	chr15	15	q26.3	101786076	101797325	7	0	-0.73784	-0.73784	4.77E-18

252152938949	368	PI-6	chr16	16	p13.3	2223923	2265578	13	0	-0.59432	-0.59432	1.11E-17
252152938949	371	PI-6	chr16	16	p13.3	4162241	4175094	6	0	-0.7782	-0.7782	7.78E-17
252152938949	372	PI-6	chr16	16	p13.2	9054847	9058938	3	0	-1.27987	-1.27987	1.80E-20
252152938949	375	PI-6	chr16	16	p11.2	28298800	28335137	15	0	-0.46157	-0.46157	1.74E-14
252152938949	376	PI-6	chr16	16	q12.1	48413813	48423323	4	0	-0.92693	-0.92693	6.81E-16
252152938949	377	PI-6	chr16	16	q12.1	50186187	50190997	3	0	-0.94623	-0.94623	9.02E-13
252152938949	378	PI-6	chr16	16	q12.2	56220623	56232232	5	0	-0.73803	-0.73803	1.73E-13
252152938949	379	PI-6	chr16	16	q21	57555055	57571441	9	0	-0.74893	-0.74893	6.85E-21
252152938949	380	PI-6	chr16	16	q21	58227960	58236439	4	0	-1.02645	-1.02645	1.16E-18
252152938949	381	PI-6	chr16	16	q22.1	67681204	67689798	4	0	-1.19002	-1.19002	2.42E-16
252152938949	382	PI-6	chr16	16	q23.2	79625286	79643620	12	0	-0.58789	-0.58789	1.58E-19
252152938949	383	PI-6	chr16	16	q23.2	80833452	80843034	5	0	-0.8765	-0.8765	6.23E-18
252152938949	384	PI-6	chr16	16	q24.2	87759646	87762259	3	0	-1.4662	-1.4662	6.69E-22
252152938949	385	PI-6	chr17	17	p13.2	4120401	4132973	6	0	-0.86851	-0.86851	8.09E-18
252152938949	386	PI-6	chr17	17	p13.2	5182104	5188354	5	0	-0.75215	-0.75215	2.26E-12
252152938949	387	PI-6	chr17	17	p12	11140998	11149214	4	0	-1.17717	-1.17717	6.23E-22
252152938949	388	PI-6	chr17	17	p11.2	18113229	18141928	14	0	-0.52405	-0.52405	6.16E-17
252152938949	391	PI-6	chr17	17	q21.32	45784656	45789434	3	0	-1.62644	-1.62644	3.78E-24
252152938949	394	PI-6	chr17	17	q23.1	57903175	57925377	26	0	-0.2898	-0.2898	1.53E-12
252152938949	395	PI-6	chr17	17	q23.2	60139533	60148466	5	0	-0.92087	-0.92087	6.27E-17
252152938949	398	PI-6	chr17	17	q24.2	65987167	65994893	4	0	-0.79037	-0.79037	3.45E-12
252152938949	399	PI-6	chr17	17	q25.1	74232394	74240537	5	0	-0.84802	-0.84802	1.82E-17
252152938949	401	PI-6	chr17	17	q25.3	76775024	76781579	5	0	-0.94771	-0.94771	3.85E-19
252152938949	402	PI-6	chr17	17	q25.3	77747699	77754689	5	0	-1.08	-1.08	5.03E-24
252152938949	404	PI-6	chr17	17	q25.3	80476337	80481025	3	0	-1.56715	-1.56715	5.30E-27
252152938949	406	PI-6	chr18	18	p11.31	5292275	5298074	3	0	-1.09551	-1.09551	9.46E-16
252152938949	407	PI-6	chr18	18	p11.22	8606407	8612475	5	0	-1.07821	-1.07821	2.38E-20
252152938949	408	PI-6	chr18	18	p11.22	9135489	9146932	6	0	-0.59278	-0.59278	6.12E-11
252152938949	409	PI-6	chr18	18	p11.22	9613158	9618145	4	0	-1.36665	-1.36665	4.69E-28
252152938949	410	PI-6	chr18	18	q12.2	33156966	33168141	6	0	-0.84734	-0.84734	5.35E-19
252152938949	411	PI-6	chr18	18	q21.1	43912416	43916566	3	0	-1.37748	-1.37748	3.65E-23
252152938949	412	PI-6	chr18	18	q21.2	48720053	48728192	5	0	-0.70892	-0.70892	1.94E-10
252152938949	413	PI-6	chr18	18	q21.2	51747178	51753258	4	0	-1.14908	-1.14908	5.48E-22
252152938949	414	PI-6	chr18	18	q21.32	56527066	56534019	4	0	-1.11806	-1.11806	4.27E-22
252152938949	416	PI-6	chr18	18	q21.33	60984221	60990528	4	0	-0.99005	-0.99005	6.27E-18
252152938949	417	PI-6	chr18	18	q22.3	72918343	72925263	4	0	-0.95929	-0.95929	1.45E-16
252152938949	419	PI-6	chr18	18	q23	74206170	74211566	4	0	-1.08792	-1.08792	1.71E-19
252152938949	420	PI-6	chr18	18	q23	76736376	76758150	11	0	-0.78346	-0.78346	4.85E-29
252152938949	428	PI-6	chr19	19	p13.3	3267330	3272558	5	0	-0.88787	-0.88787	3.92E-15
252152938949	430	PI-6	chr19	19	p13.3	6418359	6432179	7	0	-0.65354	-0.65354	2.30E-14
252152938949	431	PI-6	chr19	19	p13.2	10979040	10987305	5	0	-0.91466	-0.91466	4.24E-18
252152938949	433	PI-6	chr19	19	p13.13	13972973	13978612	6	0	-0.985	-0.985	1.79E-25
252152938949	434	PI-6	chr19	19	p13.12	14191532	14232289	21	0	-0.48311	-0.48311	1.06E-21
252152938949	435	PI-6	chr19	19	p13.12	15439338	15446236	5	0	-0.84769	-0.84769	2.79E-16
252152938949	436	PI-6	chr19	19	p13.12	15534320	15573466	34	0	-0.5115	-0.5115	3.05E-34
252152938949	440	PI-6	chr19	19	p13.11	19514961	19519948	5	0	-1.17218	-1.17218	9.49E-27
252152938949	441	PI-6	chr19	19	q12	30301243	30305837	3	0	-1.04256	-1.04256	7.50E-15
252152938949	443	PI-6	chr19	19	q13.11	34967359	34975960	5	0	-0.7266	-0.7266	1.12E-12
252152938949	444	PI-6	chr19	19	q13.2	39052840	39057486	3	0	-1.1281	-1.1281	3.56E-17
252152938949	448	PI-6	chr19	19	q13.32	45734378	45741599	5	0	-0.86134	-0.86134	3.13E-17
252152938949	453	PI-6	chr19	19	q13.33	49230736	49235045	3	0	-1.10113	-1.10113	5.60E-16
252152938949	454	PI-6	chr19	19	q13.33	50828151	50835955	4	0	-1.33707	-1.33707	2.09E-27
252152938949	455	PI-6	chr19	19	q13.41	51599773	51608914	6	0	-1.47004	-1.47004	1.92E-42
252152938949	456	PI-6	chr19	19	q13.42	54481402	54484439	4	0	-1.21431	-1.21431	1.89E-18
252152938949	459	PI-6	chr19	19	q13.43	56594133	56603908	7	0	-0.91855	-0.91855	8.04E-25
252152938949	460	PI-6	chr19	19	q13.43	57682597	57688317	5	0	-0.97339	-0.97339	4.69E-20
252152938949	462	PI-6	chr20	20	p13	642377	648189	4	0	-1.10429	-1.10429	2.53E-19
252152938949	466	PI-6	chr20	20	p11.23	19190772	19203345	7	0	-0.64159	-0.64159	5.07E-14
252152938949	467	PI-6	chr20	20	p11.23	20344619	20353360	6	0	-0.77583	-0.77583	8.65E-16
252152938949	468	PI-6	chr20	20	q11.22	33811432	33822324	7	0	-0.65894	-0.65894	1.11E-13
252152938949	469	PI-6	chr20	20	q11.23	35485118	35495687	5	0	-0.88583	-0.88583	5.89E-17
252152938949	470	PI-6	chr20	20	q12	39943286	39949675	4	0	-1.01206	-1.01206	2.78E-18
252152938949	471	PI-6	chr20	20	q13.13	47440537	47447223	4	0	-0.89984	-0.89984	2.23E-14
252152938949	472	PI-6	chr20	20	q13.13	48328237	48334030	3	0	-0.90958	-0.90958	5.17E-12
252152938949	473	PI-6	chr20	20	q13.13	49541476	49553908	8	0	-0.63305	-0.63305	8.62E-14
252152938949	474	PI-6	chr20	20	q13.2	50380940	50389993	6	0	-0.94592	-0.94592	2.46E-20
252152938949	476	PI-6	chr20	20	q13.33	59824185	59831399	4	0	-1.03321	-1.03321	3.36E-19
252152938949	482	PI-6	chr21	21	q22.11	35437719	35455335	12	0	-0.60923	-0.60923	6.73E-19
252152938949	483	PI-6	chr21	21	q22.13	38117816	38122231	4	0	-0.74697	-0.74697	2.02E-11
252152938949	484	PI-6	chr21	21	q22.13	38737227	38742471	4	0	-1.12428	-1.12428	5.15E-17
252152938949	485	PI-6	chr21	21	q22.2	42215599	42222204	6	0	-1.31099	-1.31099	1.75E-37
252152938949	486	PI-6	chr21	21	q22.3	43292913	43301444	5	0	-0.99803	-0.99803	3.34E-21
252152938949	489	PI-6	chr21	21	q22.3	46493567	46496996	3	0	-1.62233	-1.62233	8.20E-26
252152938949	490	PI-6	chr21	21	q22.3	46970389	46977962	4	0	-1.39633	-1.39633	2.18E-21
252152938949	493	PI-6	chr22	22	q11.21	19747933	19752605	4	0	-1.31109	-1.31109	9.99E-22
252152938949	494	PI-6	chr22	22	q11.22	23407298	23420471	9	0	-0.86607	-0.86607	2.25E-20
252152938949	495	PI-6	chr22	22	q11.23	23520897	23525973	4	0	-0.9844	-0.9844	1.54E-17
252152938949	496	PI-6	chr22	22	q12.1	25951368	25974200	13	0	-0.49425	-0.49425	2.16E-15
252152938949	497	PI-6	chr22	22	q12.1	29273710	29287746	11	0	-0.64453	-0.64453	9.03E-21
252152938949	502	PI-6	chr22	22	q13.1	39744824	39748341	3	0	-1.31177	-1.31177	9.63E-16
252152938949	503	PI-6	chr22	22	q13.1	40437527	40443984	4	0	-0.8265	-0.8265	3.48E-13
252152938949	504	PI-6	chr22	22	q13.2	42367453	42377107	7	0	-0.83889	-0.83889	2.56E-21
252152938949	511	PI-6	chr22	22	q13.32	48883618	48890727	5	0	-1.12244	-1.12244	4.07E-22
252152938949	513	PI-6	chr22	22	q13.33	50216379	50255802	19	0	-0.46917	-0.46917	3.13E-17
252152938951	1	PI-7	chr4	4	p14	40257693	40293500	10	0.408187	0	0.408187	9.17E-10
252152938951	2	PI-7	chr6	6	q23.1	130330834	130348250	9	0	-0.495815	-0.495815	1.42E-12
252152938951	3	PI-7	chr6	6	q27	170119250	170127040	5	0	-0.828843	-0.828843	3.77E-17
252152938951	4	PI-7	chr7	7	q22.1	101455968	101472053	9	0	-0.45802	-0.45802	9.67E-11
252152938951	6	PI-7	chr8	8	q12.1	61588520	61593702	3	0	-1.057798	-1.057798	1.15E-15
252152938951	8	PI-7	chr9	9	p24.3	2037997	2055305	10	0	-0.460062	-0.460062	5.46E-12
252152938951	9	PI-7	chr10	10	p12.2	22607561	22612702	3	0	-1.013062	-1.013062	5.37E-15
252152938951	10	PI-7	chr12	12	q13.13	52404481	52409678	3	0	-0.95197	-0.95197	1.75E-13
252152938951	12	PI-7	chr13	13	q12.3	31033785	31042977	5	0	-0.682115	-0.682115	6.60E-13
252152938951	16	PI-7	chr15	15	q13.1	29859183	29867088	5	0	-1.002948	-1.002948	4.73E-22
252152938951	17	PI-7	chr15	15	q26.3	101786076	101797325	7	0	-0.589111	-0.589111	2.62E-13
252152938951	18	PI-7	chr16	16	p13.2	9054847	9058938	3	0	-0.94255	-0.94255	7.21E-14

252152938951	20	PI-7	chr18	18	q23	76746058	76758150	7	0	-0.747369	-0.747369	2.05E-19
252152938951	21	PI-7	chr19	19	p13.2	10976359	10995287	8	0	-0.468161	-0.468161	4.25E-11
252152938951	22	PI-7	chr19	19	p13.12	14195682	14204159	6	0	-0.634451	-0.634451	5.73E-14
252152938951	23	PI-7	chr20	20	q13.33	60625605	60643318	9	0	-0.477297	-0.477297	7.32E-12
252152938951	25	PI-7	chr22	22	q13.31	47770715	47777489	4	0	-0.839194	-0.839194	1.35E-14
252152938951	26	PI-7	chr22	22	q13.32	48881938	48888205	4	0	-0.81353	-0.81353	1.64E-11
252152938951	27	PI-7	chr22	22	q13.33	51125551	51144365	9	0	-0.630214	-0.630214	7.26E-16
252152938943	4	PI-8	chr14	14	q32.12	92253960	92364089	55	0.26647	0	0.26647	3.78E-19
252152938945	2	PI-9	chr4	4	p16.3	2040751	2072425	10	0	-0.461573	-0.461573	2.16E-10
252152938945	4	PI-9	chr6	6	p25.3	1600137	1636731	17	0	-0.403499	-0.403499	5.03E-14
252152938945	7	PI-9	chr10	10	p12.2	22602135	22632965	18	0	-0.431924	-0.431924	3.10E-17
252152938945	8	PI-9	chr10	10	q26.13	124891202	124911392	11	0	-0.424635	-0.424635	5.39E-10
252152938945	9	PI-9	chr11	11	q12.1	59031718	59034891	3	0	-0.897114	-0.897114	8.68E-10
252152938945	10	PI-9	chr12	12	p13.31	7778761	7783075	3	0	-1.132916	-1.132916	1.63E-17
252152938945	11	PI-9	chr13	13	q14.11	42608658	42631144	12	0	-0.351965	-0.351965	6.83E-10
252152938945	17	PI-9	chr17	17	q25.3	77749226	77794796	24	0	-0.33186	-0.33186	1.77E-12
252152938945	18	PI-9	chr18	18	q23	76724307	76770904	24	0	-0.273444	-0.273444	2.16E-10
252152938946	1	PI-10	chr2	2	q24.1	158260532	158325556	29	0.36799	0	0.36799	5.00E-19
252152938946	2	PI-10	chr2	2	q32.3	196974418	197061104	38	0.311236	0	0.311236	5.86E-11
252152938946	3	PI-10	chr4	4	p14	40175634	40269384	43	0.303898	0	0.303898	1.83E-21
252152938946	4	PI-10	chr4	4	q25	108950537	109086214	65	0.265655	0	0.265655	1.25E-24
252152938946	5	PI-10	chr5	5	q31.1	131786136	131834358	23	0.342834	0	0.342834	5.71E-10
252152938946	6	PI-10	chr7	7	12.2 - p12.	50333095	50501756	61	0.267958	0	0.267958	4.78E-23
252152938946	8	PI-10	chr11	11	q13.1	65164138	65327265	88	0.321694	0	0.321694	4.12E-42
252152938946	9	PI-10	chr11	11	q24.3	128293898	128373504	35	0.268709	0	0.268709	4.71E-13
252152938946	11	PI-10	chr14	14	q32.12	92256429	92365960	55	0.267274	0	0.267274	3.32E-19
252152938946	13	PI-10	chr17	17	q23.3	62497650	62550273	29	0.279493	0	0.279493	8.55E-11
252152934022	2	PI-4	chr1	1	p36.33	1707749	1712762	4	0	-1.15793	-1.15793	2.08E-24
252152934022	6	PI-4	chr1	1	p36.32	3525401	3572198	21	0	-0.47503	-0.47503	2.97E-20
252152934022	7	PI-4	chr1	1	p36.31	6291928	6326289	17	0	-0.53888	-0.53888	5.42E-20
252152934022	12	PI-4	chr1	1	p36.22	9339191	9357441	11	0	-0.66969	-0.66969	8.27E-22
252152934022	38	PI-4	chr1	1	p36.12	22468255	22471726	3	0	-1.23029	-1.23029	4.98E-19
252152934022	41	PI-4	chr1	1	p36.11	25926921	25951052	11	0	-0.5526	-0.5526	4.21E-17
252152934022	43	PI-4	chr1	1	p36.11	27127015	27156287	13	0	-0.79074	-0.79074	3.56E-35
252152934022	49	PI-4	chr1	1	p35.3	29562293	29565728	3	0	-1.1101	-1.1101	5.68E-17
252152934022	52	PI-4	chr1	1	p35.2	31880882	31892388	6	0	-0.72033	-0.72033	5.82E-14
252152934022	56	PI-4	chr1	1	p35.1	33424980	33443386	9	0	-0.71493	-0.71493	3.73E-22
252152934022	60	PI-4	chr1	1	p34.3	35389722	35451509	21	0	-0.4257	-0.4257	2.40E-18
252152934022	61	PI-4	chr1	1	p34.3	36271890	36276436	3	0	-1.01608	-1.01608	5.13E-15
252152934022	63	PI-4	chr1	1	p34.3	38236474	38276764	19	0	-0.51747	-0.51747	1.30E-24
252152934022	74	PI-4	chr1	1	p34.2	43421332	43428748	4	0	-0.92501	-0.92501	3.96E-16
252152934022	76	PI-4	chr1	1	p34.1	45668562	45683636	7	0	-0.64013	-0.64013	1.06E-14
252152934022	78	PI-4	chr1	1	p33	46993626	47007821	7	0	-0.65855	-0.65855	3.60E-15
252152934022	79	PI-4	chr1	1	p33	47129380	47134706	4	0	-0.79727	-0.79727	3.08E-13
252152934022	80	PI-4	chr1	1	p33	47796164	47805367	5	0	-0.71419	-0.71419	1.43E-13
252152934022	81	PI-4	chr1	1	p33	47880566	47887014	5	0	-0.77498	-0.77498	1.11E-14
252152934022	82	PI-4	chr1	1	p33	48459077	48465244	4	0	-0.94722	-0.94722	7.22E-17
252152934022	83	PI-4	chr1	1	p32.3	51421960	51445710	14	0	-0.53368	-0.53368	1.91E-18
252152934022	86	PI-4	chr1	1	p32.3	53790801	53797465	4	0	-0.8191	-0.8191	1.56E-12
252152934022	87	PI-4	chr1	1	p32.3	54202680	54212155	5	0	-0.79875	-0.79875	2.98E-15
252152934022	88	PI-4	chr1	1	p32.3	54697776	54708166	6	0	-0.97283	-0.97283	6.83E-24
252152934022	90	PI-4	chr1	1	p32.2	57106831	57113307	5	0	-0.95747	-0.95747	1.17E-20
252152934022	91	PI-4	chr1	1	p31.3	61546348	61551920	4	0	-0.89746	-0.89746	1.42E-12
252152934022	92	PI-4	chr1	1	p31.3	62206615	62213320	3	0	-0.78453	-0.78453	7.79E-10
252152934022	93	PI-4	chr1	1	p31.3	63150311	63161066	7	0	-0.70177	-0.70177	9.07E-17
252152934022	94	PI-4	chr1	1	p31.3	63779389	63791203	5	0	-0.74789	-0.74789	7.00E-14
252152934022	95	PI-4	chr1	1	p31.3	64237782	64243464	4	0	-0.93129	-0.93129	2.12E-16
252152934022	96	PI-4	chr1	1	p31.3	65428902	65435523	4	0	-0.73179	-0.73179	1.82E-11
252152934022	97	PI-4	chr1	1	p31.3	65528552	65535482	9	0	-0.59211	-0.59211	6.10E-15
252152934022	98	PI-4	chr1	1	p31.3	65719715	65723432	3	0	-1.02721	-1.02721	1.55E-13
252152934022	99	PI-4	chr1	1	p31.1	75589808	75604854	9	0	-0.49734	-0.49734	9.09E-12
252152934022	100	PI-4	chr1	1	p31.1	76572350	76581149	5	0	-0.74147	-0.74147	4.75E-14
252152934022	102	PI-4	chr1	1	p31.1	84540354	84547548	5	0	-0.74634	-0.74634	1.97E-14
252152934022	103	PI-4	chr1	1	p22.3	85926811	85935792	6	0	-0.74574	-0.74574	4.13E-16
252152934022	105	PI-4	chr1	1	p22.3	87792557	87805324	7	0	-0.88639	-0.88639	1.55E-22
252152934022	106	PI-4	chr1	1	p22.2	88929607	88934413	3	0	-0.99771	-0.99771	5.67E-14
252152934022	107	PI-4	chr1	1	p22.2	91171663	91198922	15	0	-0.42994	-0.42994	3.08E-13
252152934022	108	PI-4	chr1	1	p22.1	92943067	92950243	4	0	-0.70816	-0.70816	3.69E-10
252152934022	110	PI-4	chr1	1	p21.3	95283566	95286607	3	0	-0.92458	-0.92458	5.84E-13
252152934022	111	PI-4	chr1	1	p21.3	95575936	95590339	9	0	-0.58022	-0.58022	1.05E-15
252152934022	112	PI-4	chr1	1	p21.2	101002217	101006789	3	0	-0.90904	-0.90904	1.17E-11
252152934022	113	PI-4	chr1	1	p13.3	109991848	110056057	26	0	-0.31545	-0.31545	5.61E-13
252152934022	114	PI-4	chr1	1	p13.3	110452601	110458342	4	0	-0.88099	-0.88099	1.70E-13
252152934022	115	PI-4	chr1	1	p13.2	112530076	112534758	3	0	-0.93378	-0.93378	1.61E-12
252152934022	117	PI-4	chr1	1	p13.2	113246836	113260432	8	0	-0.68869	-0.68869	1.23E-18
252152934022	123	PI-4	chr1	1	p13.1	117209274	117214614	6	0	-0.73698	-0.73698	6.49E-13
252152934022	124	PI-4	chr1	1	p12	117907265	117912975	4	0	-0.81401	-0.81401	4.32E-13
252152934022	125	PI-4	chr1	1	p12	120162251	120178408	10	0	-0.56034	-0.56034	9.36E-16
252152934022	127	PI-4	chr1	1	q21.2	150118635	150123509	3	0	-0.84648	-0.84648	7.04E-13
252152934022	128	PI-4	chr1	1	q21.3	151427909	151433411	4	0	-0.89709	-0.89709	7.30E-17
252152934022	133	PI-4	chr1	1	q21.3	154529603	154534270	3	0	-0.87279	-0.87279	6.38E-13
252152934022	137	PI-4	chr1	1	q24.1	166129892	166138553	10	0	-0.85462	-0.85462	1.14E-31
252152934022	138	PI-4	chr1	1	q24.1	166805276	166810880	4	0	-0.99426	-0.99426	1.07E-16
252152934022	139	PI-4	chr1	1	q24.1	167188388	167197909	5	0	-0.6532	-0.6532	3.81E-12
252152934022	140	PI-4	chr1	1	q24.2	168099097	168120656	12	0	-0.45402	-0.45402	4.23E-14
252152934022	141	PI-4	chr1	1	q25.1	173442738	173450664	5	0	-0.7517	-0.7517	3.39E-15
252152934022	142	PI-4	chr1	1	q25.1	173576840	173585830	5	0	-0.60116	-0.60116	6.43E-11
252152934022	145	PI-4	chr1	1	q25.3	184004232	184007045	3	0	-0.90435	-0.90435	6.18E-12
252152934022	146	PI-4	chr1	1	q31.3	197741987	197745923	3	0	-0.9984	-0.9984	4.15E-15
252152934022	148	PI-4	chr1	1	q32.1	202102653	202116036	8	0	-0.49684	-0.49684	8.58E-13
252152934022	150	PI-4	chr1	1	q32.1	205168910	205211442	20	0	-0.36148	-0.36148	1.56E-15
252152934022	153	PI-4	chr1	1	q32.1	206856583	206861094	4	0	-0.84062	-0.84062	2.20E-13
252152934022	154	PI-4	chr1	1	q32.2	207989881	207993482	4	0	-0.78493	-0.78493	2.20E-13
252152934022	161	PI-4	chr1	1	q32.3	212948773	212957254	5	0	-0.85809	-0.85809	4.83E-18
252152934022	163	PI-4	chr1	1	q41	215248728	215258703	7	0	-0.56556	-0.56556	8.39E-11
252152934022	164	PI-4	chr1	1	q41	220630089	220715479	36	0	-0.28666	-0.28666	2.99E-15

252152934022	169	PI-4	chr1	1	q42.12	226494462	226505081	6	0	-0.67963	-0.67963	5.72E-13
252152934022	170	PI-4	chr1	1	q42.13	227504698	227510771	4	0	-0.79387	-0.79387	3.83E-13
252152934022	171	PI-4	chr1	1	q42.13	228864069	228882842	9	0	-0.46399	-0.46399	1.56E-10
252152934022	172	PI-4	chr1	1	q42.13	229690105	229702530	8	0	-0.6609	-0.6609	4.17E-17
252152934022	176	PI-4	chr1	1	q42.2	231173681	231179520	6	0	-0.76624	-0.76624	6.72E-15
252152934022	179	PI-4	chr1	1	q42.3	234733262	234747456	10	0	-0.7605	-0.7605	2.04E-25
252152934022	182	PI-4	chr1	1	q43	237203838	237209074	4	0	-0.87333	-0.87333	3.95E-15
252152934022	184	PI-4	chr1	1	q43	242681472	242692335	6	0	-0.69892	-0.69892	6.92E-15
252152934022	185	PI-4	chr1	1	q44	244209483	244214770	4	0	-0.94764	-0.94764	6.09E-17
252152934022	186	PI-4	chr1	1	q44	247091653	247098965	6	0	-0.77253	-0.77253	1.63E-17
252152934022	188	PI-4	chr1	1	q44	247670189	247710787	17	0	-0.34331	-0.34331	4.72E-11
252152934022	190	PI-4	chr2	2	p25.3	945598	952932	4	0	-0.80853	-0.80853	1.02E-11
252152934022	191	PI-4	chr2	2	p25.3	1745982	1755641	5	0	-0.71312	-0.71312	3.29E-11
252152934022	193	PI-4	chr2	2	p25.2	5829494	5838952	4	0	-0.9048	-0.9048	2.55E-11
252152934022	194	PI-4	chr2	2	p25.2	7054409	7060934	4	0	-0.83658	-0.83658	1.84E-12
252152934022	195	PI-4	chr2	2	p25.1	8818562	8827209	6	0	-0.87819	-0.87819	8.45E-22
252152934022	196	PI-4	chr2	2	p25.1	9345470	9351641	3	0	-1.03016	-1.03016	4.12E-15
252152934022	197	PI-4	chr2	2	p25.1	11039677	11054514	8	0	-0.71636	-0.71636	5.57E-19
252152934022	198	PI-4	chr2	2	p25.1	11468119	11486791	9	0	-0.54625	-0.54625	4.28E-14
252152934022	200	PI-4	chr2	2	p25.1	11876749	11901485	12	0	-0.47008	-0.47008	6.54E-14
252152934022	203	PI-4	chr2	2	p24.3	16080065	16084723	4	0	-1.05323	-1.05323	3.65E-17
252152934022	209	PI-4	chr2	2	p23.3	24713098	24718157	3	0	-1.08739	-1.08739	1.25E-16
252152934022	210	PI-4	chr2	2	p23.3	25561139	25567949	6	0	-0.89038	-0.89038	8.24E-19
252152934022	211	PI-4	chr2	2	p23.3	26393711	26414703	10	0	-0.52625	-0.52625	2.59E-12
252152934022	212	PI-4	chr2	2	p23.3	26590069	26599089	6	0	-0.61292	-0.61292	3.96E-12
252152934022	213	PI-4	chr2	2	p23.3	27335629	27344813	6	0	-0.89913	-0.89913	1.55E-21
252152934022	214	PI-4	chr2	2	p23.3	27713867	27721023	5	0	-0.80685	-0.80685	5.68E-16
252152934022	215	PI-4	chr2	2	p23.3	27754585	27783112	12	0	-0.59709	-0.59709	3.72E-19
252152934022	216	PI-4	chr2	2	p23.2	29336357	29339295	3	0	-1.3186	-1.3186	3.18E-18
252152934022	217	PI-4	chr2	2	p22.3	32668351	32688713	12	0	-0.51695	-0.51695	1.86E-16
252152934022	218	PI-4	chr2	2	p22.3	33168330	33178696	6	0	-0.77721	-0.77721	3.36E-16
252152934022	219	PI-4	chr2	2	p22.2	36822107	36825949	4	0	-0.68336	-0.68336	4.58E-10
252152934022	220	PI-4	chr2	2	p22.1	39346574	39350971	3	0	-1.04192	-1.04192	2.11E-17
252152934022	221	PI-4	chr2	2	p21	42271583	42278166	4	0	-0.89161	-0.89161	9.27E-14
252152934022	224	PI-4	chr2	2	p21	45875493	45880447	4	0	-0.90213	-0.90213	8.56E-14
252152934022	225	PI-4	chr2	2	p21	46522771	46531279	5	0	-0.65175	-0.65175	7.02E-11
252152934022	226	PI-4	chr2	2	p21	47163934	47170671	4	0	-0.75225	-0.75225	1.19E-11
252152934022	227	PI-4	chr2	2	p16.2	54951369	54954446	3	0	-1.0521	-1.0521	4.11E-16
252152934022	228	PI-4	chr2	2	p16.1	56395136	56426699	15	0	-0.37964	-0.37964	8.90E-12
252152934022	229	PI-4	chr2	2	p16.1	60775963	60783723	4	0	-0.86267	-0.86267	3.09E-12
252152934022	231	PI-4	chr2	2	p14	64878424	64882195	3	0	-1.18828	-1.18828	1.41E-18
252152934022	233	PI-4	chr2	2	p13.3	70312607	70319336	4	0	-0.80745	-0.80745	1.28E-10
252152934022	236	PI-4	chr2	2	p13.2	73142415	73148782	4	0	-0.69038	-0.69038	2.50E-10
252152934022	238	PI-4	chr2	2	p13.1	74208046	74216010	4	0	-0.77696	-0.77696	1.64E-12
252152934022	239	PI-4	chr2	2	p13.1	74284926	74292395	5	0	-0.75309	-0.75309	2.03E-14
252152934022	240	PI-4	chr2	2	p11.2	85196363	85206936	7	0	-0.62941	-0.62941	4.23E-14
252152934022	242	PI-4	chr2	2	p11.2	86665811	86671549	4	0	-0.83162	-0.83162	6.57E-14
252152934022	243	PI-4	chr2	2	p11.2	86849532	86864052	6	0	-0.77242	-0.77242	6.09E-17
252152934022	244	PI-4	chr2	2	p11.2	88744731	88755682	6	0	-0.66749	-0.66749	1.36E-13
252152934022	246	PI-4	chr2	2	q11.2	97470883	97483722	8	0	-0.84079	-0.84079	7.76E-24
252152934022	247	PI-4	chr2	2	q11.2	99346052	99349698	3	0	-1.35092	-1.35092	3.99E-21
252152934022	248	PI-4	chr2	2	q11.2	100935735	100939766	3	0	-1.33966	-1.33966	1.68E-17
252152934022	256	PI-4	chr2	2	q13	113031037	113035865	4	0	-1.03979	-1.03979	6.88E-18
252152934022	257	PI-4	chr2	2	q13	113237561	113243627	5	0	-0.85041	-0.85041	3.91E-15
252152934022	258	PI-4	chr2	2	q13	113912817	113918193	4	0	-0.99274	-0.99274	2.07E-17
252152934022	260	PI-4	chr2	2	q14.2	119600140	119608598	5	0	-0.95444	-0.95444	2.64E-18
252152934022	264	PI-4	chr2	2	q21.3	135429833	135436972	5	0	-0.75538	-0.75538	7.24E-14
252152934022	265	PI-4	chr2	2	q21.3	135474639	135479311	3	0	-0.89212	-0.89212	1.87E-11
252152934022	267	PI-4	chr2	2	q22.3	144743574	144757560	7	0	-0.51974	-0.51974	1.44E-10
252152934022	269	PI-4	chr2	2	q23.1	149891480	149898817	5	0	-0.64133	-0.64133	3.37E-11
252152934022	272	PI-4	chr2	2	q24.1	158726275	158737387	6	0	-0.70714	-0.70714	2.19E-15
252152934022	273	PI-4	chr2	2	q24.2	162093140	162100794	5	0	-0.69353	-0.69353	3.32E-11
252152934022	274	PI-4	chr2	2	q24.3	169099929	169105801	5	0	-0.6875	-0.6875	5.87E-12
252152934022	275	PI-4	chr2	2	q31.1	170177106	170191485	7	0	-0.57729	-0.57729	1.86E-12
252152934022	276	PI-4	chr2	2	q31.1	170359041	170364581	4	0	-0.94385	-0.94385	1.83E-15
252152934022	277	PI-4	chr2	2	q31.1	170587426	170599168	5	0	-0.92774	-0.92774	7.18E-20
252152934022	281	PI-4	chr2	2	q31.1	173937480	173943470	5	0	-0.82095	-0.82095	1.72E-16
252152934022	284	PI-4	chr2	2	q31.1	175869034	175872548	3	0	-0.78679	-0.78679	6.03E-10
252152934022	285	PI-4	chr2	2	q31.1	176933003	177003927	45	0	-0.60832	-0.60832	3.21E-69
252152934022	287	PI-4	chr2	2	q31.2	180118914	180132437	7	0	-0.60971	-0.60971	2.41E-12
252152934022	288	PI-4	chr2	2	q31.3	180720354	180733649	15	0	-0.5749	-0.5749	9.75E-24
252152934022	289	PI-4	chr2	2	q32.1	185459973	185464799	4	0	-0.69661	-0.69661	8.69E-11
252152934022	290	PI-4	chr2	2	q32.2	190516424	190522575	3	0	-0.8283	-0.8283	6.56E-11
252152934022	291	PI-4	chr2	2	q32.3	192259703	192266370	4	0	-0.68793	-0.68793	2.48E-10
252152934022	292	PI-4	chr2	2	q32.3	196423078	196438302	6	0	-0.56354	-0.56354	6.98E-10
252152934022	293	PI-4	chr2	2	q32.3	197034440	197038405	3	0	-0.97744	-0.97744	1.71E-13
252152934022	294	PI-4	chr2	2	q33.1	197455313	197460545	4	0	-1.05884	-1.05884	1.45E-20
252152934022	295	PI-4	chr2	2	q33.1	198169927	198177264	5	0	-0.88581	-0.88581	4.32E-16
252152934022	303	PI-4	chr2	2	q33.3	208537179	208581944	26	0	-0.30918	-0.30918	2.01E-12
252152934022	304	PI-4	chr2	2	q34	214013299	214020099	4	0	-0.79758	-0.79758	2.48E-12
252152934022	305	PI-4	chr2	2	q35	215696001	215707951	6	0	-0.64796	-0.64796	2.58E-13
252152934022	307	PI-4	chr2	2	q36.2	225447085	225452495	4	0	-0.99343	-0.99343	5.61E-17
252152934022	308	PI-4	chr2	2	q36.2	225901360	225908462	5	0	-0.73974	-0.73974	2.52E-14
252152934022	309	PI-4	chr2	2	q36.3	227655453	227668870	8	0	-0.66796	-0.66796	1.33E-17
252152934022	328	PI-4	chr3	3	p25.2	12041877	12048847	5	0	-0.86622	-0.86622	7.79E-18
252152934022	333	PI-4	chr3	3	p25.1	15899339	15903568	5	0	-0.9156	-0.9156	1.31E-19
252152934022	334	PI-4	chr3	3	p24.3	16548964	16557063	5	0	-0.61125	-0.61125	2.19E-10
252152934022	335	PI-4	chr3	3	p24.3	16922993	16930049	4	0	-0.77773	-0.77773	1.49E-12
252152934022	336	PI-4	chr3	3	p24.3	17743125	17749185	5	0	-0.88615	-0.88615	1.01E-17
252152934022	337	PI-4	chr3	3	p24.3	18467918	18490049	11	0	-0.44616	-0.44616	1.35E-11
252152934022	338	PI-4	chr3	3	p24.3	20072303	20085689	7	0	-0.59539	-0.59539	8.70E-13
252152934022	339	PI-4	chr3	3	p24.3	23845495	23853474	5	0	-0.86307	-0.86307	6.96E-18
252152934022	340	PI-4	chr3	3	p24.2	23983335	23994450	7	0	-0.63819	-0.63819	2.29E-14
252152934022	341	PI-4	chr3	3	p24.2	25820132	25830543	5	0	-0.61086	-0.61086	2.95E-10
252152934022	342	PI-4	chr3	3	p22.3	32428018	32439833	7	0	-0.60485	-0.60485	3.30E-13
252152934022	343	PI-4	chr3	3	p22.3	32855171	32865112	5	0	-0.76862	-0.76862	1.61E-12

252152934022	344	PI-4	chr3	3	p22.2	37489726	37506781	9	0	-0.53735	-0.53735	1.04E-13
252152934022	345	PI-4	chr3	3	p22.2	38686122	38694076	4	0	-0.81116	-0.81116	4.87E-13
252152934022	346	PI-4	chr3	3	p22.1	43325893	43330505	4	0	-0.91323	-0.91323	5.83E-16
252152934022	347	PI-4	chr3	3	p21.31	44901620	44906047	6	0	-0.81773	-0.81773	1.55E-18
252152934022	348	PI-4	chr3	3	p21.31	45264355	45269773	5	0	-0.933	-0.933	1.46E-18
252152934022	353	PI-4	chr3	3	p21.31	48094781	48101738	5	0	-0.90414	-0.90414	9.75E-19
252152934022	354	PI-4	chr3	3	p21.31	49022960	49029456	6	0	-0.76945	-0.76945	1.50E-17
252152934022	358	PI-4	chr3	3	p21.2	51988474	52030161	20	0	-0.4012	-0.4012	9.53E-16
252152934022	367	PI-4	chr3	3	p14.3	58317877	58321201	3	0	-1.06382	-1.06382	1.15E-15
252152934022	368	PI-4	chr3	3	p14.3	58475161	58480285	3	0	-0.90558	-0.90558	4.67E-12
252152934022	372	PI-4	chr3	3	p14.1	67492303	67498019	4	0	-0.71102	-0.71102	8.41E-11
252152934022	373	PI-4	chr3	3	p13	71800618	71806142	4	0	-0.97674	-0.97674	7.66E-17
252152934022	374	PI-4	chr3	3	p13	72493493	72499565	4	0	-0.79902	-0.79902	4.69E-13
252152934022	375	PI-4	chr3	3	p13	72936696	72939895	3	0	-1.15624	-1.15624	3.61E-17
252152934022	379	PI-4	chr3	3	q13.31	113663759	113668404	4	0	-0.75618	-0.75618	1.12E-11
252152934022	380	PI-4	chr3	3	q21.1	123163880	123171485	4	0	-0.74903	-0.74903	2.56E-11
252152934022	381	PI-4	chr3	3	q21.1	123595305	123613828	9	0	-0.56446	-0.56446	6.38E-14
252152934022	385	PI-4	chr3	3	q21.3	127341468	127351298	5	0	-0.7554	-0.7554	1.94E-14
252152934022	386	PI-4	chr3	3	q21.3	127539248	127546706	4	0	-0.82786	-0.82786	1.03E-13
252152934022	387	PI-4	chr3	3	q22.2	133968402	133973608	4	0	-1.02393	-1.02393	5.74E-19
252152934022	389	PI-4	chr3	3	q23	141594273	141601080	5	0	-0.85588	-0.85588	8.61E-18
252152934022	391	PI-4	chr3	3	q23 - q24	142760435	142843378	33	0	-0.3165	-0.3165	1.22E-16
252152934022	392	PI-4	chr3	3	q24	148698142	148718738	9	0	-0.54676	-0.54676	1.13E-13
252152934022	393	PI-4	chr3	3	q25.1	149087228	149108642	11	0	-0.49941	-0.49941	2.42E-14
252152934022	394	PI-4	chr3	3	q25.1	149682888	149691543	5	0	-0.68084	-0.68084	5.12E-12
252152934022	395	PI-4	chr3	3	q25.33	160276111	160290063	6	0	-0.65577	-0.65577	1.59E-13
252152934022	396	PI-4	chr3	3	q26.2	170076897	170079770	3	0	-0.80148	-0.80148	1.92E-10
252152934022	397	PI-4	chr3	3	q26.31	171908174	171918918	6	0	-0.54407	-0.54407	5.63E-10
252152934022	398	PI-4	chr3	3	q26.32	176912261	176917249	3	0	-0.84783	-0.84783	1.77E-11
252152934022	400	PI-4	chr3	3	q26.33	179033815	179042020	5	0	-0.67151	-0.67151	1.51E-11
252152934022	401	PI-4	chr3	3	q26.33	179369823	179377038	4	0	-0.88798	-0.88798	1.34E-15
252152934022	403	PI-4	chr3	3	q27.1	182967949	182978151	5	0	-0.70326	-0.70326	5.62E-13
252152934022	404	PI-4	chr3	3	q27.1	183538001	183543966	3	0	-0.81548	-0.81548	1.70E-10
252152934022	405	PI-4	chr3	3	q27.1	183871254	183875594	4	0	-0.88662	-0.88662	3.02E-15
252152934022	410	PI-4	chr3	3	q29	193847833	193862149	7	0	-0.95916	-0.95916	7.35E-26
252152934022	413	PI-4	chr3	3	q29	195628785	195639586	5	0	-1.01109	-1.01109	3.24E-21
252152934022	422	PI-4	chr4	4	p16.1	8858439	8877011	21	0	-0.66642	-0.66642	3.19E-40
252152934022	423	PI-4	chr4	4	p16.1	10456045	10465209	5	0	-0.7716	-0.7716	1.45E-14
252152934022	424	PI-4	chr4	4	p15.33	13627412	13629980	3	0	-1.43019	-1.43019	7.26E-22
252152934022	425	PI-4	chr4	4	p15.33	15001524	15007275	4	0	-0.94623	-0.94623	6.24E-16
252152934022	426	PI-4	chr4	4	p15.32	15653615	15661211	5	0	-0.73132	-0.73132	7.46E-14
252152934022	427	PI-4	chr4	4	p15.32	16225080	16233105	4	0	-0.6845	-0.6845	3.89E-10
252152934022	428	PI-4	chr4	4	p15.2	21946541	21953523	5	0	-0.6478	-0.6478	2.72E-11
252152934022	429	PI-4	chr4	4	p15.2	22513948	22519252	3	0	-0.88028	-0.88028	5.05E-12
252152934022	430	PI-4	chr4	4	p15.2	24910507	24919403	5	0	-0.87207	-0.87207	2.30E-18
252152934022	431	PI-4	chr4	4	p15.2	25237399	25256743	7	0	-0.70773	-0.70773	1.92E-17
252152934022	433	PI-4	chr4	4	p15.2	26856128	26865330	5	0	-0.72588	-0.72588	1.32E-13
252152934022	434	PI-4	chr4	4	p15.1	30720057	30727220	4	0	-0.69931	-0.69931	1.37E-10
252152934022	435	PI-4	chr4	4	p14	36243261	36247229	3	0	-0.79922	-0.79922	1.44E-10
252152934022	436	PI-4	chr4	4	p14	37663985	37689159	12	0	-0.40834	-0.40834	9.88E-11
252152934022	437	PI-4	chr4	4	p14	38867364	38873403	7	0	-0.76973	-0.76973	9.95E-21
252152934022	438	PI-4	chr4	4	p14	39040148	39049212	6	0	-0.58066	-0.58066	6.73E-11
252152934022	439	PI-4	chr4	4	p14	40931255	40933891	3	0	-0.79227	-0.79227	5.41E-10
252152934022	440	PI-4	chr4	4	p13	41746504	41752222	4	0	-0.72083	-0.72083	8.49E-11
252152934022	441	PI-4	chr4	4	p12	46371394	46395671	13	0	-0.42129	-0.42129	2.59E-12
252152934022	442	PI-4	chr4	4	p11	48484329	48494547	6	0	-0.78115	-0.78115	7.15E-18
252152934022	443	PI-4	chr4	4	q12	52898838	52916714	9	0	-0.53949	-0.53949	1.21E-13
252152934022	444	PI-4	chr4	4	q12	56910884	56925269	6	0	-0.62318	-0.62318	1.98E-12
252152934022	449	PI-4	chr4	4	q21.21	79856229	79864896	6	0	-0.79805	-0.79805	4.93E-18
252152934022	450	PI-4	chr4	4	q21.23	85885034	85888775	3	0	-0.84239	-0.84239	1.78E-11
252152934022	451	PI-4	chr4	4	q22.1	88928009	88932753	4	0	-0.9052	-0.9052	2.09E-16
252152934022	452	PI-4	chr4	4	q23	99181133	99186818	3	0	-0.85472	-0.85472	1.61E-11
252152934022	454	PI-4	chr4	4	q23	100864474	100872426	5	0	-0.66085	-0.66085	1.40E-10
252152934022	455	PI-4	chr4	4	q24	103419353	103425936	5	0	-0.69665	-0.69665	1.39E-12
252152934022	456	PI-4	chr4	4	q24	105409092	105415040	5	0	-0.73368	-0.73368	1.37E-13
252152934022	457	PI-4	chr4	4	q25	109086155	109098154	7	0	-0.74062	-0.74062	3.39E-18
252152934022	458	PI-4	chr4	4	q26	120541350	120556880	8	0	-0.57047	-0.57047	5.60E-13
252152934022	459	PI-4	chr4	4	q27	123732119	123753968	10	0	-0.59109	-0.59109	1.02E-17
252152934022	460	PI-4	chr4	4	q28.1	123931741	123940224	4	0	-0.70823	-0.70823	1.65E-10
252152934022	461	PI-4	chr4	4	q28.2	128977599	129007142	13	0	-0.58226	-0.58226	3.00E-21
252152934022	462	PI-4	chr4	4	q28.2	129727517	129735518	6	0	-0.87661	-0.87661	5.82E-19
252152934022	463	PI-4	chr4	4	q31.21	145562628	145571509	6	0	-0.60251	-0.60251	6.55E-12
252152934022	464	PI-4	chr4	4	q31.21	146100515	146103777	3	0	-0.95719	-0.95719	1.40E-12
252152934022	465	PI-4	chr4	4	q31.21	146613744	146617735	3	0	-1.03126	-1.03126	3.68E-15
252152934022	466	PI-4	chr4	4	q31.22	146856809	146862108	3	0	-0.80171	-0.80171	1.72E-10
252152934022	467	PI-4	chr4	4	q31.3	152442699	152451157	5	0	-0.66791	-0.66791	4.50E-12
252152934022	468	PI-4	chr4	4	q31.3	154130767	154177365	28	0	-0.28031	-0.28031	1.65E-11
252152934022	469	PI-4	chr4	4	q31.3	154386476	154390161	3	0	-1.0079	-1.0079	8.16E-15
252152934022	470	PI-4	chr4	4	q32.1	157995532	158000885	4	0	-0.82697	-0.82697	1.93E-12
252152934022	471	PI-4	chr4	4	q32.3	165937934	165945767	4	0	-0.89689	-0.89689	1.48E-14
252152934022	472	PI-4	chr4	4	q32.3	166296198	166305227	10	0	-0.51368	-0.51368	1.31E-12
252152934022	473	PI-4	chr4	4	q33	170188837	170197970	7	0	-0.61351	-0.61351	2.76E-11
252152934022	474	PI-4	chr4	4	q34.1	174087045	174111042	12	0	-0.6675	-0.6675	3.79E-24
252152934022	475	PI-4	chr4	4	q34.1	174445945	174455071	6	0	-0.78387	-0.78387	3.61E-15
252152934022	476	PI-4	chr4	4	q34.3	177710134	177722131	5	0	-0.634	-0.634	3.66E-10
252152934022	477	PI-4	chr4	4	q34.3	183063558	183069722	6	0	-0.90093	-0.90093	1.51E-19
252152934022	481	PI-4	chr4	4	q35.1	185744797	185748493	3	0	-1.15379	-1.15379	5.58E-16
252152934022	482	PI-4	chr4	4	q35.1	186123296	186132573	6	0	-1.00707	-1.00707	7.23E-26
252152934022	483	PI-4	chr4	4	q35.1 - q35.2	187007504	187120799	50	0	-0.32035	-0.32035	1.15E-20
252152934022	484	PI-4	chr4	4	q35.2	187473308	187479459	4	0	-0.72437	-0.72437	1.28E-10
252152934022	485	PI-4	chr4	4	q35.2	187642850	187650409	4	0	-0.73757	-0.73757	8.83E-11
252152934022	486	PI-4	chr5	5	p15.33	2745603	2755695	6	0	-1.20971	-1.20971	1.33E-30
252152934022	487	PI-4	chr5	5	p15.33	3595595	3599080	3	0	-1.29571	-1.29571	2.55E-16
252152934022	488	PI-4	chr5	5	p15.31	6709608	6719319	5	0	-0.85393	-0.85393	1.10E-15
252152934022	490	PI-4	chr5	5	p15.2	10751324	10764809	8	0	-0.56105	-0.56105	4.64E-11
252152934022	491	PI-4	chr5	5	p15.2	11377931	11393727	9	0	-0.57321	-0.57321	5.19E-13

252152934022	492	PI-4	chr5	5	p15.2	11900407	11919849	11	0	-0.61624	-0.61624	4.57E-17
252152934022	495	PI-4	chr5	5	p15.2	14869647	14880657	7	0	-0.70601	-0.70601	1.16E-13
252152934022	496	PI-4	chr5	5	p15.1	17269946	17279595	7	0	-0.67938	-0.67938	1.57E-14
252152934022	497	PI-4	chr5	5	p14.2	23942021	23951125	3	0	-0.84503	-0.84503	8.99E-11
252152934022	499	PI-4	chr5	5	p13.3	32443236	32448171	4	0	-0.82091	-0.82091	7.31E-13
252152934022	500	PI-4	chr5	5	p13.2	34926929	34932061	4	0	-0.93398	-0.93398	5.47E-15
252152934022	501	PI-4	chr5	5	p13.1	38555754	38560170	3	0	-0.97233	-0.97233	2.95E-14
252152934022	502	PI-4	chr5	5	p12	45681597	45704838	12	0	-0.45964	-0.45964	2.80E-13
252152934022	504	PI-4	chr5	5	q11.2	53802193	53818069	7	0	-0.53501	-0.53501	3.15E-10
252152934022	505	PI-4	chr5	5	q11.2	54468349	54472237	7	0	-0.95503	-0.95503	2.79E-25
252152934022	506	PI-4	chr5	5	q11.2	56105453	56115746	6	0	-0.54153	-0.54153	7.73E-10
252152934022	507	PI-4	chr5	5	q12.1	59179077	59194027	9	0	-0.55279	-0.55279	1.34E-13
252152934022	508	PI-4	chr5	5	q12.1	60619639	60641055	6	0	-0.55579	-0.55579	3.44E-10
252152934022	509	PI-4	chr5	5	q12.3	65220697	65275451	27	0	-0.38876	-0.38876	4.44E-20
252152934022	510	PI-4	chr5	5	q13.2	68808690	68818232	5	0	-0.6068	-0.6068	3.27E-10
252152934022	512	PI-4	chr5	5	q13.2	72742059	72745282	3	0	-1.42479	-1.42479	1.27E-21
252152934022	513	PI-4	chr5	5	q13.2	72922693	72927938	4	0	-0.81995	-0.81995	7.89E-14
252152934022	518	PI-4	chr5	5	q14.1	79327683	79333814	4	0	-0.72043	-0.72043	2.72E-11
252152934022	519	PI-4	chr5	5	q14.3	83602324	83611384	6	0	-0.58431	-0.58431	6.54E-11
252152934022	520	PI-4	chr5	5	q15	92911737	92967287	30	0	-0.43	-0.43	1.44E-24
252152934022	521	PI-4	chr5	5	q15	94951976	94960844	6	0	-0.73833	-0.73833	4.80E-16
252152934022	522	PI-4	chr5	5	q21.3	107004043	107010185	5	0	-0.76739	-0.76739	4.13E-13
252152934022	523	PI-4	chr5	5	q21.3	107712622	107722044	5	0	-0.62666	-0.62666	6.81E-11
252152934022	524	PI-4	chr5	5	q21.3	108673080	108681873	5	0	-0.82793	-0.82793	1.58E-16
252152934022	525	PI-4	chr5	5	q23.2	122178937	122184501	4	0	-1.11751	-1.11751	1.46E-20
252152934022	526	PI-4	chr5	5	q23.2	122845059	122851344	5	0	-0.66246	-0.66246	1.13E-11
252152934022	527	PI-4	chr5	5	q23.3 - q31.1	130596794	130617758	11	0	-0.60104	-0.60104	2.44E-19
252152934022	529	PI-4	chr5	5	q31.1	132145613	132167361	13	0	-0.72112	-0.72112	2.25E-29
252152934022	534	PI-4	chr5	5	q31.3	139796573	139811648	7	0	-0.62636	-0.62636	1.93E-14
252152934022	535	PI-4	chr5	5	q31.3	141253592	141265259	7	0	-0.58733	-0.58733	4.17E-12
252152934022	538	PI-4	chr5	5	q33.3	157166954	157174629	5	0	-0.66905	-0.66905	6.50E-12
252152934022	539	PI-4	chr5	5	q34	167283031	167288784	3	0	-0.84798	-0.84798	5.18E-10
252152934022	540	PI-4	chr5	5	q34	167715822	167720463	4	0	-0.91411	-0.91411	5.00E-16
252152934022	541	PI-4	chr5	5	q34	167951830	167958053	4	0	-0.92621	-0.92621	7.02E-16
252152934022	542	PI-4	chr5	5	q34	168000172	168011390	9	0	-0.52118	-0.52118	6.68E-13
252152934022	543	PI-4	chr5	5	q35.1	168726663	168729665	3	0	-1.06895	-1.06895	5.64E-16
252152934022	544	PI-4	chr5	5	q35.1	170827317	170849587	13	0	-0.53369	-0.53369	9.81E-18
252152934022	545	PI-4	chr5	5	q35.1	171704170	171711985	5	0	-0.67724	-0.67724	3.36E-12
252152934022	546	PI-4	chr5	5	q35.1	171878961	171885507	4	0	-0.7672	-0.7672	3.73E-12
252152934022	547	PI-4	chr5	5	q35.1	172062063	172115048	26	0	-0.39748	-0.39748	9.03E-20
252152934022	560	PI-4	chr6	6	p25.3	287366	295178	5	0	-0.64925	-0.64925	3.58E-11
252152934022	561	PI-4	chr6	6	p25.3	1309409	1322976	5	0	-0.94641	-0.94641	1.31E-20
252152934022	562	PI-4	chr6	6	p25.3	1376203	1400038	12	0	-0.5552	-0.5552	6.32E-17
252152934022	563	PI-4	chr6	6	p25.3	1603954	1624100	10	0	-0.7751	-0.7751	1.29E-25
252152934022	567	PI-4	chr6	6	p25.2	3453042	3459841	4	0	-0.84585	-0.84585	1.77E-11
252152934022	568	PI-4	chr6	6	p25.2	3749197	3760175	6	0	-0.95287	-0.95287	2.50E-24
252152934022	569	PI-4	chr6	6	p25.1	4773466	4777924	3	0	-1.087	-1.087	7.59E-16
252152934022	570	PI-4	chr6	6	p24.3	7904608	7912516	4	0	-0.71165	-0.71165	6.29E-11
252152934022	571	PI-4	chr6	6	p24.3	10481501	10496579	7	0	-0.50449	-0.50449	4.70E-10
252152934022	572	PI-4	chr6	6	p24.2	11039564	11048781	6	0	-0.71453	-0.71453	4.72E-15
252152934022	573	PI-4	chr6	6	p24.2	11086580	11098331	7	0	-0.80307	-0.80307	8.28E-21
252152934022	574	PI-4	chr6	6	p24.1	12008097	12013632	4	0	-1.31765	-1.31765	1.66E-22
252152934022	575	PI-4	chr6	6	p23	13709943	13714372	3	0	-1.06096	-1.06096	1.08E-15
252152934022	576	PI-4	chr6	6	p23	13923407	13929364	3	0	-0.9302	-0.9302	1.29E-12
252152934022	577	PI-4	chr6	6	p22.3	15244447	15251230	5	0	-1.05721	-1.05721	7.65E-25
252152934022	578	PI-4	chr6	6	p22.3	15413079	15419256	4	0	-0.96006	-0.96006	1.39E-17
252152934022	579	PI-4	chr6	6	p22.3	16236989	16240985	3	0	-0.85898	-0.85898	2.71E-11
252152934022	580	PI-4	chr6	6	p22.3	17276986	17284955	5	0	-0.78703	-0.78703	9.80E-16
252152934022	581	PI-4	chr6	6	p22.3	17728000	17743845	6	0	-0.71221	-0.71221	2.26E-14
252152934022	583	PI-4	chr6	6	p22.3	18260047	18267148	4	0	-0.87358	-0.87358	9.78E-15
252152934022	584	PI-4	chr6	6	p22.3	19835409	19842250	6	0	-0.75197	-0.75197	2.12E-14
252152934022	585	PI-4	chr6	6	p22.3	21593054	21603809	7	0	-0.62376	-0.62376	2.57E-14
252152934022	589	PI-4	chr6	6	p21.33	31940860	31946312	4	0	-0.82464	-0.82464	3.46E-15
252152934022	590	PI-4	chr6	6	p21.31	33586785	33602979	9	0	-0.65943	-0.65943	6.21E-19
252152934022	591	PI-4	chr6	6	p21.31	34179897	34218075	16	0	-0.43705	-0.43705	8.15E-18
252152934022	594	PI-4	chr6	6	p21.31	35884066	35894931	6	0	-0.65696	-0.65696	4.88E-15
252152934022	597	PI-4	chr6	6	p21.2	37785349	37791957	4	0	-0.8789	-0.8789	3.50E-15
252152934022	603	PI-4	chr6	6	p21.1	43545425	43552038	4	0	-1.13249	-1.13249	4.38E-21
252152934022	605	PI-4	chr6	6	p12.3	46456278	46460312	3	0	-1.00689	-1.00689	6.34E-15
252152934022	606	PI-4	chr6	6	p12.2	51843061	51851568	5	0	-0.60639	-0.60639	2.63E-10
252152934022	607	PI-4	chr6	6	p12.2	52432428	52445634	9	0	-0.52556	-0.52556	8.09E-13
252152934022	608	PI-4	chr6	6	p12.1	53168261	53175648	4	0	-0.7412	-0.7412	2.13E-11
252152934022	609	PI-4	chr6	6	p12.1	56584355	56589411	3	0	-0.8302	-0.8302	8.79E-11
252152934022	610	PI-4	chr6	6	q13	71995521	72001868	4	0	-0.76983	-0.76983	9.45E-12
252152934022	611	PI-4	chr6	6	q14.1	79784507	79789852	4	0	-0.99344	-0.99344	2.45E-18
252152934022	613	PI-4	chr6	6	q14.3	87717828	87725773	5	0	-0.62687	-0.62687	1.12E-10
252152934022	614	PI-4	chr6	6	q15	88439950	88462126	9	0	-0.4595	-0.4595	1.65E-10
252152934022	615	PI-4	chr6	6	q16.1	99280026	99289565	6	0	-0.69342	-0.69342	2.64E-14
252152934022	616	PI-4	chr6	6	q16.2	99793834	99802228	5	0	-0.70769	-0.70769	7.61E-12
252152934022	617	PI-4	chr6	6	q21	105582741	105592924	5	0	-0.71358	-0.71358	5.68E-13
252152934022	618	PI-4	chr6	6	q21	105625169	105632155	5	0	-0.70364	-0.70364	4.05E-13
252152934022	619	PI-4	chr6	6	q21	105848758	105853164	4	0	-0.67377	-0.67377	4.77E-10
252152934022	621	PI-4	chr6	6	q21	108272561	108281377	6	0	-0.70393	-0.70393	1.19E-14
252152934022	623	PI-4	chr6	6	q21	111407939	111412801	3	0	-0.88591	-0.88591	6.15E-12
252152934022	624	PI-4	chr6	6	q21	114177937	114183824	4	0	-1.11172	-1.11172	3.45E-21
252152934022	625	PI-4	chr6	6	q22.1	118227066	118231579	3	0	-1.08422	-1.08422	5.54E-16
252152934022	626	PI-4	chr6	6	q22.31	124121057	124129366	5	0	-0.88911	-0.88911	8.33E-19
252152934022	627	PI-4	chr6	6	q23.2	131452998	131457339	3	0	-0.80814	-0.80814	6.07E-10
252152934022	628	PI-4	chr6	6	q23.3	135495448	135509460	8	0	-0.45288	-0.45288	1.28E-10
252152934022	629	PI-4	chr6	6	q23.3	136869023	136872607	3	0	-1.09927	-1.09927	1.04E-16
252152934022	630	PI-4	chr6	6	q23.3	137086103	137114704	15	0	-0.4393	-0.4393	8.92E-15
252152934022	634	PI-4	chr6	6	q25.1	150179713	150188465	5	0	-0.68014	-0.68014	2.44E-12
252152934022	636	PI-4	chr6	6	q25.1	151185146	151189293	3	0	-0.81536	-0.81536	1.54E-10
252152934022	637	PI-4	chr6	6	q25.2	153445515	153459692	8	0	-0.68548	-0.68548	2.54E-18
252152934022	640	PI-4	chr6	6	q25.3	157693068	157698905	8	0	-0.72582	-0.72582	2.23E-19
252152934022	641	PI-4	chr6	6	q25.3	158652327	158663116	4	0	-0.97892	-0.97892	2.19E-17

252152934022	642	PI-4	chr6	6	q25.3	160384952	160392521	5	0	-0.83001	-0.83001	7.82E-15
252152934022	646	PI-4	chr6	6	q27	166810788	166821796	7	0	-0.64654	-0.64654	6.51E-13
252152934022	652	PI-4	chr7	7	p22.3	1081110	1085752	6	0	-1.38222	-1.38222	3.66E-31
252152934022	653	PI-4	chr7	7	p22.3	1266051	1279052	7	0	-1.61508	-1.61508	3.22E-41
252152934022	654	PI-4	chr7	7	p22.3	2616473	2623881	5	0	-1.04524	-1.04524	5.85E-24
252152934022	655	PI-4	chr7	7	p22.2	2880961	2885896	4	0	-1.04377	-1.04377	9.74E-19
252152934022	660	PI-4	chr7	7	p22.1	6647142	6714612	31	0	-0.51945	-0.51945	6.33E-35
252152934022	662	PI-4	chr7	7	p21.3	9763073	9771937	5	0	-0.70741	-0.70741	3.21E-11
252152934022	663	PI-4	chr7	7	p21.3	10502601	10508845	4	0	-0.68951	-0.68951	2.54E-10
252152934022	666	PI-4	chr7	7	p21.1	20819365	20847855	14	0	-0.52351	-0.52351	2.64E-18
252152934022	667	PI-4	chr7	7	p15.3	22387779	22410641	12	0	-0.49322	-0.49322	4.89E-15
252152934022	670	PI-4	chr7	7	p15.3	24605165	24616405	6	0	-0.60699	-0.60699	9.61E-12
252152934022	672	PI-4	chr7	7	p15.2	26329288	26336565	6	0	-0.79748	-0.79748	6.40E-19
252152934022	673	PI-4	chr7	7	p15.2	27139893	27261612	95	0	-0.44589	-0.44589	1.16E-84
252152934022	675	PI-4	chr7	7	p15.1	28216387	28224936	5	0	-0.82903	-0.82903	1.32E-16
252152934022	683	PI-4	chr7	7	p14.1	42271561	42279753	5	0	-0.74696	-0.74696	2.31E-13
252152934022	685	PI-4	chr7	7	p13	44362013	44370247	5	0	-0.80879	-0.80879	5.03E-14
252152934022	687	PI-4	chr7	7	p13	44919730	44927821	6	0	-0.69357	-0.69357	1.15E-14
252152934022	688	PI-4	chr7	7	p13	45032614	45040773	5	0	-1.21369	-1.21369	3.54E-31
252152934022	689	PI-4	chr7	7	p12.3	45611077	45624920	7	0	-0.72618	-0.72618	1.08E-16
252152934022	690	PI-4	chr7	7	p12.3	47574280	47580917	5	0	-0.68227	-0.68227	6.23E-12
252152934022	691	PI-4	chr7	7	p12.3	47618471	47624157	4	0	-0.68098	-0.68098	4.03E-10
252152934022	692	PI-4	chr7	7	p12.2	49811104	49816304	4	0	-0.91409	-0.91409	2.18E-13
252152934022	693	PI-4	chr7	7	p12.2	50343122	50346310	3	0	-0.96943	-0.96943	3.88E-13
252152934022	694	PI-4	chr7	7	p12.1	50846702	50865598	8	0	-0.78192	-0.78192	8.97E-23
252152934022	697	PI-4	chr7	7	p11.2	56025359	56035843	7	0	-0.70866	-0.70866	3.31E-16
252152934022	698	PI-4	chr7	7	q11.21	63639563	63647019	4	0	-0.84671	-0.84671	1.25E-14
252152934022	700	PI-4	chr7	7	q11.22	70157312	70161546	3	0	-1.10609	-1.10609	1.08E-16
252152934022	702	PI-4	chr7	7	q11.23	73583467	73590414	7	0	-0.67517	-0.67517	7.75E-16
252152934022	704	PI-4	chr7	7	q21.11	77644551	77655755	7	0	-0.6497	-0.6497	4.17E-15
252152934022	705	PI-4	chr7	7	q21.12	87100948	87108002	5	0	-0.70127	-0.70127	7.50E-13
252152934022	706	PI-4	chr7	7	q21.13	90220541	90231480	7	0	-0.62506	-0.62506	4.04E-13
252152934022	709	PI-4	chr7	7	q21.3	94532156	94542174	8	0	-0.81033	-0.81033	2.42E-24
252152934022	710	PI-4	chr7	7	q21.3	97836953	97844684	4	0	-0.72618	-0.72618	3.90E-11
252152934022	711	PI-4	chr7	7	q21.3	97909997	97914003	3	0	-1.26916	-1.26916	2.80E-18
252152934022	720	PI-4	chr7	7	q22.1	101888196	101896854	8	0	-0.78825	-0.78825	1.63E-19
252152934022	726	PI-4	chr7	7	q22.3	105914384	105930563	9	0	-0.49147	-0.49147	8.39E-12
252152934022	728	PI-4	chr7	7	q31.1	107483086	107493457	6	0	-0.55255	-0.55255	3.31E-10
252152934022	730	PI-4	chr7	7	q31.2	116131714	116144941	8	0	-0.54104	-0.54104	1.68E-12
252152934022	731	PI-4	chr7	7	q31.2	116308977	116315972	6	0	-0.55187	-0.55187	5.31E-10
252152934022	732	PI-4	chr7	7	q31.2	116585803	116608143	13	0	-0.44109	-0.44109	2.46E-13
252152934022	733	PI-4	chr7	7	q31.31	119911666	119916550	4	0	-1.06247	-1.06247	8.97E-21
252152934022	734	PI-4	chr7	7	q31.33	126987532	126990366	3	0	-0.89719	-0.89719	2.29E-11
252152934022	738	PI-4	chr7	7	q32.1	129102259	129152807	24	0	-0.34249	-0.34249	2.89E-14
252152934022	739	PI-4	chr7	7	q32.2	130125921	130134249	11	0	-0.54717	-0.54717	2.28E-16
252152934022	740	PI-4	chr7	7	q32.2	130352477	130355822	3	0	-0.86818	-0.86818	4.59E-12
252152934022	742	PI-4	chr7	7	q32.3	131235076	131245047	6	0	-0.63727	-0.63727	1.58E-12
252152934022	743	PI-4	chr7	7	q34	138661481	138669417	5	0	-0.87086	-0.87086	2.44E-18
252152934022	746	PI-4	chr7	7	q34	140337142	140375836	14	0	-0.47457	-0.47457	5.54E-16
252152934022	747	PI-4	chr7	7	q35	144098121	144104974	5	0	-0.75388	-0.75388	7.89E-14
252152934022	748	PI-4	chr7	7	q36.1	148840475	148847308	5	0	-0.92933	-0.92933	1.95E-16
252152934022	749	PI-4	chr7	7	q36.1	148919532	148979684	29	0	-0.37508	-0.37508	5.97E-14
252152934022	752	PI-4	chr7	7	q36.1	150063446	150107848	22	0	-0.65369	-0.65369	3.91E-33
252152934022	755	PI-4	chr7	7	q36.1	151719755	151723323	3	0	-0.93756	-0.93756	5.83E-13
252152934022	756	PI-4	chr7	7	q36.2	153991672	154030651	23	0	-0.3639	-0.3639	8.25E-14
252152934022	758	PI-4	chr7	7	q36.3	155577275	155605712	16	0	-0.56811	-0.56811	4.13E-15
252152934022	761	PI-4	chr7	7	q36.3	157338612	157348580	10	0	-0.77592	-0.77592	2.46E-23
252152934022	768	PI-4	chr8	8	p23.1	10915544	10921103	6	0	-0.62713	-0.62713	4.14E-10
252152934022	771	PI-4	chr8	8	p22	12807108	12812396	4	0	-0.95302	-0.95302	4.44E-15
252152934022	772	PI-4	chr8	8	p22	17352781	17355718	3	0	-1.11598	-1.11598	4.27E-15
252152934022	773	PI-4	chr8	8	p22	18868138	18873560	4	0	-0.88033	-0.88033	5.31E-14
252152934022	774	PI-4	chr8	8	p21.3	20159098	20165020	4	0	-0.79993	-0.79993	3.46E-13
252152934022	775	PI-4	chr8	8	p21.3	22012095	22025085	7	0	-0.81289	-0.81289	1.23E-18
252152934022	776	PI-4	chr8	8	p21.3	22218299	22228198	6	0	-0.58169	-0.58169	7.81E-11
252152934022	778	PI-4	chr8	8	p21.2	23376719	23396002	11	0	-0.51157	-0.51157	8.91E-15
252152934022	779	PI-4	chr8	8	p21.2	25038131	25048603	7	0	-0.61668	-0.61668	7.50E-14
252152934022	780	PI-4	chr8	8	p21.2	26235983	26243888	4	0	-0.76051	-0.76051	2.78E-12
252152934022	784	PI-4	chr8	8	p21.1	28729229	28748930	10	0	-0.46829	-0.46829	3.24E-11
252152934022	785	PI-4	chr8	8	p12	29938907	29948666	5	0	-0.93591	-0.93591	7.75E-20
252152934022	787	PI-4	chr8	8	p12	30886622	30892125	4	0	-0.87799	-0.87799	2.14E-15
252152934022	788	PI-4	chr8	8	p12	31495506	31511670	9	0	-0.75177	-0.75177	2.80E-24
252152934022	792	PI-4	chr8	8	p11.21	41749522	41767114	10	0	-0.63071	-0.63071	9.72E-18
252152934022	794	PI-4	chr8	8	q11.23	54995799	55042202	14	0	-0.61719	-0.61719	1.56E-25
252152934022	798	PI-4	chr8	8	q12.1	57221048	57235886	9	0	-0.52932	-0.52932	2.46E-13
252152934022	799	PI-4	chr8	8	q12.1	57903463	57909112	4	0	-0.88908	-0.88908	4.76E-16
252152934022	800	PI-4	chr8	8	q12.1	61588520	61595100	4	0	-0.96912	-0.96912	8.05E-18
252152934022	802	PI-4	chr8	8	q13.1	66752290	66756892	4	0	-0.91163	-0.91163	4.22E-16
252152934022	803	PI-4	chr8	8	q13.1	67623906	67627238	3	0	-0.96819	-0.96819	7.56E-14
252152934022	804	PI-4	chr8	8	q13.1	67872353	67875921	3	0	-1.10394	-1.10394	2.34E-14
252152934022	805	PI-4	chr8	8	q13.2	68252887	68259278	4	0	-0.77345	-0.77345	5.09E-12
252152934022	806	PI-4	chr8	8	q13.3	71309017	71316986	5	0	-0.66789	-0.66789	1.28E-11
252152934022	807	PI-4	chr8	8	q21.11	74002955	74007274	3	0	-0.88058	-0.88058	7.73E-12
252152934022	808	PI-4	chr8	8	q21.11	74197122	74211900	7	0	-0.51838	-0.51838	2.25E-10
252152934022	809	PI-4	chr8	8	q21.13	80676557	80685083	6	0	-0.75697	-0.75697	1.95E-15
252152934022	810	PI-4	chr8	8	q21.13	81396247	81402832	4	0	-0.84634	-0.84634	1.56E-14
252152934022	811	PI-4	chr8	8	q21.2	86088759	86091715	3	0	-1.26369	-1.26369	2.02E-20
252152934022	821	PI-4	chr8	8	q22.3	103874769	103878546	4	0	-1.13634	-1.13634	1.83E-17
252152934022	822	PI-4	chr8	8	q23.1	106319150	106335008	9	0	-0.55776	-0.55776	7.15E-14
252152934022	823	PI-4	chr8	8	q23.3	117688407	117694251	3	0	-0.85769	-0.85769	2.48E-11
252152934022	825	PI-4	chr8	8	q24.12	120216326	120223875	5	0	-0.74358	-0.74358	5.85E-14
252152934022	827	PI-4	chr8	8	q24.13	124322805	124332436	6	0	-0.57962	-0.57962	3.24E-11
252152934022	830	PI-4	chr8	8	q24.22	133490673	133495998	3	0	-0.79027	-0.79027	1.22E-10
252152934022	834	PI-4	chr8	8	q24.23	139505652	139512552	5	0	-0.81697	-0.81697	3.10E-16
252152934022	835	PI-4	chr8	8	q24.3	141640540	141652704	6	0	-0.74083	-0.74083	4.75E-16
252152934022	839	PI-4	chr8	8	q24.3	144439594	144448984	5	0	-0.82673	-0.82673	1.55E-10
252152934022	842	PI-4	chr8	8	q24.3	145511620	145516280	4	0	-1.22156	-1.22156	9.46E-18

252152934022	845	PI-4	chr9	9	p24.3	2043102	2049904	5	0	-0.86643	-0.86643	9.69E-18
252152934022	846	PI-4	chr9	9	p24.1	6805980	6816980	7	0	-0.50593	-0.50593	5.49E-10
252152934022	847	PI-4	chr9	9	p24.1	8849537	8864438	9	0	-0.47291	-0.47291	4.16E-11
252152934022	848	PI-4	chr9	9	p23	13274717	13281904	5	0	-0.87022	-0.87022	1.04E-14
252152934022	856	PI-4	chr9	9	p13.1	38419583	38427110	5	0	-0.85215	-0.85215	1.00E-17
252152934022	857	PI-4	chr9	9	q21.11	71316347	71326168	6	0	-0.56889	-0.56889	1.49E-10
252152934022	858	PI-4	chr9	9	q21.11	71937907	71942782	4	0	-0.95524	-0.95524	2.76E-17
252152934022	859	PI-4	chr9	9	q21.11	72120570	72142259	10	0	-0.52441	-0.52441	1.76E-14
252152934022	860	PI-4	chr9	9	q21.13	75416470	75485560	24	0	-0.34454	-0.34454	7.07E-15
252152934022	862	PI-4	chr9	9	q21.2	80374126	80379965	3	0	-0.82167	-0.82167	9.71E-11
252152934022	863	PI-4	chr9	9	q21.2	80644003	80650305	4	0	-0.84695	-0.84695	3.93E-11
252152934022	864	PI-4	chr9	9	q21.31	82183730	82188939	4	0	-0.87423	-0.87423	1.24E-14
252152934022	865	PI-4	chr9	9	q21.32	86560455	86564205	4	0	-0.72448	-0.72448	1.42E-10
252152934022	866	PI-4	chr9	9	q21.33	89555203	89564473	6	0	-0.62606	-0.62606	9.09E-12
252152934022	867	PI-4	chr9	9	q22.1	91790359	91796056	4	0	-0.822	-0.822	8.47E-14
252152934022	869	PI-4	chr9	9	q22.31	95939991	95956100	7	0	-0.58841	-0.58841	1.94E-12
252152934022	870	PI-4	chr9	9	q22.31	96212997	96216292	3	0	-1.06375	-1.06375	7.64E-15
252152934022	873	PI-4	chr9	9	q22.32	96924824	96933017	8	0	-0.66987	-0.66987	8.42E-18
252152934022	875	PI-4	chr9	9	q22.32	98265488	98282413	10	0	-1.10054	-1.10054	6.56E-42
252152934022	876	PI-4	chr9	9	q22.33	99413144	99421189	4	0	-0.80609	-0.80609	2.16E-13
252152934022	877	PI-4	chr9	9	q22.33	100258515	100267067	6	0	-0.7499	-0.7499	2.30E-16
252152934022	878	PI-4	chr9	9	q22.33	100335648	100342536	5	0	-0.67677	-0.67677	3.19E-12
252152934022	882	PI-4	chr9	9	q22.33	101553418	101577905	12	0	-0.50677	-0.50677	4.58E-15
252152934022	883	PI-4	chr9	9	q22.33	101863999	101871663	5	0	-0.72391	-0.72391	4.18E-13
252152934022	884	PI-4	chr9	9	q22.33	102580589	102592420	6	0	-0.63281	-0.63281	2.33E-12
252152934022	886	PI-4	chr9	9	q31.1	107620525	107640169	12	0	-0.60838	-0.60838	5.83E-21
252152934022	887	PI-4	chr9	9	q31.1	108001300	108009464	5	0	-0.72565	-0.72565	1.26E-13
252152934022	889	PI-4	chr9	9	q31.3	111927306	111931247	3	0	-0.99043	-0.99043	1.59E-13
252152934022	891	PI-4	chr9	9	q31.3	112539579	112549692	6	0	-0.62077	-0.62077	2.38E-12
252152934022	893	PI-4	chr9	9	q31.3	114377132	114432913	29	0	-0.29309	-0.29309	3.06E-13
252152934022	894	PI-4	chr9	9	q32	114934775	114942700	5	0	-0.64556	-0.64556	1.04E-10
252152934022	895	PI-4	chr9	9	q32	115248045	115251453	3	0	-1.19507	-1.19507	1.56E-18
252152934022	896	PI-4	chr9	9	q32	115512321	115517036	4	0	-1.0967	-1.0967	2.00E-20
252152934022	905	PI-4	chr9	9	q33.3	126759910	126782797	11	0	-0.78582	-0.78582	3.43E-27
252152934022	918	PI-4	chr9	9	q34.11	131449302	131455424	4	0	-1.04321	-1.04321	6.17E-20
252152934022	922	PI-4	chr9	9	q34.12	133705609	133712381	5	0	-0.82746	-0.82746	1.11E-15
252152934022	923	PI-4	chr9	9	q34.13	134265101	134271587	4	0	-0.92582	-0.92582	2.09E-16
252152934022	924	PI-4	chr9	9	q34.13	134609943	134620060	5	0	-0.78532	-0.78532	5.13E-15
252152934022	925	PI-4	chr9	9	q34.13	135463797	135468587	4	0	-0.86667	-0.86667	1.31E-11
252152934022	928	PI-4	chr9	9	q34.3	137966024	137987242	10	0	-0.50148	-0.50148	2.89E-13
252152934022	929	PI-4	chr9	9	q34.3	138369004	138384638	8	0	-0.68854	-0.68854	4.99E-17
252152934022	940	PI-4	chr10	10	p15.3	178045	186810	5	0	-0.62157	-0.62157	1.55E-10
252152934022	942	PI-4	chr10	10	p15.2	3076714	3134187	25	0	-0.27796	-0.27796	3.65E-10
252152934022	947	PI-4	chr10	10	p14	8042937	8054834	7	0	-0.64853	-0.64853	2.80E-15
252152934022	949	PI-4	chr10	10	p14	11908864	11916733	5	0	-0.67999	-0.67999	4.35E-12
252152934022	950	PI-4	chr10	10	p13	12386795	12394296	4	0	-0.74416	-0.74416	7.96E-12
252152934022	952	PI-4	chr10	10	p13	13388242	13392460	3	0	-1.09004	-1.09004	1.59E-13
252152934022	953	PI-4	chr10	10	p13	13690710	13704689	7	0	-0.5033	-0.5033	8.74E-10
252152934022	954	PI-4	chr10	10	p13	14644277	14650987	3	0	-0.85533	-0.85533	6.84E-11
252152934022	956	PI-4	chr10	10	p13	15409524	15415335	4	0	-0.82052	-0.82052	1.58E-11
252152934022	957	PI-4	chr10	10	p13	16560017	16565830	5	0	-0.86906	-0.86906	3.66E-15
252152934022	958	PI-4	chr10	10	p12.33	17493955	17499710	4	0	-0.86738	-0.86738	1.46E-14
252152934022	961	PI-4	chr10	10	p12.31	21792260	21828310	32	0	-0.69658	-0.69658	2.60E-65
252152934022	962	PI-4	chr10	10	p12.2	22602135	22635726	19	0	-0.86206	-0.86206	1.27E-57
252152934022	963	PI-4	chr10	10	p12.2	23479832	23484626	4	0	-0.90955	-0.90955	2.15E-14
252152934022	964	PI-4	chr10	10	p12.2	23721982	23745890	8	0	-0.52235	-0.52235	1.05E-11
252152934022	966	PI-4	chr10	10	p12.1	25240582	25247189	4	0	-0.71576	-0.71576	5.32E-11
252152934022	970	PI-4	chr10	10	p11.23	30309575	30352380	21	0	-0.30239	-0.30239	1.19E-10
252152934022	971	PI-4	chr10	10	p11.22	32213594	32222550	5	0	-0.59987	-0.59987	7.65E-10
252152934022	972	PI-4	chr10	10	p11.22	32630670	32639879	6	0	-0.70429	-0.70429	2.74E-15
252152934022	973	PI-4	chr10	10	p11.21	35917090	35934470	8	0	-0.51848	-0.51848	8.58E-11
252152934022	974	PI-4	chr10	10	q11.21	43632389	43636004	3	0	-1.05416	-1.05416	1.85E-15
252152934022	976	PI-4	chr10	10	q11.21	43900420	43968350	25	0	-0.36316	-0.36316	3.78E-15
252152934022	977	PI-4	chr10	10	q11.21	45494605	45499960	5	0	-0.77049	-0.77049	1.61E-14
252152934022	981	PI-4	chr10	10	q11.22	49725423	49735835	5	0	-0.7624	-0.7624	1.86E-14
252152934022	982	PI-4	chr10	10	q21.1	53148868	53157451	6	0	-0.69125	-0.69125	7.62E-15
252152934022	983	PI-4	chr10	10	q21.3	65282280	65286922	4	0	-0.74813	-0.74813	6.37E-12
252152934022	984	PI-4	chr10	10	q21.3	69642083	69647235	4	0	-0.74193	-0.74193	1.10E-11
252152934022	993	PI-4	chr10	10	q23.1	82291359	82296843	4	0	-0.93334	-0.93334	6.79E-16
252152934022	994	PI-4	chr10	10	q23.1	83628655	83643337	8	0	-0.68251	-0.68251	5.93E-18
252152934022	995	PI-4	chr10	10	q23.1	86080632	86120249	19	0	-0.41413	-0.41413	4.80E-16
252152934022	999	PI-4	chr10	10	q23.31	92607245	92618536	7	0	-0.5635	-0.5635	5.80E-11
252152934022	1000	PI-4	chr10	10	q23.32	92917816	92924461	4	0	-0.9306	-0.9306	2.61E-16
252152934022	1001	PI-4	chr10	10	q23.32	93165067	93177051	7	0	-0.68906	-0.68906	2.77E-16
252152934022	1003	PI-4	chr10	10	q23.33	94604788	94619815	6	0	-0.64522	-0.64522	2.57E-13
252152934022	1004	PI-4	chr10	10	q23.33	95751962	95757535	3	0	-0.81645	-0.81645	2.01E-10
252152934022	1005	PI-4	chr10	10	q24.1	97049984	97053154	3	0	-1.04658	-1.04658	1.58E-15
252152934022	1007	PI-4	chr10	10	q24.1	98340784	98353235	7	0	-0.55062	-0.55062	1.74E-11
252152934022	1008	PI-4	chr10	10	q24.1	98588727	98595989	10	0	-0.82335	-0.82335	1.03E-28
252152934022	1013	PI-4	chr10	10	q24.2	101294355	101298352	3	0	-1.13348	-1.13348	1.02E-16
252152934022	1014	PI-4	chr10	10	q24.2	101764593	101773975	6	0	-0.64575	-0.64575	4.26E-13
252152934022	1015	PI-4	chr10	10	q24.31	102029337	102040548	6	0	-0.58227	-0.58227	4.59E-11
252152934022	1016	PI-4	chr10	10	q24.31	102474552	102495974	8	0	-0.49722	-0.49722	3.63E-10
252152934022	1017	PI-4	chr10	10	q24.31	102982411	102992376	6	0	-1.04331	-1.04331	4.45E-20
252152934022	1030	PI-4	chr10	10	q25.3	116579263	116584435	4	0	-1.10076	-1.10076	5.49E-22
252152934022	1036	PI-4	chr10	10	q26.13	123343140	123372110	14	0	-0.45659	-0.45659	4.49E-15
252152934022	1039	PI-4	chr10	10	q26.13	126845007	126851638	4	0	-1.0058	-1.0058	1.33E-15
252152934022	1042	PI-4	chr10	10	q26.3	131759054	131776585	10	0	-0.92992	-0.92992	2.74E-28
252152934022	1043	PI-4	chr10	10	q26.3	133107399	133112924	4	0	-0.98569	-0.98569	3.22E-15
252152934022	1048	PI-4	chr11	11	p15.5	559132	577920	11	0	-0.8276	-0.8276	2.84E-23
252152934022	1054	PI-4	chr11	11	p15.4	3184691	3189015	3	0	-0.87829	-0.87829	5.71E-10
252152934022	1055	PI-4	chr11	11	p15.4	3874345	3879297	4	0	-0.92953	-0.92953	1.71E-16
252152934022	1056	PI-4	chr11	11	p15.4	4154856	4160221	5	0	-0.70202	-0.70202	1.14E-12
252152934022	1061	PI-4	chr11	11	p15.3	12027274	12033463	5	0	-0.80981	-0.80981	4.16E-16
252152934022	1068	PI-4	chr11	11	p11.2	45903180	45929000	15	0	-0.49764	-0.49764	3.71E-17
252152934022	1070	PI-4	chr11	11	p11.2	46936411	46942301	4	0	-1.018	-1.018	1.84E-18

252152934022	1071	PI-4	chr11	11	p11.2	47116672	47122954	4	0	-0.72459	-0.72459	2.34E-11
252152934022	1072	PI-4	chr11	11	p11.2	47999278	48005637	4	0	-0.79557	-0.79557	6.46E-13
252152934022	1073	PI-4	chr11	11	q12.2	60581667	60585476	3	0	-0.9479	-0.9479	2.02E-13
252152934022	1074	PI-4	chr11	11	q12.2	61275757	61279974	3	0	-0.93761	-0.93761	3.43E-12
252152934022	1077	PI-4	chr11	11	q13.1	63528548	63540745	5	0	-0.83705	-0.83705	1.88E-15
252152934022	1093	PI-4	chr11	11	q13.3	70109830	70147001	33	0	-0.39393	-0.39393	1.10E-24
252152934022	1094	PI-4	chr11	11	q13.4	71931627	71959702	17	0	-0.50852	-0.50852	8.17E-19
252152934022	1095	PI-4	chr11	11	q13.4	72850066	72858811	5	0	-0.65633	-0.65633	1.52E-11
252152934022	1096	PI-4	chr11	11	q13.4	74433041	74477912	18	0	-0.39925	-0.39925	6.07E-15
252152934022	1097	PI-4	chr11	11	q13.5	75230808	75237616	4	0	-0.78245	-0.78245	3.61E-12
252152934022	1102	PI-4	chr11	11	q14.2	86508172	86513370	4	0	-0.79459	-0.79459	6.10E-13
252152934022	1103	PI-4	chr11	11	q21	93273959	93277536	3	0	-1.13908	-1.13908	7.41E-18
252152934022	1105	PI-4	chr11	11	q22.1	100988351	101000094	10	0	-0.5398	-0.5398	7.65E-15
252152934022	1106	PI-4	chr11	11	q22.3	106884480	106893357	5	0	-0.83274	-0.83274	3.88E-16
252152934022	1107	PI-4	chr11	11	q22.3	110298943	110311311	6	0	-0.66324	-0.66324	8.69E-14
252152934022	1108	PI-4	chr11	11	q23.1	110581263	110586374	3	0	-0.82603	-0.82603	5.37E-11
252152934022	1109	PI-4	chr11	11	q23.2	113739143	113748344	6	0	-0.79295	-0.79295	1.90E-18
252152934022	1110	PI-4	chr11	11	q23.3	117121240	117124657	3	0	-0.94719	-0.94719	2.34E-13
252152934022	1111	PI-4	chr11	11	q23.3	118924528	118932496	5	0	-0.81519	-0.81519	2.51E-16
252152934022	1115	PI-4	chr11	11	q23.3	120204421	120208978	4	0	-0.95131	-0.95131	8.94E-17
252152934022	1116	PI-4	chr11	11	q24.1	121319747	121326406	5	0	-0.64602	-0.64602	3.46E-11
252152934022	1122	PI-4	chr11	11	q25	131778700	131786438	5	0	-1.0321	-1.0321	8.59E-24
252152934022	1130	PI-4	chr12	12	p13.33	3178420	3211096	18	0	-0.38709	-0.38709	3.18E-14
252152934022	1133	PI-4	chr12	12	p13.31	7592349	7596114	4	0	-0.85509	-0.85509	8.46E-15
252152934022	1134	PI-4	chr12	12	p13.31	7777178	7787402	5	0	-0.74871	-0.74871	2.62E-14
252152934022	1135	PI-4	chr12	12	p13.31	8183161	8187785	3	0	-0.77705	-0.77705	5.54E-10
252152934022	1137	PI-4	chr12	12	p13.31	8845605	8853239	5	0	-0.76895	-0.76895	1.72E-14
252152934022	1138	PI-4	chr12	12	p13.2	10869583	10883409	8	0	-0.51703	-0.51703	2.10E-11
252152934022	1139	PI-4	chr12	12	p13.2	11800304	11805269	4	0	-0.87235	-0.87235	7.48E-12
252152934022	1140	PI-4	chr12	12	p12.3	19282053	19285386	3	0	-1.09001	-1.09001	1.37E-16
252152934022	1142	PI-4	chr12	12	p12.1	26264989	26282653	11	0	-0.61761	-0.61761	2.57E-20
252152934022	1143	PI-4	chr12	12	p11.23	27484679	27491755	4	0	-0.8747	-0.8747	2.86E-15
252152934022	1144	PI-4	chr12	12	p11.22	28121472	28125485	3	0	-0.92885	-0.92885	7.14E-12
252152934022	1147	PI-4	chr12	12	p11.21	30906690	30909774	3	0	-1.01831	-1.01831	4.02E-15
252152934022	1149	PI-4	chr12	12	p11.21	32551794	32555670	3	0	-0.80322	-0.80322	2.39E-10
252152934022	1150	PI-4	chr12	12	p11.21	32711213	32721846	12	0	-0.49042	-0.49042	7.47E-15
252152934022	1151	PI-4	chr12	12	q12	41580805	41584404	3	0	-1.02938	-1.02938	6.33E-15
252152934022	1152	PI-4	chr12	12	q12	42620061	42634368	6	0	-1.0529	-1.0529	3.56E-29
252152934022	1153	PI-4	chr12	12	q12	42982644	42991521	6	0	-0.70388	-0.70388	4.67E-15
252152934022	1155	PI-4	chr12	12	q13.11	48722931	48728516	3	0	-1.07067	-1.07067	4.51E-16
252152934022	1157	PI-4	chr12	12	q13.12	49929788	49935746	4	0	-1.03574	-1.03574	8.17E-19
252152934022	1158	PI-4	chr12	12	q13.12	50985586	50994046	5	0	-0.77563	-0.77563	5.01E-14
252152934022	1159	PI-4	chr12	12	q13.13	52206600	52217560	6	0	-1.01797	-1.01797	3.39E-27
252152934022	1163	PI-4	chr12	12	q13.13	54767121	54776518	5	0	-0.72752	-0.72752	4.78E-16
252152934022	1164	PI-4	chr12	12	q13.2	56135092	56143617	6	0	-0.6893	-0.6893	1.10E-16
252152934022	1166	PI-4	chr12	12	q13.3	57175974	57186362	5	0	-0.90624	-0.90624	9.24E-20
252152934022	1167	PI-4	chr12	12	q13.3	57394367	57403889	7	0	-0.64869	-0.64869	8.85E-15
252152934022	1168	PI-4	chr12	12	q13.3	57820409	57827578	5	0	-0.94981	-0.94981	7.33E-21
252152934022	1169	PI-4	chr12	12	q13.3	57914894	57917740	4	0	-1.18564	-1.18564	4.22E-22
252152934022	1170	PI-4	chr12	12	q14.1	58115294	58154075	21	0	-0.44295	-0.44295	8.59E-19
252152934022	1171	PI-4	chr12	12	q14.2	64782643	64800553	9	0	-0.50999	-0.50999	1.34E-12
252152934022	1172	PI-4	chr12	12	q14.2	65001469	65009162	8	0	-0.72152	-0.72152	4.28E-20
252152934022	1173	PI-4	chr12	12	q15	69002007	69005661	3	0	-0.95673	-0.95673	5.49E-13
252152934022	1174	PI-4	chr12	12	q15	69618626	69641285	10	0	-0.60018	-0.60018	1.05E-16
252152934022	1175	PI-4	chr12	12	q15	70127652	70155363	14	0	-0.423	-0.423	3.36E-13
252152934022	1176	PI-4	chr12	12	q22	93321395	93325083	3	0	-0.86925	-0.86925	6.08E-12
252152934022	1177	PI-4	chr12	12	q22	95625018	95635769	5	0	-0.62204	-0.62204	1.91E-10
252152934022	1179	PI-4	chr12	12	q23.1	96586372	96591892	4	0	-0.7494	-0.7494	6.74E-11
252152934022	1180	PI-4	chr12	12	q23.1	99288036	99292190	3	0	-1.02828	-1.02828	4.31E-15
252152934022	1181	PI-4	chr12	12	q23.1	100372561	100382164	6	0	-0.82445	-0.82445	1.69E-19
252152934022	1182	PI-4	chr12	12	q23.1	100684512	100690823	4	0	-0.8293	-0.8293	3.71E-14
252152934022	1189	PI-4	chr12	12	q24.11	109249404	109254077	4	0	-1.28713	-1.28713	1.57E-21
252152934022	1207	PI-4	chr12	12	q24.31	125475546	125481289	4	0	-0.98706	-0.98706	1.34E-17
252152934022	1208	PI-4	chr12	12	q24.33	130641995	130652916	7	0	-0.68942	-0.68942	7.99E-14
252152934022	1209	PI-4	chr12	12	q24.33	131301153	131392412	40	0	-0.34286	-0.34286	7.57E-16
252152934022	1216	PI-4	chr13	13	q12.11	22244841	22250288	5	0	-1.10447	-1.10447	9.53E-24
252152934022	1217	PI-4	chr13	13	q12.13	25944136	25950998	5	0	-0.98802	-0.98802	2.30E-20
252152934022	1219	PI-4	chr13	13	q12.13	27329861	27339320	7	0	-0.81244	-0.81244	4.46E-19
252152934022	1220	PI-4	chr13	13	q12.13	27744794	27747665	3	0	-1.1612	-1.1612	9.42E-17
252152934022	1225	PI-4	chr13	13	q13.1	33589780	33594207	3	0	-0.94656	-0.94656	1.50E-12
252152934022	1227	PI-4	chr13	13	q13.3	37492522	37496161	3	0	-0.94338	-0.94338	1.38E-13
252152934022	1228	PI-4	chr13	13	q14.11	41360472	41366016	3	0	-0.81556	-0.81556	1.33E-10
252152934022	1229	PI-4	chr13	13	q14.11	43537328	43544816	6	0	-0.65669	-0.65669	7.04E-13
252152934022	1230	PI-4	chr13	13	q14.11	45148934	45153985	3	0	-0.95579	-0.95579	9.24E-14
252152934022	1231	PI-4	chr13	13	q14.13	46056407	46061190	4	0	-0.70835	-0.70835	9.63E-11
252152934022	1233	PI-4	chr13	13	q14.2	50365135	50369032	3	0	-1.19118	-1.19118	2.07E-13
252152934022	1234	PI-4	chr13	13	q14.2	50567919	50574345	4	0	-0.81688	-0.81688	6.31E-14
252152934022	1240	PI-4	chr13	13	q31.1	79174029	79178668	3	0	-1.21172	-1.21172	4.49E-19
252152934022	1241	PI-4	chr13	13	q31.1	80910339	80919954	7	0	-0.67454	-0.67454	7.21E-14
252152934022	1242	PI-4	chr13	13	q31.3	91996408	92005080	11	0	-0.80208	-0.80208	1.63E-29
252152934022	1243	PI-4	chr13	13	q32.1	95361923	95366159	4	0	-1.00851	-1.00851	5.59E-15
252152934022	1244	PI-4	chr13	13	q32.1	96740042	96744223	3	0	-1.05695	-1.05695	1.23E-12
252152934022	1245	PI-4	chr13	13	q32.2	98625939	98631159	4	0	-0.91358	-0.91358	4.09E-16
252152934022	1246	PI-4	chr13	13	q32.2	98793056	98796425	3	0	-1.23489	-1.23489	1.20E-17
252152934022	1247	PI-4	chr13	13	q32.2	99227999	99231549	3	0	-1.11346	-1.11346	9.01E-17
252152934022	1250	PI-4	chr13	13	q32.3	100619381	100638825	11	0	-0.91717	-0.91717	3.94E-32
252152934022	1253	PI-4	chr13	13	q33.3	107186045	107190156	4	0	-1.15727	-1.15727	6.43E-18
252152934022	1254	PI-4	chr13	13	q33.3	108433133	108438112	4	0	-0.82601	-0.82601	1.04E-11
252152934022	1255	PI-4	chr13	13	q33.3	108863497	108871629	5	0	-0.76204	-0.76204	4.04E-12
252152934022	1257	PI-4	chr13	13	q34	111357935	111367596	6	0	-0.77004	-0.77004	2.88E-12
252152934022	1258	PI-4	chr13	13	q34	111766109	111773768	6	0	-0.73035	-0.73035	6.68E-13
252152934022	1264	PI-4	chr14	14	q11.2	21557769	21568120	6	0	-0.86828	-0.86828	2.40E-21
252152934022	1267	PI-4	chr14	14	q11.2	23514833	23530894	11	0	-0.59664	-0.59664	6.81E-19
252152934022	1268	PI-4	chr14	14	q11.2	23765478	23799437	20	0	-0.37593	-0.37593	9.09E-15
252152934022	1269	PI-4	chr14	14	q11.2	24044612	24052121	5	0	-0.82623	-0.82623	4.37E-14
252152934022	1270	PI-4	chr14	14	q12	24777360	24787001	6	0	-0.61434	-0.61434	3.95E-12

252152934022	1271	PI-4	chr14	14	q12	29231513	29241116	7	0	-0.66717	-0.66717	4.60E-14
252152934022	1273	PI-4	chr14	14	q13.1	33401486	33409722	5	0	-1.09059	-1.09059	1.23E-25
252152934022	1275	PI-4	chr14	14	q13.2	35341299	35347502	5	0	-0.82686	-0.82686	3.97E-13
252152934022	1276	PI-4	chr14	14	q13.2	35869847	35875663	5	0	-0.62749	-0.62749	1.05E-10
252152934022	1277	PI-4	chr14	14	q13.2	36287834	36302047	9	0	-0.55194	-0.55194	7.18E-14
252152934022	1278	PI-4	chr14	14	q21.1	38052340	38081215	16	0	-0.46826	-0.46826	8.57E-17
252152934022	1279	PI-4	chr14	14	q21.1	39897273	39906306	7	0	-0.61619	-0.61619	3.83E-13
252152934022	1280	PI-4	chr14	14	q21.1	42139845	42146342	4	0	-0.93225	-0.93225	6.07E-17
252152934022	1282	PI-4	chr14	14	q21.3	50694601	50704319	6	0	-0.66872	-0.66872	2.03E-13
252152934022	1283	PI-4	chr14	14	q22.1	51295640	51300049	3	0	-0.93504	-0.93504	5.63E-13
252152934022	1284	PI-4	chr14	14	q22.2	54412547	54424898	7	0	-0.54847	-0.54847	1.44E-11
252152934022	1285	PI-4	chr14	14	q22.3	55735855	55742917	5	0	-0.84605	-0.84605	3.72E-17
252152934022	1287	PI-4	chr14	14	q22.3	57262352	57287037	19	0	-0.41468	-0.41468	6.34E-16
252152934022	1300	PI-4	chr14	14	q24.3	74250771	74255111	4	0	-0.87449	-0.87449	3.22E-15
252152934022	1303	PI-4	chr14	14	q24.3	78208152	78218450	7	0	-0.56748	-0.56748	3.23E-12
252152934022	1305	PI-4	chr14	14	q31.1	81781591	81794222	8	0	-0.49289	-0.49289	1.43E-10
252152934022	1306	PI-4	chr14	14	q31.3	88786676	88791783	4	0	-0.79157	-0.79157	7.57E-13
252152934022	1307	PI-4	chr14	14	q31.3	89017312	89027307	6	0	-0.58631	-0.58631	3.50E-10
252152934022	1308	PI-4	chr14	14	q32.11	89882072	89887444	4	0	-0.82458	-0.82458	2.09E-13
252152934022	1312	PI-4	chr14	14	q32.11	91716455	91732700	10	0	-0.71491	-0.71491	7.43E-23
252152934022	1313	PI-4	chr14	14	q32.12	93578488	93586834	5	0	-0.75764	-0.75764	1.08E-11
252152934022	1314	PI-4	chr14	14	q32.12	93648640	93652614	3	0	-0.87718	-0.87718	5.82E-12
252152934022	1316	PI-4	chr14	14	q32.13	95621215	95625546	4	0	-1.08212	-1.08212	1.03E-21
252152934022	1317	PI-4	chr14	14	q32.13	95784221	95788362	3	0	-1.25269	-1.25269	5.82E-20
252152934022	1335	PI-4	chr15	15	q11.2	23929562	23933678	3	0	-0.99587	-0.99587	4.81E-13
252152934022	1337	PI-4	chr15	15	q13.1	29861670	29867088	4	0	-1.0253	-1.0253	3.75E-17
252152934022	1339	PI-4	chr15	15	q13.3	31282994	31287111	3	0	-1.11089	-1.11089	1.30E-15
252152934022	1342	PI-4	chr15	15	q14	34328703	34335526	5	0	-0.91349	-0.91349	1.86E-18
252152934022	1344	PI-4	chr15	15	q14	34653046	34664608	13	0	-0.53104	-0.53104	3.45E-16
252152934022	1345	PI-4	chr15	15	q14	35234120	35240589	5	0	-0.64154	-0.64154	3.28E-11
252152934022	1346	PI-4	chr15	15	q14	35947358	35954416	4	0	-0.87152	-0.87152	5.80E-15
252152934022	1347	PI-4	chr15	15	q14	38853585	38866388	6	0	-0.53703	-0.53703	9.07E-10
252152934022	1348	PI-4	chr15	15	q15.1	40184148	40192600	6	0	-0.5754	-0.5754	7.93E-11
252152934022	1349	PI-4	chr15	15	q15.1	40569566	40585630	10	0	-0.58428	-0.58428	3.28E-16
252152934022	1351	PI-4	chr15	15	q15.1	40730549	40736307	4	0	-1.04849	-1.04849	8.70E-19
252152934022	1354	PI-4	chr15	15	q15.1	41785091	41806648	13	0	-0.53844	-0.53844	2.10E-15
252152934022	1355	PI-4	chr15	15	q15.1	42253300	42268755	8	0	-0.51952	-0.51952	3.99E-11
252152934022	1357	PI-4	chr15	15	q15.2	43027117	43034033	5	0	-0.71908	-0.71908	1.82E-13
252152934022	1358	PI-4	chr15	15	q21.2	51382032	51391332	6	0	-0.6858	-0.6858	1.70E-14
252152934022	1359	PI-4	chr15	15	q21.2	51584126	51588921	4	0	-1.07875	-1.07875	4.96E-20
252152934022	1360	PI-4	chr15	15	q21.2	52032494	52046582	6	0	-0.71998	-0.71998	7.55E-16
252152934022	1365	PI-4	chr15	15	q21.3	56533717	56537782	4	0	-1.05795	-1.05795	4.17E-20
252152934022	1366	PI-4	chr15	15	q21.3	57667528	57671393	3	0	-0.85494	-0.85494	2.46E-11
252152934022	1367	PI-4	chr15	15	q22.1	59223714	59226879	3	0	-0.87475	-0.87475	6.58E-12
252152934022	1368	PI-4	chr15	15	q22.2	59728028	59731193	3	0	-1.03437	-1.03437	8.15E-15
252152934022	1369	PI-4	chr15	15	q22.2	62351798	62364547	9	0	-0.67808	-0.67808	3.63E-20
252152934022	1378	PI-4	chr15	15	q22.33	67357060	67360534	3	0	-1.05595	-1.05595	3.07E-15
252152934022	1380	PI-4	chr15	15	q23	71405105	71410596	4	0	-0.91394	-0.91394	4.67E-16
252152934022	1391	PI-4	chr15	15	q24.3	77709817	77716554	5	0	-0.88453	-0.88453	5.46E-19
252152934022	1392	PI-4	chr15	15	q25.1	80694072	80700327	4	0	-0.90997	-0.90997	3.19E-16
252152934022	1393	PI-4	chr15	15	q25.1	80982431	80996095	8	0	-0.51185	-0.51185	2.40E-11
252152934022	1402	PI-4	chr15	15	q26.1	89904479	89919630	20	0	-0.53603	-0.53603	3.33E-24
252152934022	1403	PI-4	chr15	15	q26.1	90186131	90211786	22	0	-0.47978	-0.47978	1.19E-20
252152934022	1404	PI-4	chr15	15	q26.1	90392263	90415827	14	0	-0.56785	-0.56785	3.79E-22
252152934022	1408	PI-4	chr15	15	q26.1	91403961	91421707	11	0	-0.55166	-0.55166	5.15E-16
252152934022	1411	PI-4	chr15	15	q26.2	95385135	95389330	3	0	-0.77546	-0.77546	8.34E-10
252152934022	1412	PI-4	chr15	15	q26.2	96866427	96885443	25	0	-0.56965	-0.56965	2.13E-33
252152934022	1413	PI-4	chr15	15	q26.2	96873020	96876018	4	0	-1.7236	-1.7236	5.04E-14
252152934022	1414	PI-4	chr15	15	q26.3	99184901	99197341	7	0	-0.63933	-0.63933	3.03E-13
252152934022	1416	PI-4	chr15	15	q26.3	99641175	99647610	4	0	-0.89061	-0.89061	4.27E-14
252152934022	1417	PI-4	chr15	15	q26.3	100101111	100111083	7	0	-0.77172	-0.77172	8.21E-18
252152934022	1420	PI-4	chr15	15	q26.3	101455610	101462918	6	0	-0.98214	-0.98214	9.71E-25
252152934022	1421	PI-4	chr15	15	q26.3	101789504	101793149	3	0	-1.14339	-1.14339	1.23E-17
252152934022	1422	PI-4	chr15	15	q26.3	102026679	102034423	5	0	-1.09896	-1.09896	5.91E-26
252152934022	1426	PI-4	chr16	16	p13.3	2031940	2075938	20	0	-0.71089	-0.71089	1.49E-22
252152934022	1429	PI-4	chr16	16	p13.3	4164240	4170423	3	0	-0.89112	-0.89112	2.29E-11
252152934022	1430	PI-4	chr16	16	p13.2	9180068	9192807	8	0	-0.538	-0.538	2.75E-12
252152934022	1432	PI-4	chr16	16	p13.13	11425689	11437781	9	0	-0.46596	-0.46596	7.30E-11
252152934022	1433	PI-4	chr16	16	p13.13	11581030	11591763	8	0	-0.535	-0.535	6.78E-12
252152934022	1434	PI-4	chr16	16	p13.13	12004539	12010888	4	0	-0.73823	-0.73823	8.41E-12
252152934022	1435	PI-4	chr16	16	p13.12	14394835	14401192	9	0	-0.60879	-0.60879	1.23E-13
252152934022	1436	PI-4	chr16	16	p13.11	15147365	15151093	3	0	-1.13285	-1.13285	1.18E-14
252152934022	1437	PI-4	chr16	16	p12.3	17558648	17566007	4	0	-0.85891	-0.85891	1.29E-14
252152934022	1438	PI-4	chr16	16	p12.3	19123854	19130354	3	0	-0.83096	-0.83096	4.22E-11
252152934022	1440	PI-4	chr16	16	p12.2	23157223	23161641	3	0	-0.94412	-0.94412	4.32E-13
252152934022	1442	PI-4	chr16	16	p12.1	25699068	25707443	5	0	-0.82983	-0.82983	7.29E-17
252152934022	1471	PI-4	chr16	16	q22.3	73078930	73103759	13	0	-0.62194	-0.62194	1.32E-22
252152934022	1472	PI-4	chr16	16	q23.2	79625286	79636091	8	0	-0.69301	-0.69301	1.59E-18
252152934022	1474	PI-4	chr16	16	q23.2	81068752	81072096	3	0	-0.95039	-0.95039	2.06E-13
252152934022	1481	PI-4	chr16	16	q24.1	86536742	86548110	6	0	-0.80464	-0.80464	1.44E-14
252152934022	1482	PI-4	chr16	16	q24.1	86595553	86615538	12	0	-0.66479	-0.66479	1.98E-23
252152934022	1486	PI-4	chr16	16	q24.3	89880964	89898890	10	0	-0.83427	-0.83427	1.96E-31
252152934022	1495	PI-4	chr17	17	p13.3	2650266	2661875	11	0	-0.79596	-0.79596	1.09E-30
252152934022	1498	PI-4	chr17	17	p13.2	3845004	3849923	4	0	-1.08284	-1.08284	4.55E-18
252152934022	1500	PI-4	chr17	17	p13.2	4480708	4491423	5	0	-0.70938	-0.70938	6.65E-13
252152934022	1501	PI-4	chr17	17	p13.2	5182104	5188354	5	0	-0.78363	-0.78363	1.18E-12
252152934022	1503	PI-4	chr17	17	p13.1	7753895	7757450	3	0	-0.96477	-0.96477	9.99E-14
252152934022	1504	PI-4	chr17	17	p12	11140998	11145660	3	0	-1.05217	-1.05217	3.30E-15
252152934022	1518	PI-4	chr17	17	q11.2	29808587	29816139	5	0	-0.76579	-0.76579	1.92E-14
252152934022	1519	PI-4	chr17	17	q11.2	29880382	29889317	9	0	-0.61442	-0.61442	1.58E-16
252152934022	1525	PI-4	chr17	17	q11.2	31146624	31159958	8	0	-0.55376	-0.55376	1.04E-12
252152934022	1528	PI-4	chr17	17	q12	35843830	35854974	7	0	-0.5829	-0.5829	1.75E-12
252152934022	1535	PI-4	chr17	17	q21.31	42253276	42326740	33	0	-0.33885	-0.33885	8.58E-18
252152934022	1543	PI-4	chr17	17	q21.32	46112708	46120214	7	0	-0.82501	-0.82501	4.30E-21
252152934022	1544	PI-4	chr17	17	q21.32	46618771	46660064	40	0	-0.51088	-0.51088	3.53E-45
252152934022	1545	PI-4	chr17	17	q21.33	47438121	47442150	3	0	-0.90413	-0.90413	2.62E-12

252152934022	1547	PI-4	chr17	17	q21.33	48941257	48945822	3	0	-0.84258	-0.84258	3.47E-11
252152934022	1548	PI-4	chr17	17	q21.33	49196414	49202190	4	0	-1.04683	-1.04683	4.52E-20
252152934022	1549	PI-4	chr17	17	q22	53497994	53510414	6	0	-0.55301	-0.55301	5.28E-10
252152934022	1551	PI-4	chr17	17	q22	56064049	56068724	3	0	-0.89674	-0.89674	1.83E-12
252152934022	1552	PI-4	chr17	17	q22	56148459	56162300	6	0	-0.72958	-0.72958	1.09E-14
252152934022	1554	PI-4	chr17	17	q22	57407190	57412581	4	0	-0.77725	-0.77725	2.81E-14
252152934022	1555	PI-4	chr17	17	q23.2	59475858	59489111	7	0	-1.06129	-1.06129	6.40E-25
252152934022	1557	PI-4	chr17	17	q23.2	61038958	61048521	6	0	-0.74422	-0.74422	2.21E-16
252152934022	1567	PI-4	chr17	17	q25.1	74232394	74266121	15	0	-0.46426	-0.46426	2.46E-16
252152934022	1568	PI-4	chr17	17	q25.1	74701184	74708999	7	0	-0.70226	-0.70226	1.69E-16
252152934022	1576	PI-4	chr17	17	q25.3	79368066	79374933	5	0	-1.21028	-1.21028	8.47E-21
252152934022	1585	PI-4	chr18	18	p11.31	5889923	5898162	4	0	-1.151	-1.151	3.18E-21
252152934022	1588	PI-4	chr18	18	p11.22	9613158	9616978	3	0	-1.15709	-1.15709	1.34E-16
252152934022	1592	PI-4	chr18	18	p11.21	12872432	12889569	7	0	-0.77412	-0.77412	1.26E-18
252152934022	1593	PI-4	chr18	18	p11.21	12977287	12982602	3	0	-0.86928	-0.86928	7.70E-11
252152934022	1594	PI-4	chr18	18	p11.21	13214829	13219924	3	0	-1.07912	-1.07912	5.27E-15
252152934022	1595	PI-4	chr18	18	q11.2	19319970	19326871	5	0	-0.94595	-0.94595	5.27E-21
252152934022	1596	PI-4	chr18	18	q11.2	19744116	19756261	7	0	-1.00727	-1.00727	1.78E-22
252152934022	1597	PI-4	chr18	18	q12.2	33156966	33164337	5	0	-0.83151	-0.83151	3.46E-16
252152934022	1604	PI-4	chr18	18	q21.1	47098245	47107233	6	0	-0.58881	-0.58881	2.90E-10
252152934022	1605	PI-4	chr18	18	q21.1	47325200	47329060	3	0	-1.15235	-1.15235	2.14E-17
252152934022	1606	PI-4	chr18	18	q21.1	48085147	48089559	3	0	-0.97859	-0.97859	5.62E-14
252152934022	1608	PI-4	chr18	18	q21.2	48555830	48560414	3	0	-0.86087	-0.86087	1.85E-11
252152934022	1609	PI-4	chr18	18	q21.2	51749096	51758058	5	0	-0.78386	-0.78386	8.50E-15
252152934022	1610	PI-4	chr18	18	q21.2	53251017	53259177	5	0	-0.68564	-0.68564	6.40E-12
252152934022	1611	PI-4	chr18	18	q21.31	54811205	54816643	3	0	-0.85872	-0.85872	1.79E-11
252152934022	1613	PI-4	chr18	18	q21.31	55708888	55716714	4	0	-0.77689	-0.77689	2.16E-12
252152934022	1614	PI-4	chr18	18	q21.32	56336464	56341909	4	0	-0.74947	-0.74947	5.99E-12
252152934022	1615	PI-4	chr18	18	q21.32	56527066	56532646	3	0	-0.77317	-0.77317	7.32E-10
252152934022	1616	PI-4	chr18	18	q21.33	59988787	59993960	4	0	-0.89381	-0.89381	2.41E-15
252152934022	1617	PI-4	chr18	18	q21.33	60049650	60057972	5	0	-0.66616	-0.66616	7.34E-12
252152934022	1618	PI-4	chr18	18	q21.33	60187607	60192468	3	0	-0.91595	-0.91595	5.24E-13
252152934022	1619	PI-4	chr18	18	q22.2	67954894	67959972	3	0	-0.9351	-0.9351	4.65E-13
252152934022	1620	PI-4	chr18	18	q22.3	72121828	72130500	6	0	-0.68047	-0.68047	1.46E-13
252152934022	1621	PI-4	chr18	18	q22.3	72914306	72925263	6	0	-0.93841	-0.93841	4.71E-23
252152934022	1640	PI-4	chr19	19	p13.2	7575096	7592244	11	0	-0.62086	-0.62086	7.35E-20
252152934022	1641	PI-4	chr19	19	p13.2	7883637	7997828	60	0	-0.29449	-0.29449	1.06E-21
252152934022	1642	PI-4	chr19	19	p13.2	10528033	10546950	14	0	-0.62771	-0.62771	3.96E-24
252152934022	1646	PI-4	chr19	19	p13.2	12944230	12953889	5	0	-0.88704	-0.88704	2.32E-17
252152934022	1647	PI-4	chr19	19	p13.2	13316350	13319207	3	0	-1.36127	-1.36127	1.71E-21
252152934022	1649	PI-4	chr19	19	p13.12	14182246	14232289	25	0	-0.41952	-0.41952	5.09E-21
252152934022	1651	PI-4	chr19	19	p13.12	15268773	15316460	25	0	-0.43067	-0.43067	3.95E-21
252152934022	1652	PI-4	chr19	19	p13.12	15439338	15444993	4	0	-1.04097	-1.04097	1.83E-18
252152934022	1653	PI-4	chr19	19	p13.12	15534320	15570906	32	0	-0.62404	-0.62404	8.53E-47
252152934022	1654	PI-4	chr19	19	p13.11	16678711	16690706	7	0	-0.68836	-0.68836	2.62E-16
252152934022	1660	PI-4	chr19	19	p13.11	18258237	18279074	11	0	-0.84134	-0.84134	3.69E-32
252152934022	1662	PI-4	chr19	19	p13.11	19141829	19146231	4	0	-0.8055	-0.8055	4.09E-13
252152934022	1663	PI-4	chr19	19	p13.11	19493932	19519948	17	0	-0.52714	-0.52714	1.21E-22
252152934022	1664	PI-4	chr19	19	p12	22285829	22292820	4	0	-0.85823	-0.85823	1.50E-14
252152934022	1667	PI-4	chr19	19	q12	30428635	30443474	8	0	-0.76436	-0.76436	6.36E-23
252152934022	1668	PI-4	chr19	19	q12	30861900	30875330	9	0	-0.59632	-0.59632	3.10E-16
252152934022	1669	PI-4	chr19	19	q12	31834910	31845724	7	0	-0.70881	-0.70881	1.12E-15
252152934022	1670	PI-4	chr19	19	q13.11	32894700	32899155	3	0	-0.93088	-0.93088	4.80E-13
252152934022	1672	PI-4	chr19	19	q13.11	33859952	33868596	6	0	-0.83091	-0.83091	4.95E-18
252152934022	1675	PI-4	chr19	19	q13.12	35752610	35767321	8	0	-0.70888	-0.70888	1.16E-19
252152934022	1680	PI-4	chr19	19	q13.2	39797218	39838353	21	0	-0.47681	-0.47681	5.58E-22
252152934022	1684	PI-4	chr19	19	q13.2	42744797	42751760	5	0	-0.8501	-0.8501	7.33E-17
252152934022	1695	PI-4	chr19	19	q13.32	47728933	47747792	13	0	-0.65569	-0.65569	4.23E-24
252152934022	1696	PI-4	chr19	19	q13.33	48180065	48214045	17	0	-0.48514	-0.48514	2.56E-17
252152934022	1701	PI-4	chr19	19	q13.33	50830225	50835955	3	0	-1.03282	-1.03282	1.49E-14
252152934022	1702	PI-4	chr19	19	q13.41	51596719	51610205	8	0	-1.03449	-1.03449	8.64E-36
252152934022	1708	PI-4	chr19	19	q13.42	56087660	56131788	26	0	-0.69061	-0.69061	3.56E-51
252152934022	1709	PI-4	chr19	19	q13.43	56594133	56638655	21	0	-0.43353	-0.43353	3.77E-18
252152934022	1712	PI-4	chr19	19	q13.43	57990926	57997014	6	0	-0.82259	-0.82259	2.88E-19
252152934022	1713	PI-4	chr19	19	q13.43	58534319	58559733	15	0	-0.37594	-0.37594	2.05E-10
252152934022	1716	PI-4	chr20	20	p13	624412	659930	17	0	-0.49906	-0.49906	1.43E-19
252152934022	1717	PI-4	chr20	20	p13	1164596	1168663	3	0	-1.0693	-1.0693	2.27E-15
252152934022	1726	PI-4	chr20	20	p11.23	20346283	20351182	4	0	-1.13172	-1.13172	4.63E-17
252152934022	1736	PI-4	chr20	20	q11.22	32259669	32290671	17	0	-0.5885	-0.5885	2.28E-25
252152934022	1746	PI-4	chr20	20	q13.12	45519744	45527022	5	0	-0.71542	-0.71542	1.84E-13
252152934022	1747	PI-4	chr20	20	q13.12	46156668	46176088	9	0	-0.44531	-0.44531	4.77E-10
252152934022	1748	PI-4	chr20	20	q13.13	46412283	46415819	3	0	-1.18174	-1.18174	2.37E-16
252152934022	1749	PI-4	chr20	20	q13.13	47442104	47450797	5	0	-0.69202	-0.69202	2.12E-12
252152934022	1752	PI-4	chr20	20	q13.13	49410818	49415807	4	0	-0.75717	-0.75717	1.04E-11
252152934022	1753	PI-4	chr20	20	q13.2	50133486	50169048	18	0	-0.31454	-0.31454	6.30E-10
252152934022	1769	PI-4	chr21	21	q21.1	16432567	16440059	5	0	-0.64567	-0.64567	2.80E-11
252152934022	1770	PI-4	chr21	21	q21.1	17098227	17106503	7	0	-0.71077	-0.71077	1.09E-17
252152934022	1771	PI-4	chr21	21	q21.3	30382191	30388267	4	0	-0.81118	-0.81118	7.16E-13
252152934022	1772	PI-4	chr21	21	q21.3	30666963	30675823	7	0	-0.61102	-0.61102	1.71E-13
252152934022	1778	PI-4	chr21	21	q22.11	35012618	35016938	3	0	-0.95493	-0.95493	2.38E-13
252152934022	1779	PI-4	chr21	21	q22.11	35440818	35449032	7	0	-0.71488	-0.71488	1.26E-15
252152934022	1780	PI-4	chr21	21	q22.12	35983072	35990686	10	0	-0.75761	-0.75761	1.51E-26
252152934022	1781	PI-4	chr21	21	q22.12	36160622	36166818	5	0	-0.85374	-0.85374	7.53E-15
252152934022	1782	PI-4	chr21	21	q22.12	36258646	36265283	6	0	-0.82298	-0.82298	1.68E-16
252152934022	1783	PI-4	chr21	21	q22.12	37620856	37654954	20	0.356016	0	0.356016	1.44E-13
252152934022	1784	PI-4	chr21	21	q22.13	37867778	37871838	5	0	-0.70825	-0.70825	3.11E-13
252152934022	1785	PI-4	chr21	21	q22.13	38113478	38123659	8	0	-0.67345	-0.67345	5.97E-18
252152934022	1786	PI-4	chr21	21	q22.13	38334436	38341057	5	0	-0.88506	-0.88506	2.68E-18
252152934022	1787	PI-4	chr21	21	q22.13	38735186	38742471	5	0	-0.9186	-0.9186	3.66E-16
252152934022	1788	PI-4	chr21	21	q22.2	40175324	40192279	12	0	-0.46968	-0.46968	6.05E-14
252152934022	1789	PI-4	chr21	21	q22.2	40717778	40747922	13	0	-0.44328	-0.44328	2.59E-12
252152934022	1790	PI-4	chr21	21	q22.2	40977432	40988857	9	0	-0.53435	-0.53435	2.26E-12
252152934022	1791	PI-4	chr21	21	q22.2	42217207	42220560	4	0	-1.04305	-1.04305	8.58E-17
252152934022	1797	PI-4	chr21	21	q22.3	44839939	44851075	7	0	-0.83239	-0.83239	3.75E-17
252152934022	1798	PI-4	chr21	21	q22.3	45719238	45723854	4	0	-0.94512	-0.94512	2.99E-14
252152934022	1802	PI-4	chr21	21	q22.3	46822915	46827999	3	0	-1.15492	-1.15492	1.25E-15

252152934022	1806	PI-4	chr22	22	q11.1	17848161	17851757	3	0	-1.02642	-1.02642	5.27E-15
252152934022	1813	PI-4	chr22	22	q11.21	20005227	20010176	6	0	-0.98077	-0.98077	3.54E-22
252152934022	1816	PI-4	chr22	22	q11.21	21307890	21320661	6	0	-0.65351	-0.65351	5.85E-13
252152934022	1817	PI-4	chr22	22	q11.21	22088145	22093215	4	0	-0.78489	-0.78489	1.38E-12
252152934022	1819	PI-4	chr22	22	q11.22	22467302	22480974	6	0	-0.57687	-0.57687	7.10E-10
252152934022	1820	PI-4	chr22	22	q11.23	23516659	23532072	11	0	-0.58251	-0.58251	4.10E-18
252152934022	1822	PI-4	chr22	22	q11.23	24711146	24715607	3	0	-0.86277	-0.86277	7.60E-12
252152934022	1823	PI-4	chr22	22	q11.23	24985412	25081694	7	0	-0.64909	-0.64909	5.42E-15
252152934022	1836	PI-4	chr22	22	q12.2	31883101	31888528	4	0	-0.90049	-0.90049	6.29E-16
252152934022	1837	PI-4	chr22	22	q12.3	33192321	33201357	8	0	-0.53784	-0.53784	2.76E-12
252152934022	1838	PI-4	chr22	22	q12.3	36420149	36426875	5	0	-0.69986	-0.69986	5.24E-15
252152934022	1839	PI-4	chr22	22	q12.3	37096552	37101511	4	0	-0.72566	-0.72566	4.45E-13
252152934022	1840	PI-4	chr22	22	q12.3	37409663	37423349	9	0	-0.62208	-0.62208	4.48E-19
252152934022	1842	PI-4	chr22	22	q13.1	38238542	38241178	5	0	-0.81663	-0.81663	9.26E-16
252152934022	1844	PI-4	chr22	22	q13.1	38475210	38488241	9	0	-0.61756	-0.61756	2.39E-14
252152934022	1847	PI-4	chr22	22	q13.1	39094108	39103243	6	0	-0.80297	-0.80297	1.20E-18
252152934022	1851	PI-4	chr22	22	q13.1	40387103	40392893	5	0	-0.87557	-0.87557	2.87E-18
252152934022	1855	PI-4	chr22	22	q13.2	42303619	42312515	9	0	-0.79146	-0.79146	1.78E-19
252152934022	1860	PI-4	chr22	22	q13.2	43360441	43376155	10	0	-0.65036	-0.65036	8.26E-21
252152934022	1862	PI-4	chr22	22	q13.2	43804711	43812404	6	0	-0.79518	-0.79518	5.80E-18
252152934022	1865	PI-4	chr22	22	q13.31	45400411	45409120	8	0	-0.67184	-0.67184	6.01E-15
252152934022	1866	PI-4	chr22	22	q13.31	46420905	46477135	33	0	-0.56421	-0.56421	1.43E-42
252152934022	1867	PI-4	chr22	22	q13.31	46655084	46659663	3	0	-1.30119	-1.30119	4.56E-19
252152934022	1871	PI-4	chr22	22	q13.33	50524890	50531831	6	0	-0.93822	-0.93822	4.04E-16
252152930760	1	PI-12	chr1	1	p34.2	43894858	43906095	8	0.616115	0	0.616115	3.28E-11
252152930760	7	PI-12	chr19	19	p13.2	8994725	9024036	17	0.426362	0	0.426362	7.19E-12
252152930762	2	PI-13	chr6	6	p21.32	32156424	32160072	3	1.023985	0	1.023985	4.10E-10
252152930762	3	PI-13	chr8	8	q24.3	143886545	143891249	3	0.803805	0	0.803805	3.39E-10
252152930761	1	PI-1	chr1	1	p36.22	10662249	10831855	76	0.282595	0	0.282595	1.04E-19
252152930761	2	PI-1	chr1	1	q21.3	153885225	153947039	37	0.27459	0	0.27459	7.45E-12
252152930761	3	PI-1	chr2	2	q12.1	105463967	105480986	9	0.52637	0	0.52637	8.20E-13
252152930761	4	PI-1	chr2	2	q31.1	176981875	177066500	77	0.259633	0	0.259633	1.17E-24
252152930761	6	PI-1	chr3	3	q21.3	128186406	128239320	24	0.321418	0	0.321418	2.37E-11
252152930761	9	PI-1	chr7	7	q32.1	128520872	128563486	18	0.354372	0	0.354372	2.85E-10
252152930761	10	PI-1	chr7	7	q36.3	156791205	156816588	13	0.429259	0	0.429259	9.25E-10
252152930761	13	PI-1	chr9	9	q34.3	138874417	139092918	82	0.298909	0	0.298909	7.02E-18
252152930761	16	PI-1	chr12	12	q13.3	57612317	57619325	5	0.759056	0	0.759056	4.75E-10
252152930761	23	PI-1	chr17	17	q23.2	59475858	59485331	5	0.788049	0	0.788049	3.16E-10
252152930761	24	PI-1	chr19	19	p13.2	9058753	9091280	20	0	-0.370144	-0.370144	2.13E-11
252152930761	25	PI-1	chr19	19	p12	21055920	21098244	14	0	-0.479442	-0.479442	1.20E-17
252152930761	28	PI-1	chr21	21	q22.3	46336245	46471967	56	0.263308	0	0.263308	3.54E-11
252152930761	29	PI-1	chr22	22	q11.22	23262225	23283115	13	0.408257	0	0.408257	8.67E-10
252152930761	30	PI-1	chr22	22	q13.2	42668193	42784749	44	0.263285	0	0.263285	1.63E-10

Dataset S4. 2. List of CNAs in TT- reactive lymphocytes of 14 tested diabetic patients (ADM-2 (LRRl0.25l, P- value ≤1x10-10) and CBS (LRRl0.25l, P-value ≤5 x 10-08)).

ID	NO.	ID	chrom	chrom	chr region	loc.start	loc.end	num.mark	Amplification	Deletions	mean LRR	pval
1489-MCG_252152938941_S01	1	TT5	chr1	1	p36.22	10685499	10784488	44	0	-0.262075	-0.262075	3.411E-17
1489-MCG_252152938941_S01	2	TT5	chr1	1	p36.13	17761695	17767851	4	0	-0.772668	-0.772668	5.35E-13
1489-MCG_252152938941_S01	3	TT5	chr1	1	p36.13	17862125	17873219	6	0	-0.63004	-0.63004	3.945E-13
1489-MCG_252152938941_S01	4	TT5	chr1	1	p36.12	22889488	22897061	4	0	-0.668404	-0.668404	6.534E-11
1489-MCG_252152938941_S01	6	TT5	chr1	1	p35.1	33426685	33433482	4	0	-0.909908	-0.909908	1.76E-17
1489-MCG_252152938941_S01	7	TT5	chr1	1	p34.2	42126009	42131241	3	0	-0.911345	-0.911345	1.701E-13
1489-MCG_252152938941_S01	8	TT5	chr1	1	p12	120160783	120171961	7	0	-0.49972	-0.49972	4.605E-10
1489-MCG_252152938941_S01	10	TT5	chr1	1	q25.1	173442738	173450664	5	0	-0.581733	-0.581733	1.547E-10
1489-MCG_252152938941_S01	11	TT5	chr1	1	q42.13	228187768	228201624	8	0	-0.793593	-0.793593	7.755E-23
1489-MCG_252152938941_S01	12	TT5	chr1	1	q42.13	228336605	228349826	5	0	-0.813001	-0.813001	2.567E-16
1489-MCG_252152938941_S01	13	TT5	chr1	1	q42.3	234741403	234747456	5	0	-0.836122	-0.836122	1.063E-17
1489-MCG_252152938941_S01	14	TT5	chr2	2	q11.2	99346052	99349698	3	0	-1.482595	-1.482595	7.684E-23
1489-MCG_252152938941_S01	15	TT5	chr2	2	q33.3	208391916	208400047	5	0	-0.94217	-0.94217	2.043E-21
1489-MCG_252152938941_S01	16	TT5	chr2	2	q37.1	231900329	231905208	3	0	-0.809115	-0.809115	6.56E-11
1489-MCG_252152938941_S01	19	TT5	chr2	2	q37.3	242150748	242158725	5	0	-0.781352	-0.781352	9.649E-14
1489-MCG_252152938941_S01	20	TT5	chr3	3	p25.2	12041877	12048847	5	0	-0.764692	-0.764692	4.467E-15
1489-MCG_252152938941_S01	21	TT5	chr3	3	p25.1	13320807	13328079	3	0	-1.079924	-1.079924	4.628E-16
1489-MCG_252152938941_S01	22	TT5	chr3	3	p22.2	37893679	37908360	9	0	-0.494565	-0.494565	3.884E-12
1489-MCG_252152938941_S01	23	TT5	chr3	3	p21.1	53072344	53086739	9	0	-0.653617	-0.653617	4.024E-20
1489-MCG_252152938941_S01	24	TT5	chr3	3	q21.3	126698025	126704964	3	0	-0.84409	-0.84409	6.017E-10
1489-MCG_252152938941_S01	25	TT5	chr3	3	q25.33	159814814	159820881	3	0	-1.08337	-1.08337	1.167E-15
1489-MCG_252152938941_S01	28	TT5	chr4	4	p16.1	7039485	7046802	4	0	-0.752236	-0.752236	3.175E-12
1489-MCG_252152938941_S01	29	TT5	chr5	5	p15.31	7392725	7400545	5	0	-0.86857	-0.86857	4.531E-18
1489-MCG_252152938941_S01	30	TT5	chr5	5	p15.2	14140937	14145463	3	0	-1.432806	-1.432806	3.571E-22
1489-MCG_252152938941_S01	31	TT5	chr5	5	p15.2	14484401	14491038	4	0	-0.691083	-0.691083	6.591E-10
1489-MCG_252152938941_S01	32	TT5	chr5	5	q34	167953640	167959937	4	0	-1.146955	-1.146955	2.94E-22
1489-MCG_252152938941_S01	34	TT5	chr6	6	q14.1	79782000	79789852	6	0	-0.8221	-0.8221	1.111E-16
1489-MCG_252152938941_S01	35	TT5	chr6	6	q24.2	143381110	143386666	4	0	-0.718257	-0.718257	5.374E-12
1489-MCG_252152938941_S01	36	TT5	chr6	6	q25.3	157093875	157104384	6	0	-0.758446	-0.758446	1.869E-17
1489-MCG_252152938941_S01	37	TT5	chr6	6	q27	170121435	170127040	4	0	-1.078001	-1.078001	7.794E-20
1489-MCG_252152938941_S01	39	TT5	chr7	7	p22.2	3338276	3347071	6	0	-0.713828	-0.713828	3.042E-13
1489-MCG_252152938941_S01	40	TT5	chr7	7	p22.1	6457386	6465906	5	0	-0.717007	-0.717007	3.394E-11
1489-MCG_252152938941_S01	41	TT5	chr7	7	p22.1	6669611	6698360	14	0	-0.469006	-0.469006	2.123E-14
1489-MCG_252152938941_S01	43	TT5	chr7	7	p12.3	45611077	45624920	7	0	-0.666736	-0.666736	4.19E-15
1489-MCG_252152938941_S01	44	TT5	chr7	7	q21.11	77644551	77652021	5	0	-0.676183	-0.676183	2.272E-12
1489-MCG_252152938941_S01	45	TT5	chr7	7	q22.1	101455968	101462497	4	0	-1.008895	-1.008895	5.506E-18
1489-MCG_252152938941_S01	46	TT5	chr7	7	q22.1	101888196	101896854	8	0	-0.886117	-0.886117	2.636E-23
1489-MCG_252152938941_S01	47	TT5	chr7	7	q32.1	128764412	128769917	4	0	-0.699984	-0.699984	3.656E-11
1489-MCG_252152938941_S01	48	TT5	chr7	7	q34	139873465	139877877	3	0	-1.20712	-1.20712	5.1E-20
1489-MCG_252152938941_S01	49	TT5	chr7	7	q36.1	149154358	149158404	3	0	-0.909293	-0.909293	7.556E-13
1489-MCG_252152938941_S01	50	TT5	chr7	7	q36.3	156795837	156811339	9	0	-0.605497	-0.605497	3.394E-14
1489-MCG_252152938941_S01	51	TT5	chr8	8	p23.3	1046077	1052100	3	0	-1.167031	-1.167031	1.104E-13
1489-MCG_252152938941_S01	52	TT5	chr8	8	p11.21	41903485	41908043	4	0	-0.819915	-0.819915	3.31E-13
1489-MCG_252152938941_S01	53	TT5	chr8	8	q12.1	61588520	61593702	3	0	-1.255532	-1.255532	6.705E-20
1489-MCG_252152938941_S01	54	TT5	chr8	8	q21.13	81784315	81790927	4	0	-0.933072	-0.933072	6.252E-15
1489-MCG_252152938941_S01	55	TT5	chr8	8	q22.2	99832651	99843368	6	0	-0.787068	-0.787068	4.307E-18
1489-MCG_252152938941_S01	56	TT5	chr8	8	q24.3	143588012	143603181	6	0	-0.703167	-0.703167	2.791E-11
1489-MCG_252152938941_S01	58	TT5	chr9	9	p24.3	2045009	2049904	4	0	-1.306087	-1.306087	7.884E-26
1489-MCG_252152938941_S01	59	TT5	chr9	9	q21.11	71937907	71944494	5	0	-0.656756	-0.656756	5.817E-12
1489-MCG_252152938941_S01	61	TT5	chr9	9	q22.31	94182549	94190452	5	0	-0.742289	-0.742289	1.089E-12
1489-MCG_252152938941_S01	62	TT5	chr9	9	q22.31	96335537	96343782	5	0	-0.793975	-0.793975	9.087E-15
1489-MCG_252152938941_S01	63	TT5	chr9	9	q31.1	103185084	103192529	5	0	-0.706715	-0.706715	1.477E-12
1489-MCG_252152938941_S01	64	TT5	chr9	9	q32	116632755	116642488	6	0	-0.7522	-0.7522	2.824E-17
1489-MCG_252152938941_S01	65	TT5	chr9	9	q33.1	118912806	118920303	5	0	-0.953323	-0.953323	1.507E-20
1489-MCG_252152938941_S01	66	TT5	chr9	9	q33.2	124455701	124465200	6	0	-0.565716	-0.565716	1.953E-10
1489-MCG_252152938941_S01	67	TT5	chr9	9	q34.11	131449302	131456708	5	0	-0.846207	-0.846207	8.098E-20
1489-MCG_252152938941_S01	68	TT5	chr9	9	q34.13	134612145	134620060	4	0	-1.003983	-1.003983	1.623E-18
1489-MCG_252152938941_S01	69	TT5	chr9	9	q34.2	137213455	137222710	5	0	-1.03892	-1.03892	2.258E-16
1489-MCG_252152938941_S01	70	TT5	chr9	9	q34.3	138602215	138607836	3	0	-0.855329	-0.855329	3.504E-10
1489-MCG_252152938941_S01	72	TT5	chr9	9	q34.3	140511505	140516179	4	0	-1.080598	-1.080598	6.159E-16
1489-MCG_252152938941_S01	73	TT5	chr10	10	p13	13388242	13394647	4	0	-0.692433	-0.692433	5.854E-10
1489-MCG_252152938941_S01	74	TT5	chr10	10	p13	13562889	13574704	7	0	-0.643418	-0.643418	5.735E-16
1489-MCG_252152938941_S01	75	TT5	chr10	10	p12.2	22606239	22615853	6	0	-1.114548	-1.114548	4.042E-33
1489-MCG_252152938941_S01	76	TT5	chr10	10	p11.21	35922572	35934470	6	0	-0.728228	-0.728228	1.984E-14
1489-MCG_252152938941_S01	77	TT5	chr10	10	q11.22	49661423	49684810	11	0	-0.549604	-0.549604	1.189E-13
1489-MCG_252152938941_S01	79	TT5	chr10	10	q23.32	92919743	92927117	4	0	-0.789087	-0.789087	6.065E-13
1489-MCG_252152938941_S01	80	TT5	chr11	11	p15.5	1306948	1313233	4	0	-1.031469	-1.031469	8.694E-12
1489-MCG_252152938941_S01	82	TT5	chr11	11	p11.2	47606064	47617180	6	0	-0.637552	-0.637552	1.581E-13
1489-MCG_252152938941_S01	83	TT5	chr11	11	q12.2	61342766	61351984	4	0	-0.646767	-0.646767	3.636E-10
1489-MCG_252152938941_S01	84	TT5	chr11	11	q13.1	65807239	65814470	4	0	-0.796868	-0.796868	7.456E-14
1489-MCG_252152938941_S01	85	TT5	chr11	11	q13.2	66494511	66498204	3	0	-1.398818	-1.398818	3.344E-24
1489-MCG_252152938941_S01	86	TT5	chr11	11	q13.2	67027356	67067067	18	0	-0.381977	-0.381977	7.116E-13
1489-MCG_252152938941_S01	87	TT5	chr11	11	q21	93273959	93277536	3	0	-0.801581	-0.801581	1.005E-10
1489-MCG_252152938941_S01	88	TT5	chr12	12	p13.31	7026930	7040293	7	0	-0.492161	-0.492161	8.148E-11
1489-MCG_252152938941_S01	89	TT5	chr12	12	p13.31	7778761	7787402	4	0	-0.809698	-0.809698	1.643E-14
1489-MCG_252152938941_S01	90	TT5	chr12	12	q13.11	47583585	47630453	23	0.333102	0	0.333102	4.902E-10
1489-MCG_252152938941_S01	91	TT5	chr12	12	q24.13	113511180	113519840	5	0	-0.82425	-0.82425	7.372E-17
1489-MCG_252152938941_S01	92	TT5	chr12	12	q24.21	116711535	116720310	5	0	-0.849996	-0.849996	2.048E-18
1489-MCG_252152938941_S01	94	TT5	chr12	12	q24.31	123871095	123875180	3	0	-1.15502	-1.15502	1.578E-17
1489-MCG_252152938941_S01	95	TT5	chr12	12	q24.33	133064406	133069525	3	0	-1.257542	-1.257542	2.626E-19
1489-MCG_252152938941_S01	97	TT5	chr13	13	q12.11	21275506	21280504	4	0	-0.969975	-0.969975	5.941E-16
1489-MCG_252152938941_S01	98	TT5	chr13	13	q12.3	31033785	31042977	5	0	-0.880347	-0.880347	6.925E-19
1489-MCG_252152938941_S01	99	TT5	chr13	13	q31.1	79170898	79181024	6	0	-0.950265	-0.950265	7.032E-23
1489-MCG_252152938941_S01	106	TT5	chr14	14	q23.2	62276772	62286106	5	0	-0.691611	-0.691611	1.12E-13
1489-MCG_252152938941_S01	107	TT5	chr14	14	q32.11	89882072	89887444	4	0	-1.119078	-1.119078	6.507E-22
1489-MCG_252152938941_S01	108	TT5	chr14	14	q32.13	95784221	95788362	3	0	-1.303503	-1.303503	1.582E-21
1489-MCG_252152938941_S01	110	TT5	chr14	14	q32.32	103240021	103247059	6	0	-0.945116	-0.945116	3.717E-21

1489-MCG_252152938941_S01	112	TT5	chr14	14	q32.33	105776904	105784047	5	0	-0.976963	-0.976963	2.693E-19
1489-MCG_252152938941_S01	113	TT5	chr15	15	q13.1	29861670	29865524	3	0	-1.629588	-1.629588	2.979E-26
1489-MCG_252152938941_S01	114	TT5	chr15	15	q26.1	90188155	90198080	11	0	-0.797337	-0.797337	6.803E-28
1489-MCG_252152938941_S01	116	TT5	chr15	15	q26.3	102026679	102032848	4	0	-1.170016	-1.170016	2.043E-23
1489-MCG_252152938941_S01	118	TT5	chr16	16	p13.3	4162241	4170423	4	0	-0.673873	-0.673873	4.181E-10
1489-MCG_252152938941_S01	119	TT5	chr16	16	p13.2	9054847	9060119	4	0	-1.192035	-1.192035	6.417E-24
1489-MCG_252152938941_S01	122	TT5	chr16	16	q21	57560930	57566184	4	0	-0.755842	-0.755842	6.959E-12
1489-MCG_252152938941_S01	123	TT5	chr16	16	q21	58230636	58238413	4	0	-0.84586	-0.84586	2.282E-13
1489-MCG_252152938941_S01	124	TT5	chr16	16	q23.2	79631778	79636091	3	0	-1.30106	-1.30106	1.224E-19
1489-MCG_252152938941_S01	125	TT5	chr16	16	q23.2	80833452	80846453	6	0	-0.904428	-0.904428	1.293E-22
1489-MCG_252152938941_S01	126	TT5	chr16	16	q24.2	87756798	87762259	4	0	-1.352127	-1.352127	1.564E-26
1489-MCG_252152938941_S01	128	TT5	chr17	17	p13.2	4123590	4126535	3	0	-1.340985	-1.340985	4.576E-15
1489-MCG_252152938941_S01	130	TT5	chr17	17	q25.3	77747699	77759937	7	0	-0.540704	-0.540704	4.844E-11
1489-MCG_252152938941_S01	131	TT5	chr17	17	q25.3	80476337	80481025	3	0	-1.34696	-1.34696	3.841E-22
1489-MCG_252152938941_S01	132	TT5	chr18	18	p11.22	9611618	9616978	4	0	-1.072127	-1.072127	8.01E-20
1489-MCG_252152938941_S01	133	TT5	chr18	18	q11.2	22925837	22947170	9	0	-0.515669	-0.515669	4.919E-13
1489-MCG_252152938941_S01	134	TT5	chr18	18	q12.1	31157460	31162296	3	0	-1.202716	-1.202716	1.193E-17
1489-MCG_252152938941_S01	135	TT5	chr18	18	q12.2	33160498	33164337	3	0	-1.597317	-1.597317	1.192E-25
1489-MCG_252152938941_S01	136	TT5	chr18	18	q21.32	56527066	56534019	4	0	-0.939342	-0.939342	4.077E-17
1489-MCG_252152938941_S01	137	TT5	chr18	18	q22.3	72914306	72928199	7	0	-0.690495	-0.690495	1.861E-16
1489-MCG_252152938941_S01	138	TT5	chr18	18	q23	76734862	76756679	11	0	-0.98676	-0.98676	1.464E-42
1489-MCG_252152938941_S01	140	TT5	chr19	19	p13.3	1648138	1656386	5	0	-0.763739	-0.763739	6.912E-13
1489-MCG_252152938941_S01	142	TT5	chr19	19	p13.3	3093251	3098084	3	0	-1.266412	-1.266412	7.083E-16
1489-MCG_252152938941_S01	144	TT5	chr19	19	p13.2	10979040	10985016	4	0	-1.068543	-1.068543	4.475E-18
1489-MCG_252152938941_S01	146	TT5	chr19	19	p13.12	14195682	14205614	7	0	-0.770899	-0.770899	8.115E-20
1489-MCG_252152938941_S01	147	TT5	chr19	19	p13.12	15539785	15546356	7	0	-1.06613	-1.06613	1.446E-30
1489-MCG_252152938941_S01	149	TT5	chr19	19	p13.11	18715895	18720332	3	0	-1.141672	-1.141672	3.928E-15
1489-MCG_252152938941_S01	150	TT5	chr19	19	q13.11	33678037	33691834	8	0	-0.594198	-0.594198	5.548E-15
1489-MCG_252152938941_S01	152	TT5	chr19	19	q13.41	51596719	51612020	9	0	-0.541753	-0.541753	2.517E-15
1489-MCG_252152938941_S01	153	TT5	chr19	19	q13.42	54482944	54489190	7	0	-0.713597	-0.713597	1.739E-18
1489-MCG_252152938941_S01	154	TT5	chr19	19	q13.43	56597559	56602764	4	0	-1.14468	-1.14468	1.711E-20
1489-MCG_252152938941_S01	155	TT5	chr19	19	q13.43	57682597	57686917	4	0	-1.289205	-1.289205	2.247E-26
1489-MCG_252152938941_S01	156	TT5	chr20	20	q11.22	33811432	33820980	6	0	-0.698472	-0.698472	1.705E-15
1489-MCG_252152938941_S01	157	TT5	chr20	20	q13.2	50380940	50389993	6	0	-0.774339	-0.774339	1.921E-16
1489-MCG_252152938941_S01	158	TT5	chr20	20	q13.32	57461685	57470482	6	0	-0.72638	-0.72638	4.409E-14
1489-MCG_252152938941_S01	159	TT5	chr20	20	q13.33	60634471	60643318	5	0	-0.957936	-0.957936	4.536E-21
1489-MCG_252152938941_S01	160	TT5	chr21	21	q22.2	42214433	42222204	7	0	-0.857616	-0.857616	6.648E-24
1489-MCG_252152938941_S01	161	TT5	chr21	21	q22.3	43296256	43301444	3	0	-1.194407	-1.194407	8.615E-18
1489-MCG_252152938941_S01	163	TT5	chr21	21	q22.3	46490681	46496996	5	0	-0.89659	-0.89659	2.621E-18
1489-MCG_252152938941_S01	164	TT5	chr21	21	q22.3	46970389	46982323	7	0	-0.691805	-0.691805	6.356E-14
1489-MCG_252152938941_S01	165	TT5	chr22	22	q11.21	19743761	19752605	6	0	-0.94326	-0.94326	1.985E-20
1489-MCG_252152938941_S01	166	TT5	chr22	22	q11.22	23409104	23423542	9	0	-0.68012	-0.68012	2.432E-16
1489-MCG_252152938941_S01	167	TT5	chr22	22	q12.1	29275657	29283212	5	0	-0.83133	-0.83133	2.83E-17
1489-MCG_252152938941_S01	168	TT5	chr22	22	q12.2	31669588	31673494	3	0	-1.543067	-1.543067	1.065E-23
1489-MCG_252152938941_S01	169	TT5	chr22	22	q13.1	39744824	39748341	3	0	-1.645644	-1.645644	5.613E-25
1489-MCG_252152938941_S01	170	TT5	chr22	22	q13.31	45630684	45638998	5	0	-0.655755	-0.655755	8.527E-11
1489-MCG_252152938941_S01	171	TT5	chr22	22	q13.32	48881938	48888205	4	0	-1.093214	-1.093214	3.889E-12
1489-MCG_252152938941_S01	172	TT5	chr22	22	q13.33	50215007	50226884	8	0	-0.630025	-0.630025	9.751E-14
1506-MCG_252152938973_S01	1	TT12	chr1	1	p36.33	2126657	2135899	4	0	-0.566383	-0.566383	6.99E-10
1506-MCG_252152938973_S01	2	TT12	chr1	1	p36.32	2352300	2383431	9	0	-0.40633	-0.40633	2.29E-11
1506-MCG_252152938973_S01	3	TT12	chr1	1	p36.22	10676838	10830533	70	0.305587	0	0.305587	1.63E-17
1506-MCG_252152938973_S01	5	TT12	chr1	1	q22	156347343	156408335	56	0.327754	0	0.327754	8.03E-12
1506-MCG_252152938973_S01	9	TT12	chr3	3	p21.31	49136309	49172251	19	0.400696	0	0.400696	9.49E-10
1506-MCG_252152938973_S01	10	TT12	chr3	3	p21.31	49677208	49745159	29	0.375073	0	0.375073	5.88E-11
1506-MCG_252152938973_S01	12	TT12	chr4	4	p16.3	552160	978936	153	0.264908	0	0.264908	1.68E-18
1506-MCG_252152938973_S01	16	TT12	chr5	5	q31.1	131787670	131836566	23	0.487037	0	0.487037	1.55E-22
1506-MCG_252152938973_S01	17	TT12	chr5	5	q35.3	176803797	176938388	57	0.295293	0	0.295293	6.02E-12
1506-MCG_252152938973_S01	18	TT12	chr7	7	p22.3	141559	194262	26	0.423563	0	0.423563	2.29E-10
1506-MCG_252152938973_S01	21	TT12	chr7	7	q11.23	75601966	75622671	10	0.629083	0	0.629083	5E-12
1506-MCG_252152938973_S01	22	TT12	chr7	7	q32.1	128478020	128566480	38	0.286262	0	0.286262	8.75E-12
1506-MCG_252152938973_S01	24	TT12	chr7	7	q36.3	156792950	156812476	11	0.536017	0	0.536017	5.58E-10
1506-MCG_252152938973_S01	25	TT12	chr8	8	p12	29916811	29959290	19	0.332157	0	0.332157	3.46E-12
1506-MCG_252152938973_S01	33	TT12	chr11	11	q13.1	65171314	65401317	122	0.292598	0	0.292598	6.37E-22
1506-MCG_252152938973_S01	34	TT12	chr11	11	q13.4	72347308	72500444	83	0.256247	0	0.256247	4.27E-11
1506-MCG_252152938973_S01	35	TT12	chr11	11	q23.3	118775267	118822120	22	0.397179	0	0.397179	2.81E-10
1506-MCG_252152938973_S01	36	TT12	chr12	12	q13.11	48123497	48211694	46	0.27473	0	0.27473	2.31E-10
1506-MCG_252152938973_S01	37	TT12	chr12	12	q13.12	49365056	49399825	17	0.400437	0	0.400437	8.3E-10
1506-MCG_252152938973_S01	39	TT12	chr12	12	q24.33	133144957	133147715	3	0	-0.915066	-0.915066	6.1E-12
1506-MCG_252152938973_S01	40	TT12	chr13	13	q34	114783408	114910140	64	0.319765	0	0.319765	2.66E-11
1506-MCG_252152938973_S01	43	TT12	chr14	14	q24.3	74155498	74239922	44	0.272894	0	0.272894	4.55E-15
1506-MCG_252152938973_S01	47	TT12	chr15	15	q11.2	25427307	25472599	15	0.453975	0	0.453975	5.87E-12
1506-MCG_252152938973_S01	48	TT12	chr15	15	q13.1	29374851	29426407	27	0.301385	0	0.301385	8.3E-12
1506-MCG_252152938973_S01	50	TT12	chr15	15	q21.1	44988478	45011224	12	0.456516	0	0.456516	9.18E-12
1506-MCG_252152938973_S01	51	TT12	chr15	15	q21.1	45406186	45487723	44	0.295261	0	0.295261	7.07E-14
1506-MCG_252152938973_S01	52	TT12	chr15	15	q24.1	75096340	75146505	25	0.364002	0	0.364002	6.33E-11
1506-MCG_252152938973_S01	54	TT12	chr16	16	p13.3	746817	759610	4	0	-0.957358	-0.957358	7.54E-12
1506-MCG_252152938973_S01	56	TT12	chr16	16	p13.13	11279376	11389754	50	0.264676	0	0.264676	2.19E-17
1506-MCG_252152938973_S01	57	TT12	chr16	16	q22.1	67179669	67232696	35	0.359473	0	0.359473	1.6E-10
1506-MCG_252152938973_S01	58	TT12	chr16	16	q22.1 - q22.2	70726401	70803518	37	0.349544	0	0.349544	1.89E-19
1506-MCG_252152938973_S01	60	TT12	chr17	17	p11.2	21186285	21320118	57	0.268085	0	0.268085	1.3E-18
1506-MCG_252152938973_S01	61	TT12	chr17	17	q21.31	43181435	43225430	22	0.429868	0	0.429868	2.77E-13
1506-MCG_252152938973_S01	63	TT12	chr17	17	q22	56373747	56414776	37	0.27349	0	0.27349	4.4E-11
1506-MCG_252152938973_S01	66	TT12	chr19	19	p13.3	1106223	1116115	5	0	-0.754392	-0.754392	1.01E-11
1506-MCG_252152938973_S01	67	TT12	chr19	19	p13.3	1816071	1826827	7	0	-0.382318	-0.382318	4.36E-10
1506-MCG_252152938973_S01	69	TT12	chr19	19	p13.3	4971110	5157796	89	0.305012	0	0.305012	9.61E-10
1506-MCG_252152938973_S01	70	TT12	chr21	21	q22.3	44764355	44815482	22	0.446022	0	0.446022	1.9E-10
1506-MCG_252152938973_S01	71	TT12	chr21	21	q22.3	46312543	46471967	66	0.294578	0	0.294578	1.71E-10
1506-MCG_252152938973_S01	73	TT12	chr22	22	q11.21	21324168	21377491	32	0.348132	0	0.348132	5.22E-11
1506-MCG_252152938973_S01	74	TT12	chr22	22	q13.1	40024172	40106186	42	0.400196	0	0.400196	6.33E-11
1506-MCG_252152938973_S01	75	TT12	chr22	22	q13.2	42668193	42833136	70	0.271174	0	0.271174	5.47E-12
1506-MCG_252152938973_S01	76	TT12	chr22	22	q13.31	47529791	47569700	23	0.422865	0	0.422865	8.34E-13
1506-MCG_252152938973_S01	77	TT12	chr22	22	q13.33	50705357	50755105	24	0	-0.309113	-0.309113	3.92E-18
1489-MCG_252152938948_S01	5	TT1	chr1	1	p35.1	33426685	33431071	3	0	-0.896923	-0.896923	1.588E-12
1489-MCG_252152938948_S01	8	TT1	chr1	1	p21.1	104062011	104093842	4	0	-0.789036	-0.789036	4.418E-11
1489-MCG_252152938948_S01	10	TT1	chr1	1	q21.3	151430573	151433411	3	0	-1.198908	-1.198908	1.023E-19
1489-MCG_252152938948_S01	15	TT1	chr2	2	p21	44079170	44096180	8	0	-0.741939	-0.741939	5.283E-18

1489-MCG_252152938948_S01	16	TT1	chr2	2	q11.2	99342816	99349698	5	0	-0.939314	-0.939314	7.079E-18
1489-MCG_252152938948_S01	17	TT1	chr2	2	q33.3	208391916	208400047	5	0	-0.728324	-0.728324	3.667E-13
1489-MCG_252152938948_S01	22	TT1	chr3	3	q25.33	159812012	159820881	5	0	-0.94189	-0.94189	3.12E-20
1489-MCG_252152938948_S01	23	TT1	chr3	3	q26.2	170066816	170079770	7	0.514317	0	0.514317	7.006E-10
1489-MCG_252152938948_S01	24	TT1	chr3	3	q29	195480960	195517225	15	0	-0.526577	-0.526577	4.239E-20
1489-MCG_252152938948_S01	25	TT1	chr4	4	p16.3	1232826	1259725	10	0	-0.524787	-0.524787	8.629E-17
1489-MCG_252152938948_S01	28	TT1	chr5	5	q13.2	72729802	72758994	14	0.3678	0	0.3678	9.669E-10
1489-MCG_252152938948_S01	29	TT1	chr5	5	q15	92899368	92931987	18	0.407467	0	0.407467	9.812E-13
1489-MCG_252152938948_S01	30	TT1	chr5	5	q31.1	132138827	132162307	13	0.417542	0	0.417542	1.302E-11
1489-MCG_252152938948_S01	31	TT1	chr5	5	q34	167953640	167964479	7	0	-0.855254	-0.855254	7.452E-23
1489-MCG_252152938948_S01	32	TT1	chr5	5	q35.3	179235424	179243160	7	0.602052	0	0.602052	6.958E-11
1489-MCG_252152938948_S01	33	TT1	chr6	6	p25.3	1592005	1635408	21	0.428219	0	0.428219	2.367E-15
1489-MCG_252152938948_S01	34	TT1	chr6	6	p22.3	17982922	17993673	7	0	-0.716428	-0.716428	2.946E-18
1489-MCG_252152938948_S01	35	TT1	chr6	6	q14.1	79784507	79789852	5	0	-0.915946	-0.915946	2.015E-15
1489-MCG_252152938948_S01	38	TT1	chr6	6	q24.2	143378370	143387979	6	0	-0.772568	-0.772568	3.469E-16
1489-MCG_252152938948_S01	39	TT1	chr6	6	q27	170119250	170132368	7	0	-0.57514	-0.57514	3.228E-12
1489-MCG_252152938948_S01	40	TT1	chr6	6	q27	170601272	170611658	6	0.803821	0	0.803821	2.547E-17
1489-MCG_252152938948_S01	41	TT1	chr7	7	p22.3	1081110	1087076	7	0.673516	0	0.673516	1.119E-10
1489-MCG_252152938948_S01	42	TT1	chr7	7	p22.1	6455091	6465906	6	0	-0.778217	-0.778217	4.906E-17
1489-MCG_252152938948_S01	44	TT1	chr7	7	p15.2	27194426	27263521	60	0.25967	0	0.25967	9.056E-19
1489-MCG_252152938948_S01	46	TT1	chr7	7	q21.11	77644551	77652021	5	0	-0.80421	-0.80421	1.337E-15
1489-MCG_252152938948_S01	47	TT1	chr7	7	q22.1	101888196	101896854	8	0	-0.916987	-0.916987	2.986E-25
1489-MCG_252152938948_S01	48	TT1	chr7	7	q34	139465802	139479047	7	0	-0.625504	-0.625504	1.525E-13
1489-MCG_252152938948_S01	49	TT1	chr7	7	q36.1	149124837	149165185	21	0	-0.383462	-0.383462	1.392E-17
1489-MCG_252152938948_S01	53	TT1	chr8	8	p23.3	1039783	1055310	5	0	-1.028011	-1.028011	1.73E-20
1489-MCG_252152938948_S01	55	TT1	chr8	8	p12	29923461	29957813	15	0.469723	0	0.469723	2.633E-16
1489-MCG_252152938948_S01	56	TT1	chr8	8	p11.21	42746896	42755506	6	0	-0.6873	-0.6873	5.781E-14
1489-MCG_252152938948_S01	57	TT1	chr8	8	q12.1	61586383	61598251	7	0	-0.719568	-0.719568	4.445E-17
1489-MCG_252152938948_S01	61	TT1	chr9	9	p24.3	2040909	2051680	7	0	-1.045432	-1.045432	1.174E-29
1489-MCG_252152938948_S01	66	TT1	chr9	9	q31.1	103185084	103192529	5	0	-0.849929	-0.849929	1.28E-15
1489-MCG_252152938948_S01	67	TT1	chr9	9	q31.3	112078026	112086535	5	0	-0.663053	-0.663053	1.75E-11
1489-MCG_252152938948_S01	70	TT1	chr9	9	q32	116635621	116642488	5	0	-0.761069	-0.761069	7.166E-14
1489-MCG_252152938948_S01	71	TT1	chr9	9	q33.1	118910949	118928038	9	0	-0.635472	-0.635472	6.489E-17
1489-MCG_252152938948_S01	73	TT1	chr9	9	q34.11	131446293	131456708	6	0	-0.627442	-0.627442	2.227E-13
1489-MCG_252152938948_S01	80	TT1	chr10	10	p13	13567770	13574704	4	0	-0.952888	-0.952888	4.955E-18
1489-MCG_252152938948_S01	81	TT1	chr10	10	p12.31	21787374	21828310	38	0.334138	0	0.334138	1.239E-19
1489-MCG_252152938948_S01	82	TT1	chr10	10	p12.2	22607561	22617629	6	0	-0.963461	-0.963461	3.151E-24
1489-MCG_252152938948_S01	91	TT1	chr11	11	q13.1	65350181	65360355	6	0	-1.25119	-1.25119	1.28E-31
1489-MCG_252152938948_S01	93	TT1	chr11	11	q13.1	65807239	65814470	4	0	-1.258493	-1.258493	3.424E-27
1489-MCG_252152938948_S01	96	TT1	chr11	11	q13.3	69435979	69535561	42	0.279598	0	0.279598	1.472E-11
1489-MCG_252152938948_S01	97	TT1	chr11	11	q14.1	77901378	77912725	7	0	-0.653002	-0.653002	7.931E-15
1489-MCG_252152938948_S01	101	TT1	chr12	12	p13.31	7777178	7787402	5	0	-0.689626	-0.689626	1.906E-13
1489-MCG_252152938948_S01	102	TT1	chr12	12	q13.13	52204405	52272874	28	0.364337	0	0.364337	6.289E-13
1489-MCG_252152938948_S01	103	TT1	chr12	12	q13.13	52407286	52412633	3	0	-1.581677	-1.581677	2.58E-22
1489-MCG_252152938948_S01	106	TT1	chr12	12	q23.1	99288036	99292190	3	0	-1.130229	-1.130229	9.744E-18
1489-MCG_252152938948_S01	108	TT1	chr12	12	q24.21	116700744	116722994	13	0	-0.52783	-0.52783	3.769E-18
1489-MCG_252152938948_S01	110	TT1	chr13	13	q12.3	31033785	31042977	5	0	-0.682265	-0.682265	4.971E-12
1489-MCG_252152938948_S01	115	TT1	chr14	14	q32.11	89877754	89887444	7	0	-0.737761	-0.737761	3.093E-18
1489-MCG_252152938948_S01	122	TT1	chr14	14	q32.33	105772413	105792476	9	0	-0.592149	-0.592149	3.552E-15
1489-MCG_252152938948_S01	125	TT1	chr15	15	q13.1	29861670	29865524	3	0	-1.364071	-1.364071	8.019E-22
1489-MCG_252152938948_S01	128	TT1	chr15	15	q26.1	89917373	89923092	7	0.547386	0	0.547386	4.983E-10
1489-MCG_252152938948_S01	130	TT1	chr15	15	q26.3	101787757	101790636	3	0	-0.875989	-0.875989	1.722E-11
1489-MCG_252152938948_S01	131	TT1	chr15	15	q26.3	102028441	102032848	3	0	-1.021986	-1.021986	2.671E-14
1489-MCG_252152938948_S01	133	TT1	chr16	16	p13.3	4156869	4179603	10	0	-0.517704	-0.517704	8.297E-15
1489-MCG_252152938948_S01	134	TT1	chr16	16	p13.2	9051756	9060119	5	0	-0.72865	-0.72865	3.244E-14
1489-MCG_252152938948_S01	137	TT1	chr16	16	q21	58227960	58233859	3	0	-1.040585	-1.040585	2.417E-15
1489-MCG_252152938948_S01	140	TT1	chr16	16	q23.2	79630430	79636091	4	0	-1.024284	-1.024284	1.589E-17
1489-MCG_252152938948_S01	142	TT1	chr16	16	q24.2	87759646	87762259	3	0	-1.744429	-1.744429	1.773E-29
1489-MCG_252152938948_S01	144	TT1	chr17	17	p13.2	4120401	4128817	5	0	-1.077849	-1.077849	4.301E-21
1489-MCG_252152938948_S01	145	TT1	chr17	17	q21.32	45784656	45789434	3	0	-1.260256	-1.260256	4.873E-19
1489-MCG_252152938948_S01	146	TT1	chr17	17	q21.32	46111279	46124549	15	0.3936	0	0.3936	5.095E-10
1489-MCG_252152938948_S01	149	TT1	chr17	17	q25.3	77770203	77807476	21	0.472796	0	0.472796	3.836E-16
1489-MCG_252152938948_S01	151	TT1	chr17	17	q25.3	80474265	80487746	8	0	-0.732002	-0.732002	3.048E-20
1489-MCG_252152938948_S01	152	TT1	chr18	18	p11.31	5290748	5298074	4	0	-0.835667	-0.835667	8.872E-14
1489-MCG_252152938948_S01	153	TT1	chr18	18	p11.22	9610119	9618145	6	0	-0.821648	-0.821648	7.655E-19
1489-MCG_252152938948_S01	154	TT1	chr18	18	q12.1	31157460	31162296	3	0	-1.138426	-1.138426	1.572E-16
1489-MCG_252152938948_S01	155	TT1	chr18	18	q12.1	31394606	31406813	3	0	-0.854587	-0.854587	6.971E-11
1489-MCG_252152938948_S01	156	TT1	chr18	18	q12.2	33160498	33164337	3	0	-1.188463	-1.188463	3.289E-17
1489-MCG_252152938948_S01	157	TT1	chr18	18	q21.32	56529328	56534019	3	0	-1.011828	-1.011828	9.66E-15
1489-MCG_252152938948_S01	158	TT1	chr18	18	q23	76738212	76756679	9	0	-0.836951	-0.836951	1.63E-25
1489-MCG_252152938948_S01	167	TT1	chr19	19	p13.2	9023977	9096906	42	0	-0.361788	-0.361788	5.517E-33
1489-MCG_252152938948_S01	170	TT1	chr19	19	p13.12	14191532	14213726	12	0	-0.472237	-0.472237	4.81E-16
1489-MCG_252152938948_S01	171	TT1	chr19	19	p13.12	15537408	15595367	44	0	-0.293334	-0.293334	6.803E-22
1489-MCG_252152938948_S01	172	TT1	chr19	19	p13.12	15541461	15544313	4	0	-1.210854	-1.210854	2.474E-11
1489-MCG_252152938948_S01	173	TT1	chr19	19	p12	21055920	21098244	14	0	-0.713848	-0.713848	6.71E-33
1489-MCG_252152938948_S01	180	TT1	chr19	19	q13.43	56596052	56603908	6	0	-1.071536	-1.071536	4.475E-29
1489-MCG_252152938948_S01	181	TT1	chr19	19	q13.43	57682597	57685722	3	0	-1.410888	-1.410888	3.423E-24
1489-MCG_252152938948_S01	182	TT1	chr20	20	q11.22	32263273	32327350	31	0.319942	0	0.319942	1.289E-12
1489-MCG_252152938948_S01	184	TT1	chr20	20	q13.12	43435228	43445722	5	0	-0.740006	-0.740006	1.687E-14
1489-MCG_252152938948_S01	186	TT1	chr20	20	q13.2	50380940	50391357	7	0	-0.654826	-0.654826	9.641E-14
1489-MCG_252152938948_S01	189	TT1	chr20	20	q13.33	62459161	62465177	3	0	-1.231611	-1.231611	4.627E-20
1489-MCG_252152938948_S01	190	TT1	chr21	21	q22.2	42214433	42222204	7	0	-0.933364	-0.933364	8.084E-27
1489-MCG_252152938948_S01	191	TT1	chr21	21	q22.3	43296256	43303812	4	0	-1.037972	-1.037972	2.105E-19
1489-MCG_252152938948_S01	197	TT1	chr22	22	q12.1	25951368	25978771	14	0	-0.372288	-0.372288	8.138E-12
1489-MCG_252152938948_S01	198	TT1	chr22	22	q12.1	29278402	29286716	7	0	-0.7614	-0.7614	1.187E-19
1489-MCG_252152938948_S01	200	TT1	chr22	22	q13.1	39744824	39748341	3	0	-1.190295	-1.190295	1.843E-15
1489-MCG_252152938948_S01	207	TT1	chr22	22	q13.33	51116128	51178283	35	0	-0.517562	-0.517562	1.438E-37
1489-MCG_252152938931_S01	1	TT7	chr6	6	q27	170119250	170127040	5	0	-0.832699	-0.832699	3.808E-17
1489-MCG_252152938931_S01	3	TT7	chr8	8	q12.1	61588520	61595100	4	0	-0.909242	-0.909242	3.497E-16
1489-MCG_252152938931_S01	5	TT7	chr9	9	p24.3	2040909	2053837	8	0	-0.474529	-0.474529	2.159E-10
1489-MCG_252152938931_S01	6	TT7	chr10	10	p12.2	22607561	22612702	3	0	-0.798528	-0.798528	5.556E-11
1489-MCG_252152938931_S01	11	TT7	chr15	15	q13.1	29861670	29867088	4	0	-0.661207	-0.661207	5.069E-10
1489-MCG_252152938931_S01	12	TT7	chr18	18	q23	76742196	76758150	9	0	-0.630256	-0.630256	1.614E-18
1489-MCG_252152938944_S01	7	TT8	chr12	12	p13.31	7777178	7787402	5	0	-0.812298	-0.812298	1.9E-14
1489-MCG_252152938944_S01	13	TT8	chr17	17	q25.1	73829036	73833506	3	1.212371	0	1.212371	6.6E-10
1489-MCG_252152938956_S01	1	TT6	chr9	9	q21.13	75737677	75774626	20	0	-0.283541	-0.283541	6.555E-10

252152934054	5	T11	chr19	19	p13.12	14193994	14204159	7	0	-0.619313	-0.619313	2.375E-15
252152934055	1	TT3	chr5	5	p15.33	2745603	2755695	6	0	-0.646656	-0.646656	6.704E-11
252152934055	3	TT3	chr7	7	q36.1	149467813	149529090	28	0	-0.313761	-0.313761	2.382E-11
252152934056	2	TT2	chr11	11	p15.5	2060612	2086591	9	0.46205	0	0.46205	1.511E-10
1506-MCG_252152938959_S01	3	TT14	chr1	1	p36.32	2323891	2337151	9	0	-0.845518	-0.845518	1.02E-13
1506-MCG_252152938959_S01	4	TT14	chr1	1	p36.32	3556574	3572198	7	0	-1.194132	-1.194132	7.47E-23
1506-MCG_252152938959_S01	7	TT14	chr1	1	p36.31	6451606	6561951	32	0	-0.515807	-0.515807	1.52E-30
1506-MCG_252152938959_S01	25	TT14	chr1	1	p36.22	10695420	10761426	29	0	-0.464997	-0.464997	2.97E-22
1506-MCG_252152938959_S01	37	TT14	chr1	1	p36.21	16160344	16175570	7	0	-0.989957	-0.989957	1.57E-26
1506-MCG_252152938959_S01	69	TT14	chr1	1	p36.11	26486488	26496077	7	0	-0.789333	-0.789333	1.69E-19
1506-MCG_252152938959_S01	70	TT14	chr1	1	p36.11	27113063	27156287	21	0	-0.661933	-0.661933	1.16E-34
1506-MCG_252152938959_S01	71	TT14	chr1	1	p36.11	27671579	27721708	25	0	-0.448124	-0.448124	1.02E-19
1506-MCG_252152938959_S01	76	TT14	chr1	1	p35.3	28284554	28288109	3	0	-0.863	-0.863	3.68E-10
1506-MCG_252152938959_S01	77	TT14	chr1	1	p35.3	28843351	28861793	11	0	-0.811739	-0.811739	1.54E-27
1506-MCG_252152938959_S01	84	TT14	chr1	1	p35.3	29562293	29565728	3	0	-1.306969	-1.306969	6.42E-20
1506-MCG_252152938959_S01	96	TT14	chr1	1	p34.3	35431221	35454727	14	0	-0.781888	-0.781888	4.49E-34
1506-MCG_252152938959_S01	108	TT14	chr1	1	p34.3 - p34.2	40096580	40106794	7	0	-1.016314	-1.016314	5.03E-26
1506-MCG_252152938959_S01	128	TT14	chr1	1	p34.1	45665567	45674158	6	0	-0.985505	-0.985505	1.17E-23
1506-MCG_252152938959_S01	137	TT14	chr1	1	p33	48938568	48948394	6	0	-1.059247	-1.059247	2.89E-27
1506-MCG_252152938959_S01	138	TT14	chr1	1	p33	50484358	50492171	5	0	-0.7328	-0.7328	8.72E-13
1506-MCG_252152938959_S01	139	TT14	chr1	1	p32.3	50883522	50890453	5	0	-1.181753	-1.181753	1.1E-19
1506-MCG_252152938959_S01	140	TT14	chr1	1	p32.3	51421960	51445710	14	0	-0.984452	-0.984452	2.08E-50
1506-MCG_252152938959_S01	156	TT14	chr1	1	p32.3	55264451	55273554	6	0	-1.213654	-1.213654	1.63E-27
1506-MCG_252152938959_S01	158	TT14	chr1	1	p32.3	55676470	55683860	5	0	-0.630757	-0.630757	6.41E-10
1506-MCG_252152938959_S01	159	TT14	chr1	1	p32.2	57108371	57113307	4	0	-1.525695	-1.525695	3.66E-31
1506-MCG_252152938959_S01	160	TT14	chr1	1	p32.2	57805141	57811130	4	0	-0.714778	-0.714778	3.82E-10
1506-MCG_252152938959_S01	161	TT14	chr1	1	p32.2	58201381	58208750	5	0	-0.794113	-0.794113	1.05E-14
1506-MCG_252152938959_S01	165	TT14	chr1	1	p31.3	62898353	62910689	7	0	-0.592644	-0.592644	7.43E-12
1506-MCG_252152938959_S01	166	TT14	chr1	1	p31.3	63132041	63171762	19	0	-0.587368	-0.587368	4.75E-28
1506-MCG_252152938959_S01	167	TT14	chr1	1	p31.3	63781851	63791203	4	0	-1.038382	-1.038382	3.63E-18
1506-MCG_252152938959_S01	169	TT14	chr1	1	p31.3	64237782	64241292	3	0	-1.338563	-1.338563	1.18E-20
1506-MCG_252152938959_S01	175	TT14	chr1	1	p31.3	65772450	65778036	4	0	-1.084934	-1.084934	3.24E-19
1506-MCG_252152938959_S01	176	TT14	chr1	1	p31.3	65989355	65993613	3	0	-1.049748	-1.049748	5.1E-15
1506-MCG_252152938959_S01	177	TT14	chr1	1	p31.3	66255255	66261009	4	0	-1.082498	-1.082498	4.95E-19
1506-MCG_252152938959_S01	180	TT14	chr1	1	p31.1	70028242	70044985	10	0	-0.478803	-0.478803	2.65E-10
1506-MCG_252152938959_S01	181	TT14	chr1	1	p31.1	71509237	71515696	8	0	-0.829509	-0.829509	1.59E-22
1506-MCG_252152938959_S01	182	TT14	chr1	1	p31.1	72744354	72751884	6	0	-0.801765	-0.801765	4.09E-16
1506-MCG_252152938959_S01	183	TT14	chr1	1	p31.1	74708373	74726514	9	0	-0.55217	-0.55217	8.54E-13
1506-MCG_252152938959_S01	184	TT14	chr1	1	p31.1	75597077	75604854	6	0	-0.93782	-0.93782	3.96E-21
1506-MCG_252152938959_S01	185	TT14	chr1	1	p31.1	76082965	76085375	3	0	-0.847296	-0.847296	1.45E-10
1506-MCG_252152938959_S01	186	TT14	chr1	1	p31.1	76537558	76542390	4	0	-1.189647	-1.189647	2.49E-23
1506-MCG_252152938959_S01	187	TT14	chr1	1	p31.1	76572350	76582780	6	0	-0.778628	-0.778628	3.34E-16
1506-MCG_252152938959_S01	188	TT14	chr1	1	p31.1	77724898	77752976	15	0	-0.565193	-0.565193	1.86E-20
1506-MCG_252152938959_S01	189	TT14	chr1	1	p31.1	77994651	78001023	4	0	-0.787634	-0.787634	4.58E-11
1506-MCG_252152938959_S01	190	TT14	chr1	1	p31.1	78333581	78339600	3	0	-0.943337	-0.943337	5.83E-12
1506-MCG_252152938959_S01	191	TT14	chr1	1	p31.1	84540354	84546316	4	0	-0.966765	-0.966765	1.12E-16
1506-MCG_252152938959_S01	192	TT14	chr1	1	p22.3	84968449	84974254	4	0	-1.0776	-1.0776	1.06E-19
1506-MCG_252152938959_S01	201	TT14	chr1	1	p22.2	88927820	88931986	3	0	-1.885531	-1.885531	3.9E-26
1506-MCG_252152938959_S01	203	TT14	chr1	1	p22.2	90451500	90462720	7	0	-0.916037	-0.916037	2E-24
1506-MCG_252152938959_S01	206	TT14	chr1	1	p22.1	92945585	92953523	5	0	-0.976934	-0.976934	2.27E-14
1506-MCG_252152938959_S01	207	TT14	chr1	1	p22.1	93248741	93251354	3	0	-1.620037	-1.620037	1.61E-24
1506-MCG_252152938959_S01	208	TT14	chr1	1	p22.1	93424353	93428550	3	0	-0.951921	-0.951921	9.03E-13
1506-MCG_252152938959_S01	209	TT14	chr1	1	p22.1	94145588	94149578	3	0	-1.045345	-1.045345	1.05E-13
1506-MCG_252152938959_S01	210	TT14	chr1	1	p22.1	94309270	94317783	10	0	-0.709264	-0.709264	1.62E-21
1506-MCG_252152938959_S01	215	TT14	chr1	1	p21.3	95283566	95286607	3	0	-1.465259	-1.465259	7.33E-24
1506-MCG_252152938959_S01	216	TT14	chr1	1	p21.3	95391075	95397570	4	0	-0.727937	-0.727937	5.13E-10
1506-MCG_252152938959_S01	217	TT14	chr1	1	p21.3	95579881	95586717	5	0	-0.77472	-0.77472	7.31E-14
1506-MCG_252152938959_S01	219	TT14	chr1	1	p21.3	97184174	97234152	22	0	-0.43944	-0.43944	1.05E-18
1506-MCG_252152938959_S01	220	TT14	chr1	1	p21.3	98384555	98390007	3	0	-0.84278	-0.84278	1.67E-10
1506-MCG_252152938959_S01	221	TT14	chr1	1	p21.3	98512809	98523348	15	0	-0.75591	-0.75591	6.65E-36
1506-MCG_252152938959_S01	226	TT14	chr1	1	p21.2	100500395	100504667	3	0	-1.19195	-1.19195	2.81E-17
1506-MCG_252152938959_S01	230	TT14	chr1	1	p13.3	109201499	109221691	7	0	-1.100923	-1.100923	1.7E-30
1506-MCG_252152938959_S01	239	TT14	chr1	1	p13.2	112146512	112166834	11	0	-0.765594	-0.765594	6.25E-27
1506-MCG_252152938959_S01	240	TT14	chr1	1	p13.2	113042698	113055533	8	0	-0.623785	-0.623785	2.54E-12
1506-MCG_252152938959_S01	241	TT14	chr1	1	p13.2	113180581	113184125	3	0	-1.372499	-1.372499	1.66E-21
1506-MCG_252152938959_S01	243	TT14	chr1	1	p13.2	113248884	113262044	8	0	-1.015583	-1.015583	8.33E-34
1506-MCG_252152938959_S01	248	TT14	chr1	1	p13.1	116182932	116187171	3	0	-1.207506	-1.207506	1.7E-17
1506-MCG_252152938959_S01	249	TT14	chr1	1	p13.1	116299697	116307687	5	0	-0.741525	-0.741525	4.75E-13
1506-MCG_252152938959_S01	250	TT14	chr1	1	p13.1	116367852	116382675	7	0	-1.044467	-1.044467	9.54E-31
1506-MCG_252152938959_S01	257	TT14	chr1	1	p12	119519032	119551722	17	0	-0.577333	-0.577333	1.46E-23
1506-MCG_252152938959_S01	258	TT14	chr1	1	p12	120162251	120198195	19	0	-0.531558	-0.531558	2.69E-23
1506-MCG_252152938959_S01	261	TT14	chr1	1	q21.1	146641601	146651819	6	0	-0.957178	-0.957178	6.02E-24
1506-MCG_252152938959_S01	262	TT14	chr1	1	q21.1	146706034	146717152	7	0	-0.896745	-0.896745	8.17E-24
1506-MCG_252152938959_S01	265	TT14	chr1	1	q21.3	150550892	150569180	10	0	-0.605254	-0.605254	2.56E-16
1506-MCG_252152938959_S01	267	TT14	chr1	1	q21.3	151567001	151588877	11	0	-0.67281	-0.67281	6.75E-25
1506-MCG_252152938959_S01	278	TT14	chr1	1	q21.3	154529603	154544764	8	0	-0.886851	-0.886851	3.88E-28
1506-MCG_252152938959_S01	283	TT14	chr1	1	q22	156180009	156188113	5	0	-0.829741	-0.829741	5.9E-17
1506-MCG_252152938959_S01	284	TT14	chr1	1	q22	156296858	156300115	3	0	-1.100248	-1.100248	2.17E-16
1506-MCG_252152938959_S01	290	TT14	chr1	1	q23.2	160033899	160071928	20	0	-0.490461	-0.490461	2.69E-25
1506-MCG_252152938959_S01	295	TT14	chr1	1	q23.3	162530134	162533692	3	0	-1.209437	-1.209437	1.07E-18
1506-MCG_252152938959_S01	296	TT14	chr1	1	q23.3	164541547	164549380	5	0	-0.924103	-0.924103	1.1E-18
1506-MCG_252152938959_S01	297	TT14	chr1	1	q23.3	165199708	165208575	6	0	-0.641589	-0.641589	7.06E-12
1506-MCG_252152938959_S01	299	TT14	chr1	1	q24.1	166131911	166139187	9	0	-0.916781	-0.916781	7.5E-28
1506-MCG_252152938959_S01	306	TT14	chr1	1	q24.2	167682828	167694285	6	0	-0.826195	-0.826195	1.74E-18
1506-MCG_252152938959_S01	307	TT14	chr1	1	q24.2	168105082	168117878	8	0	-0.852977	-0.852977	1.3E-23
1506-MCG_252152938959_S01	308	TT14	chr1	1	q24.2	168186334	168197970	7	0	-0.664226	-0.664226	7.62E-14
1506-MCG_252152938959_S01	310	TT14	chr1	1	q25.1	173445728	173449185	3	0	-1.045322	-1.045322	2E-14
1506-MCG_252152938959_S01	311	TT14	chr1	1	q25.1	173984115	173992558	4	0	-0.778397	-0.778397	1.04E-11
1506-MCG_252152938959_S01	312	TT14	chr1	1	q25.1	174124915	174130001	4	0	-0.737289	-0.737289	1.65E-10
1506-MCG_252152938959_S01	313	TT14	chr1	1	q25.1	175046140	175050450	4	0	-1.113854	-1.113854	1.22E-19
1506-MCG_252152938959_S01	319	TT14	chr1	1	q25.2	178989203	179011102	12	0	-0.626271	-0.626271	1.29E-20
1506-MCG_252152938959_S01	321	TT14	chr1	1	q25.2	179543709	179561676	11	0	-0.678082	-0.678082	3.26E-22
1506-MCG_252152938959_S01	323	TT14	chr1	1	q25.3	180879925	180930421	27	0	-0.460402	-0.460402	4.34E-22
1506-MCG_252152938959_S01	326	TT14	chr1	1	q25.3	182755842	182761813	4	0	-1.049068	-1.049068	2.96E-18
1506-MCG_252152938959_S01	330	TT14	chr1	1	q25.3	184353175	184358604	4	0	-1.088009	-1.088009	7.49E-20
1506-MCG_252152938959_S01	331	TT14	chr1	1	q25.3	184989973	185024255	13	0	-0.463678	-0.463678	1.58E-12

1506-MCG_252152938959_S01	333	TT14	chr1	1	q31.2	193073338	193079267	5	0	-1.097413	-1.097413	5.85E-24
1506-MCG_252152938959_S01	367	TT14	chr1	1	q32.2	211368632	211383015	9	0	-0.997341	-0.997341	1.74E-36
1506-MCG_252152938959_S01	379	TT14	chr1	1	q41	217260197	217265502	4	0	-1.196015	-1.196015	5.44E-21
1506-MCG_252152938959_S01	384	TT14	chr1	1	q41	220638634	220650513	6	0	-1.138795	-1.138795	2.31E-28
1506-MCG_252152938959_S01	397	TT14	chr1	1	q42.12	226594901	226599088	3	0	-1.536327	-1.536327	4.71E-25
1506-MCG_252152938959_S01	398	TT14	chr1	1	q42.13	227160505	227164467	3	0	-0.928852	-0.928852	7.5E-12
1506-MCG_252152938959_S01	399	TT14	chr1	1	q42.13	227319691	227323778	3	0	-0.867098	-0.867098	6.94E-11
1506-MCG_252152938959_S01	400	TT14	chr1	1	q42.13	227459549	227466811	4	0	-0.810087	-0.810087	1.54E-12
1506-MCG_252152938959_S01	401	TT14	chr1	1	q42.13	227502756	227507265	3	0	-1.344644	-1.344644	1.15E-21
1506-MCG_252152938959_S01	405	TT14	chr1	1	q42.13	229470060	229480436	6	0	-0.848612	-0.848612	3.86E-18
1506-MCG_252152938959_S01	406	TT14	chr1	1	q42.13	229690105	229697160	5	0	-0.855748	-0.855748	3.13E-16
1506-MCG_252152938959_S01	407	TT14	chr1	1	q42.13	229759370	229762862	3	0	-1.11031	-1.11031	2.11E-16
1506-MCG_252152938959_S01	411	TT14	chr1	1	q42.2	231173681	231179520	6	0	-0.928962	-0.928962	1.03E-18
1506-MCG_252152938959_S01	412	TT14	chr1	1	q42.2	231449141	231454868	5	0	-1.107921	-1.107921	5.35E-25
1506-MCG_252152938959_S01	418	TT14	chr1	1	q42.3	234733262	234747456	10	0	-1.005798	-1.005798	8.83E-37
1506-MCG_252152938959_S01	426	TT14	chr1	1	q43	237203838	237209074	4	0	-1.045802	-1.045802	1.56E-18
1506-MCG_252152938959_S01	437	TT14	chr1	1	q43	242684977	242692335	4	0	-1.011923	-1.011923	5.5E-18
1506-MCG_252152938959_S01	438	TT14	chr1	1	q43	243413849	243422267	6	0	-0.708467	-0.708467	3.98E-14
1506-MCG_252152938959_S01	439	TT14	chr1	1	q43	243636316	243658072	14	0	-0.728351	-0.728351	1.99E-30
1506-MCG_252152938959_S01	451	TT14	chr1	1	q44	247091653	247096020	4	0	-1.235732	-1.235732	6.04E-20
1506-MCG_252152938959_S01	457	TT14	chr1	1	q44	247799201	247806081	5	0	-0.935472	-0.935472	1.21E-13
1506-MCG_252152938959_S01	458	TT14	chr1	1	q44	248018503	248024471	4	0	-1.09698	-1.09698	4.73E-15
1506-MCG_252152938959_S01	469	TT14	chr2	2	p25.3	3735789	3757267	11	0	-0.610972	-0.610972	8.23E-14
1506-MCG_252152938959_S01	472	TT14	chr2	2	p25.1	8818562	8827209	6	0	-1.157555	-1.157555	7.18E-31
1506-MCG_252152938959_S01	483	TT14	chr2	2	p25.1	11886060	11901485	8	0	-0.947227	-0.947227	1.6E-28
1506-MCG_252152938959_S01	485	TT14	chr2	2	p24.3	15678818	15684452	5	0	-1.131885	-1.131885	1.59E-24
1506-MCG_252152938959_S01	486	TT14	chr2	2	p24.3	15749259	15753653	3	0	-1.247536	-1.247536	5.56E-19
1506-MCG_252152938959_S01	488	TT14	chr2	2	p24.2	16844397	16850569	5	0	-0.847076	-0.847076	6.25E-15
1506-MCG_252152938959_S01	489	TT14	chr2	2	p24.2	18055676	18061896	4	0	-0.763364	-0.763364	5.24E-10
1506-MCG_252152938959_S01	490	TT14	chr2	2	p24.2	18738168	18769473	13	0	-0.671698	-0.671698	5.81E-25
1506-MCG_252152938959_S01	501	TT14	chr2	2	p23.3	24713098	24718157	3	0	-1.333256	-1.333256	3.82E-21
1506-MCG_252152938959_S01	517	TT14	chr2	2	p23.1	30011744	30029095	9	0	-0.517866	-0.517866	7.18E-15
1506-MCG_252152938959_S01	518	TT14	chr2	2	p22.3	32285359	32291449	4	0	-0.811821	-0.811821	1.96E-12
1506-MCG_252152938959_S01	520	TT14	chr2	2	p22.3	32579572	32588527	5	0	-0.724456	-0.724456	1.55E-12
1506-MCG_252152938959_S01	522	TT14	chr2	2	p22.3	32974920	32983372	5	0	-0.71943	-0.71943	2.31E-12
1506-MCG_252152938959_S01	523	TT14	chr2	2	p22.3	33168330	33174938	4	0	-0.929487	-0.929487	3.08E-13
1506-MCG_252152938959_S01	524	TT14	chr2	2	p22.2	36824038	36825949	3	0	-1.31589	-1.31589	1.94E-18
1506-MCG_252152938959_S01	525	TT14	chr2	2	p22.2	36914432	36919364	3	0	-0.979599	-0.979599	3.22E-13
1506-MCG_252152938959_S01	526	TT14	chr2	2	p22.2	37382418	37395206	7	0	-0.984669	-0.984669	4.92E-22
1506-MCG_252152938959_S01	527	TT14	chr2	2	p22.2	37546362	37574841	15	0	-0.501207	-0.501207	4.25E-17
1506-MCG_252152938959_S01	528	TT14	chr2	2	p22.2	38155510	38162824	5	0	-0.968862	-0.968862	6.21E-20
1506-MCG_252152938959_S01	534	TT14	chr2	2	p22.1	38976101	38984246	5	0	-1.276465	-1.276465	6.35E-29
1506-MCG_252152938959_S01	552	TT14	chr2	2	p21	47594039	47600434	7	0	-0.980637	-0.980637	2.33E-26
1506-MCG_252152938959_S01	562	TT14	chr2	2	p16.1	55875905	55879296	3	0	-1.279311	-1.279311	1.69E-19
1506-MCG_252152938959_S01	563	TT14	chr2	2	p16.1	55924760	55934769	4	0	-0.976938	-0.976938	2.01E-17
1506-MCG_252152938959_S01	569	TT14	chr2	2	p16.1	61290383	61294284	3	0	-1.352529	-1.352529	8.91E-22
1506-MCG_252152938959_S01	576	TT14	chr2	2	p15	63271298	63293399	11	0	-0.813209	-0.813209	1.46E-28
1506-MCG_252152938959_S01	580	TT14	chr2	2	p14	64876790	64882195	4	0	-0.90384	-0.90384	1.37E-14
1506-MCG_252152938959_S01	581	TT14	chr2	2	p14	65279938	65284869	3	0	-1.080203	-1.080203	1.36E-15
1506-MCG_252152938959_S01	582	TT14	chr2	2	p14	65655923	65668725	9	0	-0.74496	-0.74496	8.06E-18
1506-MCG_252152938959_S01	583	TT14	chr2	2	p14	66648184	66672068	12	0	-0.628203	-0.628203	7.83E-21
1506-MCG_252152938959_S01	584	TT14	chr2	2	p13.3	70368081	70375177	4	0	-0.786554	-0.786554	1.49E-11
1506-MCG_252152938959_S01	587	TT14	chr2	2	p13.2 - p13.1	73489545	73522921	18	0	-0.70295	-0.70295	3.42E-35
1506-MCG_252152938959_S01	590	TT14	chr2	2	p13.1	74874254	74882406	5	0	-0.87969	-0.87969	1.76E-14
1506-MCG_252152938959_S01	591	TT14	chr2	2	p12	75057704	75063189	3	0	-0.967784	-0.967784	3.5E-13
1506-MCG_252152938959_S01	592	TT14	chr2	2	p12	75186256	75189738	4	0	-0.876634	-0.876634	4.23E-14
1506-MCG_252152938959_S01	593	TT14	chr2	2	p12	79735273	79743750	4	0	-0.855102	-0.855102	4.82E-12
1506-MCG_252152938959_S01	597	TT14	chr2	2	p11.2	85130466	85135444	4	0	-0.978378	-0.978378	6.74E-17
1506-MCG_252152938959_S01	608	TT14	chr2	2	q11.2	97470883	97483722	8	0	-1.067509	-1.067509	1.91E-30
1506-MCG_252152938959_S01	641	TT14	chr2	2	q14.2	120277678	120309514	18	0	-0.558639	-0.558639	4.02E-23
1506-MCG_252152938959_S01	649	TT14	chr2	2	q14.3	128398255	128465278	31	0	-0.548062	-0.548062	1.31E-34
1506-MCG_252152938959_S01	656	TT14	chr2	2	q21.3	136460633	136466246	4	0	-1.252466	-1.252466	4.58E-22
1506-MCG_252152938959_S01	657	TT14	chr2	2	q22.1	139257574	139261433	3	0	-1.089364	-1.089364	6.45E-14
1506-MCG_252152938959_S01	658	TT14	chr2	2	q22.1	139536907	139541164	3	0	-0.925805	-0.925805	1.35E-10
1506-MCG_252152938959_S01	666	TT14	chr2	2	q23.3	152682249	152685348	3	0	-1.289904	-1.289904	4.44E-19
1506-MCG_252152938959_S01	667	TT14	chr2	2	q23.3	153478061	153483419	4	0	-0.943184	-0.943184	6.58E-16
1506-MCG_252152938959_S01	669	TT14	chr2	2	q24.1	158726275	158737387	6	0	-0.688568	-0.688568	3.15E-13
1506-MCG_252152938959_S01	671	TT14	chr2	2	q24.2	159822651	159827602	4	0	-1.108112	-1.108112	1.73E-16
1506-MCG_252152938959_S01	673	TT14	chr2	2	q24.2	160566377	160570710	4	0	-0.830522	-0.830522	5.42E-11
1506-MCG_252152938959_S01	674	TT14	chr2	2	q24.2	160652749	160657365	4	0	-1.127198	-1.127198	9.33E-21
1506-MCG_252152938959_S01	675	TT14	chr2	2	q24.2	160759739	160763198	3	0	-0.833826	-0.833826	7.19E-10
1506-MCG_252152938959_S01	676	TT14	chr2	2	q24.2	161257405	161310109	25	0	-0.431514	-0.431514	2.48E-20
1506-MCG_252152938959_S01	677	TT14	chr2	2	q24.2	161347765	161352090	4	0	-1.192575	-1.192575	2.63E-24
1506-MCG_252152938959_S01	678	TT14	chr2	2	q24.2	162093140	162103370	6	0	-1.274392	-1.274392	3.04E-31
1506-MCG_252152938959_S01	679	TT14	chr2	2	q24.2	162269687	162287643	10	0	-0.874952	-0.874952	6.05E-28
1506-MCG_252152938959_S01	681	TT14	chr2	2	q24.3	164591385	164597096	4	0	-1.028905	-1.028905	1.61E-18
1506-MCG_252152938959_S01	682	TT14	chr2	2	q24.3	164765678	164774589	3	0	-1.015225	-1.015225	1.05E-12
1506-MCG_252152938959_S01	684	TT14	chr2	2	q24.3	166809772	166815187	4	0	-1.030935	-1.030935	1.72E-18
1506-MCG_252152938959_S01	685	TT14	chr2	2	q24.3	169099929	169105801	5	0	-0.855136	-0.855136	1.07E-14
1506-MCG_252152938959_S01	687	TT14	chr2	2	q31.1	170361100	170364581	3	0	-1.579984	-1.579984	4.26E-25
1506-MCG_252152938959_S01	689	TT14	chr2	2	q31.1	170577790	170711703	59	0	-0.368609	-0.368609	2.33E-33
1506-MCG_252152938959_S01	690	TT14	chr2	2	q31.1	170589459	170595283	3	0	-1.751923	-1.751923	1.49E-19
1506-MCG_252152938959_S01	693	TT14	chr2	2	q31.1	171621470	171632188	7	0	-0.696938	-0.696938	1.96E-15
1506-MCG_252152938959_S01	694	TT14	chr2	2	q31.1	172290054	172292145	3	0	-1.404233	-1.404233	3.96E-23
1506-MCG_252152938959_S01	706	TT14	chr2	2	q31.1	176943343	177055486	89	0	-0.69684	-0.69684	5.37E-153
1506-MCG_252152938959_S01	707	TT14	chr2	2	q31.1	176985725	177002978	17	0	-1.141768	-1.141768	1.14E-11
1506-MCG_252152938959_S01	713	TT14	chr2	2	q31.2	179339209	179348440	7	0	-0.720856	-0.720856	1.03E-15
1506-MCG_252152938959_S01	714	TT14	chr2	2	q31.3	180723225	180729821	8	0	-0.834246	-0.834246	3.28E-23
1506-MCG_252152938959_S01	718	TT14	chr2	2	q31.3	182753193	182760563	4	0	-1.018905	-1.018905	6.79E-18
1506-MCG_252152938959_S01	719	TT14	chr2	2	q32.1	183898897	183904001	3	0	-0.91969	-0.91969	7.89E-12
1506-MCG_252152938959_S01	720	TT14	chr2	2	q32.1	185461612	185471875	8	0	-0.787159	-0.787159	1.95E-21
1506-MCG_252152938959_S01	721	TT14	chr2	2	q32.1	187452428	187457376	4	0	-1.186994	-1.186994	1.34E-21
1506-MCG_252152938959_S01	723	TT14	chr2	2	q32.2	190444541	190547416	35	0	-0.397018	-0.397018	5.29E-24
1506-MCG_252152938959_S01	733	TT14	chr2	2	q33.1	197455313	197460545	4	0	-1.258193	-1.258193	2.03E-25
1506-MCG_252152938959_S01	734	TT14	chr2	2	q33.1	197787192	197793945	5	0	-0.8519	-0.8519	2.13E-16
1506-MCG_252152938959_S01	735	TT14	chr2	2	q33.1	198174779	198177264	3	0	-1.569554	-1.569554	1.54E-18

1506-MCG_252152938959_S01	746	TT14	chr2	2	q33.1	203000380	203003195	3	0	-1.550905	-1.550905	9.11E-25
1506-MCG_252152938959_S01	759	TT14	chr2	2	q33.3	208574424	208577211	3	0	-1.213492	-1.213492	9.26E-17
1506-MCG_252152938959_S01	763	TT14	chr2	2	q34	210284891	210289906	4	0	-0.987101	-0.987101	7.53E-17
1506-MCG_252152938959_S01	764	TT14	chr2	2	q34	210634779	210639660	4	0	-0.866328	-0.866328	4.68E-12
1506-MCG_252152938959_S01	765	TT14	chr2	2	q34	211033337	211037119	3	0	-0.953673	-0.953673	4.08E-12
1506-MCG_252152938959_S01	767	TT14	chr2	2	q35	215697456	215707951	5	0	-0.697152	-0.697152	9.74E-12
1506-MCG_252152938959_S01	768	TT14	chr2	2	q35	216297138	216303118	4	0	-0.915801	-0.915801	2.6E-15
1506-MCG_252152938959_S01	769	TT14	chr2	2	q35	216876434	216881097	3	0	-1.225016	-1.225016	6.1E-21
1506-MCG_252152938959_S01	773	TT14	chr2	2	q35	219260478	219273298	13	0	-0.544903	-0.544903	6.23E-13
1506-MCG_252152938959_S01	778	TT14	chr2	2	q35	220403462	220437841	16	0	-0.672576	-0.672576	7.81E-15
1506-MCG_252152938959_S01	782	TT14	chr2	2	q36.2	225447085	225452495	4	0	-1.208102	-1.208102	1.59E-21
1506-MCG_252152938959_S01	783	TT14	chr2	2	q36.2	225902497	225908462	4	0	-0.786014	-0.786014	6.59E-12
1506-MCG_252152938959_S01	784	TT14	chr2	2	q36.3	227655453	227668870	8	0	-0.968507	-0.968507	6.83E-29
1506-MCG_252152938959_S01	785	TT14	chr2	2	q36.3	230133396	230136836	3	0	-1.119262	-1.119262	1.7E-15
1506-MCG_252152938959_S01	788	TT14	chr2	2	q37.1	232258138	232278500	8	0	-0.794063	-0.794063	6.14E-19
1506-MCG_252152938959_S01	789	TT14	chr2	2	q37.1	232392597	232396012	3	0	-1.254658	-1.254658	8.14E-18
1506-MCG_252152938959_S01	793	TT14	chr2	2	q37.1	233767277	233794044	12	0	-0.704603	-0.704603	4.8E-24
1506-MCG_252152938959_S01	796	TT14	chr2	2	q37.2	236575428	236582609	4	0	-0.952728	-0.952728	1.84E-15
1506-MCG_252152938959_S01	798	TT14	chr2	2	q37.2	237120691	237150571	14	0	-0.602391	-0.602391	7.31E-21
1506-MCG_252152938959_S01	799	TT14	chr2	2	q37.3	237474924	237479062	4	0	-1.084666	-1.084666	2.21E-19
1506-MCG_252152938959_S01	811	TT14	chr3	3	p26.3	232496	244865	6	0	-0.87714	-0.87714	8.95E-17
1506-MCG_252152938959_S01	812	TT14	chr3	3	p26.3	2123694	2143793	7	0	-0.628717	-0.628717	2.06E-10
1506-MCG_252152938959_S01	813	TT14	chr3	3	p26.1	5227076	5231206	3	0	-1.501125	-1.501125	4.88E-23
1506-MCG_252152938959_S01	814	TT14	chr3	3	p26.1	6894609	6905611	7	0	-0.644662	-0.644662	1.88E-13
1506-MCG_252152938959_S01	817	TT14	chr3	3	p25.3	9436558	9445930	5	0	-0.788147	-0.788147	1.77E-14
1506-MCG_252152938959_S01	827	TT14	chr3	3	p25.1	13969351	13996627	7	0	-0.588167	-0.588167	7.72E-11
1506-MCG_252152938959_S01	828	TT14	chr3	3	p25.1	15100180	15107190	4	0	-0.930768	-0.930768	2.23E-15
1506-MCG_252152938959_S01	829	TT14	chr3	3	p25.1	15245453	15248436	3	0	-1.299819	-1.299819	2.19E-19
1506-MCG_252152938959_S01	830	TT14	chr3	3	p25.1	15779457	15785752	4	0	-0.746127	-0.746127	8.57E-11
1506-MCG_252152938959_S01	831	TT14	chr3	3	p25.1	15898124	15903568	6	0	-1.018591	-1.018591	2.47E-25
1506-MCG_252152938959_S01	842	TT14	chr3	3	p24.3	23846698	23851485	3	0	-1.556925	-1.556925	5.63E-26
1506-MCG_252152938959_S01	876	TT14	chr3	3	p21.31	47820754	47871277	23	0	-0.455228	-0.455228	1.58E-20
1506-MCG_252152938959_S01	885	TT14	chr3	3	p21.2	51420224	51431725	7	0	-0.992478	-0.992478	9.03E-25
1506-MCG_252152938959_S01	890	TT14	chr3	3	p21.2	51988474	52026149	17	0	-0.582553	-0.582553	4.1E-23
1506-MCG_252152938959_S01	892	TT14	chr3	3	p21.1	52309300	52317575	10	0	-0.756835	-0.756835	5.12E-23
1506-MCG_252152938959_S01	894	TT14	chr3	3	p21.1	52928144	52933389	4	0	-1.072282	-1.072282	7.1E-19
1506-MCG_252152938959_S01	900	TT14	chr3	3	p14.3	55499380	55529042	19	0	-0.518367	-0.518367	7.56E-22
1506-MCG_252152938959_S01	907	TT14	chr3	3	p14.3	58317877	58321201	3	0	-1.217331	-1.217331	3.53E-18
1506-MCG_252152938959_S01	922	TT14	chr3	3	p13	72934985	72941872	5	0	-1.069214	-1.069214	6.83E-23
1506-MCG_252152938959_S01	942	TT14	chr3	3	q13.12	107241277	107245211	3	0	-1.571295	-1.571295	3.01E-19
1506-MCG_252152938959_S01	946	TT14	chr3	3	q13.31	113558228	113573744	8	0	-0.76968	-0.76968	8.9E-21
1506-MCG_252152938959_S01	947	TT14	chr3	3	q13.31	113664255	113668404	3	0	-1.445412	-1.445412	1.25E-22
1506-MCG_252152938959_S01	948	TT14	chr3	3	q13.31	114527131	114533357	4	0	-1.356665	-1.356665	6.23E-26
1506-MCG_252152938959_S01	949	TT14	chr3	3	q13.31	115180708	115189856	4	0	-0.751625	-0.751625	5.34E-11
1506-MCG_252152938959_S01	950	TT14	chr3	3	q13.31	115501589	115510217	4	0	-1.018078	-1.018078	3.34E-17
1506-MCG_252152938959_S01	951	TT14	chr3	3	q13.32	118750979	118754600	3	0	-1.30026	-1.30026	2.89E-20
1506-MCG_252152938959_S01	957	TT14	chr3	3	q13.33	121404859	121410002	4	0	-1.078433	-1.078433	8.8E-20
1506-MCG_252152938959_S01	958	TT14	chr3	3	q13.33 - q21.1	121898331	121922797	13	0	-0.582028	-0.582028	1.3E-19
1506-MCG_252152938959_S01	959	TT14	chr3	3	q21.1	122465355	122469186	3	0	-1.105776	-1.105776	5.53E-16
1506-MCG_252152938959_S01	960	TT14	chr3	3	q21.1	122490415	122517830	12	0	-0.531889	-0.531889	3.12E-15
1506-MCG_252152938959_S01	967	TT14	chr3	3	q21.3	125802184	125803640	3	0	-1.476833	-1.476833	8.12E-21
1506-MCG_252152938959_S01	980	TT14	chr3	3	q22.1	130353186	130357262	3	0	-1.167554	-1.167554	7.42E-17
1506-MCG_252152938959_S01	981	TT14	chr3	3	q22.1	130581966	130621365	15	0	-0.390019	-0.390019	4.26E-11
1506-MCG_252152938959_S01	983	TT14	chr3	3	q22.1	132436934	132442567	4	0	-0.736637	-0.736637	3.07E-10
1506-MCG_252152938959_S01	984	TT14	chr3	3	q22.1	133290238	133293929	3	0	-1.18648	-1.18648	5.74E-17
1506-MCG_252152938959_S01	985	TT14	chr3	3	q22.1	133641456	133648969	6	0	-0.733889	-0.733889	3.63E-11
1506-MCG_252152938959_S01	986	TT14	chr3	3	q22.2	133968402	133971437	3	0	-1.508591	-1.508591	1.35E-23
1506-MCG_252152938959_S01	990	TT14	chr3	3	q22.3	138066818	138071607	4	0	-0.872486	-0.872486	8.79E-13
1506-MCG_252152938959_S01	991	TT14	chr3	3	q22.3	138325847	138330031	3	0	-1.108801	-1.108801	9.38E-16
1506-MCG_252152938959_S01	993	TT14	chr3	3	q23	138722783	138742314	9	0	-0.957357	-0.957357	5.81E-32
1506-MCG_252152938959_S01	1044	TT14	chr3	3	q26.33	181410275	181435409	13	0	-0.649226	-0.649226	4.94E-23
1506-MCG_252152938959_S01	1050	TT14	chr3	3	q27.1	184278257	184287854	5	0	-1.061342	-1.061342	6E-14
1506-MCG_252152938959_S01	1055	TT14	chr3	3	q27.3	187870164	187876556	3	0	-0.736586	-0.736586	5.88E-10
1506-MCG_252152938959_S01	1056	TT14	chr3	3	q28	189835795	189843093	5	0	-1.173205	-1.173205	1.24E-26
1506-MCG_252152938959_S01	1057	TT14	chr3	3	q28	190579781	190582753	3	0	-1.45822	-1.45822	5.36E-24
1506-MCG_252152938959_S01	1058	TT14	chr3	3	q28	191038864	191053192	8	0	-0.58248	-0.58248	7.91E-13
1506-MCG_252152938959_S01	1060	TT14	chr3	3	q29	192423837	192434093	4	0	-0.809787	-0.809787	1.57E-12
1506-MCG_252152938959_S01	1061	TT14	chr3	3	q29	192505209	192509774	3	0	-1.056683	-1.056683	4.71E-15
1506-MCG_252152938959_S01	1062	TT14	chr3	3	q29	192953574	192961412	5	0	-0.945044	-0.945044	1.04E-18
1506-MCG_252152938959_S01	1063	TT14	chr3	3	q29	193851204	193860162	5	0	-1.145378	-1.145378	1.71E-21
1506-MCG_252152938959_S01	1076	TT14	chr4	4	p16.3	648593	1689354	342	0	-0.360844	-0.360844	4.56E-154
1506-MCG_252152938959_S01	1077	TT14	chr4	4	p16.3	713799	741733	12	0	-1.062843	-1.062843	5.16E-21
1506-MCG_252152938959_S01	1079	TT14	chr4	4	p16.3	1978572	2059423	32	0	-0.469487	-0.469487	1.06E-24
1506-MCG_252152938959_S01	1081	TT14	chr4	4	p16.3	2756012	2766571	5	0	-0.971326	-0.971326	3.71E-18
1506-MCG_252152938959_S01	1088	TT14	chr4	4	p16.1	6973277	6990842	8	0	-0.869133	-0.869133	8.15E-24
1506-MCG_252152938959_S01	1091	TT14	chr4	4	p16.1	8858439	8877011	21	0	-0.60211	-0.60211	7.97E-27
1506-MCG_252152938959_S01	1106	TT14	chr4	4	p15.2	25237399	25256743	7	0	-0.978345	-0.978345	9.28E-26
1506-MCG_252152938959_S01	1109	TT14	chr4	4	p15.2	26856128	26865330	5	0	-1.100371	-1.100371	1.98E-22
1506-MCG_252152938959_S01	1110	TT14	chr4	4	p14	36243261	36247229	3	0	-0.995087	-0.995087	6.56E-13
1506-MCG_252152938959_S01	1111	TT14	chr4	4	p14	37453173	37457321	4	0	-0.998019	-0.998019	8.2E-16
1506-MCG_252152938959_S01	1112	TT14	chr4	4	p14	37666089	37689159	11	0	-0.542373	-0.542373	6.92E-13
1506-MCG_252152938959_S01	1115	TT14	chr4	4	p14	38867364	38873403	7	0	-0.766862	-0.766862	3.19E-17
1506-MCG_252152938959_S01	1116	TT14	chr4	4	p14	39043315	39047362	3	0	-1.204268	-1.204268	8.98E-19
1506-MCG_252152938959_S01	1117	TT14	chr4	4	p14	40142093	40151822	5	0	-0.757414	-0.757414	8.73E-14
1506-MCG_252152938959_S01	1118	TT14	chr4	4	p14	40437749	40441620	3	0	-1.155497	-1.155497	2.21E-18
1506-MCG_252152938959_S01	1119	TT14	chr4	4	p14	40931255	40933891	3	0	-1.282425	-1.282425	2.95E-18
1506-MCG_252152938959_S01	1126	TT14	chr4	4	p13	44182063	44198000	9	0	-0.792053	-0.792053	8.08E-23
1506-MCG_252152938959_S01	1127	TT14	chr4	4	p13	44445715	44452347	4	0	-0.771834	-0.771834	2.79E-10
1506-MCG_252152938959_S01	1128	TT14	chr4	4	p12	46377156	46395671	10	0	-0.837252	-0.837252	9.64E-28
1506-MCG_252152938959_S01	1131	TT14	chr4	4	p11	48484329	48494547	6	0	-0.903695	-0.903695	1.2E-19
1506-MCG_252152938959_S01	1132	TT14	chr4	4	p11	48778874	48784295	4	0	-0.86766	-0.86766	6.63E-13
1506-MCG_252152938959_S01	1133	TT14	chr4	4	q12	52902001	52919480	8	0	-0.84068	-0.84068	3E-23
1506-MCG_252152938959_S01	1135	TT14	chr4	4	q12	53725348	53729510	3	0	-1.27379	-1.27379	1.1E-18
1506-MCG_252152938959_S01	1136	TT14	chr4	4	q12	54001096	54014248	7	0	-0.716924	-0.716924	5.13E-15
1506-MCG_252152938959_S01	1137	TT14	chr4	4	q12	54101825	54124211	6	0	-0.736657	-0.736657	5.26E-14
1506-MCG_252152938959_S01	1138	TT14	chr4	4	q12	54929118	54932692	3	0	-1.163553	-1.163553	6.03E-16

1506-MCG_252152938959_S01	1139	TT14	chr4	4	q12	55011839	55024200	8	0	-0.847378	-0.847378	1.18E-22
1506-MCG_252152938959_S01	1145	TT14	chr4	4	q12	57842236	57856937	8	0	-0.727497	-0.727497	3.5E-17
1506-MCG_252152938959_S01	1155	TT14	chr4	4	q13.3	75021195	75029418	6	0	-0.89908	-0.89908	1.78E-18
1506-MCG_252152938959_S01	1156	TT14	chr4	4	q21.1	77044457	77049604	4	0	-0.922753	-0.922753	1.9E-14
1506-MCG_252152938959_S01	1161	TT14	chr4	4	q21.21	79470555	79473682	3	0	-1.375498	-1.375498	1.16E-22
1506-MCG_252152938959_S01	1162	TT14	chr4	4	q21.21	79693100	79701310	4	0	-0.784048	-0.784048	2.83E-12
1506-MCG_252152938959_S01	1164	TT14	chr4	4	q21.21	81106445	81130800	14	0	-0.570245	-0.570245	2.2E-18
1506-MCG_252152938959_S01	1169	TT14	chr4	4	q21.23	85413878	85417433	3	0	-1.461469	-1.461469	1.32E-19
1506-MCG_252152938959_S01	1170	TT14	chr4	4	q21.23	85500960	85508534	5	0	-0.660553	-0.660553	7.9E-10
1506-MCG_252152938959_S01	1171	TT14	chr4	4	q21.23	85885034	85888775	3	0	-1.235353	-1.235353	6.95E-18
1506-MCG_252152938959_S01	1172	TT14	chr4	4	q22.1	88135296	88145030	7	0	-0.777651	-0.777651	2.59E-17
1506-MCG_252152938959_S01	1173	TT14	chr4	4	q22.1	88782242	88786571	3	0	-1.056049	-1.056049	3.41E-14
1506-MCG_252152938959_S01	1174	TT14	chr4	4	q22.1	88928009	88932753	4	0	-1.218087	-1.218087	2.57E-22
1506-MCG_252152938959_S01	1214	TT14	chr4	4	q27	123732119	123753968	10	0	-0.841071	-0.841071	8.57E-28
1506-MCG_252152938959_S01	1215	TT14	chr4	4	q28.1	123935900	123940224	3	0	-1.140188	-1.140188	1.97E-15
1506-MCG_252152938959_S01	1218	TT14	chr4	4	q28.2	128965342	129008808	18	0	-0.512088	-0.512088	6.13E-18
1506-MCG_252152938959_S01	1223	TT14	chr4	4	q31.1	141071319	141076662	3	0	-1.03725	-1.03725	6.41E-14
1506-MCG_252152938959_S01	1226	TT14	chr4	4	q31.21	141673733	141684448	7	0	-0.741891	-0.741891	2.38E-15
1506-MCG_252152938959_S01	1231	TT14	chr4	4	q31.22	148277187	148281797	4	0	-0.946226	-0.946226	1.75E-16
1506-MCG_252152938959_S01	1232	TT14	chr4	4	q31.22	148399076	148403464	3	0	-0.816264	-0.816264	4.16E-10
1506-MCG_252152938959_S01	1233	TT14	chr4	4	q31.23	148648805	148657059	5	0	-0.743013	-0.743013	5.59E-13
1506-MCG_252152938959_S01	1235	TT14	chr4	4	q31.3	151873462	151883780	5	0	-0.687995	-0.687995	1.41E-11
1506-MCG_252152938959_S01	1236	TT14	chr4	4	q31.3	152131918	152177485	21	0	-0.423626	-0.423626	7.68E-17
1506-MCG_252152938959_S01	1253	TT14	chr4	4	q32.3	166296198	166303772	8	0	-1.080288	-1.080288	6.32E-36
1506-MCG_252152938959_S01	1254	TT14	chr4	4	q32.3	166793169	166797391	3	0	-1.031165	-1.031165	6.39E-13
1506-MCG_252152938959_S01	1255	TT14	chr4	4	q32.3	169797797	169805166	5	0	-0.990867	-0.990867	1.32E-19
1506-MCG_252152938959_S01	1256	TT14	chr4	4	q33	170190328	170196539	5	0	-0.993559	-0.993559	1.05E-16
1506-MCG_252152938959_S01	1260	TT14	chr4	4	q34.1	174087045	174108617	11	0	-0.942491	-0.942491	1.6E-37
1506-MCG_252152938959_S01	1262	TT14	chr4	4	q34.1	174440796	174459872	11	0	-0.679143	-0.679143	9.45E-17
1506-MCG_252152938959_S01	1263	TT14	chr4	4	q34.1	175142517	175149668	4	0	-0.863595	-0.863595	6.02E-13
1506-MCG_252152938959_S01	1264	TT14	chr4	4	q34.2	176984739	176990894	5	0	-1.116635	-1.116635	1.79E-23
1506-MCG_252152938959_S01	1265	TT14	chr4	4	q34.2	177239101	177242240	3	0	-1.251958	-1.251958	1.8E-18
1506-MCG_252152938959_S01	1272	TT14	chr4	4	q35.1	184576975	184582241	5	0	-1.152229	-1.152229	1.5E-23
1506-MCG_252152938959_S01	1276	TT14	chr4	4	q35.1	186123296	186132573	6	0	-1.10989	-1.10989	9.15E-28
1506-MCG_252152938959_S01	1279	TT14	chr4	4	q35.1 - q35.2	187009504	187118190	49	0	-0.459773	-0.459773	2.67E-35
1506-MCG_252152938959_S01	1280	TT14	chr4	4	q35.2	187470917	187479459	5	0	-1.035498	-1.035498	3.52E-21
1506-MCG_252152938959_S01	1281	TT14	chr4	4	q35.2	187642850	187648663	3	0	-1.376521	-1.376521	3.26E-20
1506-MCG_252152938959_S01	1284	TT14	chr5	5	p15.33	45617	1948661	616	0	-0.264588	-0.264588	5.99E-158
1506-MCG_252152938959_S01	1285	TT14	chr5	5	p15.33	309434	313372	3	0	-1.290454	-1.290454	2.48E-11
1506-MCG_252152938959_S01	1288	TT14	chr5	5	p15.33	2738432	2757388	10	0	-1.283214	-1.283214	5.39E-48
1506-MCG_252152938959_S01	1289	TT14	chr5	5	p15.33	3597876	3601272	3	0	-1.329329	-1.329329	7.84E-18
1506-MCG_252152938959_S01	1293	TT14	chr5	5	p15.2	10638335	10651533	8	0	-0.810109	-0.810109	2.35E-19
1506-MCG_252152938959_S01	1301	TT14	chr5	5	p15.1	16935014	16946049	6	0	-1.101134	-1.101134	1.42E-26
1506-MCG_252152938959_S01	1304	TT14	chr5	5	p15.1	17272953	17277955	4	0	-1.078343	-1.078343	4.22E-18
1506-MCG_252152938959_S01	1308	TT14	chr5	5	p13.3	32139156	32211469	33	0	-0.318746	-0.318746	2.49E-15
1506-MCG_252152938959_S01	1309	TT14	chr5	5	p13.3	32410942	32418017	6	0	-0.648855	-0.648855	4.36E-12
1506-MCG_252152938959_S01	1310	TT14	chr5	5	p13.3	32443236	32446625	3	0	-1.264931	-1.264931	2.53E-17
1506-MCG_252152938959_S01	1311	TT14	chr5	5	p13.3	33499362	33520712	11	0	-0.445438	-0.445438	1.02E-10
1506-MCG_252152938959_S01	1312	TT14	chr5	5	p13.2	34653491	34663779	6	0	-0.829335	-0.829335	2.24E-18
1506-MCG_252152938959_S01	1313	TT14	chr5	5	p13.2	34926929	34932061	4	0	-1.076848	-1.076848	1.13E-16
1506-MCG_252152938959_S01	1314	TT14	chr5	5	p13.2	37245326	37300710	19	0	-0.437164	-0.437164	5.32E-16
1506-MCG_252152938959_S01	1316	TT14	chr5	5	p13.1	38555754	38560170	3	0	-1.016518	-1.016518	3.55E-14
1506-MCG_252152938959_S01	1317	TT14	chr5	5	p13.1	38842699	38850725	6	0	-0.876545	-0.876545	3.76E-20
1506-MCG_252152938959_S01	1322	TT14	chr5	5	p13.1	42420146	42425896	5	0	-0.963156	-0.963156	3.17E-19
1506-MCG_252152938959_S01	1323	TT14	chr5	5	p12	43507604	43524292	7	0	-0.828872	-0.828872	3.13E-21
1506-MCG_252152938959_S01	1324	TT14	chr5	5	p12	43601049	43606578	4	0	-0.940893	-0.940893	4.44E-16
1506-MCG_252152938959_S01	1325	TT14	chr5	5	p12	45692999	45700416	5	0	-0.906906	-0.906906	1.8E-17
1506-MCG_252152938959_S01	1326	TT14	chr5	5	q11.1	50680528	50690001	7	0	-0.735563	-0.735563	4.1E-16
1506-MCG_252152938959_S01	1328	TT14	chr5	5	q11.2	53810919	53820374	5	0	-0.741612	-0.741612	6.38E-13
1506-MCG_252152938959_S01	1329	TT14	chr5	5	q11.2	54156688	54193568	10	0	-0.441721	-0.441721	9.5E-10
1506-MCG_252152938959_S01	1330	TT14	chr5	5	q11.2	54465378	54473374	12	0	-1.245439	-1.245439	7.5E-56
1506-MCG_252152938959_S01	1332	TT14	chr5	5	q11.2	55284032	55341020	29	0	-0.432203	-0.432203	1.83E-22
1506-MCG_252152938959_S01	1333	TT14	chr5	5	q11.2	56107595	56115746	5	0	-0.756147	-0.756147	1.77E-13
1506-MCG_252152938959_S01	1334	TT14	chr5	5	q11.2	56243770	56249458	3	0	-0.869655	-0.869655	6.81E-11
1506-MCG_252152938959_S01	1335	TT14	chr5	5	q11.2	56540984	56546883	5	0	-0.7661	-0.7661	1.01E-13
1506-MCG_252152938959_S01	1336	TT14	chr5	5	q11.2	58324649	58338989	7	0	-0.517341	-0.517341	1.89E-11
1506-MCG_252152938959_S01	1338	TT14	chr5	5	q12.1	60111219	60144338	14	0	-0.517086	-0.517086	1.32E-16
1506-MCG_252152938959_S01	1339	TT14	chr5	5	q12.3	63460981	63464467	3	0	-1.375414	-1.375414	6.75E-21
1506-MCG_252152938959_S01	1340	TT14	chr5	5	q12.3	64392234	64404541	6	0	-0.725308	-0.725308	1.02E-14
1506-MCG_252152938959_S01	1341	TT14	chr5	5	q12.3	65215015	65275451	29	0	-0.547237	-0.547237	1.14E-35
1506-MCG_252152938959_S01	1343	TT14	chr5	5	q12.3	66042530	66046071	3	0	-1.114652	-1.114652	2.5E-15
1506-MCG_252152938959_S01	1344	TT14	chr5	5	q13.1	67508101	67514146	4	0	-1.119681	-1.119681	5.26E-21
1506-MCG_252152938959_S01	1347	TT14	chr5	5	q13.2	70813405	70849943	16	0	-0.531949	-0.531949	4.4E-20
1506-MCG_252152938959_S01	1348	TT14	chr5	5	q13.2	71398860	71407094	5	0	-0.738079	-0.738079	6.21E-13
1506-MCG_252152938959_S01	1350	TT14	chr5	5	q13.2	72712633	72748668	15	0	-0.7794	-0.7794	1.99E-34
1506-MCG_252152938959_S01	1352	TT14	chr5	5	q13.3	75376946	75383162	5	0	-0.92021	-0.92021	4.74E-18
1506-MCG_252152938959_S01	1354	TT14	chr5	5	q13.3	76324796	76383268	28	0	-0.462332	-0.462332	1.32E-25
1506-MCG_252152938959_S01	1355	TT14	chr5	5	q14.1	76921797	76944403	13	0	-0.6534	-0.6534	1.73E-23
1506-MCG_252152938959_S01	1358	TT14	chr5	5	q14.1	78363042	78366553	3	0	-1.424052	-1.424052	9.21E-23
1506-MCG_252152938959_S01	1359	TT14	chr5	5	q14.1	78525943	78535164	7	0	-0.810459	-0.810459	5.98E-17
1506-MCG_252152938959_S01	1366	TT14	chr5	5	q14.1	80291943	80294293	3	0	-1.204217	-1.204217	5.27E-17
1506-MCG_252152938959_S01	1367	TT14	chr5	5	q14.1	80726565	80729661	3	0	-1.376056	-1.376056	9.5E-21
1506-MCG_252152938959_S01	1368	TT14	chr5	5	q14.1	81264022	81283919	11	0	-0.694602	-0.694602	5.84E-23
1506-MCG_252152938959_S01	1369	TT14	chr5	5	q14.3	83016598	83022603	4	0	-0.749279	-0.749279	9.49E-11
1506-MCG_252152938959_S01	1370	TT14	chr5	5	q14.3	83602324	83611384	6	0	-0.843124	-0.843124	1.68E-18
1506-MCG_252152938959_S01	1372	TT14	chr5	5	q14.3	87953363	87978049	32	0	-0.770162	-0.770162	5.16E-72
1506-MCG_252152938959_S01	1373	TT14	chr5	5	q14.3	87968374	87973133	7	0	-1.435913	-1.435913	2.06E-11
1506-MCG_252152938959_S01	1375	TT14	chr5	5	q14.3	89889913	89895542	3	0	-0.958718	-0.958718	6.62E-13
1506-MCG_252152938959_S01	1376	TT14	chr5	5	q14.3	90674208	90679698	5	0	-1.205464	-1.205464	2.48E-28
1506-MCG_252152938959_S01	1377	TT14	chr5	5	q15	92911737	92959492	27	0	-0.581157	-0.581157	1.21E-33
1506-MCG_252152938959_S01	1381	TT14	chr5	5	q15	96142747	96145530	3	0	-1.275925	-1.275925	2.81E-20
1506-MCG_252152938959_S01	1385	TT14	chr5	5	q21.3	107004043	107010185	5	0	-1.053193	-1.053193	2.58E-19
1506-MCG_252152938959_S01	1394	TT14	chr5	5	q22.3	114872274	114973740	48	0	-0.326278	-0.326278	5.61E-22
1506-MCG_252152938959_S01	1395	TT14	chr5	5	q23.1	117797077	117803119	3	0	-0.910255	-0.910255	1.44E-11
1506-MCG_252152938959_S01	1396	TT14	chr5	5	q23.1	118298734	118326831	17	0	-0.838428	-0.838428	1.67E-45
1506-MCG_252152938959_S01	1397	TT14	chr5	5	q23.1	118690066	118692451	3	0	-1.54505	-1.54505	1.2E-24

1506-MCG_252152938959_S01	1398	TT14	chr5	5	q23.1	119794955	119804374	7	0	-0.697062	-0.697062	1.22E-13
1506-MCG_252152938959_S01	1399	TT14	chr5	5	q23.1	121183533	121196914	6	0	-0.997054	-0.997054	1.35E-24
1506-MCG_252152938959_S01	1400	TT14	chr5	5	q23.2	122108822	122114532	4	0	-1.097705	-1.097705	6.62E-20
1506-MCG_252152938959_S01	1401	TT14	chr5	5	q23.2	122178937	122182302	3	0	-1.455198	-1.455198	2.53E-24
1506-MCG_252152938959_S01	1402	TT14	chr5	5	q23.2	122427356	122436216	6	0	-0.8823	-0.8823	7.46E-20
1506-MCG_252152938959_S01	1403	TT14	chr5	5	q23.2	122759805	122770927	8	0	-0.904231	-0.904231	4.67E-27
1506-MCG_252152938959_S01	1415	TT14	chr5	5	q31.1	132147370	132167361	12	0	-0.978625	-0.978625	6.9E-40
1506-MCG_252152938959_S01	1434	TT14	chr5	5	q31.3	140166702	140812764	290	0	-0.317386	-0.317386	4.03E-118
1506-MCG_252152938959_S01	1435	TT14	chr5	5	q31.3	140177147	140266130	41	0	-0.616551	-0.616551	2.39E-16
1506-MCG_252152938959_S01	1444	TT14	chr5	5	q32	148729875	148760008	17	0	-0.389055	-0.389055	9.77E-14
1506-MCG_252152938959_S01	1450	TT14	chr5	5	q33.1	151144629	151156842	7	0	-0.62603	-0.62603	4.9E-14
1506-MCG_252152938959_S01	1454	TT14	chr5	5	q33.3	158520795	158554913	15	0	-0.622694	-0.622694	8.55E-27
1506-MCG_252152938959_S01	1463	TT14	chr5	5	q34	167953640	167958053	3	0	-1.278045	-1.278045	1.16E-18
1506-MCG_252152938959_S01	1464	TT14	chr5	5	q34	168000172	168007587	7	0	-0.752431	-0.752431	7.87E-18
1506-MCG_252152938959_S01	1465	TT14	chr5	5	q35.1	168724414	168729665	4	0	-0.96293	-0.96293	5.79E-18
1506-MCG_252152938959_S01	1466	TT14	chr5	5	q35.1	169062968	169068518	4	0	-0.723079	-0.723079	7.36E-11
1506-MCG_252152938959_S01	1467	TT14	chr5	5	q35.1	170285925	170290520	4	0	-0.900546	-0.900546	1.71E-13
1506-MCG_252152938959_S01	1468	TT14	chr5	5	q35.1	170827317	170847859	12	0	-0.537347	-0.537347	2.34E-15
1506-MCG_252152938959_S01	1486	TT14	chr5	5	q35.3	176982148	176987870	3	0	-1.519604	-1.519604	2.7E-21
1506-MCG_252152938959_S01	1496	TT14	chr5	5	q35.3	180478261	180487643	5	0	-1.183459	-1.183459	3.71E-22
1506-MCG_252152938959_S01	1499	TT14	chr6	6	p25.3	387608	461482	34	0	-0.325525	-0.325525	2.49E-15
1506-MCG_252152938959_S01	1500	TT14	chr6	6	p25.3	652471	657439	3	0	-1.207536	-1.207536	4.2E-18
1506-MCG_252152938959_S01	1501	TT14	chr6	6	p25.3	1311530	1318307	3	0	-1.196701	-1.196701	1.2E-17
1506-MCG_252152938959_S01	1504	TT14	chr6	6	p25.3	1603954	1624100	10	0	-1.255684	-1.255684	2.19E-50
1506-MCG_252152938959_S01	1505	TT14	chr6	6	p25.3	2242163	2249090	5	0	-1.02188	-1.02188	9.86E-22
1506-MCG_252152938959_S01	1506	TT14	chr6	6	p25.2	2762512	2768246	4	0	-1.099533	-1.099533	6.09E-20
1506-MCG_252152938959_S01	1507	TT14	chr6	6	p25.2	2869134	2877040	4	0	-1.066383	-1.066383	6.72E-10
1506-MCG_252152938959_S01	1513	TT14	chr6	6	p25.2	3749197	3775130	12	0	-0.981755	-0.981755	8.42E-44
1506-MCG_252152938959_S01	1516	TT14	chr6	6	p25.1	4770869	4779865	6	0	-0.737662	-0.737662	1.64E-14
1506-MCG_252152938959_S01	1517	TT14	chr6	6	p25.1	5084065	5089074	3	0	-1.145185	-1.145185	5.08E-16
1506-MCG_252152938959_S01	1518	TT14	chr6	6	p25.1	6603577	6618597	6	0	-0.911297	-0.911297	8.71E-21
1506-MCG_252152938959_S01	1520	TT14	chr6	6	p24.3	7137753	7144737	6	0	-0.818184	-0.818184	2.24E-16
1506-MCG_252152938959_S01	1524	TT14	chr6	6	p24.3	10379830	10499332	57	0	-0.396426	-0.396426	2.73E-37
1506-MCG_252152938959_S01	1525	TT14	chr6	6	p24.3	10400666	10415952	8	0	-0.948636	-0.948636	4.71E-11
1506-MCG_252152938959_S01	1526	TT14	chr6	6	p24.3	10484127	10491031	4	0	-1.562879	-1.562879	2.4E-20
1506-MCG_252152938959_S01	1527	TT14	chr6	6	p24.2	11041650	11047118	4	0	-0.996307	-0.996307	1.59E-16
1506-MCG_252152938959_S01	1528	TT14	chr6	6	p24.2	11086580	11098331	7	0	-1.03849	-1.03849	7.36E-30
1506-MCG_252152938959_S01	1530	TT14	chr6	6	p24.1	12008097	12015884	5	0	-1.295232	-1.295232	9.1E-27
1506-MCG_252152938959_S01	1535	TT14	chr6	6	p23	13810823	13815309	3	0	-1.417871	-1.417871	1.05E-21
1506-MCG_252152938959_S01	1538	TT14	chr6	6	p22.3	15244447	15250079	4	0	-1.315107	-1.315107	1.99E-26
1506-MCG_252152938959_S01	1543	TT14	chr6	6	p22.3	17199142	17208964	5	0	-1.083291	-1.083291	6.74E-24
1506-MCG_252152938959_S01	1545	TT14	chr6	6	p22.3	17597931	17603252	4	0	-1.13101	-1.13101	5.5E-20
1506-MCG_252152938959_S01	1546	TT14	chr6	6	p22.3	17728000	17730704	3	0	-1.326261	-1.326261	6.89E-21
1506-MCG_252152938959_S01	1549	TT14	chr6	6	p22.3	18260047	18267148	4	0	-1.128297	-1.128297	1.11E-19
1506-MCG_252152938959_S01	1550	TT14	chr6	6	p22.3	19835409	19856347	13	0	-0.661987	-0.661987	4.54E-23
1506-MCG_252152938959_S01	1552	TT14	chr6	6	p22.3	20401064	20407436	4	0	-0.95115	-0.95115	5.29E-15
1506-MCG_252152938959_S01	1553	TT14	chr6	6	p22.3	21587759	21610977	12	0	-0.580758	-0.580758	2.82E-17
1506-MCG_252152938959_S01	1561	TT14	chr6	6	p22.1	28431359	28486657	29	0	-0.488283	-0.488283	4.84E-29
1506-MCG_252152938959_S01	1562	TT14	chr6	6	p22.1	28980549	28984750	3	0	-1.260134	-1.260134	2.5E-13
1506-MCG_252152938959_S01	1572	TT14	chr6	6	p21.31	34186940	34240127	16	0	-0.514419	-0.514419	9.74E-18
1506-MCG_252152938959_S01	1575	TT14	chr6	6	p21.31	35285310	35288210	3	0	-1.377849	-1.377849	9.48E-21
1506-MCG_252152938959_S01	1576	TT14	chr6	6	p21.31	35886756	35890624	3	0	-1.231729	-1.231729	1.03E-18
1506-MCG_252152938959_S01	1579	TT14	chr6	6	p21.2	36625325	36652374	16	0	-0.369461	-0.369461	1.86E-10
1506-MCG_252152938959_S01	1580	TT14	chr6	6	p21.2	36904038	36927933	13	0	-0.432624	-0.432624	2.15E-11
1506-MCG_252152938959_S01	1581	TT14	chr6	6	p21.2	37785349	37791957	4	0	-0.789196	-0.789196	7.31E-12
1506-MCG_252152938959_S01	1582	TT14	chr6	6	p21.2	38603682	38612022	5	0	-0.729572	-0.729572	1.18E-12
1506-MCG_252152938959_S01	1583	TT14	chr6	6	p21.2	38929229	38933631	3	0	-1.091441	-1.091441	1.11E-15
1506-MCG_252152938959_S01	1585	TT14	chr6	6	p21.1	41737017	41781081	18	0	-0.584583	-0.584583	1.47E-25
1506-MCG_252152938959_S01	1586	TT14	chr6	6	p21.1	42650890	42658774	5	0	-0.729202	-0.729202	4.05E-12
1506-MCG_252152938959_S01	1594	TT14	chr6	6	p21.1	44183964	44245449	31	0	-0.458119	-0.458119	6.68E-26
1506-MCG_252152938959_S01	1596	TT14	chr6	6	p12.3	46456278	46460312	3	0	-1.165753	-1.165753	1.93E-16
1506-MCG_252152938959_S01	1597	TT14	chr6	6	p12.3	50767598	50825881	29	0	-0.43034	-0.43034	2E-19
1506-MCG_252152938959_S01	1598	TT14	chr6	6	p12.2	51841829	51851568	6	0	-0.608385	-0.608385	9.96E-10
1506-MCG_252152938959_S01	1599	TT14	chr6	6	p12.2	52439533	52443077	3	0	-0.937341	-0.937341	4.1E-10
1506-MCG_252152938959_S01	1601	TT14	chr6	6	p12.1	53168261	53175648	4	0	-0.902228	-0.902228	4.63E-13
1506-MCG_252152938959_S01	1602	TT14	chr6	6	p12.1	53211616	53226675	7	0	-0.800993	-0.800993	2.2E-18
1506-MCG_252152938959_S01	1603	TT14	chr6	6	p12.1	53408502	53412457	3	0	-0.98589	-0.98589	4.8E-12
1506-MCG_252152938959_S01	1604	TT14	chr6	6	p12.1	56295328	56298852	3	0	-1.152952	-1.152952	2.65E-15
1506-MCG_252152938959_S01	1605	TT14	chr6	6	p12.1	56584355	56589411	3	0	-1.203508	-1.203508	7.85E-17
1506-MCG_252152938959_S01	1606	TT14	chr6	6	q12	63917839	63926079	5	0	-0.847076	-0.847076	1.23E-14
1506-MCG_252152938959_S01	1607	TT14	chr6	6	q12	64280499	64289326	5	0	-0.86549	-0.86549	1.64E-15
1506-MCG_252152938959_S01	1608	TT14	chr6	6	q12	64343817	64351910	5	0	-0.865907	-0.865907	2.12E-15
1506-MCG_252152938959_S01	1609	TT14	chr6	6	q12	69341048	69348865	5	0	-0.948983	-0.948983	2.97E-18
1506-MCG_252152938959_S01	1610	TT14	chr6	6	q12	69827579	69838112	6	0	-0.750784	-0.750784	3.44E-14
1506-MCG_252152938959_S01	1611	TT14	chr6	6	q13	72126810	72140912	14	0	-0.534835	-0.534835	5.74E-16
1506-MCG_252152938959_S01	1612	TT14	chr6	6	q13	72890425	72893122	3	0	-1.47838	-1.47838	2.37E-23
1506-MCG_252152938959_S01	1615	TT14	chr6	6	q13	74362784	74372012	5	0	-1.30988	-1.30988	3.04E-28
1506-MCG_252152938959_S01	1616	TT14	chr6	6	q14.1	76310651	76314033	3	0	-1.019745	-1.019745	4.65E-13
1506-MCG_252152938959_S01	1617	TT14	chr6	6	q14.1	79784507	79789852	4	0	-0.898601	-0.898601	9.42E-14
1506-MCG_252152938959_S01	1618	TT14	chr6	6	q14.1	83772440	83780433	6	0	-0.855817	-0.855817	5.97E-18
1506-MCG_252152938959_S01	1622	TT14	chr6	6	q14.2	84741538	84745997	4	0	-1.327973	-1.327973	6.45E-24
1506-MCG_252152938959_S01	1633	TT14	chr6	6	q15	89853054	89859086	4	0	-1.145754	-1.145754	6.72E-21
1506-MCG_252152938959_S01	1634	TT14	chr6	6	q15	90045242	90063827	11	0	-0.724941	-0.724941	2.67E-21
1506-MCG_252152938959_S01	1636	TT14	chr6	6	q16.1	96024828	96028291	3	0	-1.148406	-1.148406	2.34E-16
1506-MCG_252152938959_S01	1637	TT14	chr6	6	q16.1	97367158	97376537	5	0	-0.745323	-0.745323	5.04E-12
1506-MCG_252152938959_S01	1638	TT14	chr6	6	q16.1	99280026	99295600	8	0	-0.950604	-0.950604	3.3E-24
1506-MCG_252152938959_S01	1639	TT14	chr6	6	q16.2	100057323	100066112	5	0	-0.829268	-0.829268	1.19E-14
1506-MCG_252152938959_S01	1645	TT14	chr6	6	q21	108274071	108278822	4	0	-1.545077	-1.545077	9.15E-31
1506-MCG_252152938959_S01	1651	TT14	chr6	6	q21	109801874	109809468	5	0	-1.044073	-1.044073	2.79E-21
1506-MCG_252152938959_S01	1652	TT14	chr6	6	q21	110677214	110681221	4	0	-1.058196	-1.058196	1.88E-18
1506-MCG_252152938959_S01	1654	TT14	chr6	6	q21	113525064	113529818	3	0	-1.07986	-1.07986	2.63E-15
1506-MCG_252152938959_S01	1655	TT14	chr6	6	q21	114177937	114181892	3	0	-1.455421	-1.455421	8.46E-23
1506-MCG_252152938959_S01	1661	TT14	chr6	6	q22.31	122002043	122012450	6	0	-0.875788	-0.875788	5.36E-18
1506-MCG_252152938959_S01	1662	TT14	chr6	6	q22.31	122719659	122723660	3	0	-1.11875	-1.11875	5.38E-15
1506-MCG_252152938959_S01	1663	TT14	chr6	6	q22.31	122927982	122932983	4	0	-0.775522	-0.775522	2.53E-10
1506-MCG_252152938959_S01	1664	TT14	chr6	6	q22.31 - q22.32	126066399	126113502	23	0	-0.621213	-0.621213	8.03E-36

1506-MCG_252152938959_S01	1670	TT14	chr6	6	q23.2	131379367	131389064	6	0	-0.816442	-0.816442	1.03E-17
1506-MCG_252152938959_S01	1672	TT14	chr6	6	q23.2	132125744	132133594	5	0	-0.676783	-0.676783	4.05E-11
1506-MCG_252152938959_S01	1673	TT14	chr6	6	q23.2	132264857	132273629	6	0	-0.853776	-0.853776	1.19E-18
1506-MCG_252152938959_S01	1679	TT14	chr6	6	q23.3	136869023	136872607	3	0	-1.506479	-1.506479	3.91E-25
1506-MCG_252152938959_S01	1683	TT14	chr6	6	q23.3	138425846	138430669	4	0	-1.453573	-1.453573	4.56E-31
1506-MCG_252152938959_S01	1705	TT14	chr6	6	q25.3	157467930	158103570	90	0	-0.253306	-0.253306	5.24E-24
1506-MCG_252152938959_S01	1706	TT14	chr6	6	q25.3	157554732	157558894	5	0	-1.059838	-1.059838	1.46E-13
1506-MCG_252152938959_S01	1710	TT14	chr6	6	q25.3	160387669	160392521	4	0	-1.073154	-1.073154	3.52E-18
1506-MCG_252152938959_S01	1713	TT14	chr6	6	q26	162758137	162765311	4	0	-0.91254	-0.91254	1.25E-14
1506-MCG_252152938959_S01	1714	TT14	chr6	6	q26	163004719	163007764	3	0	-1.270366	-1.270366	2.3E-19
1506-MCG_252152938959_S01	1715	TT14	chr6	6	q27	166795249	166819327	13	0	-0.898226	-0.898226	2.67E-31
1506-MCG_252152938959_S01	1722	TT14	chr6	6	q27	169612742	169634766	12	0	-0.611234	-0.611234	1.64E-13
1506-MCG_252152938959_S01	1723	TT14	chr6	6	q27	170059093	170069353	7	0	-0.982071	-0.982071	1.1E-21
1506-MCG_252152938959_S01	1727	TT14	chr6	6	q27	170593154	170606636	7	0	-1.174225	-1.174225	4.38E-26
1506-MCG_252152938959_S01	1729	TT14	chr7	7	p22.3	149637	2699174	835	0	-0.279314	-0.279314	3.09E-231
1506-MCG_252152938959_S01	1730	TT14	chr7	7	p22.3	914213	1136767	105	0	-0.54695	-0.54695	3.89E-27
1506-MCG_252152938959_S01	1731	TT14	chr7	7	p22.3	1081110	1084900	5	0	-1.522431	-1.522431	4.99E-16
1506-MCG_252152938959_S01	1733	TT14	chr7	7	p22.3	1511244	1545943	12	0	-0.927071	-0.927071	2.55E-16
1506-MCG_252152938959_S01	1737	TT14	chr7	7	p22.3	2616473	2623881	5	0	-1.321258	-1.321258	2.9E-20
1506-MCG_252152938959_S01	1741	TT14	chr7	7	p22.1	6193292	6196520	3	0	-1.544078	-1.544078	2.7E-24
1506-MCG_252152938959_S01	1743	TT14	chr7	7	p22.1	6520530	6714612	83	0	-0.40694	-0.40694	1.3E-50
1506-MCG_252152938959_S01	1744	TT14	chr7	7	p22.1	6701900	6713163	5	0	-1.08886	-1.08886	1.58E-10
1506-MCG_252152938959_S01	1760	TT14	chr7	7	p21.1	20815539	20840703	13	0	-0.987022	-0.987022	5.41E-46
1506-MCG_252152938959_S01	1762	TT14	chr7	7	p15.3	22394702	22397913	3	0	-1.114282	-1.114282	1.03E-15
1506-MCG_252152938959_S01	1765	TT14	chr7	7	p15.3	23506574	23532939	13	0	-0.621093	-0.621093	1.09E-20
1506-MCG_252152938959_S01	1770	TT14	chr7	7	p15.2	26329288	26333612	4	0	-1.084367	-1.084367	7.01E-20
1506-MCG_252152938959_S01	1771	TT14	chr7	7	p15.2	26409579	26440233	18	0	-0.469782	-0.469782	4.67E-17
1506-MCG_252152938959_S01	1772	TT14	chr7	7	p15.2	27135496	27292752	113	0	-0.775877	-0.775877	2.62E-246
1506-MCG_252152938959_S01	1773	TT14	chr7	7	p15.2	27139893	27156158	10	0	-1.371688	-1.371688	6.58E-14
1506-MCG_252152938959_S01	1799	TT14	chr7	7	p14.1	37482996	37489118	4	0	-0.740862	-0.740862	9.02E-11
1506-MCG_252152938959_S01	1801	TT14	chr7	7	p14.1	39644075	39672106	14	0	-0.495357	-0.495357	2.54E-15
1506-MCG_252152938959_S01	1802	TT14	chr7	7	p14.1	39869979	39876354	4	0	-0.795882	-0.795882	6.15E-12
1506-MCG_252152938959_S01	1804	TT14	chr7	7	p14.1	42265337	42279753	8	0	-0.643311	-0.643311	9.67E-15
1506-MCG_252152938959_S01	1805	TT14	chr7	7	p14.1	42944511	42956576	7	0	-0.666521	-0.666521	5.59E-14
1506-MCG_252152938959_S01	1807	TT14	chr7	7	p13	43620995	43626154	5	0	-0.744205	-0.744205	3.09E-12
1506-MCG_252152938959_S01	1808	TT14	chr7	7	p13	43796266	43799448	3	0	-1.117684	-1.117684	2.6E-15
1506-MCG_252152938959_S01	1810	TT14	chr7	7	p13	44645253	44647078	3	0	-1.122664	-1.122664	7.7E-16
1506-MCG_252152938959_S01	1813	TT14	chr7	7	p13	45027696	45040773	7	0	-1.207236	-1.207236	5.49E-39
1506-MCG_252152938959_S01	1814	TT14	chr7	7	p13	45126223	45129550	3	0	-1.08213	-1.08213	1.01E-14
1506-MCG_252152938959_S01	1816	TT14	chr7	7	p12.3	47574280	47580917	5	0	-0.947638	-0.947638	1.88E-17
1506-MCG_252152938959_S01	1817	TT14	chr7	7	p12.3	48240144	48256856	4	0	-0.953217	-0.953217	3.97E-16
1506-MCG_252152938959_S01	1818	TT14	chr7	7	p12.2	49811104	49816304	4	0	-1.437906	-1.437906	2.01E-23
1506-MCG_252152938959_S01	1821	TT14	chr7	7	p12.1	50846702	50865598	8	0	-0.809296	-0.809296	1.72E-22
1506-MCG_252152938959_S01	1822	TT14	chr7	7	p11.2	54607096	54617116	6	0	-0.866397	-0.866397	1.74E-16
1506-MCG_252152938959_S01	1824	TT14	chr7	7	p11.2	55069326	55090640	11	0	-0.816431	-0.816431	2.52E-28
1506-MCG_252152938959_S01	1842	TT14	chr7	7	q11.23	73587101	73590414	4	0	-1.210803	-1.210803	4.53E-24
1506-MCG_252152938959_S01	1846	TT14	chr7	7	q11.23	76021037	76023473	3	0	-1.392857	-1.392857	1.1E-20
1506-MCG_252152938959_S01	1847	TT14	chr7	7	q21.11	77646120	77652021	4	0	-0.901086	-0.901086	4.38E-13
1506-MCG_252152938959_S01	1848	TT14	chr7	7	q21.11	78126799	78135194	7	0	-0.647696	-0.647696	5.64E-12
1506-MCG_252152938959_S01	1850	TT14	chr7	7	q21.11	80528296	80560088	15	0	-0.488409	-0.488409	5.68E-14
1506-MCG_252152938959_S01	1852	TT14	chr7	7	q21.11	82066351	82078458	6	0	-0.656706	-0.656706	4.91E-11
1506-MCG_252152938959_S01	1854	TT14	chr7	7	q21.12	86686005	86689763	3	0	-1.262705	-1.262705	1.71E-18
1506-MCG_252152938959_S01	1855	TT14	chr7	7	q21.12	87102114	87108002	4	0	-0.880224	-0.880224	2.84E-13
1506-MCG_252152938959_S01	1856	TT14	chr7	7	q21.12	87504541	87508778	3	0	-0.97704	-0.97704	1.94E-12
1506-MCG_252152938959_S01	1857	TT14	chr7	7	q21.12	87846664	87852548	4	0	-0.901294	-0.901294	3.61E-12
1506-MCG_252152938959_S01	1858	TT14	chr7	7	q21.13	89946163	89962227	8	0	-0.778534	-0.778534	4.91E-19
1506-MCG_252152938959_S01	1860	TT14	chr7	7	q21.13	90370668	90378462	5	0	-1.023883	-1.023883	6.45E-20
1506-MCG_252152938959_S01	1861	TT14	chr7	7	q21.13	90522864	90526938	3	0	-1.133612	-1.133612	1.05E-15
1506-MCG_252152938959_S01	1867	TT14	chr7	7	q21.3	94533676	94539262	5	0	-1.1631	-1.1631	1.33E-25
1506-MCG_252152938959_S01	1870	TT14	chr7	7	q21.3	96620885	96670770	26	0	-0.351849	-0.351849	7.06E-12
1506-MCG_252152938959_S01	1882	TT14	chr7	7	q22.1	100731956	100737545	4	0	-1.272992	-1.272992	1.12E-25
1506-MCG_252152938959_S01	1884	TT14	chr7	7	q22.1	101455968	101463679	5	0	-0.937126	-0.937126	2.53E-18
1506-MCG_252152938959_S01	1886	TT14	chr7	7	q22.1	102067584	102335349	27	0	-0.426353	-0.426353	3.24E-20
1506-MCG_252152938959_S01	1889	TT14	chr7	7	q22.1	103084879	103088371	3	0	-1.006111	-1.006111	1.58E-12
1506-MCG_252152938959_S01	1890	TT14	chr7	7	q22.3	104612114	104616270	3	0	-0.971944	-0.971944	4.26E-13
1506-MCG_252152938959_S01	1911	TT14	chr7	7	q31.31	119908549	119918581	6	0	-0.984598	-0.984598	3.56E-24
1506-MCG_252152938959_S01	1912	TT14	chr7	7	q31.31	120494708	120501450	4	0	-0.799816	-0.799816	2.88E-12
1506-MCG_252152938959_S01	1913	TT14	chr7	7	q31.31	120697669	120704361	4	0	-0.832814	-0.832814	9.85E-13
1506-MCG_252152938959_S01	1914	TT14	chr7	7	q31.32	121508967	121515071	4	0	-0.98736	-0.98736	1.62E-16
1506-MCG_252152938959_S01	1916	TT14	chr7	7	q31.32	121938571	121952771	9	0	-0.837851	-0.837851	3.39E-26
1506-MCG_252152938959_S01	1918	TT14	chr7	7	q31.32	123275700	123284089	6	0	-0.941306	-0.941306	5.72E-23
1506-MCG_252152938959_S01	1920	TT14	chr7	7	q31.32	123667122	123674617	5	0	-0.777944	-0.777944	1.22E-13
1506-MCG_252152938959_S01	1927	TT14	chr7	7	q32.1	128756558	128871921	56	0	-0.289501	-0.289501	2.04E-20
1506-MCG_252152938959_S01	1933	TT14	chr7	7	q32.2	130127134	130134249	10	0	-0.995885	-0.995885	2.45E-37
1506-MCG_252152938959_S01	1955	TT14	chr7	7	q34	142551520	142555932	3	0	-0.957	-0.957	4.88E-13
1506-MCG_252152938959_S01	1957	TT14	chr7	7	q35	143592785	143601429	5	0	-0.648231	-0.648231	2.97E-10
1506-MCG_252152938959_S01	1958	TT14	chr7	7	q35	144096806	144103191	5	0	-1.038181	-1.038181	2.2E-19
1506-MCG_252152938959_S01	1959	TT14	chr7	7	q35	144525891	144534728	6	0	-0.644471	-0.644471	4.97E-10
1506-MCG_252152938959_S01	1960	TT14	chr7	7	q35	145393053	145397672	4	0	-1.118126	-1.118126	7.46E-18
1506-MCG_252152938959_S01	1961	TT14	chr7	7	q35	145811624	145820353	6	0	-0.825833	-0.825833	2.77E-13
1506-MCG_252152938959_S01	1963	TT14	chr7	7	q35	146719184	146727503	5	0	-0.837031	-0.837031	1.66E-12
1506-MCG_252152938959_S01	1964	TT14	chr7	7	q35	147498198	147502097	3	0	-0.917165	-0.917165	1.99E-11
1506-MCG_252152938959_S01	1965	TT14	chr7	7	q36.1	148394712	148400324	4	0	-0.869369	-0.869369	5.76E-14
1506-MCG_252152938959_S01	1972	TT14	chr7	7	q36.1	150066573	150106229	19	0	-0.838507	-0.838507	2.1E-37
1506-MCG_252152938959_S01	1978	TT14	chr7	7	q36.1	151566488	151577426	7	0	-0.670143	-0.670143	3.2E-13
1506-MCG_252152938959_S01	1979	TT14	chr7	7	q36.1	151719755	151723323	3	0	-1.199748	-1.199748	1.46E-17
1506-MCG_252152938959_S01	1983	TT14	chr7	7	q36.3	155138022	155145717	4	0	-1.207411	-1.207411	1.27E-17
1506-MCG_252152938959_S01	1984	TT14	chr7	7	q36.3	155161696	155172050	7	0	-1.3024	-1.3024	1.53E-33
1506-MCG_252152938959_S01	1985	TT14	chr7	7	q36.3	155434904	155440625	4	0	-0.967639	-0.967639	1.38E-13
1506-MCG_252152938959_S01	1987	TT14	chr7	7	q36.3	155637907	155644057	4	0	-0.817798	-0.817798	6.61E-10
1506-MCG_252152938959_S01	1990	TT14	chr7	7	q36.3	156791205	156812476	12	0	-1.126482	-1.126482	9.46E-34
1506-MCG_252152938959_S01	1992	TT14	chr7	7	q36.3	157197628	157709199	267	0	-0.28993	-0.28993	1.46E-37
1506-MCG_252152938959_S01	1993	TT14	chr7	7	q36.3	157201751	157205965	4	0	-1.091402	-1.091402	8.98E-10
1506-MCG_252152938959_S01	1995	TT14	chr7	7	q36.3	158096063	158116271	11	0	-0.556548	-0.556548	7.84E-11
1506-MCG_252152938959_S01	1996	TT14	chr7	7	q36.3	158188970	158201521	8	0	-0.90061	-0.90061	4.31E-21
1506-MCG_252152938959_S01	2004	TT14	chr8	8	p23.3	1921265	1953478	16	0	-0.75172	-0.75172	2.14E-17

1506-MCG_252152938959_S01	2009	TT14	chr8	8	p23.1	10580900	10595443	11	0	-0.642945	-0.642945	2.02E-18
1506-MCG_252152938959_S01	2010	TT14	chr8	8	p23.1	10915544	10919887	5	0	-0.923201	-0.923201	3.84E-15
1506-MCG_252152938959_S01	2016	TT14	chr8	8	p22	16854413	16890198	18	0	-0.549015	-0.549015	7.23E-18
1506-MCG_252152938959_S01	2019	TT14	chr8	8	p22	17352781	17355718	3	0	-1.661035	-1.661035	1.3E-23
1506-MCG_252152938959_S01	2020	TT14	chr8	8	p22	18868138	18873560	4	0	-1.014077	-1.014077	1.16E-17
1506-MCG_252152938959_S01	2021	TT14	chr8	8	p21.3	19168125	19177078	5	0	-0.818136	-0.818136	3.01E-15
1506-MCG_252152938959_S01	2023	TT14	chr8	8	p21.3	20159098	20163390	3	0	-0.963599	-0.963599	1.38E-12
1506-MCG_252152938959_S01	2024	TT14	chr8	8	p21.3	21916834	22036147	59	0	-0.312357	-0.312357	3.73E-21
1506-MCG_252152938959_S01	2037	TT14	chr8	8	p12	29938907	29954567	7	0	-1.349593	-1.349593	2.08E-44
1506-MCG_252152938959_S01	2038	TT14	chr8	8	p12	30239046	30247708	5	0	-0.696657	-0.696657	1.01E-11
1506-MCG_252152938959_S01	2039	TT14	chr8	8	p12	30513039	30518129	5	0	-1.046798	-1.046798	1.68E-22
1506-MCG_252152938959_S01	2041	TT14	chr8	8	p12	31495506	31512647	10	0	-0.939661	-0.939661	1.93E-34
1506-MCG_252152938959_S01	2042	TT14	chr8	8	p12	32401414	32412980	7	0	-0.71192	-0.71192	5.96E-16
1506-MCG_252152938959_S01	2043	TT14	chr8	8	p12	35084744	35101647	9	0	-0.555632	-0.555632	3.95E-13
1506-MCG_252152938959_S01	2048	TT14	chr8	8	p11.23	38123342	38128510	5	0	-1.110645	-1.110645	2.41E-25
1506-MCG_252152938959_S01	2050	TT14	chr8	8	p11.22	39193880	39203326	4	0	-1.1388	-1.1388	5.88E-20
1506-MCG_252152938959_S01	2054	TT14	chr8	8	p11.21	41731809	41740183	5	0	-0.727737	-0.727737	5.6E-12
1506-MCG_252152938959_S01	2069	TT14	chr8	8	q11.23	54789131	54791460	3	0	-1.302689	-1.302689	2.72E-19
1506-MCG_252152938959_S01	2070	TT14	chr8	8	q11.23	55011393	55042202	10	0	-0.789044	-0.789044	3.72E-24
1506-MCG_252152938959_S01	2071	TT14	chr8	8	q11.23	55367633	55383329	8	0	-1.033408	-1.033408	2.65E-27
1506-MCG_252152938959_S01	2087	TT14	chr8	8	q12.3	65280685	65290626	13	0	-0.757514	-0.757514	5.85E-25
1506-MCG_252152938959_S01	2088	TT14	chr8	8	q12.3	65490280	65496706	4	0	-0.896608	-0.896608	1.24E-13
1506-MCG_252152938959_S01	2089	TT14	chr8	8	q12.3	65594981	65604143	5	0	-0.709794	-0.709794	4.64E-11
1506-MCG_252152938959_S01	2090	TT14	chr8	8	q12.3	65704915	65714535	7	0	-0.721266	-0.721266	1.42E-14
1506-MCG_252152938959_S01	2091	TT14	chr8	8	q13.1	66752290	66756892	4	0	-1.200111	-1.200111	2.22E-21
1506-MCG_252152938959_S01	2093	TT14	chr8	8	q13.1	67623906	67627238	3	0	-1.486922	-1.486922	8.68E-23
1506-MCG_252152938959_S01	2102	TT14	chr8	8	q21.11	74194963	74211900	8	0	-0.790971	-0.790971	2.31E-19
1506-MCG_252152938959_S01	2103	TT14	chr8	8	q21.11	74658030	74662906	3	0	-0.949233	-0.949233	2.55E-10
1506-MCG_252152938959_S01	2104	TT14	chr8	8	q21.11	74883715	74891044	5	0	-0.999472	-0.999472	2.55E-18
1506-MCG_252152938959_S01	2105	TT14	chr8	8	q21.11	75224306	75232517	5	0	-1.073986	-1.073986	5.57E-20
1506-MCG_252152938959_S01	2106	TT14	chr8	8	q21.11	76318659	76330045	6	0	-0.89744	-0.89744	6.23E-20
1506-MCG_252152938959_S01	2107	TT14	chr8	8	q21.13	80674456	80701312	15	0	-0.439708	-0.439708	2.52E-11
1506-MCG_252152938959_S01	2108	TT14	chr8	8	q21.13	81081609	81087055	4	0	-1.290843	-1.290843	1.44E-24
1506-MCG_252152938959_S01	2109	TT14	chr8	8	q21.13	81396247	81400081	3	0	-1.022499	-1.022499	3.02E-13
1506-MCG_252152938959_S01	2110	TT14	chr8	8	q21.2	85092265	85098303	4	0	-0.990161	-0.990161	4.59E-16
1506-MCG_252152938959_S01	2111	TT14	chr8	8	q21.2	86088759	86093535	4	0	-1.186216	-1.186216	8.53E-20
1506-MCG_252152938959_S01	2112	TT14	chr8	8	q21.2	86370751	86381516	6	0	-0.76645	-0.76645	1.07E-14
1506-MCG_252152938959_S01	2113	TT14	chr8	8	q21.3	87353171	87355862	3	0	-1.301912	-1.301912	5.48E-19
1506-MCG_252152938959_S01	2133	TT14	chr8	8	q22.2	101317511	101329645	7	0	-0.946632	-0.946632	2.01E-22
1506-MCG_252152938959_S01	2136	TT14	chr8	8	q22.3	102504036	102509202	4	0	-1.122198	-1.122198	7.59E-23
1506-MCG_252152938959_S01	2140	TT14	chr8	8	q22.3	103874769	103877368	3	0	-1.547245	-1.547245	2.9E-17
1506-MCG_252152938959_S01	2142	TT14	chr8	8	q22.3	105476947	105482077	5	0	-1.195124	-1.195124	4.2E-26
1506-MCG_252152938959_S01	2146	TT14	chr8	8	q23.1	107280540	107284366	4	0	-1.092744	-1.092744	8.94E-20
1506-MCG_252152938959_S01	2148	TT14	chr8	8	q23.2	110653368	110662165	6	0	-0.773637	-0.773637	2.95E-15
1506-MCG_252152938959_S01	2149	TT14	chr8	8	q23.2	110701138	110706274	4	0	-1.106561	-1.106561	1.82E-18
1506-MCG_252152938959_S01	2150	TT14	chr8	8	q23.3	114454434	114457278	3	0	-1.331771	-1.331771	1.21E-19
1506-MCG_252152938959_S01	2151	TT14	chr8	8	q23.3	117686699	117699497	6	0	-0.587108	-0.587108	3.11E-10
1506-MCG_252152938959_S01	2152	TT14	chr8	8	q24.11	117947983	117965855	10	0	-0.691966	-0.691966	6.21E-21
1506-MCG_252152938959_S01	2153	TT14	chr8	8	q24.11	119120552	119125752	3	0	-1.082065	-1.082065	9.46E-14
1506-MCG_252152938959_S01	2154	TT14	chr8	8	q24.12	120216326	120222588	4	0	-1.020318	-1.020318	8.48E-18
1506-MCG_252152938959_S01	2155	TT14	chr8	8	q24.12	120857745	120904194	24	0	-0.360793	-0.360793	3.87E-14
1506-MCG_252152938959_S01	2156	TT14	chr8	8	q24.12	121823119	121826895	3	0	-0.93166	-0.93166	6.67E-11
1506-MCG_252152938959_S01	2157	TT14	chr8	8	q24.13	122649044	122684694	13	0	-0.423273	-0.423273	3.3E-11
1506-MCG_252152938959_S01	2158	TT14	chr8	8	q24.13	123791277	123796116	4	0	-0.959486	-0.959486	3.31E-15
1506-MCG_252152938959_S01	2165	TT14	chr8	8	q24.21	129835586	129842186	4	0	-1.090301	-1.090301	3.64E-22
1506-MCG_252152938959_S01	2166	TT14	chr8	8	q24.21	131365153	131374048	5	0	-0.599317	-0.599317	1.05E-10
1506-MCG_252152938959_S01	2167	TT14	chr8	8	q24.22	132913618	132919352	4	0	-0.935986	-0.935986	4.54E-18
1506-MCG_252152938959_S01	2174	TT14	chr8	8	q24.3	141463500	141605018	60	0	-0.256432	-0.256432	2.97E-17
1506-MCG_252152938959_S01	2187	TT14	chr8	8	q24.3	146022273	146038068	9	0	-0.802616	-0.802616	4.4E-23
1506-MCG_252152938959_S01	2191	TT14	chr9	9	p24.3	973803	978104	3	0	-1.435933	-1.435933	1.49E-22
1506-MCG_252152938959_S01	2207	TT14	chr9	9	p24.1	8855658	8858550	3	0	-1.2885	-1.2885	1.11E-18
1506-MCG_252152938959_S01	2210	TT14	chr9	9	p22.3	14311332	14325297	7	0	-1.123497	-1.123497	2.59E-29
1506-MCG_252152938959_S01	2214	TT14	chr9	9	p22.1	19430094	19437090	4	0	-0.844944	-0.844944	1.75E-13
1506-MCG_252152938959_S01	2216	TT14	chr9	9	p22.1	19783655	19791545	5	0	-0.924108	-0.924108	3.14E-18
1506-MCG_252152938959_S01	2217	TT14	chr9	9	p21.3	20617752	20623005	3	0	-0.90265	-0.90265	8.51E-12
1506-MCG_252152938959_S01	2218	TT14	chr9	9	p21.3	20679665	20687828	6	0	-0.820955	-0.820955	6.58E-18
1506-MCG_252152938959_S01	2219	TT14	chr9	9	p21.3	21029271	21035261	4	0	-0.92786	-0.92786	1.22E-15
1506-MCG_252152938959_S01	2220	TT14	chr9	9	p21.3	21558354	21562382	3	0	-1.398579	-1.398579	5.97E-21
1506-MCG_252152938959_S01	2221	TT14	chr9	9	p21.3	21956186	22009029	31	0	-0.477757	-0.477757	2.64E-29
1506-MCG_252152938959_S01	2222	TT14	chr9	9	p21.3	22444682	22451204	4	0	-0.964241	-0.964241	2.5E-16
1506-MCG_252152938959_S01	2223	TT14	chr9	9	p21.3	23817986	23823653	3	0	-0.91098	-0.91098	5.67E-12
1506-MCG_252152938959_S01	2225	TT14	chr9	9	p21.2	27570498	27579551	4	0	-0.991899	-0.991899	1.26E-16
1506-MCG_252152938959_S01	2228	TT14	chr9	9	p13.3	33814505	33819068	3	0	-0.990854	-0.990854	7.44E-14
1506-MCG_252152938959_S01	2229	TT14	chr9	9	p13.3	34135223	34140346	4	0	-1.321428	-1.321428	6.11E-25
1506-MCG_252152938959_S01	2230	TT14	chr9	9	p13.3	34219024	34223145	3	0	-1.177829	-1.177829	2.3E-17
1506-MCG_252152938959_S01	2287	TT14	chr9	9	q22.32	97805863	97811608	5	0	-1.454541	-1.454541	4.52E-29
1506-MCG_252152938959_S01	2289	TT14	chr9	9	q22.32	98267289	98280517	8	0	-1.263924	-1.263924	1.8E-24
1506-MCG_252152938959_S01	2295	TT14	chr9	9	q22.33	100173622	100176217	3	0	-1.370134	-1.370134	7.22E-21
1506-MCG_252152938959_S01	2296	TT14	chr9	9	q22.33	100258515	100265778	5	0	-1.122896	-1.122896	3.23E-24
1506-MCG_252152938959_S01	2299	TT14	chr9	9	q22.33	101566957	101572111	4	0	-0.97843	-0.97843	4.21E-17
1506-MCG_252152938959_S01	2300	TT14	chr9	9	q22.33	101705631	101708393	3	0	-1.19189	-1.19189	3.04E-16
1506-MCG_252152938959_S01	2301	TT14	chr9	9	q22.33	101863999	101869385	3	0	-0.993239	-0.993239	1.45E-12
1506-MCG_252152938959_S01	2302	TT14	chr9	9	q22.33	102580589	102592420	6	0	-1.212497	-1.212497	2.4E-31
1506-MCG_252152938959_S01	2348	TT14	chr9	9	q33.3	126762818	126810130	24	0	-0.57269	-0.57269	1.6E-29
1506-MCG_252152938959_S01	2349	TT14	chr9	9	q33.3	127359334	127364589	4	0	-0.859512	-0.859512	6.79E-14
1506-MCG_252152938959_S01	2350	TT14	chr9	9	q33.3	127533747	127538325	4	0	-1.219732	-1.219732	4.17E-22
1506-MCG_252152938959_S01	2351	TT14	chr9	9	q33.3	127597888	127634517	19	0	-0.421109	-0.421109	3.23E-15
1506-MCG_252152938959_S01	2356	TT14	chr9	9	q33.3	128651323	128657515	4	0	-1.264184	-1.264184	1.03E-26
1506-MCG_252152938959_S01	2365	TT14	chr9	9	q34.11	131149596	131159862	11	0	-0.788491	-0.788491	2.94E-23
1506-MCG_252152938959_S01	2378	TT14	chr9	9	q34.2	136880863	136892259	5	0	-1.01574	-1.01574	4.59E-15
1506-MCG_252152938959_S01	2380	TT14	chr9	9	q34.3	138369004	140776585	951	0	-0.267142	-0.267142	1.11E-227
1506-MCG_252152938959_S01	2381	TT14	chr9	9	q34.3	139136704	139143102	4	0	-1.171117	-1.171117	4.42E-11
1506-MCG_252152938959_S01	2387	TT14	chr10	10	p15.3	666572	688807	13	0	-0.804132	-0.804132	2.85E-21
1506-MCG_252152938959_S01	2390	TT14	chr10	10	p15.2	3102670	3129876	13	0	-0.523688	-0.523688	3.01E-14
1506-MCG_252152938959_S01	2393	TT14	chr10	10	p15.1	5707362	5736758	13	0	-0.670251	-0.670251	5.08E-25
1506-MCG_252152938959_S01	2395	TT14	chr10	10	p15.1	6018355	6021685	3	0	-1.35072	-1.35072	9.93E-21

1506-MCG_252152938959_S01	2396	TT14	chr10	10	p15.1	6123940	6273277	69	0	-0.275549	-0.275549	4.88E-22
1506-MCG_252152938959_S01	2397	TT14	chr10	10	p14	6619639	6623812	3	0	-0.949019	-0.949019	1.76E-12
1506-MCG_252152938959_S01	2398	TT14	chr10	10	p14	7211838	7214764	3	0	-1.023221	-1.023221	4.61E-13
1506-MCG_252152938959_S01	2399	TT14	chr10	10	p14	8047731	8054834	5	0	-1.006482	-1.006482	4.81E-21
1506-MCG_252152938959_S01	2413	TT14	chr10	10	p12.33	17655390	17680901	11	0	-0.721022	-0.721022	7.93E-24
1506-MCG_252152938959_S01	2414	TT14	chr10	10	p12.33	18426356	18432032	4	0	-1.013146	-1.013146	1.97E-14
1506-MCG_252152938959_S01	2415	TT14	chr10	10	p12.31	20102290	20107688	4	0	-0.952949	-0.952949	2.29E-14
1506-MCG_252152938959_S01	2416	TT14	chr10	10	p12.31	21461367	21465684	3	0	-1.084734	-1.084734	1.67E-15
1506-MCG_252152938959_S01	2418	TT14	chr10	10	p12.31	21795837	21829711	29	0	-0.946129	-0.946129	5.63E-92
1506-MCG_252152938959_S01	2420	TT14	chr10	10	p12.2	22603928	22635726	18	0	-1.195309	-1.195309	1.68E-89
1506-MCG_252152938959_S01	2421	TT14	chr10	10	p12.2	23479832	23489189	6	0	-0.860194	-0.860194	1.54E-17
1506-MCG_252152938959_S01	2425	TT14	chr10	10	p12.1	26851965	26858737	5	0	-0.987783	-0.987783	6.1E-21
1506-MCG_252152938959_S01	2475	TT14	chr10	10	q22.1	72163628	72168229	4	0	-1.981258	-1.981258	1.14E-39
1506-MCG_252152938959_S01	2485	TT14	chr10	10	q22.2	75254852	75257828	3	0	-1.089005	-1.089005	5.53E-16
1506-MCG_252152938959_S01	2487	TT14	chr10	10	q22.2	75756398	75761836	4	0	-0.891993	-0.891993	2.21E-12
1506-MCG_252152938959_S01	2488	TT14	chr10	10	q22.2	76568563	76589992	9	0	-0.549891	-0.549891	6.43E-13
1506-MCG_252152938959_S01	2496	TT14	chr10	10	q23.1	82291359	82304288	7	0	-1.018537	-1.018537	1.1E-28
1506-MCG_252152938959_S01	2513	TT14	chr10	10	q23.33	94447927	94457619	6	0	-1.133266	-1.133266	2.09E-28
1506-MCG_252152938959_S01	2514	TT14	chr10	10	q23.33	94604788	94610667	5	0	-1.019847	-1.019847	3.07E-22
1506-MCG_252152938959_S01	2515	TT14	chr10	10	q23.33	94733936	94739363	3	0	-0.827774	-0.827774	5.11E-10
1506-MCG_252152938959_S01	2516	TT14	chr10	10	q23.33	94818006	94829179	6	0	-1.023259	-1.023259	2.65E-24
1506-MCG_252152938959_S01	2517	TT14	chr10	10	q23.33	95651827	95657211	4	0	-0.993451	-0.993451	8.13E-17
1506-MCG_252152938959_S01	2519	TT14	chr10	10	q23.33	96159912	96166308	4	0	-0.855739	-0.855739	2.17E-13
1506-MCG_252152938959_S01	2520	TT14	chr10	10	q24.1	97048849	97053154	4	0	-1.338258	-1.338258	3.63E-26
1506-MCG_252152938959_S01	2521	TT14	chr10	10	q24.1	97412505	97419847	6	0	-0.686346	-0.686346	3.11E-13
1506-MCG_252152938959_S01	2522	TT14	chr10	10	q24.1	98347582	98350841	3	0	-0.884181	-0.884181	4.45E-11
1506-MCG_252152938959_S01	2523	TT14	chr10	10	q24.1	98589399	98595152	8	0	-1.141248	-1.141248	1.41E-33
1506-MCG_252152938959_S01	2527	TT14	chr10	10	q24.2	99599558	99610913	5	0	-0.985587	-0.985587	7.33E-18
1506-MCG_252152938959_S01	2528	TT14	chr10	10	q24.2	99911230	99914897	3	0	-1.035136	-1.035136	9.74E-15
1506-MCG_252152938959_S01	2529	TT14	chr10	10	q24.2	101292509	101296194	3	0	-1.294634	-1.294634	1.07E-15
1506-MCG_252152938959_S01	2534	TT14	chr10	10	q24.31	102474552	102507331	13	0	-0.946435	-0.946435	1.68E-39
1506-MCG_252152938959_S01	2538	TT14	chr10	10	q24.32	104159864	104182994	20	0	-0.532299	-0.532299	4.2E-20
1506-MCG_252152938959_S01	2540	TT14	chr10	10	q24.32	104400463	104407266	5	0	-0.764956	-0.764956	5.05E-11
1506-MCG_252152938959_S01	2541	TT14	chr10	10	q24.32	104752691	104756173	3	0	-0.940856	-0.940856	1.31E-12
1506-MCG_252152938959_S01	2542	TT14	chr10	10	q24.32	104886986	104891087	3	0	-1.026995	-1.026995	9.44E-15
1506-MCG_252152938959_S01	2557	TT14	chr10	10	q25.3	116579263	116584435	4	0	-1.273878	-1.273878	6.53E-25
1506-MCG_252152938959_S01	2558	TT14	chr10	10	q25.3	116851374	116856352	3	0	-1.063768	-1.063768	9.71E-15
1506-MCG_252152938959_S01	2561	TT14	chr10	10	q25.3	118888898	118898501	6	0	-0.908044	-0.908044	3.99E-19
1506-MCG_252152938959_S01	2562	TT14	chr10	10	q26.11	119291707	119308473	9	0	-0.737139	-0.737139	1.02E-18
1506-MCG_252152938959_S01	2568	TT14	chr10	10	q26.13	123356483	123372110	7	0	-0.673637	-0.673637	1.41E-14
1506-MCG_252152938959_S01	2573	TT14	chr10	10	q26.13	124893503	124914883	12	0	-0.62968	-0.62968	3.7E-18
1506-MCG_252152938959_S01	2576	TT14	chr10	10	q26.13	126133261	126152928	11	0	-0.727509	-0.727509	1.76E-23
1506-MCG_252152938959_S01	2579	TT14	chr10	10	q26.2	127656436	127661280	4	0	-1.214036	-1.214036	1.8E-23
1506-MCG_252152938959_S01	2581	TT14	chr10	10	q26.3	131741542	131772350	17	0	-0.749226	-0.749226	8.35E-35
1506-MCG_252152938959_S01	2595	TT14	chr11	11	p15.4	2870132	2892711	12	0	-0.944371	-0.944371	1.69E-19
1506-MCG_252152938959_S01	2598	TT14	chr11	11	p15.4	3859946	3879297	12	0	-0.659918	-0.659918	2.23E-22
1506-MCG_252152938959_S01	2599	TT14	chr11	11	p15.4	4156274	4160221	4	0	-1.238903	-1.238903	4.06E-24
1506-MCG_252152938959_S01	2627	TT14	chr11	11	p15.1	21248520	21252067	4	0	-1.369587	-1.369587	8.67E-25
1506-MCG_252152938959_S01	2628	TT14	chr11	11	p14.1	27717104	27746606	18	0	-0.447439	-0.447439	8.83E-13
1506-MCG_252152938959_S01	2630	TT14	chr11	11	p13	31819688	31853198	15	0	-0.665492	-0.665492	5.36E-24
1506-MCG_252152938959_S01	2641	TT14	chr11	11	p13	35637057	35644045	5	0	-0.724636	-0.724636	8.15E-14
1506-MCG_252152938959_S01	2642	TT14	chr11	11	p13	35681706	35688898	4	0	-0.79719	-0.79719	1.57E-14
1506-MCG_252152938959_S01	2643	TT14	chr11	11	p13	35960550	35973960	7	0	-0.56478	-0.56478	9.59E-14
1506-MCG_252152938959_S01	2644	TT14	chr11	11	p11.2	43566785	43571831	4	0	-0.910299	-0.910299	4.29E-14
1506-MCG_252152938959_S01	2645	TT14	chr11	11	p11.2	44113923	44119706	4	0	-0.993698	-0.993698	2.3E-16
1506-MCG_252152938959_S01	2646	TT14	chr11	11	p11.2	45903180	45929000	15	0	-0.439696	-0.439696	3.68E-12
1506-MCG_252152938959_S01	2648	TT14	chr11	11	p11.2	46366345	46415124	20	0	-0.568593	-0.568593	7.03E-22
1506-MCG_252152938959_S01	2670	TT14	chr11	11	q12.2	60690879	60703155	6	0	-0.944665	-0.944665	8.07E-21
1506-MCG_252152938959_S01	2672	TT14	chr11	11	q12.2	61303739	61351984	23	0	-0.433331	-0.433331	1.11E-15
1506-MCG_252152938959_S01	2678	TT14	chr11	11	q13.1	63932100	63956373	12	0	-0.766486	-0.766486	7.44E-22
1506-MCG_252152938959_S01	2679	TT14	chr11	11	q13.1	63991419	64143273	72	0	-0.284321	-0.284321	7.37E-10
1506-MCG_252152938959_S01	2685	TT14	chr11	11	q13.1	65306264	65431718	59	0	-0.609595	-0.609595	4.08E-52
1506-MCG_252152938959_S01	2693	TT14	chr11	11	q13.2	68224758	68245889	10	0	-0.683887	-0.683887	4.91E-15
1506-MCG_252152938959_S01	2694	TT14	chr11	11	q13.3	68607815	68611893	3	0	-1.17404	-1.17404	1.1E-13
1506-MCG_252152938959_S01	2698	TT14	chr11	11	q13.3	70302169	70308262	4	0	-1.357496	-1.357496	3.56E-24
1506-MCG_252152938959_S01	2716	TT14	chr11	11	q14.1	77903747	77912725	5	0	-0.718262	-0.718262	3.8E-12
1506-MCG_252152938959_S01	2717	TT14	chr11	11	q14.1	78587420	78591804	3	0	-0.931186	-0.931186	3.27E-12
1506-MCG_252152938959_S01	2718	TT14	chr11	11	q14.1	78898511	78903872	3	0	-0.901738	-0.901738	5.24E-11
1506-MCG_252152938959_S01	2719	TT14	chr11	11	q14.1	79144123	79156183	8	0	-0.622865	-0.622865	4.73E-13
1506-MCG_252152938959_S01	2721	TT14	chr11	11	q14.1	82681207	82684689	3	0	-1.282118	-1.282118	5.92E-19
1506-MCG_252152938959_S01	2725	TT14	chr11	11	q14.2	86510313	86513370	3	0	-1.422816	-1.422816	3.82E-22
1506-MCG_252152938959_S01	2726	TT14	chr11	11	q14.2	86663483	86669223	3	0	-0.906638	-0.906638	9.15E-12
1506-MCG_252152938959_S01	2730	TT14	chr11	11	q21	93273959	93277536	3	0	-1.20581	-1.20581	2.51E-18
1506-MCG_252152938959_S01	2734	TT14	chr11	11	q21	94961093	94966741	4	0	-0.886637	-0.886637	1.5E-14
1506-MCG_252152938959_S01	2735	TT14	chr11	11	q22.1	99688416	99694175	4	0	-0.920295	-0.920295	7.37E-13
1506-MCG_252152938959_S01	2737	TT14	chr11	11	q22.2	102319527	102324330	3	0	-1.000012	-1.000012	1.15E-13
1506-MCG_252152938959_S01	2739	TT14	chr11	11	q22.3	108366253	108372054	4	0	-0.798689	-0.798689	5.06E-12
1506-MCG_252152938959_S01	2741	TT14	chr11	11	q23.1	110581263	110586374	3	0	-0.933159	-0.933159	1.84E-12
1506-MCG_252152938959_S01	2742	TT14	chr11	11	q23.1	111380935	111387769	9	0	-0.910303	-0.910303	5.96E-27
1506-MCG_252152938959_S01	2750	TT14	chr11	11	q23.2	113745707	113748344	3	0	-1.219051	-1.219051	9.29E-18
1506-MCG_252152938959_S01	2753	TT14	chr11	11	q23.3	117097602	117127625	16	0	-0.487489	-0.487489	3E-16
1506-MCG_252152938959_S01	2758	TT14	chr11	11	q23.3	119186807	119237202	24	0	-0.487375	-0.487375	4.86E-23
1506-MCG_252152938959_S01	2761	TT14	chr11	11	q23.3	120192908	120208978	10	0	-0.816241	-0.816241	8.13E-27
1506-MCG_252152938959_S01	2781	TT14	chr11	11	q25	131556686	131565395	6	0	-0.603673	-0.603673	1.71E-10
1506-MCG_252152938959_S01	2782	TT14	chr11	11	q25	131778700	131782380	3	0	-1.348205	-1.348205	3.17E-21
1506-MCG_252152938959_S01	2788	TT14	chr12	12	p13.33	294704	316663	13	0	-0.553688	-0.553688	2.73E-16
1506-MCG_252152938959_S01	2789	TT14	chr12	12	p13.33	558499	573483	9	0	-0.819638	-0.819638	1.5E-25
1506-MCG_252152938959_S01	2792	TT14	chr12	12	p13.33	1739965	1754362	10	0	-0.709894	-0.709894	8.61E-22
1506-MCG_252152938959_S01	2809	TT14	chr12	12	p13.31	7339215	7354112	6	0	-0.951099	-0.951099	1.12E-21
1506-MCG_252152938959_S01	2810	TT14	chr12	12	p13.31	7592349	7594898	3	0	-1.467041	-1.467041	4.72E-25
1506-MCG_252152938959_S01	2811	TT14	chr12	12	p13.31	7777178	7790225	6	0	-0.95494	-0.95494	4.04E-23
1506-MCG_252152938959_S01	2812	TT14	chr12	12	p13.31	7903616	7906753	3	0	-1.206074	-1.206074	2.38E-18
1506-MCG_252152938959_S01	2814	TT14	chr12	12	p13.31	8740418	8755332	8	0	-0.763264	-0.763264	1.49E-18
1506-MCG_252152938959_S01	2815	TT14	chr12	12	p13.31	8847357	8851459	3	0	-1.315274	-1.315274	3.29E-19
1506-MCG_252152938959_S01	2816	TT14	chr12	12	p13.31	9064152	9070712	4	0	-0.785171	-0.785171	6.93E-12
1506-MCG_252152938959_S01	2820	TT14	chr12	12	p13.2	12714031	12720459	4	0	-1.295807	-1.295807	5.45E-25

1506-MCG_252152938959_S01	2821	TT14	chr12	12	p13.1	12868234	12881712	8	0	-0.947252	-0.947252	6.31E-26
1506-MCG_252152938959_S01	2822	TT14	chr12	12	p13.1	12933447	12944103	9	0	-0.663897	-0.663897	4.73E-17
1506-MCG_252152938959_S01	2825	TT14	chr12	12	p12.3	15940153	15947200	5	0	-0.907481	-0.907481	5.47E-18
1506-MCG_252152938959_S01	2827	TT14	chr12	12	p12.3	18647619	18656057	5	0	-0.83229	-0.83229	7.08E-16
1506-MCG_252152938959_S01	2828	TT14	chr12	12	p12.3	19278489	19285386	4	0	-0.974844	-0.974844	1.25E-16
1506-MCG_252152938959_S01	2829	TT14	chr12	12	p12.3	19490580	19497187	5	0	-0.865588	-0.865588	9.38E-17
1506-MCG_252152938959_S01	2831	TT14	chr12	12	p12.2	20961362	20963103	3	0	-1.208026	-1.208026	3.44E-18
1506-MCG_252152938959_S01	2832	TT14	chr12	12	p12.1	21808914	21831204	12	0	-0.75372	-0.75372	2.96E-29
1506-MCG_252152938959_S01	2833	TT14	chr12	12	p12.1	22526537	22531413	3	0	-0.982781	-0.982781	2.57E-13
1506-MCG_252152938959_S01	2834	TT14	chr12	12	p12.1	24712248	24720635	4	0	-0.746209	-0.746209	3.83E-10
1506-MCG_252152938959_S01	2835	TT14	chr12	12	p12.1	25402580	25406069	3	0	-1.109219	-1.109219	2.38E-16
1506-MCG_252152938959_S01	2836	TT14	chr12	12	p12.1	25489552	25549568	45	0	-0.322609	-0.322609	4.91E-20
1506-MCG_252152938959_S01	2837	TT14	chr12	12	p12.1	26266480	26278447	8	0	-1.047561	-1.047561	2.69E-33
1506-MCG_252152938959_S01	2839	TT14	chr12	12	p11.23	26984458	26994117	5	0	-1.010976	-1.010976	1.49E-22
1506-MCG_252152938959_S01	2840	TT14	chr12	12	p11.23	27484679	27488523	3	0	-1.009006	-1.009006	9.18E-14
1506-MCG_252152938959_S01	2841	TT14	chr12	12	p11.22	28595250	28604231	6	0	-0.932797	-0.932797	2.22E-19
1506-MCG_252152938959_S01	2842	TT14	chr12	12	p11.22	29540336	29542222	3	0	-1.870828	-1.870828	3.55E-30
1506-MCG_252152938959_S01	2843	TT14	chr12	12	p11.22	29930678	29942578	6	0	-0.615997	-0.615997	4.17E-11
1506-MCG_252152938959_S01	2844	TT14	chr12	12	p11.21	30847908	30854183	5	0	-0.892701	-0.892701	7.07E-17
1506-MCG_252152938959_S01	2845	TT14	chr12	12	p11.21	30906690	30911953	4	0	-1.132508	-1.132508	5.98E-20
1506-MCG_252152938959_S01	2847	TT14	chr12	12	p11.21	32544224	32555670	6	0	-0.886676	-0.886676	1.51E-19
1506-MCG_252152938959_S01	2848	TT14	chr12	12	p11.21	32707333	32720999	14	0	-0.735274	-0.735274	5.96E-32
1506-MCG_252152938959_S01	2851	TT14	chr12	12	q12	42534716	42540492	3	0	-0.905856	-0.905856	9.59E-12
1506-MCG_252152938959_S01	2852	TT14	chr12	12	q12	42617907	42636817	8	0	-0.942453	-0.942453	2.13E-29
1506-MCG_252152938959_S01	2853	TT14	chr12	12	q12	42875508	42880727	4	0	-0.914229	-0.914229	1.04E-14
1506-MCG_252152938959_S01	2854	TT14	chr12	12	q12	42979841	42987900	5	0	-0.930503	-0.930503	1.29E-18
1506-MCG_252152938959_S01	2855	TT14	chr12	12	q12	43958112	43967870	6	0	-0.773452	-0.773452	2.93E-16
1506-MCG_252152938959_S01	2857	TT14	chr12	12	q12	45442232	45446268	4	0	-1.203328	-1.203328	9.01E-23
1506-MCG_252152938959_S01	2858	TT14	chr12	12	q13.11	46760620	46783337	14	0	-0.547233	-0.547233	5.96E-18
1506-MCG_252152938959_S01	2859	TT14	chr12	12	q13.11	47465949	47476740	6	0	-0.606285	-0.606285	8.2E-11
1506-MCG_252152938959_S01	2861	TT14	chr12	12	q13.11	48722841	48728516	4	0	-1.407688	-1.407688	9.39E-31
1506-MCG_252152938959_S01	2876	TT14	chr12	12	q13.13	53508848	53517381	4	0	-1.016432	-1.016432	3.01E-17
1506-MCG_252152938959_S01	2882	TT14	chr12	12	q13.3	56652770	56662701	5	0	-1.027467	-1.027467	1.73E-20
1506-MCG_252152938959_S01	2883	TT14	chr12	12	q13.3	57022784	57051705	15	0	-0.388489	-0.388489	8.12E-11
1506-MCG_252152938959_S01	2884	TT14	chr12	12	q13.3	57175974	57186362	5	0	-1.115575	-1.115575	1.46E-26
1506-MCG_252152938959_S01	2885	TT14	chr12	12	q13.3	57394367	57403889	7	0	-0.539064	-0.539064	2.85E-13
1506-MCG_252152938959_S01	2886	TT14	chr12	12	q13.3	57596472	57616930	14	0	-0.376257	-0.376257	1.38E-12
1506-MCG_252152938959_S01	2887	TT14	chr12	12	q13.3	57823145	57825259	3	0	-1.523128	-1.523128	2.15E-25
1506-MCG_252152938959_S01	2890	TT14	chr12	12	q13.3 - q14.1	57994071	58154075	63	0	-0.258928	-0.258928	8.18E-18
1506-MCG_252152938959_S01	2891	TT14	chr12	12	q14.1	59311114	59314863	3	0	-1.094066	-1.094066	2E-15
1506-MCG_252152938959_S01	2892	TT14	chr12	12	q14.1	62400136	62407714	4	0	-0.790889	-0.790889	4.93E-12
1506-MCG_252152938959_S01	2893	TT14	chr12	12	q14.1	62855947	62861603	4	0	-0.698144	-0.698144	9.35E-10
1506-MCG_252152938959_S01	2894	TT14	chr12	12	q14.1	62994505	62998503	7	0	-1.174643	-1.174643	3.74E-38
1506-MCG_252152938959_S01	2898	TT14	chr12	12	q14.2	65000641	65009162	9	0	-0.697573	-0.697573	1.06E-18
1506-MCG_252152938959_S01	2903	TT14	chr12	12	q15	69002007	69005661	3	0	-1.230677	-1.230677	2.42E-17
1506-MCG_252152938959_S01	2904	TT14	chr12	12	q15	69323561	69331701	5	0	-0.956468	-0.956468	5.19E-19
1506-MCG_252152938959_S01	2905	TT14	chr12	12	q15	69628122	69641285	9	0	-0.808642	-0.808642	1.06E-22
1506-MCG_252152938959_S01	2907	TT14	chr12	12	q15	70754323	70766581	7	0	-0.603322	-0.603322	3.49E-12
1506-MCG_252152938959_S01	2908	TT14	chr12	12	q15	70999702	71008066	6	0	-0.766826	-0.766826	2.11E-15
1506-MCG_252152938959_S01	2909	TT14	chr12	12	q21.1	71557451	71565029	4	0	-0.757127	-0.757127	3.57E-11
1506-MCG_252152938959_S01	2911	TT14	chr12	12	q21.1	72147512	72151762	3	0	-1.268193	-1.268193	1.45E-18
1506-MCG_252152938959_S01	2912	TT14	chr12	12	q21.1	75595711	75605657	6	0	-0.620587	-0.620587	4.5E-11
1506-MCG_252152938959_S01	2913	TT14	chr12	12	q21.2	77458282	77463587	4	0	-0.795763	-0.795763	4.31E-12
1506-MCG_252152938959_S01	2914	TT14	chr12	12	q21.2	80082053	80108240	9	0	-0.661741	-0.661741	1.71E-17
1506-MCG_252152938959_S01	2915	TT14	chr12	12	q21.31	80696499	80704558	5	0	-0.924946	-0.924946	4.15E-17
1506-MCG_252152938959_S01	2917	TT14	chr12	12	q21.31	81605370	81608586	3	0	-1.2361	-1.2361	4.69E-16
1506-MCG_252152938959_S01	2920	TT14	chr12	12	q22	93321395	93325083	3	0	-1.150348	-1.150348	3.01E-17
1506-MCG_252152938959_S01	2921	TT14	chr12	12	q22	93831641	93838970	5	0	-0.84453	-0.84453	4.43E-16
1506-MCG_252152938959_S01	2922	TT14	chr12	12	q22	94133617	94138626	4	0	-0.902972	-0.902972	1.92E-14
1506-MCG_252152938959_S01	2923	TT14	chr12	12	q22	95042916	95048520	4	0	-0.941694	-0.941694	1.33E-15
1506-MCG_252152938959_S01	2924	TT14	chr12	12	q22	95462982	95467944	4	0	-0.995442	-0.995442	9.27E-17
1506-MCG_252152938959_S01	2932	TT14	chr12	12	q23.1	99285362	99292190	4	0	-1.066861	-1.066861	1.1E-18
1506-MCG_252152938959_S01	2933	TT14	chr12	12	q23.1	100376873	100382164	4	0	-0.877963	-0.877963	2.03E-14
1506-MCG_252152938959_S01	2940	TT14	chr12	12	q23.2	103349683	103353153	3	0	-1.613351	-1.613351	5.96E-28
1506-MCG_252152938959_S01	2954	TT14	chr12	12	q23.3	108152454	108169809	10	0	-0.725895	-0.725895	6.14E-23
1506-MCG_252152938959_S01	2963	TT14	chr12	12	q24.13	112852746	112860493	4	0	-0.758848	-0.758848	3.24E-11
1506-MCG_252152938959_S01	2967	TT14	chr12	12	q24.21	115109251	115116328	4	0	-1.050243	-1.050243	1.26E-18
1506-MCG_252152938959_S01	2969	TT14	chr12	12	q24.22	117172295	117186309	8	0	-0.655005	-0.655005	1.59E-15
1506-MCG_252152938959_S01	2973	TT14	chr12	12	q24.23	118196812	118202403	5	0	-1.150422	-1.150422	6.79E-25
1506-MCG_252152938959_S01	2974	TT14	chr12	12	q24.23	118680758	118687835	5	0	-0.856244	-0.856244	1.42E-16
1506-MCG_252152938959_S01	2975	TT14	chr12	12	q24.23	118811647	118816091	3	0	-1.423991	-1.423991	1.13E-19
1506-MCG_252152938959_S01	2982	TT14	chr12	12	q24.31	122236515	122269384	16	0	-0.696656	-0.696656	6.51E-29
1506-MCG_252152938959_S01	2993	TT14	chr12	12	q24.31	125535008	125552032	8	0	-0.831914	-0.831914	5.46E-23
1506-MCG_252152938959_S01	2994	TT14	chr12	12	q24.32	127618265	127653849	10	0	-0.560441	-0.560441	2.28E-13
1506-MCG_252152938959_S01	2996	TT14	chr12	12	q24.33	130311429	130315492	4	0	-0.912119	-0.912119	3.03E-15
1506-MCG_252152938959_S01	2999	TT14	chr12	12	q24.33	132262558	133496334	485	0	-0.298345	-0.298345	1.78E-155
1506-MCG_252152938959_S01	3000	TT14	chr12	12	q24.33	132502755	132509770	5	0	-0.96398	-0.96398	2.17E-10
1506-MCG_252152938959_S01	3007	TT14	chr13	13	q12.11	21097911	21100927	3	0	-1.380348	-1.380348	1.11E-19
1506-MCG_252152938959_S01	3031	TT14	chr13	13	q12.2	28525529	28553990	17	0	-0.781397	-0.781397	2.55E-35
1506-MCG_252152938959_S01	3032	TT14	chr13	13	q12.2	28669064	28718721	22	0	-0.519304	-0.519304	1.01E-21
1506-MCG_252152938959_S01	3072	TT14	chr13	13	q14.2	50066463	50080772	10	0	-1.10006	-1.10006	1.17E-45
1506-MCG_252152938959_S01	3083	TT14	chr13	13	q14.3	53022698	53030741	5	0	-1.228652	-1.228652	1.59E-26
1506-MCG_252152938959_S01	3084	TT14	chr13	13	q14.3	53386254	53401978	13	0	-0.690432	-0.690432	3.84E-23
1506-MCG_252152938959_S01	3085	TT14	chr13	13	q14.3	53771960	53779892	4	0	-0.736394	-0.736394	6.49E-10
1506-MCG_252152938959_S01	3086	TT14	chr13	13	q21.2	60966961	60975736	6	0	-0.705397	-0.705397	7.73E-13
1506-MCG_252152938959_S01	3087	TT14	chr13	13	q21.32	67133302	67137011	3	0	-1.233578	-1.233578	3.66E-16
1506-MCG_252152938959_S01	3088	TT14	chr13	13	q21.33	72436388	72443486	5	0	-0.801006	-0.801006	5.74E-12
1506-MCG_252152938959_S01	3089	TT14	chr13	13	q22.1	73631748	73636395	3	0	-0.915422	-0.915422	2.19E-11
1506-MCG_252152938959_S01	3090	TT14	chr13	13	q22.2	76052920	76059965	5	0	-0.87508	-0.87508	4.58E-15
1506-MCG_252152938959_S01	3091	TT14	chr13	13	q22.3	77456449	77465373	7	0	-0.852864	-0.852864	7.62E-20
1506-MCG_252152938959_S01	3092	TT14	chr13	13	q22.3	77561142	77569158	6	0	-0.601981	-0.601981	9.02E-10
1506-MCG_252152938959_S01	3095	TT14	chr13	13	q31.1	79174029	79178668	3	0	-1.155592	-1.155592	4.78E-16
1506-MCG_252152938959_S01	3096	TT14	chr13	13	q31.1	79977241	79982884	5	0	-0.977266	-0.977266	1.38E-17
1506-MCG_252152938959_S01	3097	TT14	chr13	13	q31.1	80910339	80933474	16	0	-0.643828	-0.643828	3.25E-23
1506-MCG_252152938959_S01	3098	TT14	chr13	13	q31.1	82825319	82835651	3	0	-1.055922	-1.055922	2.41E-13
1506-MCG_252152938959_S01	3099	TT14	chr13	13	q31.2	88320800	88331657	5	0	-0.708169	-0.708169	3.67E-11

1506-MCG_252152938959_S01	3100	TT14	chr13	13	q31.3	90012370	90018429	4	0	-0.919466	-0.919466	2.7E-14
1506-MCG_252152938959_S01	3101	TT14	chr13	13	q31.3	91998062	92003923	8	0	-1.080467	-1.080467	3.74E-30
1506-MCG_252152938959_S01	3103	TT14	chr13	13	q31.3	94099770	94113043	9	0	-0.573337	-0.573337	1.45E-12
1506-MCG_252152938959_S01	3104	TT14	chr13	13	q32.1	95358636	95367832	7	0	-0.980068	-0.980068	6.28E-22
1506-MCG_252152938959_S01	3105	TT14	chr13	13	q32.1	95951556	95956685	4	0	-0.896305	-0.896305	6.59E-14
1506-MCG_252152938959_S01	3106	TT14	chr13	13	q32.1	96202845	96207814	4	0	-0.928098	-0.928098	8.22E-15
1506-MCG_252152938959_S01	3111	TT14	chr13	13	q32.2	98626977	98632380	4	0	-1.076819	-1.076819	1.23E-18
1506-MCG_252152938959_S01	3113	TT14	chr13	13	q32.2	99227999	99231549	3	0	-1.297585	-1.297585	2.3E-19
1506-MCG_252152938959_S01	3114	TT14	chr13	13	q32.3	99402707	99407313	3	0	-1.155394	-1.155394	8.57E-17
1506-MCG_252152938959_S01	3115	TT14	chr13	13	q32.3	100544845	100552549	5	0	-0.91372	-0.91372	6.37E-17
1506-MCG_252152938959_S01	3116	TT14	chr13	13	q32.3	100609077	100638825	15	0	-0.928457	-0.928457	3.99E-39
1506-MCG_252152938959_S01	3117	TT14	chr13	13	q33.1	102061286	102111391	27	0	-0.433493	-0.433493	3.04E-19
1506-MCG_252152938959_S01	3118	TT14	chr13	13	q33.1	102562825	102573216	7	0	-0.67087	-0.67087	3.51E-12
1506-MCG_252152938959_S01	3119	TT14	chr13	13	q33.1	103450138	103455031	4	0	-1.135114	-1.135114	4.15E-19
1506-MCG_252152938959_S01	3120	TT14	chr13	13	q33.3	107184767	107190156	5	0	-1.276461	-1.276461	1.64E-23
1506-MCG_252152938959_S01	3122	TT14	chr13	13	q33.3	108433133	108440013	5	0	-0.909081	-0.909081	3.56E-17
1506-MCG_252152938959_S01	3123	TT14	chr13	13	q33.3	108515503	108527066	6	0	-0.713156	-0.713156	9.55E-12
1506-MCG_252152938959_S01	3124	TT14	chr13	13	q33.3	108868860	108871629	3	0	-1.848893	-1.848893	6.31E-30
1506-MCG_252152938959_S01	3125	TT14	chr13	13	q33.3	109144668	109152015	4	0	-0.888728	-0.888728	2.57E-13
1506-MCG_252152938959_S01	3126	TT14	chr13	13	q33.3	109789984	109796247	4	0	-1.125316	-1.125316	1.29E-19
1506-MCG_252152938959_S01	3128	TT14	chr13	13	q34	110430371	110440771	6	0	-0.750784	-0.750784	1.76E-11
1506-MCG_252152938959_S01	3129	TT14	chr13	13	q34	110956617	110966823	6	0	-1.094809	-1.094809	3.82E-20
1506-MCG_252152938959_S01	3131	TT14	chr13	13	q34	111357935	111367596	6	0	-1.121868	-1.121868	6.98E-18
1506-MCG_252152938959_S01	3132	TT14	chr13	13	q34	112709350	112730077	10	0	-1.305142	-1.305142	1.29E-31
1506-MCG_252152938959_S01	3134	TT14	chr13	13	q34	113592971	113765453	90	0	-0.431954	-0.431954	5.18E-23
1506-MCG_252152938959_S01	3136	TT14	chr13	13	q34	114034110	114074877	14	0	-0.691613	-0.691613	5.35E-15
1506-MCG_252152938959_S01	3137	TT14	chr13	13	q34	114137698	114148380	8	0	-0.694471	-0.694471	1.73E-10
1506-MCG_252152938959_S01	3138	TT14	chr13	13	q34	114303365	114843971	139	0	-0.420077	-0.420077	4.14E-31
1506-MCG_252152938959_S01	3139	TT14	chr13	13	q34	114837880	114841752	4	0	-1.202691	-1.202691	3.75E-10
1506-MCG_252152938959_S01	3147	TT14	chr14	14	q11.2	21556436	21568120	7	0	-1.075935	-1.075935	4.58E-32
1506-MCG_252152938959_S01	3153	TT14	chr14	14	q11.2	23476981	23484956	6	0	-0.664038	-0.664038	5.38E-11
1506-MCG_252152938959_S01	3154	TT14	chr14	14	q11.2	23512844	23529670	11	0	-0.709438	-0.709438	4.12E-23
1506-MCG_252152938959_S01	3155	TT14	chr14	14	q11.2	23751381	23838990	47	0	-0.340037	-0.340037	1.3E-22
1506-MCG_252152938959_S01	3156	TT14	chr14	14	q11.2	24044612	24052121	5	0	-1.072617	-1.072617	7.7E-20
1506-MCG_252152938959_S01	3159	TT14	chr14	14	q12	24777360	24787001	6	0	-0.957068	-0.957068	2.36E-23
1506-MCG_252152938959_S01	3160	TT14	chr14	14	q12	29232583	29238842	5	0	-0.949229	-0.949229	2.99E-15
1506-MCG_252152938959_S01	3161	TT14	chr14	14	q12	30389967	30402423	8	0	-0.660123	-0.660123	4.12E-13
1506-MCG_252152938959_S01	3163	TT14	chr14	14	q12	31492580	31500862	10	0	-0.661587	-0.661587	1.24E-16
1506-MCG_252152938959_S01	3164	TT14	chr14	14	q12	31885900	31909830	13	0	-0.649256	-0.649256	2.08E-20
1506-MCG_252152938959_S01	3165	TT14	chr14	14	q12	32541770	32547674	4	0	-1.019099	-1.019099	2.31E-15
1506-MCG_252152938959_S01	3166	TT14	chr14	14	q12	32922319	32925470	3	0	-1.113853	-1.113853	1.95E-15
1506-MCG_252152938959_S01	3167	TT14	chr14	14	q13.1	33401486	33409722	5	0	-1.142309	-1.142309	1.45E-23
1506-MCG_252152938959_S01	3168	TT14	chr14	14	q13.1	34266757	34271220	3	0	-1.038792	-1.038792	1.17E-13
1506-MCG_252152938959_S01	3169	TT14	chr14	14	q13.1	34929695	34935643	5	0	-1.031349	-1.031349	3.11E-19
1506-MCG_252152938959_S01	3170	TT14	chr14	14	q13.1	35182815	35188236	3	0	-1.246521	-1.246521	1.17E-17
1506-MCG_252152938959_S01	3174	TT14	chr14	14	q13.2	36289917	36297265	5	0	-1.084449	-1.084449	5.1E-20
1506-MCG_252152938959_S01	3175	TT14	chr14	14	q13.3	36971273	36988926	9	0	-0.605591	-0.605591	1.02E-12
1506-MCG_252152938959_S01	3176	TT14	chr14	14	q13.3	37048038	37054351	8	0	-0.88037	-0.88037	1.48E-18
1506-MCG_252152938959_S01	3177	TT14	chr14	14	q21.1	38049086	38095632	23	0	-0.56326	-0.56326	1.37E-25
1506-MCG_252152938959_S01	3179	TT14	chr14	14	q21.1	42139845	42144964	3	0	-1.208777	-1.208777	1.45E-17
1506-MCG_252152938959_S01	3180	TT14	chr14	14	q21.2	45365166	45387047	14	0	-0.776207	-0.776207	2.51E-31
1506-MCG_252152938959_S01	3181	TT14	chr14	14	q21.2	45548554	45554035	4	0	-1.315293	-1.315293	5.59E-26
1506-MCG_252152938959_S01	3183	TT14	chr14	14	q21.3	48089266	48149684	30	0	-0.451703	-0.451703	1.41E-21
1506-MCG_252152938959_S01	3184	TT14	chr14	14	q21.3	48093914	48097812	3	0	-1.418246	-1.418246	3.75E-11
1506-MCG_252152938959_S01	3200	TT14	chr14	14	q22.2	54411087	54422318	7	0	-1.062089	-1.062089	3.07E-31
1506-MCG_252152938959_S01	3206	TT14	chr14	14	q22.3	57262352	57285751	18	0	-0.989956	-0.989956	4.41E-62
1506-MCG_252152938959_S01	3244	TT14	chr14	14	q24.3	77168143	77290652	52	0	-0.352717	-0.352717	1.98E-27
1506-MCG_252152938959_S01	3245	TT14	chr14	14	q24.3	77225464	77230131	4	0	-1.109321	-1.109321	1.15E-10
1506-MCG_252152938959_S01	3248	TT14	chr14	14	q24.3	77839031	77848064	5	0	-0.734568	-0.734568	7.71E-13
1506-MCG_252152938959_S01	3249	TT14	chr14	14	q24.3	77963201	77967339	4	0	-0.829744	-0.829744	1.23E-12
1506-MCG_252152938959_S01	3250	TT14	chr14	14	q24.3	78081347	78084421	3	0	-1.388925	-1.388925	2.25E-21
1506-MCG_252152938959_S01	3251	TT14	chr14	14	q24.3	78210979	78218450	5	0	-0.815298	-0.815298	2.1E-15
1506-MCG_252152938959_S01	3252	TT14	chr14	14	q31.1	81677205	81716636	14	0	-0.425345	-0.425345	5.74E-12
1506-MCG_252152938959_S01	3253	TT14	chr14	14	q31.1	81781591	81789434	5	0	-0.692458	-0.692458	1.33E-11
1506-MCG_252152938959_S01	3254	TT14	chr14	14	q31.3	88456906	88462310	4	0	-0.933038	-0.933038	1.49E-15
1506-MCG_252152938959_S01	3255	TT14	chr14	14	q31.3	88786676	88794244	6	0	-0.887877	-0.887877	1.69E-18
1506-MCG_252152938959_S01	3256	TT14	chr14	14	q31.3	89017312	89030206	8	0	-0.78723	-0.78723	6.38E-20
1506-MCG_252152938959_S01	3271	TT14	chr14	14	q32.12	92411817	92416548	4	0	-1.136052	-1.136052	3.32E-22
1506-MCG_252152938959_S01	3272	TT14	chr14	14	q32.12	93183557	93186424	3	0	-1.232883	-1.232883	1.5E-17
1506-MCG_252152938959_S01	3273	TT14	chr14	14	q32.12	93376244	93413568	22	0	-0.429329	-0.429329	5.11E-16
1506-MCG_252152938959_S01	3285	TT14	chr14	14	q32.2	97260112	97268472	7	0	-0.9363	-0.9363	1.26E-25
1506-MCG_252152938959_S01	3286	TT14	chr14	14	q32.2	99638171	99643585	3	0	-1.131742	-1.131742	3.46E-14
1506-MCG_252152938959_S01	3287	TT14	chr14	14	q32.2	99734781	99743808	7	0	-0.935105	-0.935105	1.92E-23
1506-MCG_252152938959_S01	3304	TT14	chr14	14	q32.33	105176602	105189610	8	0	-0.989587	-0.989587	1.43E-17
1506-MCG_252152938959_S01	3305	TT14	chr14	14	q32.33	105260853	105266448	3	0	-1.718308	-1.718308	1.34E-11
1506-MCG_252152938959_S01	3307	TT14	chr15	15	q11.2	23929562	23933678	3	0	-1.273131	-1.273131	7.7E-16
1506-MCG_252152938959_S01	3310	TT14	chr15	15	q12	27004000	27249917	113	0	-0.353303	-0.353303	3.53E-57
1506-MCG_252152938959_S01	3311	TT14	chr15	15	q12	27127747	27132472	3	0	-1.254199	-1.254199	1.05E-10
1506-MCG_252152938959_S01	3314	TT14	chr15	15	q12	27783426	27788309	4	0	-1.259522	-1.259522	5.74E-25
1506-MCG_252152938959_S01	3315	TT14	chr15	15	q13.1	28321191	28365786	18	0	-0.586359	-0.586359	1.35E-24
1506-MCG_252152938959_S01	3320	TT14	chr15	15	q13.3	31280817	31287111	4	0	-1.369652	-1.369652	2.47E-27
1506-MCG_252152938959_S01	3323	TT14	chr15	15	q13.3	33006246	33012222	5	0	-0.972434	-0.972434	2.49E-18
1506-MCG_252152938959_S01	3324	TT14	chr15	15	q14	33602378	33606095	4	0	-0.792567	-0.792567	5.66E-11
1506-MCG_252152938959_S01	3325	TT14	chr15	15	q14	34328703	34331727	3	0	-1.481015	-1.481015	2.83E-21
1506-MCG_252152938959_S01	3326	TT14	chr15	15	q14	34498530	34505572	5	0	-0.986775	-0.986775	8.55E-20
1506-MCG_252152938959_S01	3327	TT14	chr15	15	q14	34628280	34631417	4	0	-1.426614	-1.426614	2.59E-25
1506-MCG_252152938959_S01	3332	TT14	chr15	15	q14	35947358	35954416	4	0	-1.180133	-1.180133	2.07E-22
1506-MCG_252152938959_S01	3333	TT14	chr15	15	q14	37389105	37396371	5	0	-0.747403	-0.747403	1.15E-11
1506-MCG_252152938959_S01	3334	TT14	chr15	15	q14	38542171	38546350	3	0	-1.037697	-1.037697	1.21E-14
1506-MCG_252152938959_S01	3335	TT14	chr15	15	q14	38855065	38859762	4	0	-1.137834	-1.137834	1.62E-20
1506-MCG_252152938959_S01	3337	TT14	chr15	15	q15.1	40394780	40402020	5	0	-0.958152	-0.958152	1.09E-17
1506-MCG_252152938959_S01	3350	TT14	chr15	15	q15.2	43027117	43030034	3	0	-1.380513	-1.380513	1.16E-20
1506-MCG_252152938959_S01	3359	TT14	chr15	15	q21.1	45955564	45961721	4	0	-0.752487	-0.752487	1.37E-10
1506-MCG_252152938959_S01	3360	TT14	chr15	15	q21.1	48006696	48013919	5	0	-0.965875	-0.965875	1.87E-15
1506-MCG_252152938959_S01	3361	TT14	chr15	15	q21.1	48469685	48473115	3	0	-1.232344	-1.232344	6.6E-19
1506-MCG_252152938959_S01	3362	TT14	chr15	15	q21.1	48933825	48941122	5	0	-1.040482	-1.040482	3.12E-19

1506-MCG_252152938959_S01	3363	TT14	chr15	15	q21.1	49266014	49270441	4	0	-1.042162	-1.042162	6.38E-18
1506-MCG_252152938959_S01	3364	TT14	chr15	15	q21.2	49656988	49661645	4	0	-1.311735	-1.311735	5.14E-27
1506-MCG_252152938959_S01	3365	TT14	chr15	15	q21.2	50468785	50482044	10	0	-0.616259	-0.616259	2.42E-17
1506-MCG_252152938959_S01	3367	TT14	chr15	15	q21.2	51582544	51589977	6	0	-0.852239	-0.852239	8.91E-19
1506-MCG_252152938959_S01	3368	TT14	chr15	15	q21.2	51631638	51635883	4	0	-1.075512	-1.075512	1.65E-19
1506-MCG_252152938959_S01	3369	TT14	chr15	15	q21.2	52027853	52046582	8	0	-0.876674	-0.876674	2.32E-26
1506-MCG_252152938959_S01	3371	TT14	chr15	15	q21.2	52176080	52179609	3	0	-1.179607	-1.179607	2.14E-16
1506-MCG_252152938959_S01	3373	TT14	chr15	15	q21.2	52577201	52590077	14	0	-0.891523	-0.891523	5.81E-41
1506-MCG_252152938959_S01	3374	TT14	chr15	15	q21.2	52817185	52824788	6	0	-0.819504	-0.819504	1.09E-16
1506-MCG_252152938959_S01	3375	TT14	chr15	15	q21.3	53075292	53098895	14	0	-0.48895	-0.48895	2.13E-13
1506-MCG_252152938959_S01	3376	TT14	chr15	15	q21.3	54044274	54064733	9	0	-0.599873	-0.599873	5.09E-14
1506-MCG_252152938959_S01	3377	TT14	chr15	15	q21.3	54396507	54413902	9	0	-0.493418	-0.493418	1.25E-10
1506-MCG_252152938959_S01	3378	TT14	chr15	15	q21.3	55580873	55593587	5	0	-0.845477	-0.845477	4.26E-16
1506-MCG_252152938959_S01	3379	TT14	chr15	15	q21.3	55878001	55883032	4	0	-1.211012	-1.211012	4.03E-18
1506-MCG_252152938959_S01	3380	TT14	chr15	15	q21.3	56028685	56038081	6	0	-0.776412	-0.776412	4.1E-16
1506-MCG_252152938959_S01	3381	TT14	chr15	15	q21.3	56284557	56298732	8	0	-0.688017	-0.688017	1.8E-16
1506-MCG_252152938959_S01	3382	TT14	chr15	15	q21.3	56532615	56537782	5	0	-1.065741	-1.065741	2.42E-23
1506-MCG_252152938959_S01	3388	TT14	chr15	15	q22.1	59223714	59226879	3	0	-1.350235	-1.350235	1.13E-20
1506-MCG_252152938959_S01	3389	TT14	chr15	15	q22.2	59572200	59577123	4	0	-0.923191	-0.923191	4.17E-15
1506-MCG_252152938959_S01	3391	TT14	chr15	15	q22.2	61236287	61242042	8	0	-1.010628	-1.010628	1.37E-31
1506-MCG_252152938959_S01	3392	TT14	chr15	15	q22.2	61363087	61365215	3	0	-1.171757	-1.171757	1.41E-17
1506-MCG_252152938959_S01	3393	TT14	chr15	15	q22.2	62350092	62364547	10	0	-0.812716	-0.812716	8.68E-27
1506-MCG_252152938959_S01	3394	TT14	chr15	15	q22.2	62449514	62525172	25	0	-0.448812	-0.448812	2.25E-21
1506-MCG_252152938959_S01	3406	TT14	chr15	15	q22.31	65575412	65597673	12	0	-0.636957	-0.636957	2.15E-19
1506-MCG_252152938959_S01	3409	TT14	chr15	15	q22.33	67357060	67360534	3	0	-1.227232	-1.227232	1.34E-17
1506-MCG_252152938959_S01	3410	TT14	chr15	15	q23	67810023	67842467	17	0	-0.50502	-0.50502	4.4E-19
1506-MCG_252152938959_S01	3411	TT14	chr15	15	q23	68117437	68134218	10	0	-0.60145	-0.60145	1.12E-14
1506-MCG_252152938959_S01	3412	TT14	chr15	15	q23	68510121	68576842	30	0	-0.389606	-0.389606	3.24E-19
1506-MCG_252152938959_S01	3415	TT14	chr15	15	q23	69704215	69711555	5	0	-0.864272	-0.864272	5.26E-17
1506-MCG_252152938959_S01	3417	TT14	chr15	15	q23	71141150	71183446	21	0	-0.485765	-0.485765	1.77E-21
1506-MCG_252152938959_S01	3423	TT14	chr15	15	q23	72562519	72586742	15	0	-0.623609	-0.623609	1.61E-24
1506-MCG_252152938959_S01	3437	TT14	chr15	15	q24.3	76628429	76640635	8	0	-1.191522	-1.191522	1.36E-32
1506-MCG_252152938959_S01	3439	TT14	chr15	15	q24.3	77360863	77364085	3	0	-1.578959	-1.578959	4.53E-24
1506-MCG_252152938959_S01	3440	TT14	chr15	15	q24.3	77709817	77714605	4	0	-1.22462	-1.22462	1.11E-23
1506-MCG_252152938959_S01	3459	TT14	chr15	15	q25.3	86300132	86303772	6	0	-0.991939	-0.991939	6.82E-21
1506-MCG_252152938959_S01	3460	TT14	chr15	15	q25.3	86335581	86340444	5	0	-0.750695	-0.750695	9.96E-12
1506-MCG_252152938959_S01	3461	TT14	chr15	15	q25.3	86927851	86931688	3	0	-1.198073	-1.198073	2.75E-18
1506-MCG_252152938959_S01	3465	TT14	chr15	15	q26.1	89901498	89923092	26	0	-0.696136	-0.696136	4.41E-42
1506-MCG_252152938959_S01	3466	TT14	chr15	15	q26.1	90191005	90213125	17	0	-0.730989	-0.730989	1.74E-30
1506-MCG_252152938959_S01	3468	TT14	chr15	15	q26.1	90393461	90415827	13	0	-0.740182	-0.740182	1.04E-29
1506-MCG_252152938959_S01	3469	TT14	chr15	15	q26.1	90743533	90747488	3	0	-1.039597	-1.039597	1.62E-14
1506-MCG_252152938959_S01	3476	TT14	chr15	15	q26.1	92457058	92461954	4	0	-1.242243	-1.242243	1.32E-23
1506-MCG_252152938959_S01	3477	TT14	chr15	15	q26.1	93608090	93635178	16	0	-0.691845	-0.691845	6.93E-28
1506-MCG_252152938959_S01	3478	TT14	chr15	15	q26.2	95386703	95402240	7	0	-1.285396	-1.285396	7.54E-42
1506-MCG_252152938959_S01	3479	TT14	chr15	15	q26.2	96862256	96910411	50	0	-0.520618	-0.520618	6.95E-49
1506-MCG_252152938959_S01	3480	TT14	chr15	15	q26.2	96873020	96876347	5	0	-1.96201	-1.96201	2.48E-17
1506-MCG_252152938959_S01	3483	TT14	chr15	15	q26.2 - q26.3	98499656	98507009	5	0	-1.056214	-1.056214	1.02E-22
1506-MCG_252152938959_S01	3484	TT14	chr15	15	q26.3	98628330	98652509	7	0	-0.585291	-0.585291	1.1E-10
1506-MCG_252152938959_S01	3485	TT14	chr15	15	q26.3	99540304	99554091	7	0	-1.110669	-1.110669	1.17E-34
1506-MCG_252152938959_S01	3491	TT14	chr15	15	q26.3	101083535	101101920	10	0	-0.878053	-0.878053	6.86E-29
1506-MCG_252152938959_S01	3492	TT14	chr15	15	q26.3	101455610	101462918	6	0	-1.043085	-1.043085	3.44E-24
1506-MCG_252152938959_S01	3494	TT14	chr15	15	q26.3	101624783	101629506	3	0	-1.170304	-1.170304	3.83E-17
1506-MCG_252152938959_S01	3495	TT14	chr15	15	q26.3	101789504	101840768	26	0	-0.542655	-0.542655	7.51E-32
1506-MCG_252152938959_S01	3496	TT14	chr15	15	q26.3	102028441	102034423	4	0	-1.187613	-1.187613	1.45E-21
1506-MCG_252152938959_S01	3498	TT14	chr15	15	q26.3	102263359	102266016	3	0	-1.127158	-1.127158	8.33E-16
1506-MCG_252152938959_S01	3500	TT14	chr16	16	p13.3	185195	3353610	1238	0	-0.278038	-0.278038	4.900e-324
1506-MCG_252152938959_S01	3501	TT14	chr16	16	p13.3	668276	672126	3	0	-1.622076	-1.622076	3.66E-15
1506-MCG_252152938959_S01	3506	TT14	chr16	16	p13.3	2006856	2099068	40	0	-0.599042	-0.599042	1.22E-14
1506-MCG_252152938959_S01	3507	TT14	chr16	16	p13.3	2722049	2732132	5	0	-1.06627	-1.06627	1.55E-12
1506-MCG_252152938959_S01	3509	TT14	chr16	16	p13.3	3657088	3664903	6	0	-0.86885	-0.86885	2.12E-19
1506-MCG_252152938959_S01	3510	TT14	chr16	16	p13.3	3764864	3768085	3	0	-1.029871	-1.029871	8.7E-14
1506-MCG_252152938959_S01	3513	TT14	chr16	16	p13.3	6530097	6534173	3	0	-1.090444	-1.090444	1.01E-14
1506-MCG_252152938959_S01	3514	TT14	chr16	16	p13.3	6595689	6602026	5	0	-0.696483	-0.696483	3.74E-11
1506-MCG_252152938959_S01	3515	TT14	chr16	16	p13.3	7046160	7078751	17	0	-0.54958	-0.54958	2.05E-22
1506-MCG_252152938959_S01	3516	TT14	chr16	16	p13.3	7697965	7707912	6	0	-0.673332	-0.673332	7.74E-13
1506-MCG_252152938959_S01	3519	TT14	chr16	16	p13.2	9271042	9280048	4	0	-0.86273	-0.86273	3.76E-13
1506-MCG_252152938959_S01	3520	TT14	chr16	16	p13.2	10073774	10086128	8	0	-0.539106	-0.539106	1.31E-12
1506-MCG_252152938959_S01	3521	TT14	chr16	16	p13.13	11343885	11352749	5	0	-0.944048	-0.944048	3.44E-16
1506-MCG_252152938959_S01	3522	TT14	chr16	16	p13.13	11423004	11441629	12	0	-0.556337	-0.556337	2.9E-18
1506-MCG_252152938959_S01	3523	TT14	chr16	16	p13.13	11586017	11593925	5	0	-0.957	-0.957	7.88E-20
1506-MCG_252152938959_S01	3524	TT14	chr16	16	p13.13	12006530	12012499	4	0	-1.095904	-1.095904	2.88E-18
1506-MCG_252152938959_S01	3525	TT14	chr16	16	p13.12	14377515	14400719	23	0	-0.410574	-0.410574	6.39E-19
1506-MCG_252152938959_S01	3526	TT14	chr16	16	p13.11	15147365	15151093	3	0	-1.379532	-1.379532	4.65E-19
1506-MCG_252152938959_S01	3527	TT14	chr16	16	p13.11	15737765	15746483	11	0	-0.842511	-0.842511	5.17E-33
1506-MCG_252152938959_S01	3528	TT14	chr16	16	p13.11	15949527	15956209	5	0	-0.845796	-0.845796	1.21E-16
1506-MCG_252152938959_S01	3530	TT14	chr16	16	p12.3	18994598	18996301	3	0	-1.666131	-1.666131	4.2E-28
1506-MCG_252152938959_S01	3533	TT14	chr16	16	p12.3	20049860	20055652	5	0	-0.989191	-0.989191	5.66E-22
1506-MCG_252152938959_S01	3541	TT14	chr16	16	p12.1	24548742	24590151	20	0	-0.455431	-0.455431	3.06E-21
1506-MCG_252152938959_S01	3551	TT14	chr16	16	p11.2	30903627	30915107	6	0	-0.935011	-0.935011	9.6E-11
1506-MCG_252152938959_S01	3552	TT14	chr16	16	p11.2	30903627	31244505	157	0	-0.317777	-0.317777	8.42E-23
1506-MCG_252152938959_S01	3553	TT14	chr16	16	p11.2	30936116	30942057	4	0	-1.653742	-1.653742	3.36E-16
1506-MCG_252152938959_S01	3555	TT14	chr16	16	p11.2	31227281	31244505	9	0	-0.894473	-0.894473	2.97E-12
1506-MCG_252152938959_S01	3556	TT14	chr16	16	p11.2	31435768	31487258	24	0	-0.64268	-0.64268	2.93E-25
1506-MCG_252152938959_S01	3557	TT14	chr16	16	p11.2	34206074	34213224	6	0	-1.137233	-1.137233	1.91E-24
1506-MCG_252152938959_S01	3558	TT14	chr16	16	q11.2	46726341	46729920	5	0	-1.580859	-1.580859	2.48E-42
1506-MCG_252152938959_S01	3562	TT14	chr16	16	q12.1	48515183	48520527	3	0	-0.880812	-0.880812	3.46E-11
1506-MCG_252152938959_S01	3563	TT14	chr16	16	q12.1	49510642	49548926	21	0	-0.454938	-0.454938	4.64E-19
1506-MCG_252152938959_S01	3564	TT14	chr16	16	q12.1	49870854	49877273	4	0	-0.957471	-0.957471	3.57E-16
1506-MCG_252152938959_S01	3578	TT14	chr16	16	q13	56911366	56914633	4	0	-1.091481	-1.091481	2.14E-18
1506-MCG_252152938959_S01	3579	TT14	chr16	16	q13	57233681	57237847	3	0	-1.089818	-1.089818	3.23E-16
1506-MCG_252152938959_S01	3580	TT14	chr16	16	q13	57274367	57280954	6	0	-0.917673	-0.917673	3.82E-21
1506-MCG_252152938959_S01	3581	TT14	chr16	16	q21	57560930	57571441	6	0	-0.947402	-0.947402	2.29E-20
1506-MCG_252152938959_S01	3588	TT14	chr16	16	q22.1	67183753	67234597	34	0	-0.699873	-0.699873	2.62E-55
1506-MCG_252152938959_S01	3597	TT14	chr16	16	q22.1	69416221	69425615	6	0	-0.88128	-0.88128	5.16E-19
1506-MCG_252152938959_S01	3598	TT14	chr16	16	q22.1	69596835	69604594	10	0	-0.853724	-0.853724	5.2E-26
1506-MCG_252152938959_S01	3600	TT14	chr16	16	q22.2	71472654	71478764	4	0	-0.946788	-0.946788	3.94E-16

1506-MCG_252152938959_S01	3602	TT14	chr16	16	q22.3	73078930	73099761	11	0	-0.767605	-0.767605	1.53E-23
1506-MCG_252152938959_S01	3605	TT14	chr16	16	q23.1	77465234	77472120	5	0	-0.948885	-0.948885	8.6E-19
1506-MCG_252152938959_S01	3606	TT14	chr16	16	q23.1	78635994	78642849	4	0	-0.900763	-0.900763	2.28E-14
1506-MCG_252152938959_S01	3607	TT14	chr16	16	q23.2	79620939	79640486	12	0	-0.548381	-0.548381	7.04E-16
1506-MCG_252152938959_S01	3608	TT14	chr16	16	q23.2	80833452	80843034	5	0	-0.693591	-0.693591	1.23E-11
1506-MCG_252152938959_S01	3609	TT14	chr16	16	q23.2	81068752	81072096	3	0	-1.172237	-1.172237	2.95E-17
1506-MCG_252152938959_S01	3610	TT14	chr16	16	q23.2	81127047	81134497	5	0	-1.100411	-1.100411	3.21E-23
1506-MCG_252152938959_S01	3617	TT14	chr16	16	q24.1	85931720	85956742	15	0	-0.398166	-0.398166	2.34E-11
1506-MCG_252152938959_S01	3618	TT14	chr16	16	q24.1	86524459	86616736	48	0	-0.376853	-0.376853	1.97E-26
1506-MCG_252152938959_S01	3619	TT14	chr16	16	q24.1	86538734	86548110	5	0	-1.302944	-1.302944	1.96E-11
1506-MCG_252152938959_S01	3628	TT14	chr17	17	p13.3	1170540	1176469	4	0	-1.18992	-1.18992	1.88E-18
1506-MCG_252152938959_S01	3638	TT14	chr17	17	p13.3	2594489	2632895	23	0	-0.44297	-0.44297	2.22E-15
1506-MCG_252152938959_S01	3639	TT14	chr17	17	p13.3	2650266	2661875	11	0	-0.84704	-0.84704	5.94E-28
1506-MCG_252152938959_S01	3640	TT14	chr17	17	p13.2	3369261	3377180	5	0	-1.299434	-1.299434	6.16E-30
1506-MCG_252152938959_S01	3641	TT14	chr17	17	p13.2	3748524	3756524	4	0	-1.169207	-1.169207	1.67E-20
1506-MCG_252152938959_S01	3648	TT14	chr17	17	p13.2	5013730	5049888	13	0	-0.649625	-0.649625	6.91E-20
1506-MCG_252152938959_S01	3655	TT14	chr17	17	p13.1	7295160	7311225	8	0	-0.840484	-0.840484	3.59E-12
1506-MCG_252152938959_S01	3661	TT14	chr17	17	p13.1	9142056	9146306	3	0	-0.948134	-0.948134	8.3E-10
1506-MCG_252152938959_S01	3662	TT14	chr17	17	p13.1	9547123	9549743	3	0	-1.009898	-1.009898	4.3E-10
1506-MCG_252152938959_S01	3663	TT14	chr17	17	p13.1	10100621	10103782	3	0	-1.162682	-1.162682	4.51E-13
1506-MCG_252152938959_S01	3664	TT14	chr17	17	p13.1	10592866	10604587	7	0	-0.593703	-0.593703	2.78E-12
1506-MCG_252152938959_S01	3665	TT14	chr17	17	p12	11142803	11149214	3	0	-1.119161	-1.119161	2.04E-15
1506-MCG_252152938959_S01	3666	TT14	chr17	17	p12	11499945	11503170	3	0	-1.290131	-1.290131	3.29E-20
1506-MCG_252152938959_S01	3667	TT14	chr17	17	p12	11899624	11927378	15	0	-0.537172	-0.537172	1.17E-19
1506-MCG_252152938959_S01	3668	TT14	chr17	17	p12	12691006	12694596	3	0	-1.25627	-1.25627	5.14E-19
1506-MCG_252152938959_S01	3671	TT14	chr17	17	p12	14201443	14213458	6	0	-0.892511	-0.892511	4.58E-18
1506-MCG_252152938959_S01	3674	TT14	chr17	17	p12	15900975	15903878	3	0	-1.346454	-1.346454	1.2E-19
1506-MCG_252152938959_S01	3676	TT14	chr17	17	p11.2	16212697	16216627	3	0	-1.132385	-1.132385	5.7E-16
1506-MCG_252152938959_S01	3679	TT14	chr17	17	p11.2	17705510	17746898	32	0	-0.512477	-0.512477	9.32E-26
1506-MCG_252152938959_S01	3681	TT14	chr17	17	p11.2	18084877	18090030	4	0	-0.749847	-0.749847	6.46E-10
1506-MCG_252152938959_S01	3683	TT14	chr17	17	p11.2	18200354	18210039	9	0	-0.980106	-0.980106	1.3E-32
1506-MCG_252152938959_S01	3702	TT14	chr17	17	q11.2	29876002	29888598	13	0	-0.764327	-0.764327	4.39E-31
1506-MCG_252152938959_S01	3704	TT14	chr17	17	q11.2	30242551	30244833	3	0	-1.480446	-1.480446	8.14E-23
1506-MCG_252152938959_S01	3706	TT14	chr17	17	q11.2	30666760	30671145	6	0	-1.138148	-1.138148	3.9E-27
1506-MCG_252152938959_S01	3722	TT14	chr17	17	q12	37758808	37773133	9	0	-0.639373	-0.639373	2.62E-15
1506-MCG_252152938959_S01	3724	TT14	chr17	17	q21.2	38970019	38979083	5	0	-0.874697	-0.874697	1.34E-16
1506-MCG_252152938959_S01	3730	TT14	chr17	17	q21.2	40682904	40688958	3	0	-1.439587	-1.439587	3.16E-22
1506-MCG_252152938959_S01	3741	TT14	chr17	17	q21.31	42388509	42456979	34	0	-0.366221	-0.366221	3.07E-18
1506-MCG_252152938959_S01	3754	TT14	chr17	17	q21.32	46618771	46717643	101	0	-0.575264	-0.575264	1.39E-120
1506-MCG_252152938959_S01	3755	TT14	chr17	17	q21.32	46653704	46660064	9	0	-1.226327	-1.226327	1.4E-13
1506-MCG_252152938959_S01	3772	TT14	chr17	17	q22	56564078	56567605	3	0	-1.357559	-1.357559	1.67E-20
1506-MCG_252152938959_S01	3793	TT14	chr17	17	q24.2	65984595	66291531	61	0	-0.326104	-0.326104	4.29E-26
1506-MCG_252152938959_S01	3794	TT14	chr17	17	q24.2	65987167	65991512	3	0	-1.319506	-1.319506	8.75E-12
1506-MCG_252152938959_S01	3807	TT14	chr17	17	q25.1	72885149	72890773	3	0	-1.372475	-1.372475	3.29E-11
1506-MCG_252152938959_S01	3824	TT14	chr17	17	q25.3	78558343	78568272	6	0	-0.819338	-0.819338	5.11E-17
1506-MCG_252152938959_S01	3837	TT14	chr18	18	p11.32	2831810	2890205	23	0	-0.353502	-0.353502	1.8E-13
1506-MCG_252152938959_S01	3839	TT14	chr18	18	p11.31	5487802	5493556	5	0	-1.012651	-1.012651	8.1E-19
1506-MCG_252152938959_S01	3840	TT14	chr18	18	p11.31	5889923	5898162	4	0	-1.06759	-1.06759	8.15E-17
1506-MCG_252152938959_S01	3841	TT14	chr18	18	p11.31 - p11.23	7094699	7120084	13	0	-0.511426	-0.511426	1.01E-12
1506-MCG_252152938959_S01	3842	TT14	chr18	18	p11.23	7565876	7570888	3	0	-1.262308	-1.262308	9.3E-17
1506-MCG_252152938959_S01	3844	TT14	chr18	18	p11.22	9333152	9337255	3	0	-1.321838	-1.321838	3.2E-18
1506-MCG_252152938959_S01	3852	TT14	chr18	18	p11.21	12775366	12779543	3	0	-1.419308	-1.419308	3.6E-20
1506-MCG_252152938959_S01	3853	TT14	chr18	18	p11.21	12872432	12913481	15	0	-0.753785	-0.753785	2.49E-29
1506-MCG_252152938959_S01	3855	TT14	chr18	18	p11.21	13214829	13219924	3	0	-1.100197	-1.100197	3.29E-14
1506-MCG_252152938959_S01	3856	TT14	chr18	18	p11.21	13384159	13396141	8	0	-0.82045	-0.82045	8.5E-20
1506-MCG_252152938959_S01	3860	TT14	chr18	18	q11.2	19319970	19323804	4	0	-1.131522	-1.131522	1.1E-21
1506-MCG_252152938959_S01	3861	TT14	chr18	18	q11.2	19744116	19756261	7	0	-1.28339	-1.28339	4.01E-31
1506-MCG_252152938959_S01	3877	TT14	chr18	18	q12.2	35102221	35107044	4	0	-0.936079	-0.936079	9.02E-16
1506-MCG_252152938959_S01	3878	TT14	chr18	18	q12.3	42471633	42477932	5	0	-0.755476	-0.755476	2.72E-13
1506-MCG_252152938959_S01	3879	TT14	chr18	18	q12.3	42641042	42646272	4	0	-1.07697	-1.07697	3.11E-20
1506-MCG_252152938959_S01	3880	TT14	chr18	18	q12.3	43413639	43420504	5	0	-0.9648	-0.9648	9.76E-19
1506-MCG_252152938959_S01	3917	TT14	chr18	18	q23	74767608	74773879	4	0	-1.026482	-1.026482	3.53E-15
1506-MCG_252152938959_S01	3918	TT14	chr18	18	q23	75988860	77926204	694	0	-0.277283	-0.277283	2.26E-205
1506-MCG_252152938959_S01	3920	TT14	chr18	18	q23	77130486	77663749	204	0	-0.49987	-0.49987	4.68E-38
1506-MCG_252152938959_S01	3921	TT14	chr18	18	q23	77146135	77172940	11	0	-1.008701	-1.008701	2.04E-10
1506-MCG_252152938959_S01	3923	TT14	chr19	19	p13.3	288700	5270277	2294	0	-0.26641	-0.26641	4.900e-324
1506-MCG_252152938959_S01	3924	TT14	chr19	19	p13.3	495517	1514855	427	0	-0.503001	-0.503001	3.59E-74
1506-MCG_252152938959_S01	3925	TT14	chr19	19	p13.3	571351	585172	8	0	-1.171254	-1.171254	2.1E-10
1506-MCG_252152938959_S01	3937	TT14	chr19	19	p13.3	4908313	4913792	5	0	-1.058277	-1.058277	3.3E-11
1506-MCG_252152938959_S01	3938	TT14	chr19	19	p13.3	5221818	5248218	14	0	-0.781354	-0.781354	5.18E-16
1506-MCG_252152938959_S01	3946	TT14	chr19	19	p13.3	6735194	6755544	12	0	-0.492744	-0.492744	7.79E-13
1506-MCG_252152938959_S01	3947	TT14	chr19	19	p13.2	7194928	7201142	4	0	-0.818238	-0.818238	7.1E-14
1506-MCG_252152938959_S01	3953	TT14	chr19	19	p13.2	7939840	7953774	7	0	-0.972602	-0.972602	7.17E-23
1506-MCG_252152938959_S01	3954	TT14	chr19	19	p13.2	7966891	7970710	5	0	-0.86521	-0.86521	1.99E-13
1506-MCG_252152938959_S01	3964	TT14	chr19	19	p13.2	10528923	10628886	52	0	-0.379367	-0.379367	6.97E-21
1506-MCG_252152938959_S01	3980	TT14	chr19	19	p13.12	15088698	15091182	3	0	-1.37415	-1.37415	7.68E-19
1506-MCG_252152938959_S01	3981	TT14	chr19	19	p13.12	15217860	15223038	4	0	-1.175537	-1.175537	5.35E-19
1506-MCG_252152938959_S01	3982	TT14	chr19	19	p13.12	15268773	15314099	24	0	-0.587737	-0.587737	1.06E-24
1506-MCG_252152938959_S01	3984	TT14	chr19	19	p13.12	15469480	15582592	69	0	-0.445643	-0.445643	2.89E-36
1506-MCG_252152938959_S01	3985	TT14	chr19	19	p13.12	15536848	15542081	5	0	-1.246528	-1.246528	6.06E-11
1506-MCG_252152938959_S01	3988	TT14	chr19	19	p13.11	16684052	16688687	4	0	-1.243888	-1.243888	5.82E-24
1506-MCG_252152938959_S01	3997	TT14	chr19	19	p13.11	18258237	18283245	12	0	-1.223321	-1.223321	7.57E-50
1506-MCG_252152938959_S01	3999	TT14	chr19	19	p13.11	18648900	18732521	40	0	-0.463244	-0.463244	3.05E-23
1506-MCG_252152938959_S01	4000	TT14	chr19	19	p13.11	18778315	18798520	10	0	-0.574604	-0.574604	3.42E-10
1506-MCG_252152938959_S01	4005	TT14	chr19	19	p13.11	19728480	19757666	17	0	-0.719884	-0.719884	2.92E-25
1506-MCG_252152938959_S01	4014	TT14	chr19	19	q12	30428635	30443474	8	0	-0.903688	-0.903688	2.89E-28
1506-MCG_252152938959_S01	4015	TT14	chr19	19	q12	30861900	30873867	8	0	-0.765014	-0.765014	8.27E-20
1506-MCG_252152938959_S01	4016	TT14	chr19	19	q12	30931727	30937918	4	0	-0.951405	-0.951405	1.5E-15
1506-MCG_252152938959_S01	4017	TT14	chr19	19	q12	31834910	31845724	7	0	-0.60317	-0.60317	5.15E-11
1506-MCG_252152938959_S01	4018	TT14	chr19	19	q13.11	32893671	32899155	4	0	-0.876311	-0.876311	7.33E-14
1506-MCG_252152938959_S01	4019	TT14	chr19	19	q13.11	33065889	33072964	4	0	-1.085398	-1.085398	9.74E-19
1506-MCG_252152938959_S01	4031	TT14	chr19	19	q13.12	36423501	36437513	8	0	-1.053697	-1.053697	6.17E-27
1506-MCG_252152938959_S01	4035	TT14	chr19	19	q13.2	38875552	38896432	13	0	-0.802633	-0.802633	3.29E-21
1506-MCG_252152938959_S01	4038	TT14	chr19	19	q13.2	39339761	39347583	4	0	-1.46025	-1.46025	6.59E-21
1506-MCG_252152938959_S01	4041	TT14	chr19	19	q13.2	39795612	39812413	10	0	-0.922315	-0.922315	9.11E-29
1506-MCG_252152938959_S01	4046	TT14	chr19	19	q13.2	40789612	40792519	4	0	-1.266783	-1.266783	2.26E-19

1506-MCG_252152938959_S01	4047	TT14	chr19	19	q13.2	40926626	41194629	133	0	-0.371922	-0.371922	2.59E-48
1506-MCG_252152938959_S01	4048	TT14	chr19	19	q13.2	41018077	41026585	5	0	-1.158311	-1.158311	1.68E-13
1506-MCG_252152938959_S01	4049	TT14	chr19	19	q13.2	41678215	41690433	7	0	-0.761507	-0.761507	1.55E-15
1506-MCG_252152938959_S01	4066	TT14	chr19	19	q13.32	47248031	47261657	7	0	-0.795211	-0.795211	1.93E-15
1506-MCG_252152938959_S01	4067	TT14	chr19	19	q13.32	47503586	47578271	35	0	-0.444551	-0.444551	1.19E-20
1506-MCG_252152938959_S01	4068	TT14	chr19	19	q13.32	47728933	47768679	21	0	-0.670886	-0.670886	1.52E-28
1506-MCG_252152938959_S01	4071	TT14	chr19	19	q13.33	48669775	48700898	16	0	-0.474215	-0.474215	1.23E-21
1506-MCG_252152938959_S01	4075	TT14	chr19	19	q13.33	49606839	49621729	8	0	-1.071166	-1.071166	3.21E-27
1506-MCG_252152938959_S01	4078	TT14	chr19	19	q13.33	50101694	50105669	4	0	-1.453488	-1.453488	6.19E-28
1506-MCG_252152938959_S01	4079	TT14	chr19	19	q13.33	50344327	50394702	29	0	-0.494133	-0.494133	1.39E-20
1506-MCG_252152938959_S01	4083	TT14	chr19	19	q13.41	51596719	51610205	8	0	-1.072991	-1.072991	1.73E-30
1506-MCG_252152938959_S01	4086	TT14	chr19	19	q13.41	52216314	52220593	6	0	-1.024284	-1.024284	6.32E-24
1506-MCG_252152938959_S01	4087	TT14	chr19	19	q13.41	52452099	52457801	4	0	-0.960226	-0.960226	9.64E-15
1506-MCG_252152938959_S01	4088	TT14	chr19	19	q13.41	52796766	52801969	8	0	-0.729692	-0.729692	1.78E-13
1506-MCG_252152938959_S01	4089	TT14	chr19	19	q13.42	54627749	54722892	50	0	-0.336677	-0.336677	3.58E-15
1506-MCG_252152938959_S01	4091	TT14	chr19	19	q13.42	54959209	54979536	11	0	-0.830439	-0.830439	2.13E-23
1506-MCG_252152938959_S01	4093	TT14	chr19	19	q13.42	55768555	56204645	209	0	-0.366808	-0.366808	3.65E-69
1506-MCG_252152938959_S01	4094	TT14	chr19	19	q13.42	55814531	55822997	6	0	-1.194045	-1.194045	5.67E-15
1506-MCG_252152938959_S01	4104	TT14	chr19	19	q13.43	57682597	57685722	3	0	-1.276551	-1.276551	5.35E-18
1506-MCG_252152938959_S01	4105	TT14	chr19	19	q13.43	57990926	58000730	9	0	-1.029911	-1.029911	4.6E-31
1506-MCG_252152938959_S01	4106	TT14	chr19	19	q13.43	58172355	58179629	5	0	-0.866756	-0.866756	1.13E-13
1506-MCG_252152938959_S01	4107	TT14	chr19	19	q13.43	58534319	58674433	74	0	-0.291819	-0.291819	1.15E-16
1506-MCG_252152938959_S01	4112	TT14	chr20	20	p13	620050	657717	17	0	-0.608342	-0.608342	1.29E-24
1506-MCG_252152938959_S01	4128	TT14	chr20	20	p12.2	10011657	10016978	3	0	-1.42064	-1.42064	2.12E-22
1506-MCG_252152938959_S01	4129	TT14	chr20	20	p12.2	10651987	10656015	3	0	-1.189257	-1.189257	6.59E-13
1506-MCG_252152938959_S01	4131	TT14	chr20	20	p12.1	13738458	13743018	3	0	-1.176962	-1.176962	4.21E-17
1506-MCG_252152938959_S01	4132	TT14	chr20	20	p12.1	13965376	13978474	7	0	-0.896201	-0.896201	1.85E-21
1506-MCG_252152938959_S01	4145	TT14	chr20	20	p11.22	21370101	21379933	6	0	-1.27876	-1.27876	4.3E-37
1506-MCG_252152938959_S01	4146	TT14	chr20	20	p11.22	21484313	21505810	10	0	-0.842343	-0.842343	5E-25
1506-MCG_252152938959_S01	4147	TT14	chr20	20	p11.21	22559497	22566370	5	0	-1.491709	-1.491709	6.28E-30
1506-MCG_252152938959_S01	4148	TT14	chr20	20	p11.21	23009461	23032779	12	0	-0.480153	-0.480153	3.05E-12
1506-MCG_252152938959_S01	4149	TT14	chr20	20	p11.21	23330322	23349961	10	0	-0.700105	-0.700105	1.37E-20
1506-MCG_252152938959_S01	4165	TT14	chr20	20	q11.22	32249319	32290671	21	0	-0.620047	-0.620047	2.45E-30
1506-MCG_252152938959_S01	4166	TT14	chr20	20	q11.22	32398707	32400457	3	0	-1.201139	-1.201139	1.36E-16
1506-MCG_252152938959_S01	4173	TT14	chr20	20	q11.22	33412231	33415628	3	0	-1.450683	-1.450683	6.53E-22
1506-MCG_252152938959_S01	4175	TT14	chr20	20	q11.22	33579730	33590989	10	0	-0.713015	-0.713015	8.22E-17
1506-MCG_252152938959_S01	4198	TT14	chr20	20	q13.12	45521224	45527022	4	0	-1.011746	-1.011746	4.46E-18
1506-MCG_252152938959_S01	4199	TT14	chr20	20	q13.12	46156668	46178857	11	0	-0.451203	-0.451203	2.3E-14
1506-MCG_252152938959_S01	4200	TT14	chr20	20	q13.13	46412283	46415819	3	0	-1.25902	-1.25902	1.46E-17
1506-MCG_252152938959_S01	4201	TT14	chr20	20	q13.13	47536848	47556371	9	0	-0.63362	-0.63362	1.49E-15
1506-MCG_252152938959_S01	4204	TT14	chr20	20	q13.13	48531131	48553686	10	0	-0.830006	-0.830006	6.59E-27
1506-MCG_252152938959_S01	4207	TT14	chr20	20	q13.13	49410818	49415807	4	0	-1.054757	-1.054757	3.48E-18
1506-MCG_252152938959_S01	4208	TT14	chr20	20	q13.13	49620164	49643017	11	0	-0.663729	-0.663729	8.75E-20
1506-MCG_252152938959_S01	4213	TT14	chr20	20	q13.31	55921291	55927689	4	0	-1.301798	-1.301798	3.32E-25
1506-MCG_252152938959_S01	4232	TT14	chr21	21	q21.1	16432567	16441757	6	0	-0.836107	-0.836107	2.18E-18
1506-MCG_252152938959_S01	4233	TT14	chr21	21	q21.1	18981740	18989268	6	0	-0.902484	-0.902484	1.05E-20
1506-MCG_252152938959_S01	4234	TT14	chr21	21	q21.1	19616585	19618883	3	0	-1.456656	-1.456656	4.96E-20
1506-MCG_252152938959_S01	4235	TT14	chr21	21	q21.1	22369527	22374553	4	0	-1.028491	-1.028491	7.68E-15
1506-MCG_252152938959_S01	4236	TT14	chr21	21	q21.3	27062149	27071233	6	0	-0.70912	-0.70912	5.32E-14
1506-MCG_252152938959_S01	4237	TT14	chr21	21	q21.3	27148030	27152893	3	0	-1.089643	-1.089643	3.61E-15
1506-MCG_252152938959_S01	4238	TT14	chr21	21	q21.3	30368049	30390975	13	0	-0.653766	-0.653766	1.04E-23
1506-MCG_252152938959_S01	4239	TT14	chr21	21	q21.3	30666963	30674465	6	0	-0.852563	-0.852563	6.68E-19
1506-MCG_252152938959_S01	4240	TT14	chr21	21	q22.11	32873718	32877739	4	0	-0.84074	-0.84074	9.76E-13
1506-MCG_252152938959_S01	4242	TT14	chr21	21	q22.11	33028342	33037627	6	0	-0.8187	-0.8187	7.07E-18
1506-MCG_252152938959_S01	4245	TT14	chr21	21	q22.11	34391464	34407144	9	0	-0.633956	-0.633956	3.56E-16
1506-MCG_252152938959_S01	4252	TT14	chr21	21	q22.12	35983448	35990686	9	0	-0.836027	-0.836027	8.92E-27
1506-MCG_252152938959_S01	4254	TT14	chr21	21	q22.12	36258646	36265283	6	0	-0.938741	-0.938741	1.22E-19
1506-MCG_252152938959_S01	4257	TT14	chr21	21	q22.12	37685379	37697586	6	0	-0.887036	-0.887036	5.73E-20
1506-MCG_252152938959_S01	4258	TT14	chr21	21	q22.12	37756452	37766158	6	0	-0.942477	-0.942477	4.65E-23
1506-MCG_252152938959_S01	4259	TT14	chr21	21	q22.13	37865668	37871838	7	0	-0.789495	-0.789495	2.31E-19
1506-MCG_252152938959_S01	4260	TT14	chr21	21	q22.13	38117816	38125435	6	0	-0.864473	-0.864473	3.69E-19
1506-MCG_252152938959_S01	4262	TT14	chr21	21	q22.13	38444592	38448355	3	0	-0.947355	-0.947355	2.77E-12
1506-MCG_252152938959_S01	4263	TT14	chr21	21	q22.13	38737227	38742471	4	0	-0.977811	-0.977811	2.4E-13
1506-MCG_252152938959_S01	4264	TT14	chr21	21	q22.2	40028977	40052981	14	0	-0.566446	-0.566446	9.64E-20
1506-MCG_252152938959_S01	4265	TT14	chr21	21	q22.2	40172472	40194594	14	0	-0.653678	-0.653678	1.74E-25
1506-MCG_252152938959_S01	4266	TT14	chr21	21	q22.2	40527006	40565579	22	0	-0.400681	-0.400681	3.25E-16
1506-MCG_252152938959_S01	4267	TT14	chr21	21	q22.2	40681403	40688465	5	0	-0.72911	-0.72911	5.49E-12
1506-MCG_252152938959_S01	4272	TT14	chr21	21	q22.2	42215599	42222204	6	0	-1.120141	-1.120141	3.64E-28
1506-MCG_252152938959_S01	4273	TT14	chr21	21	q22.2	42537209	42542691	4	0	-0.877546	-0.877546	2.65E-13
1506-MCG_252152938959_S01	4274	TT14	chr21	21	q22.3	42673420	42693538	11	0	-0.594528	-0.594528	3.01E-16
1506-MCG_252152938959_S01	4277	TT14	chr21	21	q22.3	43653036	43658230	4	0	-0.993328	-0.993328	4.59E-16
1506-MCG_252152938959_S01	4281	TT14	chr21	21	q22.3	44836490	44851075	10	0	-0.847729	-0.847729	2.74E-14
1506-MCG_252152938959_S01	4282	TT14	chr21	21	q22.3	45078216	45080822	3	0	-1.52234	-1.52234	4.24E-19
1506-MCG_252152938959_S01	4287	TT14	chr21	21	q22.3	46807835	46935612	62	0	-0.483052	-0.483052	1.75E-20
1506-MCG_252152938959_S01	4292	TT14	chr22	22	q11.1	17586293	17603644	11	0	-0.719761	-0.719761	2.25E-20
1506-MCG_252152938959_S01	4294	TT14	chr22	22	q11.1	17848161	17851757	3	0	-1.033766	-1.033766	2.48E-14
1506-MCG_252152938959_S01	4305	TT14	chr22	22	q11.21	21919686	21924995	5	0	-0.917141	-0.917141	1.62E-16
1506-MCG_252152938959_S01	4307	TT14	chr22	22	q11.21	22086648	22093215	5	0	-0.79188	-0.79188	2.4E-14
1506-MCG_252152938959_S01	4309	TT14	chr22	22	q11.22	22219333	22236660	13	0	-0.626814	-0.626814	1.59E-21
1506-MCG_252152938959_S01	4310	TT14	chr22	22	q11.22	22473014	22475952	3	0	-1.045593	-1.045593	1.95E-15
1506-MCG_252152938959_S01	4311	TT14	chr22	22	q11.22	22859095	22869748	7	0	-0.618188	-0.618188	6.65E-14
1506-MCG_252152938959_S01	4312	TT14	chr22	22	q11.22	23358080	23360910	3	0	-1.26543	-1.26543	2.51E-20
1506-MCG_252152938959_S01	4315	TT14	chr22	22	q11.23	24091038	24137258	28	0	-0.357379	-0.357379	1.91E-17
1506-MCG_252152938959_S01	4316	TT14	chr22	22	q11.23	24711146	24715607	3	0	-1.192141	-1.192141	8.53E-19
1506-MCG_252152938959_S01	4317	TT14	chr22	22	q11.23	24986438	25087825	8	0	-0.91236	-0.91236	2.38E-29
1506-MCG_252152938959_S01	4318	TT14	chr22	22	q11.23	25672585	25679662	4	0	-1.242584	-1.242584	1.52E-26
1506-MCG_252152938959_S01	4319	TT14	chr22	22	q11.23	25799523	25834421	14	0	-0.540316	-0.540316	1.34E-20
1506-MCG_252152938959_S01	4320	TT14	chr22	22	q12.1	26982528	26993700	10	0	-0.512786	-0.512786	5.45E-13
1506-MCG_252152938959_S01	4322	TT14	chr22	22	q12.1	29161649	29203833	27	0	-0.440361	-0.440361	1.68E-25
1506-MCG_252152938959_S01	4331	TT14	chr22	22	q12.2	31361826	31369235	7	0	-0.828159	-0.828159	4.85E-21
1506-MCG_252152938959_S01	4333	TT14	chr22	22	q12.2	31883101	31888528	4	0	-1.004779	-1.004779	2.56E-18
1506-MCG_252152938959_S01	4334	TT14	chr22	22	q12.3	32864784	32873786	7	0	-0.612994	-0.612994	6.92E-14
1506-MCG_252152938959_S01	4335	TT14	chr22	22	q12.3	33194565	33201357	6	0	-0.821395	-0.821395	6.53E-19
1506-MCG_252152938959_S01	4336	TT14	chr22	22	q12.3	33451774	33458492	6	0	-0.689263	-0.689263	1.73E-14
1506-MCG_252152938959_S01	4337	TT14	chr22	22	q12.3	35649462	35656565	5	0	-0.905097	-0.905097	9.71E-18
1506-MCG_252152938959_S01	4342	TT14	chr22	22	q12.3	37413935	37421692	5	0	-1.152996	-1.152996	1.17E-23

1506-MCG_252152938959_S01	4350	TT14	chr22	22	q13.1	39096121	39103243	5	0	-1.364119	-1.364119	7.46E-34
1506-MCG_252152938959_S01	4353	TT14	chr22	22	q13.1	40268063	40273069	3	0	-1.090764	-1.090764	1.95E-15
1506-MCG_252152938959_S01	4354	TT14	chr22	22	q13.1	40390055	40392893	3	0	-1.143535	-1.143535	8.31E-16
1506-MCG_252152938959_S01	4355	TT14	chr22	22	q13.1	40439770	40443984	3	0	-1.212627	-1.212627	2.59E-18
1506-MCG_252152938959_S01	4357	TT14	chr22	22	q13.1	40930766	40934812	3	0	-1.409878	-1.409878	1.14E-20
1506-MCG_252152938959_S01	4358	TT14	chr22	22	q13.2	41030874	41034145	4	0	-1.092256	-1.092256	2.45E-19
1506-MCG_252152938959_S01	4367	TT14	chr22	22	q13.2	43363424	43381645	10	0	-0.755571	-0.755571	3.57E-24
1506-MCG_252152938959_S01	4368	TT14	chr22	22	q13.2	43409417	43413606	3	0	-0.815201	-0.815201	6.33E-10
1506-MCG_252152938959_S01	4369	TT14	chr22	22	q13.2	43473628	43548087	39	0	-0.330581	-0.330581	1.12E-17
1506-MCG_252152938959_S01	4382	TT14	chr22	22	q13.31	46420905	46502454	55	0	-0.697393	-0.697393	2.54E-90
252,152,934,024	6	TT4	chr5	5	q14.1	79395648	79531972	65	0.258023	0	0.258023	5.172E-18
252,152,934,024	24	TT4	chr15	15	q11.2	25427307	25496803	24	0	-0.361211	-0.361211	1.557E-12
252,152,934,024	42	TT4	chr22	22	q13.32	48894274	49058215	98	0	-0.259865	-0.259865	3.754E-16
252,152,934,024	43	TT4	chr22	22	q13.33	50693890	50762762	33	0	-0.34677	-0.34677	5.969E-10
252,152,934,026	1	TT9	chr1	1	p36.23	9165285	9194338	13	0	-0.553557	-0.553557	3.121E-20
252,152,934,026	2	TT9	chr1	1	p36.22	10234074	10253660	7	0	-0.582038	-0.582038	2.511E-13
252,152,934,026	3	TT9	chr1	1	p34.1	45233563	45272485	18	0	-0.452856	-0.452856	8.364E-18
252,152,934,026	5	TT9	chr1	1	p31.1	70377337	70388337	7	0	-0.766179	-0.766179	1.566E-20
252,152,934,026	6	TT9	chr1	1	p31.1	76331387	76393109	29	0	-0.301331	-0.301331	1.27E-14
252,152,934,026	7	TT9	chr1	1	p22.3	87254644	87264606	6	0	-0.671772	-0.671772	2.303E-13
252,152,934,026	8	TT9	chr1	1	q24.3	171060485	171070542	8	0	-0.636656	-0.636656	1.97E-16
252,152,934,026	9	TT9	chr1	1	q31.2	191967525	191976273	4	0	-0.839321	-0.839321	1.693E-12
252,152,934,026	10	TT9	chr1	1	q31.2	193120160	193134679	13	0	-0.464858	-0.464858	3.044E-12
252,152,934,026	11	TT9	chr1	1	q41	215371422	215387375	10	0	-0.713675	-0.713675	7.074E-25
252,152,934,026	12	TT9	chr1	1	q43	238649511	238671100	11	0	-0.691624	-0.691624	1.109E-24
252,152,934,026	14	TT9	chr2	2	p22.3	36170518	36201670	16	0	-0.361101	-0.361101	4.748E-12
252,152,934,026	15	TT9	chr2	2	p21	43725872	43749858	11	0	-0.439104	-0.439104	3.338E-12
252,152,934,026	16	TT9	chr2	2	p13.3	68661328	68753578	39	0	-0.283292	-0.283292	3.402E-16
252,152,934,026	17	TT9	chr2	2	p11.2	85108592	85123503	9	0	-0.543441	-0.543441	4.446E-14
252,152,934,026	18	TT9	chr2	2	q11.2	100641538	100663114	12	0	-0.500641	-0.500641	1.126E-15
252,152,934,026	19	TT9	chr2	2	q12.1	102960337	102979229	9	0	-0.598312	-0.598312	7.699E-16
252,152,934,026	20	TT9	chr2	2	q12.1	104004087	104055623	8	0	-0.613692	-0.613692	1.078E-15
252,152,934,026	21	TT9	chr2	2	q12.1	105458161	105483080	13	0	-0.401848	-0.401848	2.18E-11
252,152,934,026	23	TT9	chr2	2	q24.1	155784102	155810530	11	0	-0.541182	-0.541182	1.214E-16
252,152,934,026	27	TT9	chr2	2	q31.1	171498625	171510814	8	0	-0.541904	-0.541904	1.417E-11
252,152,934,026	28	TT9	chr2	2	q31.1	175111074	175144901	15	0	-0.455604	-0.455604	1.164E-15
252,152,934,026	29	TT9	chr2	2	q32.2	191818280	191889589	37	0.292114	0	0.292114	3.16E-17
252,152,934,026	30	TT9	chr3	3	p26.3	552102	579869	9	0	-0.541396	-0.541396	1.563E-14
252,152,934,026	31	TT9	chr3	3	p26.3	1740913	1758915	8	0	-0.466416	-0.466416	5.117E-10
252,152,934,026	32	TT9	chr3	3	p26.3	2744616	2751712	5	0	-0.720453	-0.720453	1.011E-13
252,152,934,026	35	TT9	chr3	3	p24.3	21179054	21190317	5	0	-0.722109	-0.722109	8.4E-12
252,152,934,026	36	TT9	chr3	3	p22.3	32975713	33002583	12	0	-0.472164	-0.472164	3.808E-15
252,152,934,026	37	TT9	chr3	3	p22.1	40228562	40251165	12	0	-0.547046	-0.547046	2.181E-19
252,152,934,026	38	TT9	chr3	3	p21.31	49629420	49647140	9	0	-0.45771	-0.45771	1.176E-11
252,152,934,026	39	TT9	chr3	3	p14.3	56995001	57008878	7	0	-0.507734	-0.507734	5.039E-11
252,152,934,026	40	TT9	chr3	3	p12.3	77360018	77380453	10	0	-0.495843	-0.495843	4.12E-11
252,152,934,026	41	TT9	chr3	3	q11.2	94635798	94659751	12	0	-0.657819	-0.657819	8.366E-25
252,152,934,026	42	TT9	chr3	3	q11.2	96335013	96341451	3	0	-1.11633	-1.11633	5.66E-14
252,152,934,026	43	TT9	chr3	3	q21.3	126997779	127024561	12	0	-0.613459	-0.613459	3.557E-23
252,152,934,026	44	TT9	chr3	3	q22.1	131688292	131712054	11	0	-0.39168	-0.39168	8.782E-10
252,152,934,026	46	TT9	chr3	3	q25.2	154762809	154793001	13	0	-0.466328	-0.466328	2.32E-15
252,152,934,026	47	TT9	chr3	3	q25.33	160021656	160036239	9	0	-0.677143	-0.677143	1.346E-20
252,152,934,026	48	TT9	chr3	3	q26.2	169481395	169495598	8	0	-0.773043	-0.773043	1.262E-22
252,152,934,026	49	TT9	chr3	3	q26.31	175381708	175395905	7	0	-0.691984	-0.691984	2.072E-17
252,152,934,026	51	TT9	chr3	3	q28	187908677	187938792	17	0	-0.28262	-0.28262	6.332E-12
252,152,934,026	52	TT9	chr3	3	q28	190560789	190611223	22	0	-0.286268	-0.286268	1.068E-10
252,152,934,026	54	TT9	chr4	4	q13.3	73387015	73402588	8	0	-0.58931	-0.58931	4.532E-15
252,152,934,026	58	TT9	chr4	4	q21.23	86785710	86805308	10	0	-0.569871	-0.569871	6.466E-17
252,152,934,026	59	TT9	chr4	4	q22.1	88135296	88157767	13	0	-0.595762	-0.595762	1.964E-23
252,152,934,026	60	TT9	chr4	4	q22.1	89287349	89312078	11	0	-0.596358	-0.596358	1.258E-19
252,152,934,026	61	TT9	chr4	4	q28.2	130925233	130942126	4	0	-0.790162	-0.790162	1.695E-11
252,152,934,026	62	TT9	chr4	4	q31.23	148680328	148716512	19	0	-0.321511	-0.321511	1.833E-11
252,152,934,026	63	TT9	chr4	4	q32.1	158269304	158281030	7	0	-0.772343	-0.772343	4.171E-17
252,152,934,026	64	TT9	chr4	4	q32.3	168008629	168152471	65	0	-0.258601	-0.258601	4.113E-18
252,152,934,026	65	TT9	chr4	4	q32.3	169070647	169081168	6	0	-1.000597	-1.000597	6.501E-24
252,152,934,026	66	TT9	chr4	4	q34.1	174391839	174410419	7	0	-0.613705	-0.613705	4.668E-13
252,152,934,026	67	TT9	chr5	5	p15.2	10338078	10360982	10	0	-0.705396	-0.705396	3.31E-25
252,152,934,026	68	TT9	chr5	5	p15.2	11114765	11138819	13	0	-0.419986	-0.419986	1.877E-12
252,152,934,026	69	TT9	chr5	5	p14.3	21698936	21732035	14	0	-0.5161	-0.5161	1.613E-13
252,152,934,026	70	TT9	chr5	5	p14.1	28598313	28640741	16	0	-0.666804	-0.666804	5.625E-27
252,152,934,026	71	TT9	chr5	5	p12	43028154	43050641	11	0	-0.867154	-0.867154	1.455E-35
252,152,934,026	72	TT9	chr5	5	p12	45362306	45385445	12	0	-0.564016	-0.564016	4.394E-19
252,152,934,026	74	TT9	chr5	5	q11.2	57880034	57891728	6	0	-0.540496	-0.540496	1.293E-11
252,152,934,026	75	TT9	chr5	5	q12.1	60326891	60350525	12	0	-0.415305	-0.415305	6.948E-12
252,152,934,026	76	TT9	chr5	5	q12.3	65816288	65834094	9	0	-0.455081	-0.455081	1.227E-10
252,152,934,026	77	TT9	chr5	5	q14.1	79893245	79905362	6	0	-0.571848	-0.571848	5.141E-11
252,152,934,026	80	TT9	chr5	5	q14.3	90001372	90025652	14	0	-0.374149	-0.374149	7.075E-11
252,152,934,026	81	TT9	chr5	5	q23.2	124229373	124237622	3	0	-0.886717	-0.886717	3.205E-12
252,152,934,026	82	TT9	chr5	5	q31.1	131499380	131516574	8	0	-0.531894	-0.531894	4.253E-14
252,152,934,026	83	TT9	chr5	5	q31.1	131791093	131834358	21	0.333802	0	0.333802	8.462E-11
252,152,934,026	84	TT9	chr5	5	q31.3	142814452	142834709	9	0	-0.451653	-0.451653	5.736E-12
252,152,934,026	85	TT9	chr5	5	q33.3	156600702	156686277	42	0.255418	0	0.255418	1.038E-12
252,152,934,026	87	TT9	chr5	5	q35.3	180629866	180652442	11	0	-0.484919	-0.484919	9.816E-13
252,152,934,026	88	TT9	chr6	6	p22.3	24355977	24362855	6	0	-1.072798	-1.072798	1.992E-28
252,152,934,026	89	TT9	chr6	6	p22.1	28676590	28689924	9	0	-0.659649	-0.659649	9.309E-20
252,152,934,026	91	TT9	chr6	6	p12.3	49859234	49870369	3	0	-0.845089	-0.845089	4.788E-11
252,152,934,026	92	TT9	chr6	6	p12.1	55946676	56006887	27	0	-0.475616	-0.475616	1.576E-30
252,152,934,026	94	TT9	chr6	6	q16.3	102192848	102224850	17	0	-0.496626	-0.496626	1.532E-17
252,152,934,026	95	TT9	chr6	6	q16.3	105466208	105482171	9	0	-0.611015	-0.611015	9.14E-14
252,152,934,026	96	TT9	chr6	6	q23.3	135222186	135232002	5	0	-0.660702	-0.660702	4.311E-12
252,152,934,026	98	TT9	chr6	6	q25.1	149040202	149076049	13	0	-0.425426	-0.425426	9.046E-13
252,152,934,026	99	TT9	chr6	6	q25.3	158237516	158250063	7	0	-0.738365	-0.738365	1.828E-17
252,152,934,026	100	TT9	chr6	6	q26	161685190	161791081	35	0	-0.318536	-0.318536	3.819E-19
252,152,934,026	101	TT9	chr6	6	q26	162290562	162306103	8	0	-0.709868	-0.709868	7.218E-20
252,152,934,026	102	TT9	chr6	6	q26	162425016	162438672	8	0	-0.555807	-0.555807	2.254E-11
252,152,934,026	105	TT9	chr7	7	p21.3	7709906	7727347	9	0	-0.537753	-0.537753	1.285E-13

252,152,934,026	106	TT9	chr7	7	p21.3	11207201	11224316	8	0	-0.645027	-0.645027	1.319E-15
252,152,934,026	107	TT9	chr7	7	p21.2	14591374	14617314	14	0	-0.49125	-0.49125	4.023E-15
252,152,934,026	108	TT9	chr7	7	p12.2	50009047	50031197	9	0	-0.818374	-0.818374	8.61E-25
252,152,934,026	109	TT9	chr7	7	p11.2	54461730	54470406	4	0	-0.762953	-0.762953	7.685E-10
252,152,934,026	113	TT9	chr7	7	q11.23	75887412	75900355	9	0	-0.976919	-0.976919	3.915E-31
252,152,934,026	114	TT9	chr7	7	q21.11	82719740	82732741	7	0	-0.758389	-0.758389	2.457E-16
252,152,934,026	115	TT9	chr7	7	q31.1	113669866	113727908	24	0	-0.402678	-0.402678	1.882E-17
252,152,934,026	116	TT9	chr7	7	q31.31	119601237	119629418	11	0	-0.431338	-0.431338	6.236E-10
252,152,934,026	118	TT9	chr7	7	q33	135248329	135267925	11	0	-0.462452	-0.462452	1.457E-12
252,152,934,026	119	TT9	chr7	7	q34	140081340	140094796	8	0	-0.536641	-0.536641	9.527E-13
252,152,934,026	120	TT9	chr7	7	q34	141820464	141845891	13	0	-0.532551	-0.532551	4.416E-19
252,152,934,026	121	TT9	chr8	8	p23.3	1912203	1928356	9	0	-0.491651	-0.491651	1.932E-10
252,152,934,026	122	TT9	chr8	8	p23.2	3222837	3271253	25	0	-0.30154	-0.30154	5.209E-10
252,152,934,026	124	TT9	chr8	8	p22	16029571	16058901	15	0	-0.568347	-0.568347	2.495E-20
252,152,934,026	125	TT9	chr8	8	p22	17731832	17746094	9	0	-0.577306	-0.577306	2.387E-13
252,152,934,026	126	TT9	chr8	8	p21.2	25855297	25863854	7	0	-0.718606	-0.718606	1.478E-18
252,152,934,026	127	TT9	chr8	8	p21.2	26095321	26110051	9	0	-0.492045	-0.492045	5.666E-12
252,152,934,026	128	TT9	chr8	8	p12	35099009	35117125	11	0	-0.612076	-0.612076	5.018E-21
252,152,934,026	130	TT9	chr8	8	p11.22	38359166	38387839	15	0	-0.393663	-0.393663	2.965E-13
252,152,934,026	131	TT9	chr8	8	q12.3	64028340	64044681	6	0	-0.60925	-0.60925	9.491E-12
252,152,934,026	132	TT9	chr8	8	q21.3	88133390	88161853	13	0	-0.650198	-0.650198	7.268E-26
252,152,934,026	134	TT9	chr8	8	q22.2	101053749	101072348	12	0	-0.43451	-0.43451	1.399E-12
252,152,934,026	136	TT9	chr8	8	q23.1	106878667	106897464	5	0	-0.631209	-0.631209	1.191E-10
252,152,934,026	137	TT9	chr9	9	p24.2	3497920	3515015	9	0	-0.627411	-0.627411	1.665E-17
252,152,934,026	138	TT9	chr9	9	p21.1	28858017	28869102	14	0	-0.458804	-0.458804	4.754E-11
252,152,934,026	139	TT9	chr9	9	p13.3	35491273	35501782	5	0	-0.710446	-0.710446	7.072E-13
252,152,934,026	140	TT9	chr9	9	p13.2	37795091	37827193	15	0	-0.494026	-0.494026	2.648E-18
252,152,934,026	142	TT9	chr9	9	q31.1	104243874	104267252	10	0	-0.476054	-0.476054	9.349E-13
252,152,934,026	143	TT9	chr9	9	q31.3	113438155	113471004	15	0	-0.662569	-0.662569	1.164E-31
252,152,934,026	145	TT9	chr10	10	p13	13148823	13160924	8	0	-0.500757	-0.500757	1.329E-11
252,152,934,026	146	TT9	chr10	10	p12.31	19514893	19614519	19	0	-0.356481	-0.356481	4.279E-13
252,152,934,026	148	TT9	chr10	10	q24.32	103110386	103148645	20	0	-0.294098	-0.294098	3.963E-10
252,152,934,026	149	TT9	chr10	10	q24.32	104385694	104426127	22	0	-0.478581	-0.478581	1.345E-25
252,152,934,026	150	TT9	chr10	10	q26.13	126152869	126178032	12	0	-0.441722	-0.441722	7.072E-13
252,152,934,026	151	TT9	chr10	10	q26.2	128243295	128274623	13	0	-0.438088	-0.438088	3.154E-13
252,152,934,026	152	TT9	chr11	11	p15.4	8567027	8601260	16	0	-0.323022	-0.323022	6.153E-10
252,152,934,026	153	TT9	chr11	11	p15.4	9686182	9704106	10	0	-0.776141	-0.776141	1.823E-27
252,152,934,026	154	TT9	chr11	11	p15.1	18063905	18084373	9	0	-0.428722	-0.428722	3.921E-10
252,152,934,026	155	TT9	chr11	11	p12	43320318	43339039	10	0	-0.651117	-0.651117	5.149E-21
252,152,934,026	156	TT9	chr11	11	p11.12	50127774	50141738	5	0	-0.715815	-0.715815	5.047E-13
252,152,934,026	157	TT9	chr11	11	q13.4	71980287	71987235	4	0	-0.831278	-0.831278	1.219E-12
252,152,934,026	158	TT9	chr11	11	q13.4	72960668	72967523	4	0	-1.02139	-1.02139	1.039E-18
252,152,934,026	159	TT9	chr11	11	q22.1	97525885	97544807	9	0	-0.590494	-0.590494	2.996E-13
252,152,934,026	160	TT9	chr11	11	q23.2 - q23.3	114452469	114537625	21	0	-0.283246	-0.283246	1.007E-11
252,152,934,026	161	TT9	chr12	12	p13.31	7012559	7040293	15	0	-0.41001	-0.41001	4.328E-14
252,152,934,026	162	TT9	chr12	12	p13.31	9907267	9926351	9	0.487419	0	0.487419	1.037E-11
252,152,934,026	164	TT9	chr12	12	p12.1	23983182	24006615	13	0	-0.46493	-0.46493	3.553E-15
252,152,934,026	165	TT9	chr12	12	q12	44540298	44554041	9	0	-0.506919	-0.506919	4.998E-13
252,152,934,026	166	TT9	chr12	12	q15	69212940	69236356	14	0	-0.456576	-0.456576	8.892E-16
252,152,934,026	167	TT9	chr12	12	q21.31	86260574	86339569	21	0	-0.377495	-0.377495	1.108E-11
252,152,934,026	168	TT9	chr12	12	q24.31	121339601	121380173	13	0	-0.378855	-0.378855	7.003E-11
252,152,934,026	169	TT9	chr13	13	q12.2	28494825	28583443	45	0	-0.297838	-0.297838	3.593E-20
252,152,934,026	170	TT9	chr13	13	q13.3	39553351	39573661	9	0	-0.544259	-0.544259	3.923E-14
252,152,934,026	171	TT9	chr13	13	q14.13	45988336	46007401	15	0	-0.569993	-0.569993	2.443E-24
252,152,934,026	173	TT9	chr13	13	q31.1	79938156	79961205	14	0	-0.598822	-0.598822	3.107E-21
252,152,934,026	175	TT9	chr13	13	q31.1	86910414	86926030	8	0	-0.626539	-0.626539	1.143E-10
252,152,934,026	176	TT9	chr13	13	q31.3	93252593	93281525	17	0	-0.394026	-0.394026	1.26E-11
252,152,934,026	178	TT9	chr13	13	q33.3	109664292	109682659	9	0	-0.465848	-0.465848	3.371E-11
252,152,934,026	179	TT9	chr14	14	q11.2	20697414	20716833	9	0	-0.679815	-0.679815	2.202E-20
252,152,934,026	183	TT9	chr14	14	q22.1	52985402	53003251	12	0	-0.670381	-0.670381	1.256E-25
252,152,934,026	184	TT9	chr14	14	q31.3	89255433	89270404	8	0	-0.635339	-0.635339	5.382E-15
252,152,934,026	185	TT9	chr14	14	q32.12	93004731	93022741	9	0	-0.45775	-0.45775	3.31E-11
252,152,934,026	187	TT9	chr15	15	q15.2	42839654	42862250	16	0	-0.381494	-0.381494	1.41E-12
252,152,934,026	189	TT9	chr15	15	q25.3	87507721	87542032	22	0	-0.353395	-0.353395	2.055E-15
252,152,934,026	190	TT9	chr16	16	p13.3	6677158	6700697	13	0	-0.393017	-0.393017	1.146E-11
252,152,934,026	191	TT9	chr16	16	p13.3	6815332	6842236	12	0	-0.470869	-0.470869	1.332E-14
252,152,934,026	192	TT9	chr16	16	p11.1	34774258	34786127	6	0	-0.879912	-0.879912	3.299E-20
252,152,934,026	194	TT9	chr17	17	q12	37087537	37113474	15	0	-0.598361	-0.598361	1.268E-26
252,152,934,026	195	TT9	chr17	17	q21.31	43970762	43993293	12	0	-0.445354	-0.445354	1.693E-12
252,152,934,026	197	TT9	chr17	17	q23.2	59850540	59871032	11	0	-0.68522	-0.68522	1.848E-24
252,152,934,026	199	TT9	chr18	18	q21.1	45367254	45388189	11	0	-0.602658	-0.602658	2.445E-20
252,152,934,026	200	TT9	chr18	18	q21.2	50936882	50966992	16	0	-0.513589	-0.513589	1.843E-21
252,152,934,026	201	TT9	chr18	18	q22.1	66505951	66525356	9	0	-0.607846	-0.607846	3.261E-13
252,152,934,026	202	TT9	chr19	19	p13.2	7064859	7070469	5	0	-0.651456	-0.651456	3.018E-10
252,152,934,026	203	TT9	chr19	19	p13.2	7924966	7976400	26	0	-0.374494	-0.374494	1.225E-13
252,152,934,026	205	TT9	chr19	19	q13.11	33608694	33625464	10	0	-0.503171	-0.503171	3.006E-11
252,152,934,026	206	TT9	chr19	19	q13.31	43896675	43914287	9	0	-0.528868	-0.528868	1.044E-11
252,152,934,026	208	TT9	chr19	19	q13.33	50188988	50216338	18	0	-0.400567	-0.400567	9.874E-13
252,152,934,026	209	TT9	chr19	19	q13.33	51216944	51251429	17	0	-0.405058	-0.405058	2.65E-12
252,152,934,026	211	TT9	chr20	20	p12.3	8622848	8649522	15	0	-0.399754	-0.399754	1.452E-13
252,152,934,026	212	TT9	chr20	20	p12.1	14931823	14950564	10	0	-0.608717	-0.608717	1.02E-18
252,152,934,026	213	TT9	chr20	20	q13.12	42751457	42777780	14	0	-0.38606	-0.38606	1.136E-12
252,152,934,026	214	TT9	chr21	21	q21.1	17725089	17770917	24	0	-0.296289	-0.296289	4.194E-12
252,152,934,026	215	TT9	chr21	21	q21.1	19614098	19644728	26	0	-0.577205	-0.577205	2.492E-29
252,152,934,026	216	TT9	chr21	21	q21.1	22808584	22920901	62	0	-0.283028	-0.283028	2.562E-12
252,152,934,026	217	TT9	chr21	21	q21.2	24792729	24808653	8	0	-0.634004	-0.634004	4.476E-12
252,152,934,026	218	TT9	chr21	21	q22.11	31926707	31982011	27	0	-0.354465	-0.354465	4.513E-18
252,152,934,026	219	TT9	chr21	21	q22.11	34688902	34699955	5	0	-0.623942	-0.623942	1.965E-10
252,152,934,026	220	TT9	chr21	21	q22.3	44295943	44321188	15	0	-0.405449	-0.405449	1.915E-10
252,152,934,023	1	TT13	chr1	1	p36.33 - p36.32	837386	3711729	1009	0	-0.5455	-0.5455	4.900e-324
252,152,934,023	2	TT13	chr1	1	p36.33	903766	916634	5	0	-1.456403	-1.456403	4.76E-11
252,152,934,023	13	TT13	chr1	1	p36.33	2099931	2124738	14	0	-1.218297	-1.218297	1.002E-19
252,152,934,023	35	TT13	chr1	1	p36.32	3812363	3822284	5	0	-0.833286	-0.833286	3.606E-15
252,152,934,023	39	TT13	chr1	1	p36.31	6038009	6698570	272	0	-0.376288	-0.376288	3.023E-104
252,152,934,023	40	TT13	chr1	1	p36.31	6124968	6130435	4	0	-1.97222	-1.97222	6.463E-23
252,152,934,023	46	TT13	chr1	1	p36.31	6659729	6696508	19	0	-0.924942	-0.924942	6.784E-22

252,152,934,023	48	TT13	chr1	1	p36.31	6842596	6849062	4	0	-1.377384	-1.377384	7.156E-26
252,152,934,023	49	TT13	chr1	1	p36.31	7019181	7025791	4	0	-1.195881	-1.195881	4.168E-20
252,152,934,023	52	TT13	chr1	1	p36.23	7826748	7848371	10	0	-1.076654	-1.076654	1.38E-42
252,152,934,023	53	TT13	chr1	1	p36.23	7885280	7890277	4	0	-1.252251	-1.252251	5.476E-22
252,152,934,023	54	TT13	chr1	1	p36.23	8009450	8024247	8	0	-1.278378	-1.278378	2.101E-44
252,152,934,023	57	TT13	chr1	1	p36.23	8377847	8403665	13	0	-0.741263	-0.741263	5.606E-25
252,152,934,023	58	TT13	chr1	1	p36.23	8480673	8486959	5	0	-1.138776	-1.138776	1.795E-22
252,152,934,023	60	TT13	chr1	1	p36.23	8759587	8766451	5	0	-1.367601	-1.367601	1.036E-30
252,152,934,023	63	TT13	chr1	1	p36.23	8971146	8973048	3	0	-1.966807	-1.966807	1.456E-39
252,152,934,023	73	TT13	chr1	1	p36.22	10087094	10094740	5	0	-1.869282	-1.869282	1.446E-47
252,152,934,023	74	TT13	chr1	1	p36.22	10482720	10490014	4	0	-1.693892	-1.693892	8.51E-30
252,152,934,023	75	TT13	chr1	1	p36.22	10586560	10596275	7	0	-0.880098	-0.880098	2.228E-21
252,152,934,023	76	TT13	chr1	1	p36.22	10687365	10767400	37	0	-1.053013	-1.053013	6.654E-100
252,152,934,023	77	TT13	chr1	1	p36.22	10694013	10724147	14	0	-1.936212	-1.936212	1.091E-22
252,152,934,023	93	TT13	chr1	1	p36.22	12598992	12611699	9	0	-1.075085	-1.075085	2.811E-37
252,152,934,023	94	TT13	chr1	1	p36.22	12654184	12680578	13	0	-0.656446	-0.656446	2.042E-20
252,152,934,023	100	TT13	chr1	1	p36.21	14921030	14929967	6	0	-0.995244	-0.995244	1.837E-29
252,152,934,023	101	TT13	chr1	1	p36.21	15246658	15252877	4	0	-0.991329	-0.991329	7.04E-18
252,152,934,023	103	TT13	chr1	1	p36.21	15476594	15484358	5	0	-0.72579	-0.72579	1.325E-13
252,152,934,023	104	TT13	chr1	1	p36.21	15569705	15578059	5	0	-1.198227	-1.198227	3.653E-33
252,152,934,023	105	TT13	chr1	1	p36.21	15732787	15759606	14	0	-0.549309	-0.549309	3.459E-14
252,152,934,023	108	TT13	chr1	1	p36.21	15943078	15948486	4	0	-1.30086	-1.30086	5.673E-25
252,152,934,023	109	TT13	chr1	1	p36.21	16059692	16091866	14	0	-0.706262	-0.706262	2.607E-23
252,152,934,023	110	TT13	chr1	1	p36.21	16160344	16177397	8	0	-1.43983	-1.43983	2.701E-49
252,152,934,023	113	TT13	chr1	1	p36.13	16473571	16496926	11	0	-0.958041	-0.958041	7.464E-33
252,152,934,023	114	TT13	chr1	1	p36.13	16531036	16564424	17	0	-1.199178	-1.199178	1.085E-65
252,152,934,023	117	TT13	chr1	1	p36.13	17276005	17312224	16	0	-1.246888	-1.246888	4.74E-64
252,152,934,023	125	TT13	chr1	1	p36.13	18955412	18974422	11	0	-1.625001	-1.625001	3.776E-69
252,152,934,023	128	TT13	chr1	1	p36.13	19224874	19231939	10	0	-1.118338	-1.118338	2.195E-42
252,152,934,023	130	TT13	chr1	1	p36.13	19594971	19670722	34	0	-0.460824	-0.460824	2.177E-23
252,152,934,023	131	TT13	chr1	1	p36.13	19637504	19641386	3	0	-1.587148	-1.587148	6.312E-11
252,152,934,023	134	TT13	chr1	1	p36.13	19965857	20010200	21	0	-0.715756	-0.715756	2.608E-36
252,152,934,023	135	TT13	chr1	1	p36.13	20202479	20215729	8	0	-0.805465	-0.805465	9.727E-29
252,152,934,023	136	TT13	chr1	1	p36.13	20304950	20315059	5	0	-0.633024	-0.633024	2.367E-12
252,152,934,023	137	TT13	chr1	1	p36.12	20509275	20514726	4	0	-1.11233	-1.11233	1.552E-24
252,152,934,023	140	TT13	chr1	1	p36.12	20809150	20814586	3	0	-1.714112	-1.714112	1.104E-27
252,152,934,023	142	TT13	chr1	1	p36.12	21029140	21145327	54	0	-0.415756	-0.415756	2.883E-29
252,152,934,023	143	TT13	chr1	1	p36.12	21138966	21145327	4	0	-1.387351	-1.387351	2.749E-14
252,152,934,023	149	TT13	chr1	1	p36.12	21825029	21837784	7	0	-1.329949	-1.329949	3.236E-38
252,152,934,023	151	TT13	chr1	1	p36.12	21976661	21997717	10	0	-1.001155	-1.001155	4.523E-33
252,152,934,023	155	TT13	chr1	1	p36.12	22139855	22154083	6	0	-1.452832	-1.452832	3.289E-16
252,152,934,023	160	TT13	chr1	1	p36.12	22887170	22933522	24	0	-0.758734	-0.758734	4.311E-38
252,152,934,023	161	TT13	chr1	1	p36.12	23490124	23507240	10	0	-1.155026	-1.155026	5.47E-44
252,152,934,023	172	TT13	chr1	1	p36.11	24511795	24524682	8	0	-1.107201	-1.107201	3.877E-32
252,152,934,023	190	TT13	chr1	1	p36.11	26605263	26610012	3	0	-1.837723	-1.837723	1.481E-22
252,152,934,023	195	TT13	chr1	1	p36.11	27110170	27154631	21	0	-1.012014	-1.012014	3.694E-46
252,152,934,023	201	TT13	chr1	1	p36.11	27675488	27694046	8	0	-1.731699	-1.731699	7.26E-47
252,152,934,023	202	TT13	chr1	1	p36.11	27710878	27721708	6	0	-0.999255	-0.999255	8.228E-14
252,152,934,023	208	TT13	chr1	1	p35.3	28177740	28182544	3	0	-1.525292	-1.525292	1.338E-17
252,152,934,023	213	TT13	chr1	1	p35.3	28907123	28919697	6	0	-1.162438	-1.162438	8.537E-28
252,152,934,023	217	TT13	chr1	1	p35.3	29240316	29245682	4	0	-1.273387	-1.273387	2.075E-23
252,152,934,023	218	TT13	chr1	1	p35.3	29447324	29463384	8	0	-1.016356	-1.016356	3.609E-22
252,152,934,023	219	TT13	chr1	1	p35.3	29506218	29509628	3	0	-1.426272	-1.426272	6.453E-21
252,152,934,023	220	TT13	chr1	1	p35.3	29562293	29565728	3	0	-2.064768	-2.064768	7.263E-32
252,152,934,023	224	TT13	chr1	1	p35.2	31647344	31653720	4	0	-2.085066	-2.085066	1.733E-44
252,152,934,023	229	TT13	chr1	1	p35.2	32192705	32239771	24	0	-1.286942	-1.286942	2.135E-101
252,152,934,023	230	TT13	chr1	1	p35.2	32211581	32218938	5	0	-0.462511	-0.462511	1.647E-15
252,152,934,023	233	TT13	chr1	1	p35.1	32707331	32717736	6	0	-0.875706	-0.875706	1.119E-10
252,152,934,023	235	TT13	chr1	1	p35.1	32799418	32829866	16	0	-0.736731	-0.736731	4.686E-16
252,152,934,023	239	TT13	chr1	1	p35.1	33205824	33238880	16	0	-0.86699	-0.86699	7.466E-24
252,152,934,023	245	TT13	chr1	1	p35.1	33812229	33825029	8	0	-1.355752	-1.355752	6.208E-37
252,152,934,023	248	TT13	chr1	1	p35.1	34545245	34551848	4	0	-1.343557	-1.343557	2.202E-26
252,152,934,023	249	TT13	chr1	1	p34.3	34624767	34646451	12	0	-0.845141	-0.845141	2.171E-31
252,152,934,023	251	TT13	chr1	1	p34.3	35322436	35354997	18	0	-0.842913	-0.842913	1.323E-41
252,152,934,023	252	TT13	chr1	1	p34.3	35393703	35457462	22	0	-1.163264	-1.163264	2.246E-100
252,152,934,023	253	TT13	chr1	1	p34.3	35492060	35497693	5	0	-0.92081	-0.92081	1.022E-17
252,152,934,023	254	TT13	chr1	1	p34.3	35731457	35736567	3	0	-1.072691	-1.072691	2.808E-14
252,152,934,023	255	TT13	chr1	1	p34.3	36020004	36043564	13	0	-1.174413	-1.174413	2.497E-53
252,152,934,023	256	TT13	chr1	1	p34.3	36168228	36185996	10	0	-0.788814	-0.788814	2.3E-21
252,152,934,023	258	TT13	chr1	1	p34.3	36270106	36276436	4	0	-1.166296	-1.166296	7.34E-21
252,152,934,023	259	TT13	chr1	1	p34.3	36347373	36351533	3	0	-1.027738	-1.027738	3.374E-13
252,152,934,023	260	TT13	chr1	1	p34.3	36392094	36400997	7	0	-1.08089	-1.08089	1.668E-28
252,152,934,023	261	TT13	chr1	1	p34.3	36545763	36648780	54	0	-0.581261	-0.581261	1.344E-55
252,152,934,023	262	TT13	chr1	1	p34.3	36548138	36557195	6	0	-1.467484	-1.467484	1.06E-15
252,152,934,023	266	TT13	chr1	1	p34.3	37496328	37501157	3	0	-1.325525	-1.325525	5.053E-24
252,152,934,023	290	TT13	chr1	1	p34.2	41956054	41984193	14	0	-1.044328	-1.044328	3.065E-43
252,152,934,023	291	TT13	chr1	1	p34.2	42123905	42134441	6	0	-0.716071	-0.716071	3.331E-20
252,152,934,023	292	TT13	chr1	1	p34.2	42380507	42386883	4	0	-1.096031	-1.096031	4.876E-16
252,152,934,023	293	TT13	chr1	1	p34.2	42500766	42504848	3	0	-1.307756	-1.307756	4.136E-18
252,152,934,023	295	TT13	chr1	1	p34.2	42917296	42925694	6	0	-0.935874	-0.935874	3.38E-21
252,152,934,023	296	TT13	chr1	1	p34.2	43143795	43154781	7	0	-1.075016	-1.075016	4.749E-30
252,152,934,023	297	TT13	chr1	1	p34.2	43204485	43254040	26	0	-0.632374	-0.632374	3.441E-37
252,152,934,023	308	TT13	chr1	1	p34.1	44441473	44446139	3	0	-2.007766	-2.007766	1.048E-15
252,152,934,023	310	TT13	chr1	1	p34.1	44868987	44889109	10	0	-1.051452	-1.051452	1.952E-39
252,152,934,023	315	TT13	chr1	1	p34.1	45307093	45311756	4	0	-1.446806	-1.446806	1.061E-28
252,152,934,023	316	TT13	chr1	1	p34.1	45338443	45346136	4	0	-1.199556	-1.199556	7.694E-22
252,152,934,023	317	TT13	chr1	1	p34.1	45474508	45478139	3	0	-1.257588	-1.257588	5.38E-17
252,152,934,023	320	TT13	chr1	1	p34.1	45791572	45807730	9	0	-1.147166	-1.147166	3.76E-38
252,152,934,023	321	TT13	chr1	1	p34.1	45955635	45966863	7	0	-0.885224	-0.885224	2.269E-20
252,152,934,023	323	TT13	chr1	1	p34.1	46187369	46233671	19	0	-1.23219	-1.23219	5.417E-89
252,152,934,023	324	TT13	chr1	1	p34.1	46266753	46271562	3	0	-1.362743	-1.362743	9.473E-20
252,152,934,023	331	TT13	chr1	1	p33	47684314	47699646	8	0	-1.476588	-1.476588	7.522E-52
252,152,934,023	332	TT13	chr1	1	p33	47796164	47803642	4	0	-1.055623	-1.055623	1.185E-17
252,152,934,023	333	TT13	chr1	1	p33	47875766	47911230	20	0	-0.540837	-0.540837	4.66E-20
252,152,934,023	337	TT13	chr1	1	p33	48449542	48468186	10	0	-1.220874	-1.220874	5.225E-49
252,152,934,023	338	TT13	chr1	1	p33	48845995	48851961	4	0	-1.486979	-1.486979	2.545E-29

252,152,934,023	339	TT13	chr1	1	p33	48936274	48950588	8	0	-1.515579	-1.515579	1.28E-57
252,152,934,023	340	TT13	chr1	1	p33	49239647	49244731	3	0	-1.219309	-1.219309	3.046E-17
252,152,934,023	341	TT13	chr1	1	p33	50005250	50020229	6	0	-1.063315	-1.063315	2.945E-24
252,152,934,023	343	TT13	chr1	1	p32.3	50794231	50801542	4	0	-1.283255	-1.283255	1.059E-23
252,152,934,023	344	TT13	chr1	1	p32.3	50883522	50890453	4	0	-2.11152	-2.11152	3.546E-39
252,152,934,023	345	TT13	chr1	1	p32.3	51286881	51315378	15	0	-0.709427	-0.709427	3.408E-29
252,152,934,023	346	TT13	chr1	1	p32.3	51416501	51445710	17	0	-1.536777	-1.536777	2.257E-119
252,152,934,023	363	TT13	chr1	1	p32.3	53385554	53397292	7	0	-1.379996	-1.379996	4.579E-44
252,152,934,023	364	TT13	chr1	1	p32.3	53523687	53547875	13	0	-0.950386	-0.950386	1.633E-35
252,152,934,023	370	TT13	chr1	1	p32.3	53902733	53905952	3	0	-2.097375	-2.097375	4.254E-14
252,152,934,023	371	TT13	chr1	1	p32.3	53902733	53939179	19	0	-0.822558	-0.822558	3.64E-40
252,152,934,023	381	TT13	chr1	1	p32.3	54939315	54966118	14	0	-0.881354	-0.881354	7.005E-35
252,152,934,023	382	TT13	chr1	1	p32.3	55006213	55030131	11	0	-0.861337	-0.861337	1.306E-25
252,152,934,023	383	TT13	chr1	1	p32.3	55178990	55183527	3	0	-1.358417	-1.358417	2.957E-19
252,152,934,023	384	TT13	chr1	1	p32.3	55227034	55273554	24	0	-0.727706	-0.727706	3.378E-40
252,152,934,023	386	TT13	chr1	1	p32.3	55348952	55355878	4	0	-0.759406	-0.759406	1.587E-10
252,152,934,023	387	TT13	chr1	1	p32.3	55440938	55463739	12	0	-0.704137	-0.704137	1.066E-18
252,152,934,023	388	TT13	chr1	1	p32.3	55500471	55525888	12	0	-0.67874	-0.67874	3.682E-18
252,152,934,023	389	TT13	chr1	1	p32.3	55674778	55683860	6	0	-1.063736	-1.063736	1.285E-30
252,152,934,023	391	TT13	chr1	1	p32.2	57106831	57115304	6	0	-1.221676	-1.221676	3.427E-35
252,152,934,023	392	TT13	chr1	1	p32.2	57807434	57811130	3	0	-1.986347	-1.986347	9.684E-35
252,152,934,023	393	TT13	chr1	1	p32.2	57883121	57890776	5	0	-1.034589	-1.034589	2.71E-19
252,152,934,023	394	TT13	chr1	1	p32.2	58712705	58718702	4	0	-1.430186	-1.430186	1.112E-29
252,152,934,023	395	TT13	chr1	1	p32.1	59009058	59013177	3	0	-1.460536	-1.460536	2.235E-25
252,152,934,023	401	TT13	chr1	1	p31.3	61509974	61520999	6	0	-1.879284	-1.879284	2.568E-52
252,152,934,023	402	TT13	chr1	1	p31.3	61546348	61551920	4	0	-1.363163	-1.363163	3.161E-21
252,152,934,023	403	TT13	chr1	1	p31.3	62116563	62121278	4	0	-1.579468	-1.579468	1.979E-30
252,152,934,023	404	TT13	chr1	1	p31.3	62659040	62663713	3	0	-1.39652	-1.39652	3.37E-20
252,152,934,023	405	TT13	chr1	1	p31.3	62899291	62908181	5	0	-1.163747	-1.163747	8.492E-26
252,152,934,023	406	TT13	chr1	1	p31.3	63132041	63157208	14	0	-0.961088	-0.961088	3.226E-46
252,152,934,023	407	TT13	chr1	1	p31.3	63781851	63791203	4	0	-2.400039	-2.400039	9.766E-50
252,152,934,023	408	TT13	chr1	1	p31.3	63827865	63840469	7	0	-0.852934	-0.852934	5.072E-21
252,152,934,023	413	TT13	chr1	1	p31.3	64932690	64938418	4	0	-1.134596	-1.134596	5.659E-19
252,152,934,023	415	TT13	chr1	1	p31.3	65207212	65215916	7	0	-1.081768	-1.081768	2.721E-28
252,152,934,023	416	TT13	chr1	1	p31.3	65428902	65435523	4	0	-1.352125	-1.352125	1.574E-25
252,152,934,023	418	TT13	chr1	1	p31.3	65528552	65535482	9	0	-0.974727	-0.974727	3.3E-30
252,152,934,023	419	TT13	chr1	1	p31.3	65719715	65735198	10	0	-1.223872	-1.223872	6.256E-50
252,152,934,023	421	TT13	chr1	1	p31.3	65881049	65891101	6	0	-1.052724	-1.052724	1.807E-25
252,152,934,023	422	TT13	chr1	1	p31.3	65987339	65993613	4	0	-1.374193	-1.374193	8.548E-28
252,152,934,023	423	TT13	chr1	1	p31.3	66251765	66261009	6	0	-1.178555	-1.178555	1.008E-30
252,152,934,023	424	TT13	chr1	1	p31.3	67386921	67400730	8	0	-1.209498	-1.209498	1.04E-41
252,152,934,023	425	TT13	chr1	1	p31.3	67515525	67522664	5	0	-1.075379	-1.075379	1.702E-22
252,152,934,023	426	TT13	chr1	1	p31.3	67767864	67777383	6	0	-0.991914	-0.991914	1.228E-22
252,152,934,023	427	TT13	chr1	1	p31.3	68148514	68154962	5	0	-1.271845	-1.271845	1.996E-24
252,152,934,023	431	TT13	chr1	1	p31.1	70028242	70038721	7	0	-1.029971	-1.029971	8.758E-26
252,152,934,023	432	TT13	chr1	1	p31.1	70684050	70689588	5	0	-1.463506	-1.463506	2.744E-36
252,152,934,023	433	TT13	chr1	1	p31.1	71510281	71516744	8	0	-1.018396	-1.018396	1.923E-28
252,152,934,023	434	TT13	chr1	1	p31.1	72746468	72751884	5	0	-1.343206	-1.343206	1.935E-29
252,152,934,023	435	TT13	chr1	1	p31.1	74711847	74721306	5	0	-1.525101	-1.525101	4.059E-37
252,152,934,023	436	TT13	chr1	1	p31.1	74927884	74935397	5	0	-1.040855	-1.040855	5.813E-21
252,152,934,023	437	TT13	chr1	1	p31.1	75584687	75610598	14	0	-0.75681	-0.75681	8.045E-30
252,152,934,023	449	TT13	chr1	1	p31.1	79469472	79474835	4	0	-1.629136	-1.629136	1.415E-34
252,152,934,023	451	TT13	chr1	1	p31.1	84322972	84328932	5	0	-1.325496	-1.325496	6.669E-31
252,152,934,023	452	TT13	chr1	1	p31.1	84459833	84468317	5	0	-1.221903	-1.221903	5.458E-28
252,152,934,023	453	TT13	chr1	1	p31.1	84540354	84550695	6	0	-1.174962	-1.174962	1.358E-31
252,152,934,023	454	TT13	chr1	1	p31.1	84763939	84767665	3	0	-1.40374	-1.40374	4.879E-21
252,152,934,023	455	TT13	chr1	1	p22.3	84968449	84974254	4	0	-1.426332	-1.426332	1.036E-28
252,152,934,023	461	TT13	chr1	1	p22.3	85926811	85933781	5	0	-1.330292	-1.330292	7.425E-31
252,152,934,023	464	TT13	chr1	1	p22.3	86619706	86625104	4	0	-1.134956	-1.134956	1.005E-19
252,152,934,023	465	TT13	chr1	1	p22.3	87167872	87172276	3	0	-1.578607	-1.578607	1.9E-26
252,152,934,023	466	TT13	chr1	1	p22.3	87360612	87382643	12	0	-1.036316	-1.036316	1.638E-46
252,152,934,023	467	TT13	chr1	1	p22.3	87427752	87431399	3	0	-1.471408	-1.471408	7.685E-24
252,152,934,023	468	TT13	chr1	1	p22.3	87595137	87599410	3	0	-1.328178	-1.328178	3.244E-19
252,152,934,023	469	TT13	chr1	1	p22.3	87792557	87803061	6	0	-2.024893	-2.024893	1.378E-49
252,152,934,023	470	TT13	chr1	1	p22.2	88927820	88934413	4	0	-1.914982	-1.914982	2.402E-31
252,152,934,023	471	TT13	chr1	1	p22.2	89147566	89153259	4	0	-1.348838	-1.348838	4.183E-27
252,152,934,023	474	TT13	chr1	1	p22.2	90092884	90103434	7	0	-0.982164	-0.982164	4.232E-25
252,152,934,023	475	TT13	chr1	1	p22.2	90259829	90313799	27	0	-0.591309	-0.591309	1.877E-32
252,152,934,023	476	TT13	chr1	1	p22.2	90285181	90289998	3	0	-1.666647	-1.666647	9.154E-12
252,152,934,023	477	TT13	chr1	1	p22.2	90451500	90462720	7	0	-1.576272	-1.576272	7.768E-59
252,152,934,023	478	TT13	chr1	1	p22.2	91171663	91198922	15	0	-1.241156	-1.241156	6.988E-67
252,152,934,023	480	TT13	chr1	1	p22.2	91483664	91490590	5	0	-1.447961	-1.447961	7.475E-36
252,152,934,023	481	TT13	chr1	1	p22.2	91866603	91871537	3	0	-1.458972	-1.458972	2.546E-22
252,152,934,023	482	TT13	chr1	1	p22.2	91959810	91997169	20	0	-0.370711	-0.370711	1.648E-10
252,152,934,023	483	TT13	chr1	1	p22.1	92000948	92013306	6	0	-1.243249	-1.243249	3.895E-32
252,152,934,023	484	TT13	chr1	1	p22.1	92349389	92355194	5	0	-1.292078	-1.292078	6.481E-25
252,152,934,023	485	TT13	chr1	1	p22.1	92487293	92502231	8	0	-1.145808	-1.145808	1.319E-37
252,152,934,023	492	TT13	chr1	1	p22.1	93809183	93816756	4	0	-1.126938	-1.126938	6.594E-18
252,152,934,023	493	TT13	chr1	1	p22.1	93908664	93917838	5	0	-1.09781	-1.09781	1.813E-24
252,152,934,023	494	TT13	chr1	1	p22.1	94145588	94149578	3	0	-1.729639	-1.729639	1.622E-24
252,152,934,023	495	TT13	chr1	1	p22.1	94309270	94317636	9	0	-1.140578	-1.140578	1.3E-38
252,152,934,023	497	TT13	chr1	1	p21.3	94700316	94718466	9	0	-1.118482	-1.118482	2.183E-42
252,152,934,023	498	TT13	chr1	1	p21.3	94879726	94888512	6	0	-1.156644	-1.156644	8.496E-31
252,152,934,023	499	TT13	chr1	1	p21.3	95003639	95010118	4	0	-1.210784	-1.210784	3.207E-22
252,152,934,023	502	TT13	chr1	1	p21.3	95579881	95586717	5	0	-1.25795	-1.25795	1.891E-29
252,152,934,023	503	TT13	chr1	1	p21.3	95696324	95704254	5	0	-1.028692	-1.028692	3.256E-20
252,152,934,023	504	TT13	chr1	1	p21.3	96688620	96692541	3	0	-1.214813	-1.214813	5.71E-17
252,152,934,023	505	TT13	chr1	1	p21.3	97227002	97231484	3	0	-1.520627	-1.520627	8.823E-25
252,152,934,023	506	TT13	chr1	1	p21.3	98383049	98390007	4	0	-1.211054	-1.211054	1.752E-22
252,152,934,023	507	TT13	chr1	1	p21.3	98506372	98523952	24	0	-1.269424	-1.269424	4.166E-127
252,152,934,023	508	TT13	chr1	1	p21.3	99125353	99128667	3	0	-1.880318	-1.880318	1.477E-30
252,152,934,023	512	TT13	chr1	1	p21.2	100312623	100324593	7	0	-1.598017	-1.598017	1.034E-54
252,152,934,023	517	TT13	chr1	1	p21.2	101360110	101364539	4	0	-1.144822	-1.144822	1.766E-20
252,152,934,023	518	TT13	chr1	1	p13.3	107583922	107594854	5	0	-0.905076	-0.905076	9.299E-17
252,152,934,023	519	TT13	chr1	1	p13.3	107680569	107687426	4	0	-0.853099	-0.853099	2.683E-12
252,152,934,023	520	TT13	chr1	1	p13.3	108021671	108028146	5	0	-0.821831	-0.821831	2.798E-14

252,152,934,023	521	TT13	chr1	1	p13.3	108504977	108513882	5	0	-0.988297	-0.988297	9.831E-20
252,152,934,023	524	TT13	chr1	1	p13.3	109100537	109105616	4	0	-1.291345	-1.291345	3.667E-23
252,152,934,023	526	TT13	chr1	1	p13.3	109201499	109209795	6	0	-1.749756	-1.749756	1.791E-49
252,152,934,023	532	TT13	chr1	1	p13.3	109790306	109818339	14	0	-1.037529	-1.037529	2.336E-44
252,152,934,023	534	TT13	chr1	1	p13.3	110007052	110056057	25	0	-0.720378	-0.720378	6.559E-41
252,152,934,023	535	TT13	chr1	1	p13.3	110156958	110167704	11	0	-0.513166	-0.513166	1.035E-11
252,152,934,023	539	TT13	chr1	1	p13.3	110524995	110530422	4	0	-1.405946	-1.405946	4.437E-26
252,152,934,023	540	TT13	chr1	1	p13.3	110609117	110628846	11	0	-1.07691	-1.07691	4.668E-40
252,152,934,023	547	TT13	chr1	1	p13.3	111743459	111752592	6	0	-0.817151	-0.817151	1.792E-14
252,152,934,023	549	TT13	chr1	1	p13.2	112146512	112168333	12	0	-0.96864	-0.96864	5.706E-41
252,152,934,023	550	TT13	chr1	1	p13.2	112276952	112302000	16	0	-0.715434	-0.715434	9.081E-28
252,152,934,023	551	TT13	chr1	1	p13.2	112341471	112344486	3	0	-0.999443	-0.999443	1.03E-12
252,152,934,023	552	TT13	chr1	1	p13.2	112523566	112534758	6	0	-1.369061	-1.369061	5.925E-35
252,152,934,023	553	TT13	chr1	1	p13.2	113042314	113052607	7	0	-1.211784	-1.211784	2.475E-28
252,152,934,023	554	TT13	chr1	1	p13.2	113179404	113187552	6	0	-1.243009	-1.243009	2.286E-34
252,152,934,023	556	TT13	chr1	1	p13.2	113248884	113262044	8	0	-1.724988	-1.724988	1.146E-64
252,152,934,023	577	TT13	chr1	1	p13.1	117073563	117215320	37	0	-0.536652	-0.536652	1.408E-35
252,152,934,023	578	TT13	chr1	1	p13.1	117209274	117213167	4	0	-1.761598	-1.761598	1.717E-14
252,152,934,023	585	TT13	chr1	1	p12	119520903	119554429	17	0	-1.422932	-1.422932	3.364E-108
252,152,934,023	587	TT13	chr1	1	p12	120160783	120194981	19	0	-0.908394	-0.908394	3.206E-64
252,152,934,023	591	TT13	chr1	1	q21.1	145072001	145100373	18	0	-0.813416	-0.813416	1.223E-45
252,152,934,023	592	TT13	chr1	1	q21.1	145469857	145480547	7	0	-1.464985	-1.464985	8.313E-40
252,152,934,023	593	TT13	chr1	1	q21.1	145557868	145577280	11	0	-0.732884	-0.732884	1.356E-21
252,152,934,023	597	TT13	chr1	1	q21.1	146641601	146651819	6	0	-1.531208	-1.531208	1.164E-51
252,152,934,023	598	TT13	chr1	1	q21.1	146706034	146717152	7	0	-1.284938	-1.284938	6.69E-41
252,152,934,023	601	TT13	chr1	1	q21.2	149887097	149890122	3	0	-1.149525	-1.149525	1.997E-15
252,152,934,023	602	TT13	chr1	1	q21.2	149979356	149986986	5	0	-1.071656	-1.071656	5.185E-22
252,152,934,023	605	TT13	chr1	1	q21.3	150516582	150561532	24	0	-0.502811	-0.502811	4.522E-20
252,152,934,023	606	TT13	chr1	1	q21.3	150520901	150523505	3	0	-1.751868	-1.751868	4.381E-10
252,152,934,023	607	TT13	chr1	1	q21.3	150693133	150705611	7	0	-1.388381	-1.388381	6.792E-43
252,152,934,023	608	TT13	chr1	1	q21.3	150751541	150760236	5	0	-0.943785	-0.943785	1.542E-18
252,152,934,023	609	TT13	chr1	1	q21.3	150816820	150853253	21	0	-0.578709	-0.578709	6.778E-27
252,152,934,023	610	TT13	chr1	1	q21.3	151016220	151035348	12	0	-0.840644	-0.840644	6.136E-32
252,152,934,023	615	TT13	chr1	1	q21.3	151569463	151588877	10	0	-1.03907	-1.03907	3.178E-39
252,152,934,023	616	TT13	chr1	1	q21.3	151691317	151694445	3	0	-1.543865	-1.543865	3.388E-24
252,152,934,023	617	TT13	chr1	1	q21.3	151734656	151744379	6	0	-1.477631	-1.477631	4.93E-45
252,152,934,023	620	TT13	chr1	1	q21.3	151877441	151883288	3	0	-1.801339	-1.801339	4.115E-30
252,152,934,023	624	TT13	chr1	1	q21.3	152161011	152171565	4	0	-1.120353	-1.120353	9.489E-20
252,152,934,023	625	TT13	chr1	1	q21.3	153230866	153238397	4	0	-1.084866	-1.084866	1.064E-19
252,152,934,023	626	TT13	chr1	1	q21.3	153348561	153358430	5	0	-0.668899	-0.668899	5.978E-12
252,152,934,023	627	TT13	chr1	1	q21.3	153546661	153558157	6	0	-1.557749	-1.557749	9.853E-45
252,152,934,023	630	TT13	chr1	1	q21.3	153892092	153952825	38	0	-0.650949	-0.650949	9.659E-53
252,152,934,023	631	TT13	chr1	1	q21.3	153915801	153920113	3	0	-1.863181	-1.863181	3.638E-14
252,152,934,023	646	TT13	chr1	1	q22	155291322	155298127	7	0	-1.037413	-1.037413	3.49E-18
252,152,934,023	647	TT13	chr1	1	q22	155525343	155536874	6	0	-0.81883	-0.81883	4.501E-16
252,152,934,023	663	TT13	chr1	1	q23.1	156879156	156898941	17	0	-0.957916	-0.957916	3.374E-44
252,152,934,023	664	TT13	chr1	1	q23.1	156889753	156892304	3	0	-2.160736	-2.160736	4.636E-12
252,152,934,023	668	TT13	chr1	1	q23.1	157946367	157966884	9	0	-0.762326	-0.762326	6.082E-26
252,152,934,023	669	TT13	chr1	1	q23.1	158078978	158085844	4	0	-1.287938	-1.287938	8.077E-24
252,152,934,023	670	TT13	chr1	1	q23.1	158146670	158152424	4	0	-1.209293	-1.209293	3.069E-22
252,152,934,023	673	TT13	chr1	1	q23.2	159744431	159754284	6	0	-0.845893	-0.845893	1.684E-17
252,152,934,023	677	TT13	chr1	1	q23.2	160038546	160071928	17	0	-0.794291	-0.794291	5.063E-37
252,152,934,023	679	TT13	chr1	1	q23.2	160337732	160374070	15	0	-0.638586	-0.638586	7.673E-23
252,152,934,023	682	TT13	chr1	1	q23.3	161045927	161151165	55	0	-0.677786	-0.677786	1.326E-88
252,152,934,023	683	TT13	chr1	1	q23.3	161100423	161113372	7	0	-1.479304	-1.479304	3.996E-18
252,152,934,023	687	TT13	chr1	1	q23.3	161990628	161995589	3	0	-1.076854	-1.076854	2.308E-14
252,152,934,023	688	TT13	chr1	1	q23.3	162037113	162042820	3	0	-1.277009	-1.277009	6.544E-18
252,152,934,023	690	TT13	chr1	1	q23.3	162401289	162404591	4	0	-2.123097	-2.123097	4.599E-17
252,152,934,023	691	TT13	chr1	1	q23.3	162401289	162470087	23	0	-0.841808	-0.841808	1.958E-56
252,152,934,023	693	TT13	chr1	1	q23.3	164287051	164295429	4	0	-0.916331	-0.916331	2.428E-14
252,152,934,023	694	TT13	chr1	1	q23.3	164543795	164547036	3	0	-1.685055	-1.685055	2.946E-27
252,152,934,023	695	TT13	chr1	1	q23.3	164759409	164763933	3	0	-0.917611	-0.917611	1.833E-14
252,152,934,023	696	TT13	chr1	1	q23.3	165202916	165208575	4	0	-1.241275	-1.241275	1.819E-23
252,152,934,023	697	TT13	chr1	1	q23.3	165324564	165327890	3	0	-1.536726	-1.536726	9.315E-23
252,152,934,023	700	TT13	chr1	1	q24.1	165663753	165671934	6	0	-1.037841	-1.037841	4.527E-25
252,152,934,023	701	TT13	chr1	1	q24.1	165794058	165799972	4	0	-1.610346	-1.610346	8.426E-31
252,152,934,023	702	TT13	chr1	1	q24.1	166131911	166139187	9	0	-1.071828	-1.071828	7.674E-34
252,152,934,023	706	TT13	chr1	1	q24.1	167188388	167193371	3	0	-1.548636	-1.548636	4.992E-25
252,152,934,023	707	TT13	chr1	1	q24.2	167420811	167427028	5	0	-0.911644	-0.911644	3.844E-15
252,152,934,023	708	TT13	chr1	1	q24.2	167521513	167525793	3	0	-1.477973	-1.477973	1.064E-21
252,152,934,023	711	TT13	chr1	1	q24.2	167682828	167694285	6	0	-1.578641	-1.578641	2.64E-48
252,152,934,023	713	TT13	chr1	1	q24.2	167902933	167908383	5	0	-1.522296	-1.522296	3.489E-33
252,152,934,023	715	TT13	chr1	1	q24.2	168171225	168197970	12	0	-0.752973	-0.752973	1.553E-26
252,152,934,023	716	TT13	chr1	1	q24.2	169072404	169077569	3	0	-1.538042	-1.538042	3.472E-23
252,152,934,023	717	TT13	chr1	1	q24.2	169303045	169308834	4	0	-1.326994	-1.326994	3.391E-25
252,152,934,023	718	TT13	chr1	1	q24.2	169452266	169459014	4	0	-1.151081	-1.151081	5.265E-22
252,152,934,023	720	TT13	chr1	1	q24.2	170213726	170222178	4	0	-0.891824	-0.891824	6.428E-14
252,152,934,023	721	TT13	chr1	1	q24.2	170381041	170390909	3	0	-1.042592	-1.042592	1.981E-14
252,152,934,023	723	TT13	chr1	1	q24.3	171709946	171716277	4	0	-1.203869	-1.203869	2.773E-23
252,152,934,023	724	TT13	chr1	1	q24.3	171808796	171815084	4	0	-1.273596	-1.273596	1.521E-24
252,152,934,023	725	TT13	chr1	1	q24.3	172500204	172503822	3	0	-1.797022	-1.797022	4.172E-30
252,152,934,023	739	TT13	chr1	1	q25.2	178006048	178008955	3	0	-1.801104	-1.801104	1.259E-28
252,152,934,023	740	TT13	chr1	1	q25.2	178059012	178067193	5	0	-1.193756	-1.193756	9.911E-27
252,152,934,023	742	TT13	chr1	1	q25.2	178691308	178697827	4	0	-1.491735	-1.491735	9.743E-32
252,152,934,023	743	TT13	chr1	1	q25.2	178991736	179014416	12	0	-0.953574	-0.953574	6.2E-41
252,152,934,023	748	TT13	chr1	1	q25.2	179541375	179564086	14	0	-1.310732	-1.310732	8.048E-78
252,152,934,023	751	TT13	chr1	1	q25.2	179922073	179927296	4	0	-1.64156	-1.64156	3.439E-35
252,152,934,023	753	TT13	chr1	1	q25.2	180197137	180207114	7	0	-1.218817	-1.218817	1.044E-32
252,152,934,023	754	TT13	chr1	1	q25.2	180218809	180230208	6	0	-0.649762	-0.649762	8.853E-11
252,152,934,023	756	TT13	chr1	1	q25.3	180598712	180604429	3	0	-1.1272	-1.1272	2.305E-16
252,152,934,023	757	TT13	chr1	1	q25.3	180879925	180925035	25	0	-0.608048	-0.608048	4.156E-28
252,152,934,023	760	TT13	chr1	1	q25.3	181450113	181453394	3	0	-1.278399	-1.278399	8.686E-16
252,152,934,023	762	TT13	chr1	1	q25.3	182358004	182364533	5	0	-1.164039	-1.164039	2.133E-20
252,152,934,023	763	TT13	chr1	1	q25.3	182406556	182412069	3	0	-1.047995	-1.047995	7.03E-14
252,152,934,023	764	TT13	chr1	1	q25.3	182475419	182475648	3	0	-1.100709	-1.100709	6.838E-16
252,152,934,023	765	TT13	chr1	1	q25.3	182571337	182586714	9	0	-1.000138	-1.000138	1.79E-32

252,152,934,023	767	TT13	chr1	1	q25.3	182909554	182925655	10	0	-1.253332	-1.253332	7.121E-54
252,152,934,023	768	TT13	chr1	1	q25.3	182991007	182995786	3	0	-1.494009	-1.494009	5.36E-24
252,152,934,023	769	TT13	chr1	1	q25.3	183392116	183398969	4	0	-0.982652	-0.982652	5.108E-16
252,152,934,023	770	TT13	chr1	1	q25.3	183437154	183448169	7	0	-0.939491	-0.939491	2.284E-25
252,152,934,023	772	TT13	chr1	1	q25.3	183772809	183777495	3	0	-1.344461	-1.344461	2.479E-21
252,152,934,023	775	TT13	chr1	1	q25.3	184719447	184734633	11	0	-0.719751	-0.719751	4.813E-22
252,152,934,023	779	TT13	chr1	1	q25.3	185283000	185292856	5	0	-1.812046	-1.812046	1.852E-42
252,152,934,023	781	TT13	chr1	1	q25.3	185702905	185705341	3	0	-1.863792	-1.863792	1.368E-31
252,152,934,023	790	TT13	chr1	1	q31.2	193073338	193095297	19	0	-1.077089	-1.077089	1.972E-77
252,152,934,023	791	TT13	chr1	1	q31.2	193078411	193084522	6	0	-0.375616	-0.375616	6.641E-15
252,152,934,023	799	TT13	chr1	1	q31.3	198122838	198128690	4	0	-1.456259	-1.456259	3.272E-28
252,152,934,023	800	TT13	chr1	1	q32.1	199868196	199881873	9	0	-0.715494	-0.715494	7.892E-19
252,152,934,023	801	TT13	chr1	1	q32.1	199996777	200012950	8	0	-1.283892	-1.283892	5.545E-45
252,152,934,023	802	TT13	chr1	1	q32.1	200115418	200119095	3	0	-1.854267	-1.854267	6.526E-31
252,152,934,023	805	TT13	chr1	1	q32.1	200704832	200712243	6	0	-1.31752	-1.31752	7.498E-37
252,152,934,023	806	TT13	chr1	1	q32.1	200837402	200889665	27	0	-0.898899	-0.898899	2.262E-70
252,152,934,023	807	TT13	chr1	1	q32.1	200982405	200995762	7	0	-0.798728	-0.798728	1.041E-16
252,152,934,023	809	TT13	chr1	1	q32.1	201083044	201086280	3	0	-1.431709	-1.431709	5.48E-21
252,152,934,023	815	TT13	chr1	1	q32.1	201795174	201803409	8	0	-1.049698	-1.049698	8.376E-34
252,152,934,023	823	TT13	chr1	1	q32.1	202891016	202998954	52	0	-0.492727	-0.492727	5.507E-43
252,152,934,023	824	TT13	chr1	1	q32.1	202924210	202937875	9	0	-1.191445	-1.191445	2.319E-15
252,152,934,023	826	TT13	chr1	1	q32.1	202975028	202977793	3	0	-1.655219	-1.655219	4.296E-15
252,152,934,023	829	TT13	chr1	1	q32.1	203593771	203620702	13	0	-0.598535	-0.598535	1.156E-25
252,152,934,023	830	TT13	chr1	1	q32.1	203867547	203887644	10	0	-0.985757	-0.985757	3.744E-42
252,152,934,023	863	TT13	chr1	1	q32.2	211305242	211310158	4	0	-1.430656	-1.430656	1.422E-29
252,152,934,023	864	TT13	chr1	1	q32.2	211368632	211385370	11	0	-1.229807	-1.229807	1.118E-60
252,152,934,023	865	TT13	chr1	1	q32.2	211430062	211436093	5	0	-1.459534	-1.459534	1.75E-30
252,152,934,023	872	TT13	chr1	1	q32.3	212186052	212191123	4	0	-1.467634	-1.467634	3.976E-31
252,152,934,023	876	TT13	chr1	1	q32.3	212778347	212784703	5	0	-1.198072	-1.198072	3.823E-24
252,152,934,023	882	TT13	chr1	1	q32.3	214155563	214159733	3	0	-2.355298	-2.355298	1.305E-37
252,152,934,023	883	TT13	chr1	1	q41	214722147	214728271	4	0	-1.239232	-1.239232	3.266E-23
252,152,934,023	888	TT13	chr1	1	q41	215738712	215744832	5	0	-1.427728	-1.427728	7.687E-31
252,152,934,023	889	TT13	chr1	1	q41	216772622	216776933	3	0	-1.497489	-1.497489	4.959E-25
252,152,934,023	890	TT13	chr1	1	q41	217258046	217265502	5	0	-1.117494	-1.117494	3.009E-23
252,152,934,023	892	TT13	chr1	1	q41	217693862	217701165	4	0	-1.447672	-1.447672	3.114E-29
252,152,934,023	893	TT13	chr1	1	q41	218517954	218521047	3	0	-1.628327	-1.628327	3.336E-26
252,152,934,023	894	TT13	chr1	1	q41	219343742	219349499	4	0	-1.342634	-1.342634	3.349E-27
252,152,934,023	895	TT13	chr1	1	q41	220096698	220105725	6	0	-1.175532	-1.175532	8.271E-31
252,152,934,023	898	TT13	chr1	1	q41	220638634	220652017	7	0	-1.382545	-1.382545	1.922E-44
252,152,934,023	905	TT13	chr1	1	q41	222635852	222641351	4	0	-1.451497	-1.451497	4.584E-28
252,152,934,023	912	TT13	chr1	1	q42.11	224532826	224548084	8	0	-1.476407	-1.476407	1.627E-54
252,152,934,023	913	TT13	chr1	1	q42.12	224615265	224626236	7	0	-1.018026	-1.018026	5.816E-29
252,152,934,023	914	TT13	chr1	1	q42.12	224802852	224808627	4	0	-0.951977	-0.951977	1.549E-14
252,152,934,023	915	TT13	chr1	1	q42.12	225115022	225118051	3	0	-1.484322	-1.484322	1.733E-21
252,152,934,023	916	TT13	chr1	1	q42.12	225613830	225621443	5	0	-2.435047	-2.435047	1.826E-55
252,152,934,023	953	TT13	chr1	1	q42.13	229759370	229765103	4	0	-1.318114	-1.318114	2.193E-25
252,152,934,023	962	TT13	chr1	1	q42.2	231452462	231454868	3	0	-1.717662	-1.717662	4.187E-28
252,152,934,023	964	TT13	chr1	1	q42.2	231552492	231568582	8	0	-1.129336	-1.129336	1.393E-35
252,152,934,023	965	TT13	chr1	1	q42.2	231758121	231780975	12	0	-0.867032	-0.867032	1.087E-33
252,152,934,023	966	TT13	chr1	1	q42.2	232938895	232944709	4	0	-1.325167	-1.325167	2.106E-25
252,152,934,023	972	TT13	chr1	1	q42.2	234348088	234411269	33	0	-0.49525	-0.49525	5.355E-30
252,152,934,023	973	TT13	chr1	1	q42.2	234491523	234496516	4	0	-0.82851	-0.82851	1.774E-11
252,152,934,023	974	TT13	chr1	1	q42.3	234734915	234747456	9	0	-1.545253	-1.545253	9.018E-66
252,152,934,023	1005	TT13	chr1	1	q43	243636316	243663113	17	0	-1.280098	-1.280098	1.975E-91
252,152,934,023	1006	TT13	chr1	1	q44	244011390	244017016	4	0	-1.322218	-1.322218	1.586E-26
252,152,934,023	1007	TT13	chr1	1	q44	244209483	244216663	5	0	-1.431286	-1.431286	8.828E-36
252,152,934,023	1008	TT13	chr1	1	q44	244609660	244627372	9	0	-1.216709	-1.216709	1.185E-46
252,152,934,023	1009	TT13	chr1	1	q44	244815534	244819749	3	0	-1.320606	-1.320606	4.577E-18
252,152,934,023	1011	TT13	chr1	1	q44	245025588	245029222	3	0	-1.693531	-1.693531	1.861E-26
252,152,934,023	1021	TT13	chr1	1	q44	247092877	247096020	3	0	-1.860255	-1.860255	9.731E-31
252,152,934,023	1025	TT13	chr1	1	q44	247371885	247388514	8	0	-1.416784	-1.416784	1.772E-26
252,152,934,023	1026	TT13	chr1	1	q44	247491772	247494243	3	0	-2.043395	-2.043395	6.485E-28
252,152,934,023	1029	TT13	chr1	1	q44	247801063	247809763	6	0	-1.000862	-1.000862	1.643E-21
252,152,934,023	1030	TT13	chr1	1	q44	248015143	248026065	6	0	-0.972994	-0.972994	7.35E-22
252,152,934,023	1031	TT13	chr1	1	q44	248093829	248103873	7	0	-0.778329	-0.778329	8.368E-15
252,152,934,023	1032	TT13	chr1	1	q44	248835637	248858438	12	0	-0.978083	-0.978083	4.414E-41
252,152,934,023	1033	TT13	chr1	1	q44	249120745	249158835	19	0	-1.190573	-1.190573	4.601E-84
252,152,934,023	1034	TT13	chr1	1	q44	249145130	249150185	3	0	-0.385091	-0.385091	3.792E-10
252,152,934,023	1058	TT13	chr2	2	p25.3	2187412	2192644	4	0	-1.522198	-1.522198	1.72E-30
252,152,934,023	1060	TT13	chr2	2	p25.3	2724494	2751381	9	0	-0.533832	-0.533832	1.304E-15
252,152,934,023	1063	TT13	chr2	2	p25.3	3283020	3292141	6	0	-1.815207	-1.815207	2.719E-47
252,152,934,023	1064	TT13	chr2	2	p25.3	3322703	3330608	4	0	-1.070258	-1.070258	8.255E-17
252,152,934,023	1073	TT13	chr2	2	p25.2	4979621	4989572	6	0	-0.720426	-0.720426	1.804E-12
252,152,934,023	1074	TT13	chr2	2	p25.2	5824754	5849174	9	0	-1.265037	-1.265037	8.105E-46
252,152,934,023	1077	TT13	chr2	2	p25.1	7567444	7573530	3	0	-1.139575	-1.139575	4.807E-19
252,152,934,023	1078	TT13	chr2	2	p25.1	8816165	8836746	11	0	-1.567553	-1.567553	2.578E-76
252,152,934,023	1079	TT13	chr2	2	p25.1	8972573	8979688	5	0	-1.016422	-1.016422	2.662E-20
252,152,934,023	1080	TT13	chr2	2	p25.1	9602768	9618798	8	0	-1.341177	-1.341177	1.041E-47
252,152,934,023	1084	TT13	chr2	2	p25.1	10137980	10268996	55	0	-0.413951	-0.413951	4.337E-32
252,152,934,023	1085	TT13	chr2	2	p25.1	10144932	10156508	5	0	-1.147258	-1.147258	2.267E-10
252,152,934,023	1094	TT13	chr2	2	p25.1	11597259	11626058	11	0	-0.716855	-0.716855	3.715E-21
252,152,934,023	1096	TT13	chr2	2	p25.1	11793596	11813978	10	0	-0.77521	-0.77521	2.54E-23
252,152,934,023	1097	TT13	chr2	2	p25.1	11884743	11901485	9	0	-0.956036	-0.956036	2.019E-29
252,152,934,023	1098	TT13	chr2	2	p24.3	12852215	12862617	7	0	-0.996841	-0.996841	3.971E-25
252,152,934,023	1099	TT13	chr2	2	p24.3	14769620	14776645	5	0	-1.534549	-1.534549	3.938E-34
252,152,934,023	1100	TT13	chr2	2	p24.3	15677113	15684452	6	0	-1.329933	-1.329933	1.252E-37
252,152,934,023	1107	TT13	chr2	2	p24.2	17930279	17938074	5	0	-1.42976	-1.42976	1.74E-35
252,152,934,023	1108	TT13	chr2	2	p24.2	18055676	18063582	5	0	-1.037133	-1.037133	3.863E-18
252,152,934,023	1109	TT13	chr2	2	p24.2	18738168	18769473	13	0	-0.93765	-0.93765	4.591E-40
252,152,934,023	1119	TT13	chr2	2	p24.1	23859618	23888994	16	0	-0.467431	-0.467431	4.534E-13
252,152,934,023	1123	TT13	chr2	2	p23.3	24343890	24347393	3	0	-1.371092	-1.371092	1.271E-20
252,152,934,023	1124	TT13	chr2	2	p23.3	24396177	24400507	4	0	-1.575661	-1.575661	3.513E-27
252,152,934,023	1125	TT13	chr2	2	p23.3	24581970	24585106	3	0	-1.425297	-1.425297	1.484E-21
252,152,934,023	1126	TT13	chr2	2	p23.3	24711131	24718157	4	0	-1.427749	-1.427749	2.643E-29
252,152,934,023	1127	TT13	chr2	2	p23.3	25052222	25078480	12	0	-0.569292	-0.569292	1.861E-15
252,152,934,023	1131	TT13	chr2	2	p23.3	25381892	25393934	8	0	-1.26435	-1.26435	1.784E-42

252,152,934,023	1132	TT13	chr2	2	p23.3	25426397	25441071	6	0	-1.16715	-1.16715	3.697E-29
252,152,934,023	1153	TT13	chr2	2	p23.3	27191357	27197346	4	0	-1.358891	-1.358891	8.765E-23
252,152,934,023	1157	TT13	chr2	2	p23.3	27432727	27441058	7	0	-1.676326	-1.676326	4.481E-46
252,152,934,023	1165	TT13	chr2	2	p23.2	28610460	28619574	5	0	-1.310675	-1.310675	1.67E-28
252,152,934,023	1166	TT13	chr2	2	p23.2	28969372	28977289	5	0	-1.170894	-1.170894	2.161E-24
252,152,934,023	1167	TT13	chr2	2	p23.2	29031908	29035420	3	0	-2.049139	-2.049139	8.598E-33
252,152,934,023	1178	TT13	chr2	2	p22.3	32285359	32291449	4	0	-1.3454	-1.3454	1.698E-26
252,152,934,023	1179	TT13	chr2	2	p22.3	32500386	32523205	12	0	-1.048385	-1.048385	6.34E-48
252,152,934,023	1180	TT13	chr2	2	p22.3	32668351	32675071	4	0	-1.311735	-1.311735	1.354E-26
252,152,934,023	1184	TT13	chr2	2	p22.3	33980797	34006009	12	0	-0.834849	-0.834849	7.451E-32
252,152,934,023	1185	TT13	chr2	2	p22.3	34354488	34372054	8	0	-1.041388	-1.041388	1.653E-33
252,152,934,023	1192	TT13	chr2	2	p22.2	37378000	37387610	5	0	-1.277762	-1.277762	2.991E-29
252,152,934,023	1193	TT13	chr2	2	p22.2	37419986	37426749	4	0	-1.03783	-1.03783	1.966E-17
252,152,934,023	1194	TT13	chr2	2	p22.2	37546362	37574841	15	0	-0.796621	-0.796621	2.704E-36
252,152,934,023	1195	TT13	chr2	2	p22.2	37896781	37903093	4	0	-1.191816	-1.191816	9.168E-17
252,152,934,023	1196	TT13	chr2	2	p22.2	38148738	38162824	8	0	-1.613809	-1.613809	6.298E-66
252,152,934,023	1197	TT13	chr2	2	p22.2	38190309	38208530	8	0	-0.890914	-0.890914	2.993E-26
252,152,934,023	1201	TT13	chr2	2	p22.1	38623160	38633463	5	0	-1.55589	-1.55589	3.674E-39
252,152,934,023	1206	TT13	chr2	2	p22.1	38976101	38984246	5	0	-1.633663	-1.633663	2.351E-39
252,152,934,023	1207	TT13	chr2	2	p22.1	39182491	39189762	4	0	-1.005949	-1.005949	5.926E-17
252,152,934,023	1208	TT13	chr2	2	p22.1	39346574	39352336	4	0	-2.184263	-2.184263	2.239E-47
252,152,934,023	1212	TT13	chr2	2	p22.1	39854108	39858884	3	0	-1.413391	-1.413391	9.219E-23
252,152,934,023	1213	TT13	chr2	2	p22.1	39888884	39898290	6	0	-0.943447	-0.943447	4.184E-19
252,152,934,023	1214	TT13	chr2	2	p22.1	40005666	40008877	3	0	-1.5973	-1.5973	6.97E-19
252,152,934,023	1215	TT13	chr2	2	p22.1	40675228	40683601	5	0	-0.904388	-0.904388	7.881E-17
252,152,934,023	1218	TT13	chr2	2	p21	42827507	42853832	12	0	-0.872873	-0.872873	2.582E-33
252,152,934,023	1219	TT13	chr2	2	p21	42831655	42835689	3	0	-1.908861	-1.908861	7.24E-11
252,152,934,023	1220	TT13	chr2	2	p21	43018579	43041057	11	0	-0.863666	-0.863666	1.388E-26
252,152,934,023	1221	TT13	chr2	2	p21	43285674	43331874	20	0	-0.569412	-0.569412	9.142E-24
252,152,934,023	1226	TT13	chr2	2	p21	43901640	43907665	5	0	-1.486218	-1.486218	1.807E-37
252,152,934,023	1227	TT13	chr2	2	p21	44218718	44224667	4	0	-1.087138	-1.087138	1.967E-19
252,152,934,023	1229	TT13	chr2	2	p21	44391204	44398394	5	0	-1.294035	-1.294035	2.627E-29
252,152,934,023	1232	TT13	chr2	2	p21	44993639	44996704	3	0	-1.643187	-1.643187	1.29E-25
252,152,934,023	1234	TT13	chr2	2	p21	45154762	45183302	15	0	-1.439678	-1.439678	1.073E-84
252,152,934,023	1236	TT13	chr2	2	p21	45392396	45402598	5	0	-1.040696	-1.040696	1.746E-22
252,152,934,023	1237	TT13	chr2	2	p21	45868238	45880447	8	0	-1.659174	-1.659174	2.352E-57
252,152,934,023	1238	TT13	chr2	2	p21	46142013	46147310	4	0	-1.452114	-1.452114	2.932E-29
252,152,934,023	1247	TT13	chr2	2	p21	47594039	47600950	8	0	-1.301957	-1.301957	1.178E-46
252,152,934,023	1248	TT13	chr2	2	p21	47657018	47663118	4	0	-1.315196	-1.315196	9.967E-26
252,152,934,023	1249	TT13	chr2	2	p21 - p16.3	47792517	47802594	5	0	-0.974044	-0.974044	4.323E-19
252,152,934,023	1250	TT13	chr2	2	p16.3	48009122	48014589	4	0	-1.004123	-1.004123	2.033E-15
252,152,934,023	1251	TT13	chr2	2	p16.3	48129009	48136112	5	0	-1.121332	-1.121332	1.522E-20
252,152,934,023	1252	TT13	chr2	2	p16.3	48539255	48544662	4	0	-1.418878	-1.418878	2.194E-28
252,152,934,023	1257	TT13	chr2	2	p16.3	50636896	50639619	3	0	-2.212557	-2.212557	5.835E-36
252,152,934,023	1258	TT13	chr2	2	p16.3	51052121	51059433	4	0	-1.386186	-1.386186	4.435E-28
252,152,934,023	1259	TT13	chr2	2	p16.3	51253713	51257067	3	0	-2.161893	-2.161893	2.882E-36
252,152,934,023	1260	TT13	chr2	2	p16.3	51373091	51382872	3	0	-0.880269	-0.880269	9.151E-11
252,152,934,023	1261	TT13	chr2	2	p16.3	52004351	52011552	5	0	-1.407554	-1.407554	1.109E-35
252,152,934,023	1273	TT13	chr2	2	p16.2	54935266	54954446	9	0	-1.179954	-1.179954	5.125E-45
252,152,934,023	1274	TT13	chr2	2	p16.1	55270530	55280020	7	0	-0.938507	-0.938507	2.955E-25
252,152,934,023	1276	TT13	chr2	2	p16.1	55507561	55512132	3	0	-1.415555	-1.415555	6.543E-23
252,152,934,023	1277	TT13	chr2	2	p16.1	55644987	55649298	3	0	-1.244911	-1.244911	4.193E-19
252,152,934,023	1278	TT13	chr2	2	p16.1	55875905	55879296	3	0	-1.885976	-1.885976	1.884E-30
252,152,934,023	1279	TT13	chr2	2	p16.1	55929338	55934769	3	0	-1.309955	-1.309955	2.253E-20
252,152,934,023	1280	TT13	chr2	2	p16.1	56146850	56153510	4	0	-1.150976	-1.150976	4.329E-20
252,152,934,023	1282	TT13	chr2	2	p16.1	58269764	58278754	5	0	-1.358089	-1.358089	1.109E-31
252,152,934,023	1283	TT13	chr2	2	p16.1	58465793	58481066	8	0	-1.000141	-1.000141	2.313E-31
252,152,934,023	1284	TT13	chr2	2	p16.1	58651861	58657693	3	0	-1.310259	-1.310259	5.769E-20
252,152,934,023	1285	TT13	chr2	2	p16.1	59289705	59296510	3	0	-1.19688	-1.19688	4.236E-17
252,152,934,023	1287	TT13	chr2	2	p16.1	60774846	60783723	5	0	-1.566779	-1.566779	3.359E-33
252,152,934,023	1298	TT13	chr2	2	p15	63273315	63291714	9	0	-1.71638	-1.71638	7.692E-70
252,152,934,023	1303	TT13	chr2	2	p14	64734375	64754421	10	0	-1.146127	-1.146127	9.545E-45
252,152,934,023	1305	TT13	chr2	2	p14	64878424	64882195	3	0	-2.130086	-2.130086	7.693E-35
252,152,934,023	1315	TT13	chr2	2	p14	66650780	66676576	13	0	-1.302039	-1.302039	1.878E-77
252,152,934,023	1316	TT13	chr2	2	p14	66797644	66807687	6	0	-0.63477	-0.63477	1.062E-10
252,152,934,023	1317	TT13	chr2	2	p14	67624164	67629480	4	0	-0.823163	-0.823163	3.929E-12
252,152,934,023	1319	TT13	chr2	2	p14	68541645	68549266	5	0	-0.885132	-0.885132	5.338E-16
252,152,934,023	1320	TT13	chr2	2	p13.3	68690754	68696613	5	0	-1.452083	-1.452083	2.659E-35
252,152,934,023	1322	TT13	chr2	2	p13.3	68870085	68873119	3	0	-1.557344	-1.557344	2.112E-23
252,152,934,023	1323	TT13	chr2	2	p13.3	69235643	69246181	6	0	-0.747083	-0.747083	1.366E-19
252,152,934,023	1324	TT13	chr2	2	p13.3	69610216	69615950	4	0	-1.207861	-1.207861	1.465E-22
252,152,934,023	1329	TT13	chr2	2	p13.3	70368081	70377055	5	0	-1.60284	-1.60284	1.657E-37
252,152,934,023	1330	TT13	chr2	2	p13.3	70484492	70492953	9	0	-1.258388	-1.258388	2.533E-47
252,152,934,023	1331	TT13	chr2	2	p13.3	70525124	70533341	6	0	-1.093005	-1.093005	7.22E-27
252,152,934,023	1332	TT13	chr2	2	p13.3	70779162	70783525	3	0	-1.448059	-1.448059	2.204E-22
252,152,934,023	1333	TT13	chr2	2	p13.3	70991971	71021163	16	0	-0.682877	-0.682877	2.514E-27
252,152,934,023	1334	TT13	chr2	2	p13.3	71112326	71131619	10	0	-0.979961	-0.979961	2.689E-34
252,152,934,023	1335	TT13	chr2	2	p13.3	71189107	71224554	17	0	-0.866695	-0.866695	6.983E-41
252,152,934,023	1344	TT13	chr2	2	p13.2	73146637	73152441	4	0	-2.315152	-2.315152	4.57E-47
252,152,934,023	1351	TT13	chr2	2	p13.1	73610737	73615386	4	0	-1.749803	-1.749803	1.026E-38
252,152,934,023	1352	TT13	chr2	2	p13.1	74205415	74218368	6	0	-0.804162	-0.804162	6.62E-16
252,152,934,023	1353	TT13	chr2	2	p13.1	74287557	74296506	6	0	-1.151409	-1.151409	2.079E-29
252,152,934,023	1356	TT13	chr2	2	p13.1	74600136	74783040	84	0	-0.774553	-0.774553	1.243E-158
252,152,934,023	1357	TT13	chr2	2	p13.1	74640892	74647483	4	0	-2.296956	-2.296956	1.786E-18
252,152,934,023	1361	TT13	chr2	2	p13.1	74874254	74882406	5	0	-2.016746	-2.016746	1.007E-44
252,152,934,023	1368	TT13	chr2	2	p12	80136377	80138910	3	0	-1.691211	-1.691211	1.278E-28
252,152,934,023	1369	TT13	chr2	2	p12	80524073	80552347	14	0	-0.804946	-0.804946	1.154E-32
252,152,934,023	1370	TT13	chr2	2	p12	81689052	81707108	6	0	-0.715375	-0.715375	1.217E-13
252,152,934,023	1371	TT13	chr2	2	p12	82552094	82556679	3	0	-1.5784	-1.5784	4.277E-26
252,152,934,023	1372	TT13	chr2	2	p11.2	85103795	85144438	21	0	-0.710221	-0.710221	6.86E-39
252,152,934,023	1373	TT13	chr2	2	p11.2	85196363	85206936	7	0	-0.797992	-0.797992	9.641E-19
252,152,934,023	1374	TT13	chr2	2	p11.2	85357157	85366828	6	0	-0.916223	-0.916223	2.379E-18
252,152,934,023	1375	TT13	chr2	2	p11.2	85559034	85563862	3	0	-1.303986	-1.303986	1.583E-19
252,152,934,023	1381	TT13	chr2	2	p11.2	86111368	86118035	4	0	-1.220361	-1.220361	1.886E-22
252,152,934,023	1384	TT13	chr2	2	p11.2	86660975	86678026	11	0	-0.81912	-0.81912	1.632E-29
252,152,934,023	1390	TT13	chr2	2	p11.2	88748583	88755682	4	0	-1.521872	-1.521872	3.4E-31

252,152,934,023	1394	TT13	chr2	2	p11.2	89216986	89229669	7	0	-1.354762	-1.354762	1.114E-43
252,152,934,023	1402	TT13	chr2	2	q11.2	96986192	97002970	10	0	-1.398766	-1.398766	1.383E-61
252,152,934,023	1403	TT13	chr2	2	q11.2	97131348	97218387	39	0	-0.638317	-0.638317	2.363E-58
252,152,934,023	1404	TT13	chr2	2	q11.2	97166849	97176964	6	0	-1.408252	-1.408252	6.62E-12
252,152,934,023	1405	TT13	chr2	2	q11.2	97468779	97540319	34	0	-0.71321	-0.71321	6.344E-62
252,152,934,023	1406	TT13	chr2	2	q11.2	97526630	97528082	3	0	-2.382113	-2.382113	9.472E-18
252,152,934,023	1409	TT13	chr2	2	q11.2	98276737	98281710	4	0	-1.1073	-1.1073	2.96E-19
252,152,934,023	1410	TT13	chr2	2	q11.2	98336082	98356423	12	0	-0.737765	-0.737765	7.831E-29
252,152,934,023	1420	TT13	chr2	2	q11.2	99752635	99777115	14	0	-0.83177	-0.83177	2.03E-42
252,152,934,023	1425	TT13	chr2	2	q11.2	101031541	101040305	5	0	-1.299892	-1.299892	2.684E-33
252,152,934,023	1426	TT13	chr2	2	q11.2	101173187	101180196	5	0	-0.914485	-0.914485	3.723E-18
252,152,934,023	1428	TT13	chr2	2	q11.2	101608534	101612812	4	0	-1.547393	-1.547393	2.457E-32
252,152,934,023	1431	TT13	chr2	2	q11.2	102311073	102318092	5	0	-0.995318	-0.995318	9.119E-20
252,152,934,023	1432	TT13	chr2	2	q11.2	102639541	102643001	3	0	-1.076607	-1.076607	5.818E-16
252,152,934,023	1433	TT13	chr2	2	q12.1	102755134	102762688	4	0	-1.022986	-1.022986	3.037E-18
252,152,934,023	1437	TT13	chr2	2	q12.1	103230900	103244838	9	0	-0.739474	-0.739474	1.69E-21
252,152,934,023	1438	TT13	chr2	2	q12.1	103348563	103354390	4	0	-0.967616	-0.967616	2.475E-16
252,152,934,023	1439	TT13	chr2	2	q12.1	105458161	105492773	16	0	-1.476281	-1.476281	1.019E-93
252,152,934,023	1440	TT13	chr2	2	q12.1	105470985	105480986	5	0	-2.49548	-2.49548	6.838E-11
252,152,934,023	1441	TT13	chr2	2	q12.1	105857796	105869089	8	0	-1.369011	-1.369011	2.493E-44
252,152,934,023	1443	TT13	chr2	2	q12.2	106013217	106016024	3	0	-1.292336	-1.292336	1.134E-19
252,152,934,023	1444	TT13	chr2	2	q12.2	106495958	106513533	10	0	-1.061586	-1.061586	5.261E-44
252,152,934,023	1469	TT13	chr2	2	q13 - q14.1	114032378	114525112	62	0	-0.386435	-0.386435	6.436E-31
252,152,934,023	1470	TT13	chr2	2	q14.1	114645738	114655058	5	0	-1.058579	-1.058579	1.841E-22
252,152,934,023	1471	TT13	chr2	2	q14.1	114731764	114740984	5	0	-0.920076	-0.920076	5.523E-17
252,152,934,023	1472	TT13	chr2	2	q14.1	115408046	115425393	10	0	-0.519345	-0.519345	1.181E-14
252,152,934,023	1473	TT13	chr2	2	q14.1	115916975	115921077	3	0	-1.409135	-1.409135	3.88E-21
252,152,934,023	1474	TT13	chr2	2	q14.1	117812772	117830337	3	0	-1.6719	-1.6719	2.977E-24
252,152,934,023	1477	TT13	chr2	2	q14.2	119592767	119617643	12	0	-1.548784	-1.548784	2.546E-70
252,152,934,023	1478	TT13	chr2	2	q14.2	120002696	120008075	4	0	-1.093787	-1.093787	2.431E-17
252,152,934,023	1480	TT13	chr2	2	q14.2	120277678	120305249	15	0	-0.864479	-0.864479	1.364E-38
252,152,934,023	1481	TT13	chr2	2	q14.2	120433321	120438056	3	0	-1.220268	-1.220268	6.077E-17
252,152,934,023	1482	TT13	chr2	2	q14.2	120513365	120524838	7	0	-1.047018	-1.047018	7.695E-30
252,152,934,023	1483	TT13	chr2	2	q14.2	120752287	120777355	14	0	-0.823653	-0.823653	3.471E-35
252,152,934,023	1485	TT13	chr2	2	q14.2	121007665	121020400	5	0	-1.295681	-1.295681	8.247E-30
252,152,934,023	1486	TT13	chr2	2	q14.2	121099120	121107673	6	0	-0.76741	-0.76741	6.123E-12
252,152,934,023	1488	TT13	chr2	2	q14.2	121410978	121415357	3	0	-1.277218	-1.277218	1.103E-20
252,152,934,023	1489	TT13	chr2	2	q14.2	121491202	121500257	3	0	-1.39018	-1.39018	1.558E-23
252,152,934,023	1493	TT13	chr2	2	q14.2	121736879	121750198	7	0	-0.940203	-0.940203	2.482E-24
252,152,934,023	1495	TT13	chr2	2	q14.2	122037567	122045977	5	0	-0.9884	-0.9884	6.31E-21
252,152,934,023	1496	TT13	chr2	2	q14.2	122285562	122288797	3	0	-0.841373	-0.841373	1.791E-11
252,152,934,023	1498	TT13	chr2	2	q14.3	122489793	122517421	12	0	-0.826122	-0.826122	2.614E-35
252,152,934,023	1500	TT13	chr2	2	q14.3	127411661	127416235	3	0	-1.37725	-1.37725	3.245E-22
252,152,934,023	1505	TT13	chr2	2	q14.3	128419281	128462866	20	0	-0.897113	-0.897113	1.04E-51
252,152,934,023	1506	TT13	chr2	2	q14.3	128452004	128460215	4	0	-1.893379	-1.893379	2.233E-14
252,152,934,023	1525	TT13	chr2	2	q21.2	133400439	133434642	21	0	-0.608505	-0.608505	2.133E-27
252,152,934,023	1527	TT13	chr2	2	q21.2	134864890	134890462	6	0	-1.023009	-1.023009	1.126E-27
252,152,934,023	1528	TT13	chr2	2	q21.3	135473425	135479311	4	0	-1.406167	-1.406167	1.34E-28
252,152,934,023	1529	TT13	chr2	2	q21.3	135674860	135678509	3	0	-1.762272	-1.762272	1.334E-31
252,152,934,023	1530	TT13	chr2	2	q21.3	135785502	135795727	6	0	-0.841866	-0.841866	3.451E-20
252,152,934,023	1532	TT13	chr2	2	q21.3	136286389	136291913	4	0	-1.328331	-1.328331	4.11E-28
252,152,934,023	1533	TT13	chr2	2	q21.3	136495905	136501685	4	0	-1.522941	-1.522941	2.699E-32
252,152,934,023	1535	TT13	chr2	2	q22.1	136870595	136877665	5	0	-0.767323	-0.767323	7.793E-14
252,152,934,023	1536	TT13	chr2	2	q22.1	137514964	137520905	3	0	-1.612228	-1.612228	3.116E-29
252,152,934,023	1537	TT13	chr2	2	q22.1	138086151	138096092	4	0	-0.830262	-0.830262	2.774E-13
252,152,934,023	1538	TT13	chr2	2	q22.1	139254546	139262686	5	0	-1.247947	-1.247947	2.463E-29
252,152,934,023	1539	TT13	chr2	2	q22.1	139531378	139541164	5	0	-0.995684	-0.995684	1.846E-21
252,152,934,023	1540	TT13	chr2	2	q22.1	141438262	141445879	5	0	-0.746335	-0.746335	6.375E-14
252,152,934,023	1541	TT13	chr2	2	q22.3	144675512	144699635	12	0	-0.921295	-0.921295	7.909E-37
252,152,934,023	1542	TT13	chr2	2	q22.3	144743574	144751738	5	0	-1.377861	-1.377861	6.999E-35
252,152,934,023	1543	TT13	chr2	2	q22.3	145087227	145092498	3	0	-1.255404	-1.255404	1.259E-17
252,152,934,023	1544	TT13	chr2	2	q22.3	145269116	145284491	10	0	-1.160976	-1.160976	3.107E-41
252,152,934,023	1545	TT13	chr2	2	q22.3	147341389	147348193	5	0	-1.235425	-1.235425	1.359E-27
252,152,934,023	1546	TT13	chr2	2	q22.3	148259609	148267954	3	0	-0.892979	-0.892979	1.027E-10
252,152,934,023	1547	TT13	chr2	2	q22.3	148598844	148608010	6	0	-1.047741	-1.047741	1.465E-23
252,152,934,023	1548	TT13	chr2	2	q23.1	149396960	149442212	21	0	-0.516818	-0.516818	1.083E-20
252,152,934,023	1549	TT13	chr2	2	q23.1	149631077	149648450	10	0	-0.988989	-0.988989	1.221E-33
252,152,934,023	1550	TT13	chr2	2	q23.1	149891480	149899991	7	0	-0.955786	-0.955786	4.697E-23
252,152,934,023	1551	TT13	chr2	2	q23.2	150173758	150190869	5	0	-1.149185	-1.149185	3.73E-25
252,152,934,023	1552	TT13	chr2	2	q23.3	152115742	152119966	4	0	-1.286062	-1.286062	8.532E-24
252,152,934,023	1553	TT13	chr2	2	q23.3	152145401	152156219	6	0	-1.705278	-1.705278	3.978E-47
252,152,934,023	1554	TT13	chr2	2	q23.3	152682249	152685348	3	0	-1.778673	-1.778673	1.206E-27
252,152,934,023	1555	TT13	chr2	2	q23.3	152731077	152734587	3	0	-1.812899	-1.812899	1.798E-25
252,152,934,023	1556	TT13	chr2	2	q23.3	152952082	152957508	4	0	-1.449863	-1.449863	6.793E-29
252,152,934,023	1557	TT13	chr2	2	q23.3	153190023	153196019	3	0	-1.343029	-1.343029	7.398E-20
252,152,934,023	1558	TT13	chr2	2	q23.3	153571812	153577125	4	0	-1.104524	-1.104524	2.799E-19
252,152,934,023	1559	TT13	chr2	2	q23.3	154329149	154338522	8	0	-0.843107	-0.843107	1.149E-20
252,152,934,023	1560	TT13	chr2	2	q23.3	154723353	154734018	5	0	-0.807659	-0.807659	8.57E-14
252,152,934,023	1561	TT13	chr2	2	q24.1	155143026	155153081	4	0	-0.9021	-0.9021	1.041E-13
252,152,934,023	1564	TT13	chr2	2	q24.1	157181872	157315067	53	0	-0.58017	-0.58017	1.885E-60
252,152,934,023	1565	TT13	chr2	2	q24.1	157185021	157200651	8	0	-1.322392	-1.322392	8.491E-14
252,152,934,023	1568	TT13	chr2	2	q24.1	158253548	158334100	34	0.341447	0	0.341447	2.961E-24
252,152,934,023	1569	TT13	chr2	2	q24.1	158482196	158487502	3	0	-1.303092	-1.303092	7.797E-20
252,152,934,023	1570	TT13	chr2	2	q24.1	158730603	158737387	4	0	-1.231153	-1.231153	3.777E-23
252,152,934,023	1571	TT13	chr2	2	q24.1	159311234	159316503	3	0	-1.330741	-1.330741	1.279E-19
252,152,934,023	1572	TT13	chr2	2	q24.2	159820009	159829639	7	0	-0.949476	-0.949476	3.6E-22
252,152,934,023	1573	TT13	chr2	2	q24.2	160136690	160148346	7	0	-0.583183	-0.583183	8.057E-10
252,152,934,023	1575	TT13	chr2	2	q24.2	160563081	160572520	6	0	-1.150277	-1.150277	9.775E-26
252,152,934,023	1576	TT13	chr2	2	q24.2	160652749	160657365	4	0	-1.614136	-1.614136	1.285E-33
252,152,934,023	1577	TT13	chr2	2	q24.2	160756051	160764366	6	0	-1.179668	-1.179668	2.599E-29
252,152,934,023	1578	TT13	chr2	2	q24.2	160916664	160922194	3	0	-1.10293	-1.10293	5.179E-15
252,152,934,023	1579	TT13	chr2	2	q24.2	161125034	161128576	3	0	-0.945955	-0.945955	2.608E-11
252,152,934,023	1580	TT13	chr2	2	q24.2	161260559	161267012	3	0	-1.019749	-1.019749	2.773E-13
252,152,934,023	1581	TT13	chr2	2	q24.2	161293974	161308713	8	0	-1.088483	-1.088483	9.267E-36
252,152,934,023	1583	TT13	chr2	2	q24.2	162090722	162103370	8	0	-1.369522	-1.369522	3.089E-43
252,152,934,023	1584	TT13	chr2	2	q24.2	162191668	162204049	4	0	-0.872516	-0.872516	2.452E-13

252,152,934,023	1585	TT13	chr2	2	q24.2	162269687	162287643	10	0	-2.00411	-2.00411	3.307E-91
252,152,934,023	1586	TT13	chr2	2	q24.2	163169395	163208948	22	0	-0.576919	-0.576919	2.551E-26
252,152,934,023	1587	TT13	chr2	2	q24.2	163320063	163330106	6	0	-0.642839	-0.642839	6.075E-11
252,152,934,023	1588	TT13	chr2	2	q24.3	164586461	164597096	6	0	-1.255895	-1.255895	9.708E-35
252,152,934,023	1589	TT13	chr2	2	q24.3	165476180	165480873	3	0	-1.374807	-1.374807	2.741E-17
252,152,934,023	1590	TT13	chr2	2	q24.3	165693497	165703487	6	0	-0.992878	-0.992878	6.234E-20
252,152,934,023	1591	TT13	chr2	2	q24.3	166646761	166653833	5	0	-1.249948	-1.249948	4.964E-30
252,152,934,023	1592	TT13	chr2	2	q24.3	166809772	166815187	4	0	-2.39645	-2.39645	1.315E-50
252,152,934,023	1593	TT13	chr2	2	q24.3	168142761	168154115	4	0	-0.838277	-0.838277	7.542E-15
252,152,934,023	1594	TT13	chr2	2	q24.3	169099929	169105801	5	0	-1.289587	-1.289587	3.535E-28
252,152,934,023	1595	TT13	chr2	2	q24.3	169308127	169315509	6	0	-0.968697	-0.968697	2.66E-21
252,152,934,023	1596	TT13	chr2	2	q31.1	170175251	170720069	222	0	-0.311684	-0.311684	2.737E-65
252,152,934,023	1597	TT13	chr2	2	q31.1	170182094	170187690	3	0	-1.627478	-1.627478	2.796E-19
252,152,934,023	1606	TT13	chr2	2	q31.1	171623584	171630779	5	0	-1.204798	-1.204798	7.85E-26
252,152,934,023	1607	TT13	chr2	2	q31.1	171676232	171680824	4	0	-1.337298	-1.337298	4.637E-23
252,152,934,023	1608	TT13	chr2	2	q31.1	171783004	171787124	3	0	-1.584349	-1.584349	4.704E-25
252,152,934,023	1609	TT13	chr2	2	q31.1	172012121	172018644	3	0	-1.123187	-1.123187	1.109E-15
252,152,934,023	1610	TT13	chr2	2	q31.1	172288759	172292145	4	0	-1.949102	-1.949102	2.598E-41
252,152,934,023	1611	TT13	chr2	2	q31.1	172370855	172386992	11	0	-1.222239	-1.222239	8.863E-57
252,152,934,023	1626	TT13	chr2	2	q31.1	175199086	175209911	6	0	-2.13276	-2.13276	7.468E-55
252,152,934,023	1628	TT13	chr2	2	q31.1	175347952	175358038	6	0	-1.099634	-1.099634	3.061E-28
252,152,934,023	1629	TT13	chr2	2	q31.1	175544502	175549990	4	0	-1.585888	-1.585888	1.601E-33
252,152,934,023	1630	TT13	chr2	2	q31.1	175575459	175586675	7	0	-1.035625	-1.035625	5.18E-28
252,152,934,023	1631	TT13	chr2	2	q31.1	175866678	175872548	4	0	-1.46737	-1.46737	3.598E-30
252,152,934,023	1632	TT13	chr2	2	q31.1	175967761	175979170	6	0	-0.906384	-0.906384	2.478E-20
252,152,934,023	1634	TT13	chr2	2	q31.1	176863767	176869338	4	0	-1.333747	-1.333747	6.418E-26
252,152,934,023	1635	TT13	chr2	2	q31.1	176926359	176941472	9	0	-0.515896	-0.515896	5.309E-10
252,152,934,023	1636	TT13	chr2	2	q31.1	176943343	177055486	89	0	-1.287859	-1.287859	4.900e-324
252,152,934,023	1637	TT13	chr2	2	q31.1	176955723	177002978	34	0	-1.671477	-1.671477	1.724E-14
252,152,934,023	1639	TT13	chr2	2	q31.1	177017907	177025840	9	0	-2.176336	-2.176336	2.083E-17
252,152,934,023	1662	TT13	chr2	2	q32.1	186598972	186610227	7	0	-1.092284	-1.092284	2.168E-31
252,152,934,023	1663	TT13	chr2	2	q32.1	187450207	187457376	5	0	-1.009127	-1.009127	7.41E-20
252,152,934,023	1664	TT13	chr2	2	q32.1	187555979	187561991	4	0	-1.305377	-1.305377	3.648E-26
252,152,934,023	1665	TT13	chr2	2	q32.1	188417871	188420416	3	0	-1.223341	-1.223341	2.612E-17
252,152,934,023	1666	TT13	chr2	2	q32.2	190441011	190693739	108	0	-0.339542	-0.339542	1.113E-39
252,152,934,023	1667	TT13	chr2	2	q32.2	190444541	190447844	3	0	-1.578752	-1.578752	1.174E-17
252,152,934,023	1676	TT13	chr2	2	q32.3	192106737	192113927	5	0	-1.212639	-1.212639	3.819E-27
252,152,934,023	1677	TT13	chr2	2	q32.3	192259703	192266370	4	0	-1.2136	-1.2136	6.571E-23
252,152,934,023	1678	TT13	chr2	2	q32.3	192541496	192548014	5	0	-1.242301	-1.242301	1.424E-26
252,152,934,023	1679	TT13	chr2	2	q32.3	193052835	193062886	6	0	-0.871958	-0.871958	1.091E-17
252,152,934,023	1680	TT13	chr2	2	q32.3	196376569	196436760	17	0	-0.725794	-0.725794	6.463E-33
252,152,934,023	1681	TT13	chr2	2	q32.3	196520111	196525377	4	0	-1.227137	-1.227137	2.739E-23
252,152,934,023	1682	TT13	chr2	2	q32.3	197031944	197038405	5	0	-0.845429	-0.845429	8.255E-18
252,152,934,023	1683	TT13	chr2	2	q33.1	197453251	197460545	5	0	-1.470687	-1.470687	2.138E-35
252,152,934,023	1684	TT13	chr2	2	q33.1	197789147	197792242	3	0	-1.674412	-1.674412	3.585E-28
252,152,934,023	1685	TT13	chr2	2	q33.1	198025658	198031823	4	0	-1.098922	-1.098922	2.931E-19
252,152,934,023	1686	TT13	chr2	2	q33.1	198172505	198177264	4	0	-1.489312	-1.489312	9.573E-24
252,152,934,023	1687	TT13	chr2	2	q33.1	198229477	198242590	7	0	-0.637154	-0.637154	2.931E-12
252,152,934,023	1688	TT13	chr2	2	q33.1	198312594	198319311	5	0	-1.039508	-1.039508	3.698E-21
252,152,934,023	1689	TT13	chr2	2	q33.1	198362195	198384060	13	0	-0.941976	-0.941976	5.31E-41
252,152,934,023	1691	TT13	chr2	2	q33.1	198643238	198672015	16	0	-0.800823	-0.800823	5.914E-36
252,152,934,023	1692	TT13	chr2	2	q33.1	198784785	198792734	5	0	-1.113451	-1.113451	1.326E-23
252,152,934,023	1693	TT13	chr2	2	q33.1	200317722	200338365	12	0	-1.357022	-1.357022	1.233E-62
252,152,934,023	1694	TT13	chr2	2	q33.1	200773670	200780677	5	0	-1.301489	-1.301489	5.141E-31
252,152,934,023	1705	TT13	chr2	2	q33.1	202505354	202509894	4	0	-1.980835	-1.980835	1.285E-40
252,152,934,023	1722	TT13	chr2	2	q33.2	204646914	204653650	5	0	-0.9659	-0.9659	2.265E-19
252,152,934,023	1730	TT13	chr2	2	q33.3	208030028	208033995	3	0	-1.388938	-1.388938	1.281E-19
252,152,934,023	1738	TT13	chr2	2	q34	210286002	210292026	4	0	-1.340176	-1.340176	3.921E-25
252,152,934,023	1740	TT13	chr2	2	q34	210862109	210870887	5	0	-1.155395	-1.155395	4.121E-26
252,152,934,023	1741	TT13	chr2	2	q34	211087538	211092258	3	0	-1.45166	-1.45166	8.235E-23
252,152,934,023	1742	TT13	chr2	2	q34	212383543	212387800	3	0	-0.866567	-0.866567	2.123E-10
252,152,934,023	1743	TT13	chr2	2	q34	213396831	213404373	5	0	-1.102117	-1.102117	2.428E-21
252,152,934,023	1744	TT13	chr2	2	q34	214013299	214020099	4	0	-1.161221	-1.161221	5.855E-21
252,152,934,023	1745	TT13	chr2	2	q34	214580415	214586420	3	0	-0.975288	-0.975288	5.92E-12
252,152,934,023	1746	TT13	chr2	2	q35	215669423	215704185	20	0	-0.751234	-0.751234	2.19E-42
252,152,934,023	1761	TT13	chr2	2	q35	219254416	219273298	19	0	-0.846267	-0.846267	1.829E-33
252,152,934,023	1766	TT13	chr2	2	q35	219846005	219868439	24	0	-1.240839	-1.240839	5.368E-41
252,152,934,023	1770	TT13	chr2	2	q35	220128212	220138349	8	0.272331	0	0.272331	1.862E-18
252,152,934,023	1775	TT13	chr2	2	q35	220405562	220421188	9	0	-1.890245	-1.890245	1.55E-47
252,152,934,023	1776	TT13	chr2	2	q36.1	222755757	222761104	3	0	-1.235822	-1.235822	1.269E-17
252,152,934,023	1777	TT13	chr2	2	q36.1	223153184	223158739	4	0	-1.570802	-1.570802	1.307E-32
252,152,934,023	1778	TT13	chr2	2	q36.1	223175574	223187382	5	0	-1.136248	-1.136248	6.919E-24
252,152,934,023	1779	TT13	chr2	2	q36.1	223284901	223293357	5	0	-1.175324	-1.175324	2.801E-22
252,152,934,023	1780	TT13	chr2	2	q36.1	223532547	223540737	5	0	-1.007706	-1.007706	1.437E-20
252,152,934,023	1782	TT13	chr2	2	q36.1	223917004	223920435	3	0	-1.135756	-1.135756	5.699E-14
252,152,934,023	1783	TT13	chr2	2	q36.1	224806879	224811961	4	0	-1.453786	-1.453786	1.305E-28
252,152,934,023	1784	TT13	chr2	2	q36.1	224898393	224906247	5	0	-0.89666	-0.89666	5.627E-16
252,152,934,023	1785	TT13	chr2	2	q36.2	225442529	225472911	14	0	-0.702573	-0.702573	3.911E-26
252,152,934,023	1786	TT13	chr2	2	q36.2	225904703	225908462	3	0	-1.379977	-1.379977	5.875E-21
252,152,934,023	1787	TT13	chr2	2	q36.3	226442435	226452630	8	0	-1.163033	-1.163033	3.881E-40
252,152,934,023	1789	TT13	chr2	2	q36.3	227652999	227668870	9	0	-1.295761	-1.295761	2.742E-47
252,152,934,023	1790	TT13	chr2	2	q36.3	227697835	227705777	5	0	-1.182068	-1.182068	4.22E-23
252,152,934,023	1791	TT13	chr2	2	q36.3	228021292	228032268	6	0	-1.053038	-1.053038	4.685E-25
252,152,934,023	1792	TT13	chr2	2	q36.3	228181111	228193385	7	0	-1.136803	-1.136803	1.492E-32
252,152,934,023	1793	TT13	chr2	2	q36.3	228335457	228342178	5	0	-1.052677	-1.052677	1.082E-20
252,152,934,023	1794	TT13	chr2	2	q36.3	228451351	228487773	18	0	-1.108317	-1.108317	1.306E-78
252,152,934,023	1795	TT13	chr2	2	q36.3	228478718	228482943	3	0	-2.202616	-2.202616	8.567E-11
252,152,934,023	1796	TT13	chr2	2	q36.3	228588383	228593831	4	0	-1.940446	-1.940446	2.492E-40
252,152,934,023	1815	TT13	chr2	2	q37.1	232642237	232655386	8	0	-1.384434	-1.384434	6.703E-50
252,152,934,023	1818	TT13	chr2	2	q37.1	233209733	233280219	21	0	-0.53697	-0.53697	1.948E-20
252,152,934,023	1819	TT13	chr2	2	q37.1	233320624	233329616	4	0	-0.875942	-0.875942	9.77E-12
252,152,934,023	1830	TT13	chr2	2	q37.1	234350991	234383684	18	0	-0.807678	-0.807678	2.438E-39
252,152,934,023	1838	TT13	chr2	2	q37.2	236575428	236582609	5	0	-1.491309	-1.491309	6.413E-34
252,152,934,023	1840	TT13	chr2	2	q37.2	237026256	237034961	5	0	-1.185762	-1.185762	8.284E-27
252,152,934,023	1841	TT13	chr2	2	q37.2	237066359	237089257	12	0	-1.720915	-1.720915	1.828E-71
252,152,934,023	1842	TT13	chr2	2	q37.2	237120691	237126402	5	0	-1.389667	-1.389667	6.765E-30

252,152,934,023	1843	TT13	chr2	2	q37.3	237413976	237417138	3	0	-1.623074	-1.623074	6.253E-24
252,152,934,023	1844	TT13	chr2	2	q37.3	237473689	237479062	5	0	-1.062188	-1.062188	3.246E-21
252,152,934,023	1846	TT13	chr2	2	q37.3	238383533	238403170	9	0	-0.732686	-0.732686	5.544E-22
252,152,934,023	1863	TT13	chr2	2	q37.3	240192395	240218557	13	0	-0.752233	-0.752233	1.495E-27
252,152,934,023	1874	TT13	chr2	2	q37.3	241769058	241774720	4	0	-1.752755	-1.752755	2.049E-26
252,152,934,023	1883	TT13	chr2	2	q37.3	242476947	242848137	67	0	-0.841103	-0.841103	1.871E-59
252,152,934,023	1885	TT13	chr3	3	p26.3	232496	244865	6	0	-1.367959	-1.367959	4.815E-40
252,152,934,023	1889	TT13	chr3	3	p26.2	3167078	3172217	4	0	-1.26336	-1.26336	3.787E-25
252,152,934,023	1890	TT13	chr3	3	p26.2	3219127	3221793	3	0	-1.394726	-1.394726	4.508E-22
252,152,934,023	1891	TT13	chr3	3	p26.2	3836563	3845497	6	0	-1.014975	-1.014975	1.063E-21
252,152,934,023	1892	TT13	chr3	3	p26.1	4340481	4348855	4	0	-0.94812	-0.94812	1.34E-16
252,152,934,023	1893	TT13	chr3	3	p26.1	4505621	4511483	3	0	-1.033827	-1.033827	2.158E-14
252,152,934,023	1894	TT13	chr3	3	p26.1	4909132	4913330	3	0	-1.246288	-1.246288	3.347E-19
252,152,934,023	1895	TT13	chr3	3	p26.1	5016406	5028188	5	0	-0.777003	-0.777003	1.024E-14
252,152,934,023	1896	TT13	chr3	3	p26.1	5134162	5166686	15	0	-0.814557	-0.814557	1.546E-41
252,152,934,023	1897	TT13	chr3	3	p26.1	5227076	5233504	4	0	-1.404641	-1.404641	2.965E-27
252,152,934,023	1898	TT13	chr3	3	p26.1	6900133	6909590	7	0	-0.989718	-0.989718	2.603E-29
252,152,934,023	1903	TT13	chr3	3	p25.3	9021876	9034194	7	0	-0.715771	-0.715771	2.655E-15
252,152,934,023	1905	TT13	chr3	3	p25.3	9436558	9441240	3	0	-1.599463	-1.599463	3.326E-28
252,152,934,023	1911	TT13	chr3	3	p25.3	9972193	9995122	11	0	-1.497129	-1.497129	6.2E-65
252,152,934,023	1913	TT13	chr3	3	p25.3	10179706	10185766	3	0	-1.916354	-1.916354	4.891E-32
252,152,934,023	1914	TT13	chr3	3	p25.3	10274256	10294067	10	0	-0.704292	-0.704292	8.671E-23
252,152,934,023	1917	TT13	chr3	3	p25.3	10744520	10753626	5	0	-0.869745	-0.869745	2.283E-17
252,152,934,023	1918	TT13	chr3	3	p25.3	10857068	10861338	3	0	-1.206053	-1.206053	2.583E-17
252,152,934,023	1919	TT13	chr3	3	p25.3	11030157	11061987	16	0	-0.545342	-0.545342	2.357E-21
252,152,934,023	1922	TT13	chr3	3	p25.2	12041877	12050170	6	0	-1.239776	-1.239776	2.293E-35
252,152,934,023	1923	TT13	chr3	3	p25.2	12198399	12202823	3	0	-1.459594	-1.459594	6.809E-23
252,152,934,023	1924	TT13	chr3	3	p25.2	12324819	12333013	4	0	-1.224324	-1.224324	7.842E-24
252,152,934,023	1925	TT13	chr3	3	p25.2	12523977	12529123	4	0	-1.148755	-1.148755	6.086E-22
252,152,934,023	1926	TT13	chr3	3	p25.2	12596391	12599555	3	0	-1.707512	-1.707512	1.219E-28
252,152,934,023	1927	TT13	chr3	3	p25.2	12700329	12707704	5	0	-0.959135	-0.959135	2.2E-18
252,152,934,023	1928	TT13	chr3	3	p25.2	12805316	12946488	57	0	-0.463228	-0.463228	6.949E-50
252,152,934,023	1929	TT13	chr3	3	p25.2	12911951	12923874	5	0	-1.315396	-1.315396	1.231E-13
252,152,934,023	1948	TT13	chr3	3	p25.1	15889786	15923912	25	0	-0.807765	-0.807765	3.671E-67
252,152,934,023	1949	TT13	chr3	3	p25.1	15899339	15902692	4	0	-1.929172	-1.929172	1.832E-16
252,152,934,023	1950	TT13	chr3	3	p24.3	16550795	16559126	5	0	-1.096377	-1.096377	4.699E-25
252,152,934,023	1961	TT13	chr3	3	p24.3	23845495	23853474	5	0	-1.743268	-1.743268	1.996E-47
252,152,934,023	1962	TT13	chr3	3	p24.2	23910783	23926378	10	0	-1.130223	-1.130223	1.657E-48
252,152,934,023	1963	TT13	chr3	3	p24.2	23983335	23990976	5	0	-1.255571	-1.255571	2.608E-31
252,152,934,023	1980	TT13	chr3	3	p22.3	32431106	32446977	8	0	-1.088681	-1.088681	1.569E-32
252,152,934,023	1982	TT13	chr3	3	p22.3	32609709	32623981	7	0	-1.540576	-1.540576	1.622E-50
252,152,934,023	1986	TT13	chr3	3	p22.3	32978020	32982707	3	0	-1.553835	-1.553835	1.923E-23
252,152,934,023	1987	TT13	chr3	3	p22.3	33062601	33072383	7	0	-1.008653	-1.008653	2.216E-25
252,152,934,023	1988	TT13	chr3	3	p22.3	33131453	33162199	16	0	-0.697477	-0.697477	1.779E-23
252,152,934,023	1989	TT13	chr3	3	p22.3	33756698	33764060	5	0	-1.143725	-1.143725	4.086E-24
252,152,934,023	1990	TT13	chr3	3	p22.3	33838710	33842552	3	0	-1.319823	-1.319823	1.26E-18
252,152,934,023	1992	TT13	chr3	3	p22.3	36414320	36425584	7	0	-1.121056	-1.121056	9.562E-31
252,152,934,023	1995	TT13	chr3	3	p22.2	37271537	37288600	10	0	-1.166629	-1.166629	4.884E-48
252,152,934,023	1997	TT13	chr3	3	p22.2	37489726	37497495	5	0	-0.890188	-0.890188	2.737E-15
252,152,934,023	1998	TT13	chr3	3	p22.2	37897612	37906740	5	0	-1.086564	-1.086564	7.178E-25
252,152,934,023	1999	TT13	chr3	3	p22.2	38036630	38041222	4	0	-1.400216	-1.400216	3.614E-24
252,152,934,023	2022	TT13	chr3	3	p22.1	42622363	42645020	11	0	-0.86412	-0.86412	2.654E-27
252,152,934,023	2024	TT13	chr3	3	p22.1	42947282	42952208	3	0	-2.701382	-2.701382	8.555E-42
252,152,934,023	2036	TT13	chr3	3	p21.31	44901620	44904959	5	0	-1.811299	-1.811299	8.923E-43
252,152,934,023	2037	TT13	chr3	3	p21.31	45015500	45031546	10	0	-1.211015	-1.211015	5.287E-47
252,152,934,023	2039	TT13	chr3	3	p21.31	45264355	45269773	5	0	-1.449927	-1.449927	3.778E-30
252,152,934,023	2041	TT13	chr3	3	p21.31	45633477	45639062	5	0	-1.1478	-1.1478	1.49E-20
252,152,934,023	2044	TT13	chr3	3	p21.31	45819942	45840739	12	0	-0.729834	-0.729834	1.383E-22
252,152,934,023	2049	TT13	chr3	3	p21.31	46789430	46886005	21	0	-0.938575	-0.938575	6.83E-58
252,152,934,023	2050	TT13	chr3	3	p21.31	46792761	46799535	5	0	-1.906518	-1.906518	1.33E-14
252,152,934,023	2074	TT13	chr3	3	p21.31	49025931	49029456	4	0	-1.451468	-1.451468	1.929E-10
252,152,934,023	2075	TT13	chr3	3	p21.31	49025931	49069718	40	0	-0.652107	-0.652107	1.633E-48
252,152,934,023	2088	TT13	chr3	3	p21.31	50189627	50430382	126	0	-0.514123	-0.514123	3.743E-82
252,152,934,023	2089	TT13	chr3	3	p21.31	50306317	50311960	4	0	-1.485723	-1.485723	6.633E-12
252,152,934,023	2094	TT13	chr3	3	p21.2	50649937	50654126	3	0	-1.608476	-1.608476	1.119E-19
252,152,934,023	2095	TT13	chr3	3	p21.2	50709671	50717567	5	0	-1.052692	-1.052692	2.861E-19
252,152,934,023	2096	TT13	chr3	3	p21.2	50824511	50879171	16	0	-0.466068	-0.466068	5.285E-12
252,152,934,023	2098	TT13	chr3	3	p21.2	51417985	51431725	8	0	-1.356444	-1.356444	1.814E-37
252,152,934,023	2102	TT13	chr3	3	p21.2	51704369	51707771	3	0	-1.771866	-1.771866	2.814E-24
252,152,934,023	2103	TT13	chr3	3	p21.2	51739114	51746075	4	0	-0.907194	-0.907194	1.046E-11
252,152,934,023	2104	TT13	chr3	3	p21.2	51983601	52030161	22	0	-0.947729	-0.947729	5.501E-57
252,152,934,023	2105	TT13	chr3	3	p21.2	52080642	52094281	7	0	-0.527502	-0.527502	7.544E-13
252,152,934,023	2106	TT13	chr3	3	p21.2	52254639	52281553	16	0	-1.017279	-1.017279	1.367E-48
252,152,934,023	2107	TT13	chr3	3	p21.1	52306632	52315157	11	0	-1.288843	-1.288843	1.674E-55
252,152,934,023	2111	TT13	chr3	3	p21.1	52514291	52564795	25	0	-0.440596	-0.440596	4.939E-13
252,152,934,023	2112	TT13	chr3	3	p21.1	52566539	52571607	4	0	-2.702119	-2.702119	3.523E-29
252,152,934,023	2113	TT13	chr3	3	p21.1	52715549	52746252	18	0	-0.778621	-0.778621	8.62E-35
252,152,934,023	2114	TT13	chr3	3	p21.1	52799873	52806408	4	0	-1.096789	-1.096789	1.872E-18
252,152,934,023	2118	TT13	chr3	3	p21.1	53286661	53295108	5	0	-0.824784	-0.824784	8.135E-16
252,152,934,023	2119	TT13	chr3	3	p21.1	53526391	53531514	3	0	-1.078317	-1.078317	7.703E-16
252,152,934,023	2120	TT13	chr3	3	p21.1	53855586	53858820	3	0	-1.239916	-1.239916	9.25E-14
252,152,934,023	2123	TT13	chr3	3	p21.1	54153542	54158830	3	0	-1.585804	-1.585804	2.718E-25
252,152,934,023	2125	TT13	chr3	3	p14.3	56713899	56729392	8	0	-1.220785	-1.220785	2.731E-47
252,152,934,023	2126	TT13	chr3	3	p14.3	56832950	56836802	3	0	-1.59819	-1.59819	7.251E-26
252,152,934,023	2130	TT13	chr3	3	p14.3	57256124	57265928	7	0	-1.039401	-1.039401	8.968E-33
252,152,934,023	2133	TT13	chr3	3	p14.3	57728568	57743275	8	0	-1.288707	-1.288707	5.895E-46
252,152,934,023	2137	TT13	chr3	3	p14.3	58316453	58321201	4	0	-1.929179	-1.929179	3.835E-43
252,152,934,023	2139	TT13	chr3	3	p14.3	58569648	58573572	3	0	-1.705413	-1.705413	7.512E-28
252,152,934,023	2141	TT13	chr3	3	p14.2	59032868	59039576	5	0	-1.304751	-1.304751	1.974E-32
252,152,934,023	2142	TT13	chr3	3	p14.2	61550730	61554076	3	0	-1.389428	-1.389428	1.181E-21
252,152,934,023	2143	TT13	chr3	3	p14.2	62185407	62194160	7	0	-0.753215	-0.753215	7.836E-19
252,152,934,023	2144	TT13	chr3	3	p14.2	62355339	62365509	6	0	-1.948125	-1.948125	3.099E-59
252,152,934,023	2145	TT13	chr3	3	p14.2	62856559	62865882	5	0	-1.054519	-1.054519	2.779E-24
252,152,934,023	2146	TT13	chr3	3	p14.1	63847939	63852530	3	0	-1.521661	-1.521661	1.761E-23
252,152,934,023	2147	TT13	chr3	3	p14.1	63895315	63899837	3	0	-1.721714	-1.721714	3.607E-30
252,152,934,023	2148	TT13	chr3	3	p14.1	64006604	64010856	4	0	-1.487836	-1.487836	2.049E-32

252,152,934,023	2149	TT13	chr3	3	p14.1	64670316	64677708	5	0	-1.082299	-1.082299	1.002E-21
252,152,934,023	2150	TT13	chr3	3	p14.1	65335620	65369610	18	0	-0.761349	-0.761349	2.32E-43
252,152,934,023	2172	TT13	chr3	3	p13	72934985	72939895	4	0	-1.43105	-1.43105	3.679E-21
252,152,934,023	2181	TT13	chr3	3	p12.3	79064353	79072762	6	0	-1.177379	-1.177379	4.637E-33
252,152,934,023	2185	TT13	chr3	3	p12.2	81809574	81818957	5	0	-1.94857	-1.94857	8.427E-53
252,152,934,023	2186	TT13	chr3	3	p12.1	85003932	85015312	5	0	-0.845195	-0.845195	2.572E-17
252,152,934,023	2187	TT13	chr3	3	p12.1	85180560	85189549	5	0	-1.000831	-1.000831	3.816E-20
252,152,934,023	2188	TT13	chr3	3	p12.1	85551347	85557383	4	0	-1.280717	-1.280717	1.228E-25
252,152,934,023	2189	TT13	chr3	3	p12.1	86059106	86066452	5	0	-1.125939	-1.125939	2.099E-27
252,152,934,023	2190	TT13	chr3	3	p12.1	87035745	87044348	6	0	-1.148575	-1.148575	4.366E-32
252,152,934,023	2191	TT13	chr3	3	p11.1	88060529	88067442	4	0	-1.137121	-1.137121	5.083E-22
252,152,934,023	2192	TT13	chr3	3	p11.1	88195451	88202695	4	0	-1.279888	-1.279888	5.323E-26
252,152,934,023	2193	TT13	chr3	3	q11.1	93691065	93695740	4	0	-1.408831	-1.408831	1.195E-26
252,152,934,023	2194	TT13	chr3	3	q11.1	93762254	93771347	5	0	-0.816766	-0.816766	8.74E-14
252,152,934,023	2195	TT13	chr3	3	q11.2	94224317	94229943	3	0	-1.139402	-1.139402	2.321E-15
252,152,934,023	2196	TT13	chr3	3	q11.2	94655364	94659751	4	0	-1.408109	-1.408109	1.231E-27
252,152,934,023	2197	TT13	chr3	3	q11.2	96528594	96536833	5	0	-1.34582	-1.34582	3.652E-32
252,152,934,023	2198	TT13	chr3	3	q11.2	97195140	97201760	4	0	-0.960196	-0.960196	6.662E-16
252,152,934,023	2199	TT13	chr3	3	q11.2	97537155	97544073	4	0	-1.260803	-1.260803	1.476E-22
252,152,934,023	2200	TT13	chr3	3	q11.2	97689990	97699768	6	0	-0.907898	-0.907898	8.492E-20
252,152,934,023	2207	TT13	chr3	3	q12.1	99591299	99597878	5	0	-1.10493	-1.10493	9.891E-23
252,152,934,023	2209	TT13	chr3	3	q12.2	100049410	100062597	8	0	-0.691839	-0.691839	1.24E-15
252,152,934,023	2210	TT13	chr3	3	q12.2	100117628	100121879	4	0	-1.557494	-1.557494	2.365E-32
252,152,934,023	2211	TT13	chr3	3	q12.2	100387984	100434461	19	0	-0.552434	-0.552434	3.393E-22
252,152,934,023	2212	TT13	chr3	3	q12.3	101157472	101159987	3	0	-1.466476	-1.466476	7.277E-19
252,152,934,023	2213	TT13	chr3	3	q12.3	101230230	101234736	3	0	-0.937042	-0.937042	6.152E-12
252,152,934,023	2214	TT13	chr3	3	q12.3	101393682	101396550	3	0	-1.800058	-1.800058	4.403E-24
252,152,934,023	2215	TT13	chr3	3	q12.3	101565130	101569434	3	0	-1.204804	-1.204804	1.421E-16
252,152,934,023	2216	TT13	chr3	3	q13.11	102971907	102992355	5	0	-0.666762	-0.666762	4.447E-10
252,152,934,023	2217	TT13	chr3	3	q13.11	105581981	105591368	6	0	-1.132396	-1.132396	5.206E-29
252,152,934,023	2221	TT13	chr3	3	q13.13	108834643	108845139	5	0	-1.698547	-1.698547	1.1E-43
252,152,934,023	2224	TT13	chr3	3	q13.2	111572251	111583356	8	0	-0.865785	-0.865785	2.143E-23
252,152,934,023	2226	TT13	chr3	3	q13.2	112048170	112055766	6	0	-0.714555	-0.714555	9.859E-13
252,152,934,023	2227	TT13	chr3	3	q13.2	112272885	112282313	5	0	-1.657222	-1.657222	1.638E-42
252,152,934,023	2228	TT13	chr3	3	q13.2	112732866	112767762	12	0	-0.719979	-0.719979	4.508E-24
252,152,934,023	2229	TT13	chr3	3	q13.2	112928414	112935693	5	0	-1.072598	-1.072598	3.814E-21
252,152,934,023	2230	TT13	chr3	3	q13.2	113249321	113253681	3	0	-1.047531	-1.047531	2.508E-14
252,152,934,023	2231	TT13	chr3	3	q13.2	113412557	113418919	4	0	-1.622753	-1.622753	1.061E-32
252,152,934,023	2232	TT13	chr3	3	q13.2	113458528	113468762	7	0	-0.965755	-0.965755	2.758E-23
252,152,934,023	2233	TT13	chr3	3	q13.31	113555854	113573744	9	0	-1.129822	-1.129822	3.614E-41
252,152,934,023	2241	TT13	chr3	3	q13.31	115501589	115512325	5	0	-1.871662	-1.871662	9.078E-48
252,152,934,023	2256	TT13	chr3	3	q13.33	121404859	121410002	4	0	-1.693169	-1.693169	4.412E-35
252,152,934,023	2257	TT13	chr3	3	q13.33	121737890	121743412	4	0	-1.260459	-1.260459	4.462E-20
252,152,934,023	2258	TT13	chr3	3	q13.33 - q21.1	121889279	121922797	15	0	-0.937588	-0.937588	2.031E-49
252,152,934,023	2264	TT13	chr3	3	q21.1	122743076	122751945	6	0	-0.583069	-0.583069	1.98E-14
252,152,934,023	2265	TT13	chr3	3	q21.1	123162474	123171485	5	0	-0.834202	-0.834202	1.287E-18
252,152,934,023	2267	TT13	chr3	3	q21.1	123592500	123607315	9	0	-0.732537	-0.732537	7.049E-18
252,152,934,023	2269	TT13	chr3	3	q21.2	124082367	124107637	13	0	-0.917287	-0.917287	8.603E-40
252,152,934,023	2270	TT13	chr3	3	q21.2	124300476	124309786	5	0	-0.933558	-0.933558	3.029E-18
252,152,934,023	2272	TT13	chr3	3	q21.2	125072818	125099412	15	0	-0.841033	-0.841033	6.028E-37
252,152,934,023	2274	TT13	chr3	3	q21.2	125308523	125315178	6	0	-1.262272	-1.262272	5.159E-34
252,152,934,023	2283	TT13	chr3	3	q21.3	126106521	126114896	6	0	-1.740329	-1.740329	1.107E-41
252,152,934,023	2287	TT13	chr3	3	q21.3	127011703	127031341	9	0	-0.987188	-0.987188	4.929E-32
252,152,934,023	2292	TT13	chr3	3	q21.3	127310509	127324645	7	0	-1.705588	-1.705588	4.045E-57
252,152,934,023	2305	TT13	chr3	3	q21.3	128708598	128792851	43	0	-0.633812	-0.633812	5.266E-57
252,152,934,023	2306	TT13	chr3	3	q21.3	128710649	128721415	8	0	-1.202524	-1.202524	8.748E-11
252,152,934,023	2311	TT13	chr3	3	q22.1	129264129	129267874	3	0	-1.02413	-1.02413	8.876E-13
252,152,934,023	2312	TT13	chr3	3	q22.1	129606445	129614295	4	0	-1.217962	-1.217962	9.916E-23
252,152,934,023	2313	TT13	chr3	3	q22.1	130530230	130536677	4	0	-0.915656	-0.915656	4.975E-15
252,152,934,023	2315	TT13	chr3	3	q22.1	131095573	131104555	5	0	-0.694404	-0.694404	1.498E-10
252,152,934,023	2316	TT13	chr3	3	q22.1	131668445	131675888	3	0	-0.912169	-0.912169	2.104E-11
252,152,934,023	2317	TT13	chr3	3	q22.1	132107099	132145764	20	0	-0.767618	-0.767618	8.639E-44
252,152,934,023	2318	TT13	chr3	3	q22.1	132113453	132116317	3	0	-1.910964	-1.910964	4.344E-13
252,152,934,023	2321	TT13	chr3	3	q22.1	132438414	132445155	4	0	-1.395656	-1.395656	2.108E-25
252,152,934,023	2322	TT13	chr3	3	q22.1	132754139	132760443	4	0	-1.330209	-1.330209	2.584E-27
252,152,934,023	2323	TT13	chr3	3	q22.1	132882943	132888686	3	0	-1.209294	-1.209294	9.729E-18
252,152,934,023	2324	TT13	chr3	3	q22.1	133265846	133300703	15	0	-0.65345	-0.65345	6.041E-24
252,152,934,023	2325	TT13	chr3	3	q22.1	133377907	133396137	9	0	-1.034571	-1.034571	2.829E-33
252,152,934,023	2333	TT13	chr3	3	q22.2	134204456	134208301	4	0	-1.679329	-1.679329	9.77E-34
252,152,934,023	2334	TT13	chr3	3	q22.2	134508360	134518836	6	0	-0.757016	-0.757016	7.848E-14
252,152,934,023	2335	TT13	chr3	3	q22.2	134633851	134638029	3	0	-1.242103	-1.242103	1.228E-20
252,152,934,023	2336	TT13	chr3	3	q22.2	134755839	134761661	3	0	-0.88866	-0.88866	1.713E-14
252,152,934,023	2337	TT13	chr3	3	q22.2	135683027	135687628	3	0	-1.544117	-1.544117	1.667E-24
252,152,934,023	2338	TT13	chr3	3	q22.3	135909409	135920284	5	0	-1.206104	-1.206104	1.143E-23
252,152,934,023	2339	TT13	chr3	3	q22.3	135967054	135971857	4	0	-0.965157	-0.965157	9.593E-16
252,152,934,023	2344	TT13	chr3	3	q22.3	136701240	136708717	4	0	-0.960483	-0.960483	5.184E-15
252,152,934,023	2345	TT13	chr3	3	q22.3	137830032	137851175	12	0	-0.809691	-0.809691	6.675E-27
252,152,934,023	2346	TT13	chr3	3	q22.3	138045642	138071607	15	0	-0.759758	-0.759758	1.875E-31
252,152,934,023	2348	TT13	chr3	3	q22.3	138145167	138175729	18	0	-0.640665	-0.640665	2.829E-26
252,152,934,023	2350	TT13	chr3	3	q22.3 - q23	138633814	138766376	54	0	-0.743888	-0.743888	1.242E-97
252,152,934,023	2351	TT13	chr3	3	q22.3	138647279	138681550	18	0	-1.254875	-1.254875	1.344E-16
252,152,934,023	2352	TT13	chr3	3	q23	139256160	139261310	4	0	-1.277228	-1.277228	3.487E-23
252,152,934,023	2353	TT13	chr3	3	q23	139650312	139657692	4	0	-1.318659	-1.318659	1.049E-26
252,152,934,023	2354	TT13	chr3	3	q23	140660014	140663316	3	0	-1.414423	-1.414423	1.664E-20
252,152,934,023	2355	TT13	chr3	3	q23	140738584	140788806	16	0	-0.933658	-0.933658	2.365E-48
252,152,934,023	2369	TT13	chr3	3	q24	143689533	143698434	5	0	-0.968916	-0.968916	7.199E-19
252,152,934,023	2370	TT13	chr3	3	q24	145808680	145820549	6	0	-0.876158	-0.876158	1.968E-18
252,152,934,023	2371	TT13	chr3	3	q24	145875764	145880825	4	0	-1.564649	-1.564649	6.04E-30
252,152,934,023	2372	TT13	chr3	3	q24	145935204	145973159	16	0	-0.680343	-0.680343	1.052E-27
252,152,934,023	2373	TT13	chr3	3	q24	146182422	146221172	12	0	-0.841912	-0.841912	4.404E-31
252,152,934,023	2374	TT13	chr3	3	q24	147108273	147144346	19	0	-1.005575	-1.005575	1.472E-61
252,152,934,023	2375	TT13	chr3	3	q24	147109641	147113536	3	0	-2.431688	-2.431688	2.446E-11
252,152,934,023	2378	TT13	chr3	3	q24	148814097	148854594	16	0	-0.692475	-0.692475	7.931E-28
252,152,934,023	2381	TT13	chr3	3	q25.1	149372133	149378277	5	0	-1.541998	-1.541998	3.609E-34
252,152,934,023	2382	TT13	chr3	3	q25.1	149682888	149706205	10	0	-1.020857	-1.020857	6.68E-38
252,152,934,023	2387	TT13	chr3	3	q25.1	150800913	150807129	4	0	-1.672557	-1.672557	1.146E-34

252,152,934,023	2389	TT13	chr3	3	q25.2	152548048	152558368	6	0	-0.867297	-0.867297	1.055E-16
252,152,934,023	2390	TT13	chr3	3	q25.2	152870310	152881714	6	0	-1.443438	-1.443438	5.843E-42
252,152,934,023	2391	TT13	chr3	3	q25.2	153086194	153097418	4	0	-1.538664	-1.538664	1.18E-32
252,152,934,023	2392	TT13	chr3	3	q25.2	153802367	153808306	3	0	-1.55873	-1.55873	7.399E-12
252,152,934,023	2393	TT13	chr3	3	q25.2	153802367	153851260	22	0	-0.566309	-0.566309	6.483E-26
252,152,934,023	2394	TT13	chr3	3	q25.2	154796135	154799711	3	0	-1.739938	-1.739938	3.854E-29
252,152,934,023	2397	TT13	chr3	3	q25.31	155586458	155592165	4	0	-1.212896	-1.212896	1.048E-19
252,152,934,023	2400	TT13	chr3	3	q25.31	155944524	155945863	3	0	-1.177767	-1.177767	9.301E-18
252,152,934,023	2401	TT13	chr3	3	q25.31	156269452	156276924	6	0	-0.824161	-0.824161	4.258E-17
252,152,934,023	2402	TT13	chr3	3	q25.31	156385326	156406483	11	0	-0.837566	-0.837566	1.614E-28
252,152,934,023	2403	TT13	chr3	3	q25.31	156453507	156464528	5	0	-1.055805	-1.055805	4.357E-22
252,152,934,023	2404	TT13	chr3	3	q25.31	156531689	156547487	8	0	-1.871085	-1.871085	5.936E-80
252,152,934,023	2407	TT13	chr3	3	q25.32	157257364	157263926	5	0	-0.944664	-0.944664	1.192E-18
252,152,934,023	2408	TT13	chr3	3	q25.32	157809797	157830050	11	0	-1.700567	-1.700567	4.442E-80
252,152,934,023	2409	TT13	chr3	3	q25.32	157811709	157816521	3	0	-2.956379	-2.956379	2.239E-10
252,152,934,023	2410	TT13	chr3	3	q25.32	158447757	158452899	4	0	-1.253169	-1.253169	5.236E-22
252,152,934,023	2411	TT13	chr3	3	q25.32	158518645	158523486	4	0	-1.574486	-1.574486	5.869E-33
252,152,934,023	2412	TT13	chr3	3	q25.33	159477095	159486345	6	0	-0.956814	-0.956814	6.526E-22
252,152,934,023	2416	TT13	chr3	3	q25.33	160116110	160122146	10	0	-1.540206	-1.540206	1.488E-70
252,152,934,023	2417	TT13	chr3	3	q25.33	160279160	160295026	7	0	-1.3729	-1.3729	7.634E-47
252,152,934,023	2419	TT13	chr3	3	q26.1	160817886	160945845	32	0	-0.501124	-0.501124	1.151E-28
252,152,934,023	2420	TT13	chr3	3	q26.1	160820736	160823964	3	0	-1.705986	-1.705986	1.294E-15
252,152,934,023	2448	TT13	chr3	3	q26.32	177519702	177530282	3	0	-0.98167	-0.98167	1.215E-12
252,152,934,023	2457	TT13	chr3	3	q26.33	180306320	180309433	3	0	-1.303985	-1.303985	1.745E-20
252,152,934,023	2458	TT13	chr3	3	q26.33	180544194	180550949	3	0	-1.191591	-1.191591	4.133E-17
252,152,934,023	2459	TT13	chr3	3	q26.33	181410275	181445947	17	0	-1.163368	-1.163368	3.635E-79
252,152,934,023	2461	TT13	chr3	3	q26.33 - q27.1	182696947	182702029	3	0	-1.329272	-1.329272	7.229E-20
252,152,934,023	2462	TT13	chr3	3	q27.1	182816593	182822376	3	0	-2.236812	-2.236812	3.471E-35
252,152,934,023	2463	TT13	chr3	3	q27.1	182878799	182900260	9	0	-0.996698	-0.996698	3.668E-32
252,152,934,023	2464	TT13	chr3	3	q27.1	182967949	182974958	4	0	-1.26322	-1.26322	7.501E-24
252,152,934,023	2471	TT13	chr3	3	q27.1	183864787	184109225	140	0	-0.623885	-0.623885	1.504E-167
252,152,934,023	2472	TT13	chr3	3	q27.1	183890057	183893802	3	0	-1.96914	-1.96914	1.509E-14
252,152,934,023	2473	TT13	chr3	3	q27.1	183944109	183983164	38	0	-1.061828	-1.061828	7.232E-25
252,152,934,023	2474	TT13	chr3	3	q27.1	183976706	183980149	4	0	-2.085226	-2.085226	8.813E-10
252,152,934,023	2478	TT13	chr3	3	q27.1	184240699	184246438	3	0	-1.442998	-1.442998	5.044E-22
252,152,934,023	2479	TT13	chr3	3	q27.1	184276454	184302725	14	0	-0.992965	-0.992965	3.434E-44
252,152,934,023	2488	TT13	chr3	3	q27.2	185908971	185913816	4	0	-1.186374	-1.186374	3.958E-22
252,152,934,023	2489	TT13	chr3	3	q27.3	186075010	186083188	6	0	-1.183653	-1.183653	1.161E-26
252,152,934,023	2490	TT13	chr3	3	q27.3	186283333	186287845	4	0	-1.520381	-1.520381	8.038E-29
252,152,934,023	2491	TT13	chr3	3	q27.3	186486313	186505263	17	0	-1.083553	-1.083553	3.858E-67
252,152,934,023	2495	TT13	chr3	3	q27.3	186914883	186920420	4	0	-1.344531	-1.344531	2.007E-28
252,152,934,023	2501	TT13	chr3	3	q28	190037245	190040959	3	0	-1.417319	-1.417319	4.734E-21
252,152,934,023	2502	TT13	chr3	3	q28	190230568	190235840	3	0	-1.441968	-1.441968	4.02E-22
252,152,934,023	2503	TT13	chr3	3	q28	190577350	190584525	5	0	-1.222351	-1.222351	9.538E-29
252,152,934,023	2504	TT13	chr3	3	q28	191031984	191053192	12	0	-1.192367	-1.192367	1.497E-60
252,152,934,023	2512	TT13	chr3	3	q29	193851204	193860162	5	0	-1.740104	-1.740104	1.026E-38
252,152,934,023	2517	TT13	chr3	3	q29	194115999	194127935	7	0	-1.299556	-1.299556	2.68E-38
252,152,934,023	2524	TT13	chr3	3	q29	194979152	194997936	10	0	-1.063103	-1.063103	9.765E-41
252,152,934,023	2548	TT13	chr3	3	q29	197452592	197483637	13	0	-0.861422	-0.861422	2.687E-33
252,152,934,023	2559	TT13	chr4	4	p16.3	1103859	1111092	5	0	-1.017101	-1.017101	1.092E-18
252,152,934,023	2560	TT13	chr4	4	p16.3	1198402	1244582	19	0	-1.504828	-1.504828	4.529E-25
252,152,934,023	2568	TT13	chr4	4	p16.3	1856892	1876590	9	0	-1.077692	-1.077692	1.708E-22
252,152,934,023	2569	TT13	chr4	4	p16.3	1980253	1984568	6	0	-2.16169	-2.16169	1.493E-14
252,152,934,023	2570	TT13	chr4	4	p16.3	1980253	2069821	34	0	-1.204342	-1.204342	1.627E-96
252,152,934,023	2571	TT13	chr4	4	p16.3	2159508	2164905	3	0	-1.153682	-1.153682	1.979E-11
252,152,934,023	2574	TT13	chr4	4	p16.3	2462753	2472212	5	0	-1.630921	-1.630921	1.028E-26
252,152,934,023	2576	TT13	chr4	4	p16.3	2756012	2770339	6	0	-1.374209	-1.374209	1.479E-28
252,152,934,023	2577	TT13	chr4	4	p16.3	2930679	2937493	3	0	-1.214966	-1.214966	1.05E-11
252,152,934,023	2579	TT13	chr4	4	p16.3	3073750	3104913	11	0	-0.580136	-0.580136	2.035E-17
252,152,934,023	2581	TT13	chr4	4	p16.3	3292577	3297588	3	0	-1.320863	-1.320863	1.694E-12
252,152,934,023	2582	TT13	chr4	4	p16.3	3363511	3535755	68	0	-0.831527	-0.831527	4.467E-76
252,152,934,023	2583	TT13	chr4	4	p16.3	3377801	3409695	12	0	-0.379093	-0.379093	1.242E-12
252,152,934,023	2613	TT13	chr4	4	p16.1	8580204	8657552	26	0	-0.907897	-0.907897	5.56E-68
252,152,934,023	2614	TT13	chr4	4	p16.1	8857904	8878518	28	0	-1.070205	-1.070205	3.456E-101
252,152,934,023	2615	TT13	chr4	4	p16.1	8871820	8874117	3	0	-0.268833	-0.268833	2.473E-10
252,152,934,023	2616	TT13	chr4	4	p16.1	8891244	8898811	8	0	-0.836143	-0.836143	5.332E-14
252,152,934,023	2617	TT13	chr4	4	p16.1	10457251	10465209	4	0	-1.936999	-1.936999	9.502E-40
252,152,934,023	2620	TT13	chr4	4	p15.33	13410855	13552046	53	0	-0.487497	-0.487497	4.04E-44
252,152,934,023	2621	TT13	chr4	4	p15.33	13483020	13488008	3	0	-1.46891	-1.46891	1.24E-12
252,152,934,023	2622	TT13	chr4	4	p15.33	13542775	13550313	4	0	-1.907875	-1.907875	3.952E-22
252,152,934,023	2627	TT13	chr4	4	p15.32	15653615	15661211	5	0	-1.363373	-1.363373	5.515E-34
252,152,934,023	2628	TT13	chr4	4	p15.32	15701746	15708228	4	0	-0.91706	-0.91706	1.137E-14
252,152,934,023	2629	TT13	chr4	4	p15.32	15779157	15789989	6	0	-1.388492	-1.388492	5.817E-40
252,152,934,023	2630	TT13	chr4	4	p15.32	16083537	16088073	3	0	-1.362422	-1.362422	1.019E-20
252,152,934,023	2631	TT13	chr4	4	p15.32	16225080	16230754	3	0	-1.211843	-1.211843	1.004E-17
252,152,934,023	2633	TT13	chr4	4	p15.32	17508730	17516301	4	0	-1.124051	-1.124051	1E-19
252,152,934,023	2634	TT13	chr4	4	p15.32	17767111	17788280	11	0	-1.054444	-1.054444	2.382E-43
252,152,934,023	2644	TT13	chr4	4	p15.2	25237399	25254093	6	0	-1.865838	-1.865838	2.261E-55
252,152,934,023	2645	TT13	chr4	4	p15.2	25311992	25315638	3	0	-1.303877	-1.303877	9.244E-18
252,152,934,023	2646	TT13	chr4	4	p15.2	25375285	25385060	5	0	-0.881504	-0.881504	1.183E-15
252,152,934,023	2647	TT13	chr4	4	p15.2	25655427	25659324	3	0	-1.59067	-1.59067	8.182E-25
252,152,934,023	2648	TT13	chr4	4	p15.2	25861385	25866507	3	0	-1.515384	-1.515384	9.929E-24
252,152,934,023	2650	TT13	chr4	4	p15.2	26358941	26364054	3	0	-1.29997	-1.29997	1.333E-19
252,152,934,023	2651	TT13	chr4	4	p15.2	26856128	26865330	5	0	-1.712342	-1.712342	6.889E-40
252,152,934,023	2653	TT13	chr4	4	p15.1	28826219	28832539	4	0	-1.367366	-1.367366	6.448E-28
252,152,934,023	2654	TT13	chr4	4	p15.1	29117740	29124091	3	0	-1.320983	-1.320983	4.769E-21
252,152,934,023	2655	TT13	chr4	4	p15.1	30716667	30732727	8	0	-0.923839	-0.923839	4.394E-26
252,152,934,023	2656	TT13	chr4	4	p14	36243261	36250447	5	0	-1.16141	-1.16141	2.713E-26
252,152,934,023	2657	TT13	chr4	4	p14	37243159	37250311	5	0	-1.111278	-1.111278	4.148E-21
252,152,934,023	2658	TT13	chr4	4	p14	37453173	37458796	5	0	-1.280595	-1.280595	2.027E-30
252,152,934,023	2660	TT13	chr4	4	p14	37819462	37830652	5	0	-1.494151	-1.494151	2.516E-37
252,152,934,023	2662	TT13	chr4	4	p14	38013569	38018898	4	0	-1.447276	-1.447276	3.359E-26
252,152,934,023	2664	TT13	chr4	4	p14	38664083	38668695	3	0	-1.533256	-1.533256	3.003E-20
252,152,934,023	2665	TT13	chr4	4	p14	38800573	38874931	43	0	-0.516092	-0.516092	1.124E-41
252,152,934,023	2666	TT13	chr4	4	p14	38867364	38872564	6	0	-1.091827	-1.091827	9.572E-10
252,152,934,023	2672	TT13	chr4	4	p14	39694512	39725347	15	0	-0.775018	-0.775018	6.946E-33

252,152,934,023	2675	TT13	chr4	4	p14	40054604	40061331	4	0	-1.341318	-1.341318	1.866E-26
252,152,934,023	2677	TT13	chr4	4	p14	40437749	40443561	4	0	-1.874943	-1.874943	1.944E-40
252,152,934,023	2685	TT13	chr4	4	p13	41489458	41498171	5	0	-0.826609	-0.826609	4.684E-14
252,152,934,023	2686	TT13	chr4	4	p13	41642809	41649753	5	0	-1.167249	-1.167249	3.314E-25
252,152,934,023	2687	TT13	chr4	4	p13	41746504	41755594	6	0	-1.836448	-1.836448	8.536E-57
252,152,934,023	2688	TT13	chr4	4	p13	41870549	41884768	4	0	-1.45129	-1.45129	6.114E-29
252,152,934,023	2691	TT13	chr4	4	p13	42346658	42402725	18	0	-0.564239	-0.564239	4.494E-22
252,152,934,023	2692	TT13	chr4	4	p13	42656266	42662044	4	0	-1.248485	-1.248485	3.682E-23
252,152,934,023	2694	TT13	chr4	4	p13	44164372	44187489	10	0	-0.935009	-0.935009	7.922E-35
252,152,934,023	2695	TT13	chr4	4	p13	44445715	44454443	5	0	-1.028594	-1.028594	6.951E-21
252,152,934,023	2696	TT13	chr4	4	p12	44677755	44682491	4	0	-1.53142	-1.53142	1.841E-28
252,152,934,023	2697	TT13	chr4	4	p12	45457451	45482965	10	0	-0.922008	-0.922008	1.606E-33
252,152,934,023	2700	TT13	chr4	4	p12	46780085	46840005	24	0	-0.68932	-0.68932	2.269E-43
252,152,934,023	2701	TT13	chr4	4	p12	46992735	47001317	5	0	-0.696917	-0.696917	1.623E-10
252,152,934,023	2706	TT13	chr4	4	p12	48187166	48192793	4	0	-1.276681	-1.276681	5.196E-25
252,152,934,023	2707	TT13	chr4	4	p11	48269552	48371908	34	0	-0.531748	-0.531748	6.581E-35
252,152,934,023	2708	TT13	chr4	4	p11	48270873	48273572	3	0	-1.638774	-1.638774	9.239E-13
252,152,934,023	2709	TT13	chr4	4	p11	48484329	48494547	6	0	-1.734744	-1.734744	7.419E-56
252,152,934,023	2710	TT13	chr4	4	p11	48674895	48679916	3	0	-1.460978	-1.460978	1.031E-22
252,152,934,023	2711	TT13	chr4	4	p11	48778874	48784295	4	0	-1.391012	-1.391012	2.158E-27
252,152,934,023	2715	TT13	chr4	4	q12	52902001	52919480	8	0	-1.094135	-1.094135	5.658E-38
252,152,934,023	2716	TT13	chr4	4	q12	53272939	53283846	4	0	-0.781055	-0.781055	7.776E-11
252,152,934,023	2718	TT13	chr4	4	q12	53574168	53590837	9	0	-1.133007	-1.133007	1.09E-41
252,152,934,023	2720	TT13	chr4	4	q12	53725348	53733074	6	0	-1.089636	-1.089636	6.124E-25
252,152,934,023	2723	TT13	chr4	4	q12	54101825	54124211	6	0	-1.3612	-1.3612	1.279E-39
252,152,934,023	2724	TT13	chr4	4	q12	54216523	54250863	20	0	-0.69592	-0.69592	1.03E-34
252,152,934,023	2727	TT13	chr4	4	q12	55011839	55022924	7	0	-1.455154	-1.455154	2.36E-47
252,152,934,023	2728	TT13	chr4	4	q12	55093859	55102376	6	0	-1.164667	-1.164667	1.272E-25
252,152,934,023	2730	TT13	chr4	4	q12	55491943	55527471	15	0	-0.554541	-0.554541	8.051E-17
252,152,934,023	2731	TT13	chr4	4	q12	55987235	55994742	4	0	-0.992141	-0.992141	8.637E-17
252,152,934,023	2733	TT13	chr4	4	q12	56261067	56265619	3	0	-1.974152	-1.974152	2.494E-31
252,152,934,023	2739	TT13	chr4	4	q12	57179879	57183552	3	0	-2.101635	-2.101635	8.561E-33
252,152,934,023	2745	TT13	chr4	4	q12	57842236	57852558	6	0	-1.461116	-1.461116	2.991E-42
252,152,934,023	2748	TT13	chr4	4	q13.1	60379018	60388523	4	0	-0.912938	-0.912938	4.873E-14
252,152,934,023	2749	TT13	chr4	4	q13.1	60892801	60917162	4	0	-0.847612	-0.847612	1.318E-12
252,152,934,023	2750	TT13	chr4	4	q13.1	63677772	63686545	4	0	-1.023192	-1.023192	3.163E-16
252,152,934,023	2751	TT13	chr4	4	q13.1	66527921	66539114	6	0	-0.853001	-0.853001	1.856E-17
252,152,934,023	2752	TT13	chr4	4	q13.2	68497618	68507698	6	0	-1.056443	-1.056443	1.025E-25
252,152,934,023	2753	TT13	chr4	4	q13.2	68565040	68570507	4	0	-1.315515	-1.315515	5.084E-24
252,152,934,023	2754	TT13	chr4	4	q13.2	68759700	68767162	4	0	-1.468417	-1.468417	4.444E-28
252,152,934,023	2755	TT13	chr4	4	q13.2	69213721	69218674	4	0	-1.438257	-1.438257	1.63E-29
252,152,934,023	2767	TT13	chr4	4	q13.3	74903374	74908398	4	0	-1.483759	-1.483759	3.095E-30
252,152,934,023	2773	TT13	chr4	4	q21.1	76963541	76972697	4	0	-2.024709	-2.024709	3.121E-41
252,152,934,023	2784	TT13	chr4	4	q21.21	79470555	79473682	3	0	-2.369638	-2.369638	1.618E-38
252,152,934,023	2785	TT13	chr4	4	q21.21	79690402	79703822	8	0	-0.820166	-0.820166	2.467E-21
252,152,934,023	2787	TT13	chr4	4	q21.21	80882204	80894160	5	0	-1.107205	-1.107205	7.73E-21
252,152,934,023	2788	TT13	chr4	4	q21.21	80990513	80996757	5	0	-1.109305	-1.109305	2.991E-20
252,152,934,023	2789	TT13	chr4	4	q21.21	81102398	81127694	14	0	-1.160574	-1.160574	1.625E-58
252,152,934,023	2799	TT13	chr4	4	q21.22	83808010	83825922	9	0	-1.236908	-1.236908	8.832E-48
252,152,934,023	2804	TT13	chr4	4	q21.23	84456490	84460765	4	0	-1.377988	-1.377988	1.703E-25
252,152,934,023	2805	TT13	chr4	4	q21.23	85413878	85420930	4	0	-1.929769	-1.929769	3.586E-27
252,152,934,023	2806	TT13	chr4	4	q21.23	85500960	85506860	4	0	-1.198271	-1.198271	1.384E-21
252,152,934,023	2808	TT13	chr4	4	q21.23	85885034	85888775	3	0	-1.867642	-1.867642	3.236E-31
252,152,934,023	2809	TT13	chr4	4	q21.3	86933481	86954006	8	0	-0.563824	-0.563824	3.504E-10
252,152,934,023	2810	TT13	chr4	4	q21.3	87466376	87470140	3	0	-1.640516	-1.640516	1.46E-25
252,152,934,023	2812	TT13	chr4	4	q21.3	87912691	87935555	11	0	-0.90165	-0.90165	1.526E-32
252,152,934,023	2813	TT13	chr4	4	q22.1	88137799	88145030	5	0	-1.240457	-1.240457	6.916E-29
252,152,934,023	2814	TT13	chr4	4	q22.1	88313144	88320283	4	0	-1.10448	-1.10448	2.609E-19
252,152,934,023	2815	TT13	chr4	4	q22.1	88779295	88788610	5	0	-1.109385	-1.109385	2.838E-23
252,152,934,023	2816	TT13	chr4	4	q22.1	88928009	88932753	4	0	-1.628382	-1.628382	3.344E-33
252,152,934,023	2817	TT13	chr4	4	q22.1	89078744	89080664	3	0	-2.386708	-2.386708	6.894E-37
252,152,934,023	2822	TT13	chr4	4	q22.1	90031426	90035217	3	0	-1.787761	-1.787761	3.248E-28
252,152,934,023	2823	TT13	chr4	4	q22.1	90219840	90231195	7	0	-1.043444	-1.043444	4.887E-26
252,152,934,023	2825	TT13	chr4	4	q22.1	93223614	93231288	5	0	-1.481438	-1.481438	2.1E-37
252,152,934,023	2826	TT13	chr4	4	q22.2	94743940	94755187	8	0	-0.642321	-0.642321	4.627E-13
252,152,934,023	2827	TT13	chr4	4	q22.2	95081191	95095516	6	0	-1.228854	-1.228854	2.696E-31
252,152,934,023	2829	TT13	chr4	4	q22.3	95676916	95683995	5	0	-1.370483	-1.370483	6.774E-33
252,152,934,023	2837	TT13	chr4	4	q23	100811632	100818237	5	0	-1.203631	-1.203631	7.297E-26
252,152,934,023	2839	TT13	chr4	4	q24	101107899	101120412	7	0	-1.307513	-1.307513	2.309E-41
252,152,934,023	2840	TT13	chr4	4	q24	102263932	102271129	6	0	-1.444983	-1.444983	1.728E-43
252,152,934,023	2855	TT13	chr4	4	q25	108910313	108913481	3	0	-2.04885	-2.04885	7.288E-33
252,152,934,023	2856	TT13	chr4	4	q25	108996777	109000920	3	0	-1.214534	-1.214534	1.27E-16
252,152,934,023	2858	TT13	chr4	4	q25	109086155	109098154	7	0	-1.362492	-1.362492	2.261E-40
252,152,934,023	2859	TT13	chr4	4	q25	109680229	109686084	5	0	-1.482808	-1.482808	1.488E-35
252,152,934,023	2865	TT13	chr4	4	q25	110594147	110657838	34	0	-0.426967	-0.426967	2.919E-21
252,152,934,023	2866	TT13	chr4	4	q25	111112756	111121311	6	0	-1.026347	-1.026347	2.009E-22
252,152,934,023	2867	TT13	chr4	4	q25	111528886	111559992	17	0	-1.382885	-1.382885	2.757E-91
252,152,934,023	2868	TT13	chr4	4	q25	111541639	111544856	3	0	-2.607573	-2.607573	1.477E-10
252,152,934,023	2869	TT13	chr4	4	q25	113063509	113069309	4	0	-1.194558	-1.194558	4.508E-20
252,152,934,023	2870	TT13	chr4	4	q25	113140906	113156973	8	0	-1.353383	-1.353383	1.333E-51
252,152,934,023	2871	TT13	chr4	4	q25	113204970	113210139	4	0	-1.44367	-1.44367	3.578E-27
252,152,934,023	2873	TT13	chr4	4	q25	113433605	113446033	9	0	-1.564442	-1.564442	8.154E-57
252,152,934,023	2874	TT13	chr4	4	q25	113624752	113630257	4	0	-0.982464	-0.982464	2.998E-13
252,152,934,023	2875	TT13	chr4	4	q25	113747980	113756755	4	0	-1.094747	-1.094747	2.404E-17
252,152,934,023	2876	TT13	chr4	4	q25	113875008	113880722	4	0	-1.500348	-1.500348	1.924E-30
252,152,934,023	2877	TT13	chr4	4	q26	114678010	114700082	10	0	-0.95222	-0.95222	7.459E-34
252,152,934,023	2886	TT13	chr4	4	q26	120090986	120097828	5	0	-1.377376	-1.377376	1.794E-32
252,152,934,023	2887	TT13	chr4	4	q26	120546934	120553074	4	0	-1.602861	-1.602861	3.527E-24
252,152,934,023	2888	TT13	chr4	4	q27	121835544	121846773	6	0	-1.145272	-1.145272	8.55E-29
252,152,934,023	2899	TT13	chr4	4	q28.1	123841316	123850118	6	0	-0.909976	-0.909976	1.853E-18
252,152,934,023	2900	TT13	chr4	4	q28.1	123935900	123940224	3	0	-1.449875	-1.449875	3.099E-22
252,152,934,023	2902	TT13	chr4	4	q28.1	124314650	124323020	6	0	-1.073991	-1.073991	1.49E-22
252,152,934,023	2903	TT13	chr4	4	q28.1	125570475	125575019	3	0	-1.52	-1.52	2.349E-24
252,152,934,023	2904	TT13	chr4	4	q28.1	125627133	125634891	5	0	-1.199801	-1.199801	8.665E-22
252,152,934,023	2905	TT13	chr4	4	q28.1	126198432	126247471	16	0	-0.553105	-0.553105	3.409E-18
252,152,934,023	2906	TT13	chr4	4	q28.1	128543700	128547525	3	0	-1.628125	-1.628125	9.269E-25

252,152,934,023	2907	TT13	chr4	4	q28.1	128647359	128657016	5	0	-1.296461	-1.296461	5.15E-29
252,152,934,023	2908	TT13	chr4	4	q28.1	128700976	128707248	4	0	-1.414946	-1.414946	4.505E-28
252,152,934,023	2909	TT13	chr4	4	q28.2	128882479	128887653	3	0	-1.189243	-1.189243	3.073E-16
252,152,934,023	2910	TT13	chr4	4	q28.2	128963394	129012722	20	0	-0.841076	-0.841076	3.229E-49
252,152,934,023	2912	TT13	chr4	4	q28.2	129727517	129736822	7	0	-1.122206	-1.122206	8.192E-30
252,152,934,023	2915	TT13	chr4	4	q28.3	135120438	135126110	4	0	-1.445559	-1.445559	8.035E-26
252,152,934,023	2919	TT13	chr4	4	q31.1	140096300	140100082	3	0	-1.94725	-1.94725	4.784E-32
252,152,934,023	2930	TT13	chr4	4	q31.1 - q31.21	141488394	141502541	9	0	-1.295149	-1.295149	1.716E-49
252,152,934,023	2933	TT13	chr4	4	q31.21	142132976	142143531	6	0	-1.161818	-1.161818	1.5E-29
252,152,934,023	2936	TT13	chr4	4	q31.21	143763548	143773080	6	0	-1.131165	-1.131165	3.372E-26
252,152,934,023	2937	TT13	chr4	4	q31.21	144103220	144111803	5	0	-1.19681	-1.19681	7.451E-27
252,152,934,023	2938	TT13	chr4	4	q31.21	144256293	144274627	10	0	-1.126625	-1.126625	7.735E-45
252,152,934,023	2939	TT13	chr4	4	q31.21	144432936	144438586	4	0	-1.257193	-1.257193	3.031E-23
252,152,934,023	2940	TT13	chr4	4	q31.21	144474789	144483864	5	0	-0.948931	-0.948931	4.6E-17
252,152,934,023	2941	TT13	chr4	4	q31.21	144616499	144625890	5	0	-0.880428	-0.880428	7.749E-16
252,152,934,023	2942	TT13	chr4	4	q31.21	145564882	145570370	4	0	-1.226606	-1.226606	1.465E-22
252,152,934,023	2945	TT13	chr4	4	q31.21	146538098	146542708	3	0	-1.291201	-1.291201	5.778E-19
252,152,934,023	2946	TT13	chr4	4	q31.21	146613744	146617735	3	0	-1.870933	-1.870933	1.112E-30
252,152,934,023	2947	TT13	chr4	4	q31.21	146650383	146657185	5	0	-1.110375	-1.110375	1.959E-21
252,152,934,023	2948	TT13	chr4	4	q31.22	146853564	146860598	4	0	-1.256296	-1.256296	6.281E-24
252,152,934,023	2949	TT13	chr4	4	q31.22	147093883	147100603	4	0	-1.307184	-1.307184	2.335E-24
252,152,934,023	2950	TT13	chr4	4	q31.22	147557367	147581599	12	0	-1.067123	-1.067123	3.673E-44
252,152,934,023	2951	TT13	chr4	4	q31.22	148275808	148282909	6	0	-1.353218	-1.353218	5.14E-38
252,152,934,023	2954	TT13	chr4	4	q31.23	149359594	149370955	6	0	-0.871305	-0.871305	3.585E-17
252,152,934,023	2955	TT13	chr4	4	q31.23	150997830	151002843	3	0	-1.045581	-1.045581	3.856E-12
252,152,934,023	2956	TT13	chr4	4	q31.3	151173447	151179626	4	0	-1.169104	-1.169104	5.349E-19
252,152,934,023	2957	TT13	chr4	4	q31.3	151498630	151503983	4	0	-1.461976	-1.461976	2.813E-25
252,152,934,023	2958	TT13	chr4	4	q31.3	151576855	151584460	5	0	-1.174554	-1.174554	1.538E-24
252,152,934,023	2959	TT13	chr4	4	q31.3	151871020	151887399	7	0	-1.300593	-1.300593	1.048E-42
252,152,934,023	2960	TT13	chr4	4	q31.3	152131918	152177485	21	0	-0.653408	-0.653408	2.292E-31
252,152,934,023	2966	TT13	chr4	4	q31.3	153853945	153859421	5	0	-1.437353	-1.437353	6.242E-28
252,152,934,023	2969	TT13	chr4	4	q31.3	154384996	154390161	4	0	-1.523802	-1.523802	2.312E-32
252,152,934,023	2986	TT13	chr4	4	q32.1	160301033	160315301	5	0	-1.082828	-1.082828	4.324E-23
252,152,934,023	2988	TT13	chr4	4	q32.2	164069516	164088875	12	0	-1.264859	-1.264859	5.841E-65
252,152,934,023	2989	TT13	chr4	4	q32.2	164248116	164271409	12	0	-1.011772	-1.011772	2.509E-44
252,152,934,023	2990	TT13	chr4	4	q32.3	165937934	165943540	3	0	-1.301275	-1.301275	7.705E-18
252,152,934,023	2991	TT13	chr4	4	q32.3	166028830	166052897	12	0	-0.777538	-0.777538	6.315E-26
252,152,934,023	2992	TT13	chr4	4	q32.3	166123615	166132145	6	0	-0.902064	-0.902064	2.86E-17
252,152,934,023	2994	TT13	chr4	4	q32.3	166296198	166303772	8	0	-1.313943	-1.313943	6.784E-48
252,152,934,023	2995	TT13	chr4	4	q32.3	166793169	166799100	4	0	-1.47481	-1.47481	2.664E-28
252,152,934,023	2996	TT13	chr4	4	q32.3	167760603	167766877	4	0	-1.130769	-1.130769	1.384E-19
252,152,934,023	2997	TT13	chr4	4	q32.3	169550091	169555394	4	0	-1.414826	-1.414826	2.357E-28
252,152,934,023	2998	TT13	chr4	4	q32.3	169749790	169756233	5	0	-1.303289	-1.303289	1.78E-29
252,152,934,023	3000	TT13	chr4	4	q33	170188837	170196539	5	0	-1.448899	-1.448899	7.57E-35
252,152,934,023	3005	TT13	chr4	4	q33	171008194	171014158	4	0	-1.488116	-1.488116	9.008E-26
252,152,934,023	3007	TT13	chr4	4	q34.1	173398939	173407815	5	0	-1.101556	-1.101556	3.627E-23
252,152,934,023	3008	TT13	chr4	4	q34.1	174087045	174111042	12	0	-1.008588	-1.008588	8.433E-44
252,152,934,023	3009	TT13	chr4	4	q34.1	174242675	174298976	27	0	-0.6167	-0.6167	1.555E-36
252,152,934,023	3010	TT13	chr4	4	q34.1	174253742	174258021	3	0	-1.919189	-1.919189	1.784E-15
252,152,934,023	3011	TT13	chr4	4	q34.1	174419768	174461922	20	0	-1.2275	-1.2275	6.485E-84
252,152,934,023	3012	TT13	chr4	4	q34.1	175441267	175444210	3	0	-1.719231	-1.719231	8.592E-27
252,152,934,023	3013	TT13	chr4	4	q34.1	175611556	175618843	4	0	-0.900417	-0.900417	1.634E-13
252,152,934,023	3014	TT13	chr4	4	q34.2	176984739	176989239	4	0	-1.785295	-1.785295	3.515E-38
252,152,934,023	3015	TT13	chr4	4	q34.2	177239101	177244441	4	0	-1.797464	-1.797464	5.528E-40
252,152,934,023	3018	TT13	chr4	4	q34.3	183060607	183071211	9	0	-1.069039	-1.069039	1.257E-32
252,152,934,023	3019	TT13	chr4	4	q35.1	183364544	183373094	5	0	-1.095545	-1.095545	1.503E-23
252,152,934,023	3020	TT13	chr4	4	q35.1	183527879	183532496	4	0	-1.615588	-1.615588	9.217E-30
252,152,934,023	3023	TT13	chr4	4	q35.1	183960540	183968833	4	0	-1.827731	-1.827731	4.318E-41
252,152,934,023	3024	TT13	chr4	4	q35.1	184018370	184022501	3	0	-1.838567	-1.838567	1.105E-22
252,152,934,023	3025	TT13	chr4	4	q35.1	184260085	184265217	3	0	-0.890903	-0.890903	2.366E-10
252,152,934,023	3026	TT13	chr4	4	q35.1	184316291	184434034	52	0	-0.595886	-0.595886	8.116E-62
252,152,934,023	3027	TT13	chr4	4	q35.1	184423469	184428191	3	0	-1.673993	-1.673993	2.558E-13
252,152,934,023	3028	TT13	chr4	4	q35.1	184576975	184583636	6	0	-1.433476	-1.433476	2.586E-38
252,152,934,023	3029	TT13	chr4	4	q35.1	184639121	184672904	14	0	-1.077087	-1.077087	1.041E-54
252,152,934,023	3038	TT13	chr4	4	q35.1	186123296	186132573	6	0	-1.762582	-1.762582	1.796E-53
252,152,934,023	3044	TT13	chr4	4	q35.1	187009504	187037651	12	0	-0.935371	-0.935371	1.118E-36
252,152,934,023	3045	TT13	chr4	4	q35.1	187065047	187068952	3	0	-1.487939	-1.487939	1.048E-22
252,152,934,023	3048	TT13	chr4	4	q35.2	187642850	187650409	4	0	-1.765401	-1.765401	3.585E-36
252,152,934,023	3052	TT13	chr4	4	q35.2	188576606	188581306	3	0	-1.509509	-1.509509	5.981E-24
252,152,934,023	3057	TT13	chr4	4	q35.2	190274349	190286473	4	0	-1.280421	-1.280421	1.791E-24
252,152,934,023	3061	TT13	chr5	5	p15.33	50014	1891216	596	0	-0.548583	-0.548583	4.900e-324
252,152,934,023	3062	TT13	chr5	5	p15.33	75303	92999	6	0	-1.712455	-1.712455	1.24E-21
252,152,934,023	3076	TT13	chr5	5	p15.33	1512873	1864764	107	0	-0.252525	-0.252525	1.02E-39
252,152,934,023	3077	TT13	chr5	5	p15.33	1727462	1748349	6	0	-0.903773	-0.903773	8.508E-11
252,152,934,023	3078	TT13	chr5	5	p15.33	1799098	1803839	4	0	-1.730056	-1.730056	5.204E-27
252,152,934,023	3079	TT13	chr5	5	p15.33	1873641	1884801	7	0	-2.003171	-2.003171	1.155E-20
252,152,934,023	3083	TT13	chr5	5	p15.33	2738432	2757388	10	0	-2.070042	-2.070042	5.313E-97
252,152,934,023	3086	TT13	chr5	5	p15.33	3589087	3608655	11	0	-1.324606	-1.324606	9.527E-53
252,152,934,023	3087	TT13	chr5	5	p15.32	5137267	5142818	3	0	-1.486051	-1.486051	1.837E-24
252,152,934,023	3092	TT13	chr5	5	p15.31	6628500	6636326	5	0	-1.032406	-1.032406	5.63E-22
252,152,934,023	3094	TT13	chr5	5	p15.31	6751387	6756906	5	0	-1.433215	-1.433215	2.246E-37
252,152,934,023	3095	TT13	chr5	5	p15.31	6771768	6777667	3	0	-1.028214	-1.028214	1.231E-13
252,152,934,023	3096	TT13	chr5	5	p15.31	7392725	7399384	4	0	-1.378495	-1.378495	3.272E-28
252,152,934,023	3098	TT13	chr5	5	p15.31	7849456	7881742	17	0	-0.709868	-0.709868	4.465E-38
252,152,934,023	3099	TT13	chr5	5	p15.31	7981051	7986151	4	0	-1.170411	-1.170411	2.585E-23
252,152,934,023	3102	TT13	chr5	5	p15.2	10245144	10255004	7	0	-1.141015	-1.141015	1.706E-34
252,152,934,023	3103	TT13	chr5	5	p15.2	10305166	10382257	36	0	-0.734883	-0.734883	7.347E-79
252,152,934,023	3111	TT13	chr5	5	p15.2	14438319	14465426	14	0	-1.183075	-1.183075	5.501E-63
252,152,934,023	3112	TT13	chr5	5	p15.2	14454589	14462083	5	0	-2.215719	-2.215719	5.069E-14
252,152,934,023	3113	TT13	chr5	5	p15.2	14575236	14583860	5	0	-1.650613	-1.650613	3.636E-42
252,152,934,023	3114	TT13	chr5	5	p15.2	14658601	14668238	4	0	-0.965146	-0.965146	4.578E-16
252,152,934,023	3115	TT13	chr5	5	p15.2	14869647	14874163	4	0	-1.379832	-1.379832	2.123E-22
252,152,934,023	3116	TT13	chr5	5	p15.1	15495765	15504061	4	0	-1.021152	-1.021152	1.415E-17
252,152,934,023	3117	TT13	chr5	5	p15.1	15929071	15941706	18	0	-0.881411	-0.881411	1.238E-50
252,152,934,023	3119	TT13	chr5	5	p15.1	16933739	16939189	4	0	-1.427012	-1.427012	3.308E-28
252,152,934,023	3121	TT13	chr5	5	p15.1	17269946	17281195	8	0	-1.029738	-1.029738	2.714E-33

252,152,934,023	3122	TT13	chr5	5	p15.1	17351344	17358438	5	0	-1.188073	-1.188073	8.59E-27
252,152,934,023	3123	TT13	chr5	5	p14.3	20293943	20313728	9	0	-0.619431	-0.619431	1.752E-14
252,152,934,023	3124	TT13	chr5	5	p14.2	24168324	24173388	3	0	-1.442733	-1.442733	1.789E-23
252,152,934,023	3126	TT13	chr5	5	p14.1	27117652	27122235	3	0	-1.616021	-1.616021	1.063E-26
252,152,934,023	3129	TT13	chr5	5	p13.3	28924660	28932611	5	0	-1.414113	-1.414113	1.105E-36
252,152,934,023	3132	TT13	chr5	5	p13.3	32135766	32213816	36	0	-0.469456	-0.469456	1.176E-28
252,152,934,023	3133	TT13	chr5	5	p13.3	32141590	32145951	3	0	-1.47582	-1.47582	2.111E-12
252,152,934,023	3161	TT13	chr5	5	p13.1	39071013	39077693	6	0	-1.152236	-1.152236	9.153E-26
252,152,934,023	3162	TT13	chr5	5	p13.1	39331902	39337604	4	0	-1.229825	-1.229825	1.856E-22
252,152,934,023	3163	TT13	chr5	5	p13.1	40666517	40808782	64	0	-0.46996	-0.46996	1.881E-48
252,152,934,023	3164	TT13	chr5	5	p13.1	40678957	40685203	5	0	-1.484186	-1.484186	4.587E-17
252,152,934,023	3167	TT13	chr5	5	p13.1	42421778	42425896	4	0	-1.61496	-1.61496	9.555E-33
252,152,934,023	3168	TT13	chr5	5	p12	42833326	42839085	3	0	-1.265698	-1.265698	2.866E-18
252,152,934,023	3178	TT13	chr5	5	p12	44805486	44813305	5	0	-1.117216	-1.117216	1.54E-24
252,152,934,023	3179	TT13	chr5	5	p12	45692999	45699220	4	0	-1.282159	-1.282159	8.184E-25
252,152,934,023	3180	TT13	chr5	5	q11.1	49735462	49762843	7	0	-1.093524	-1.093524	5.053E-31
252,152,934,023	3181	TT13	chr5	5	q11.1	50060206	50079965	10	0	-0.613858	-0.613858	6.913E-15
252,152,934,023	3182	TT13	chr5	5	q11.1	50676490	50696460	14	0	-1.157434	-1.157434	5.518E-62
252,152,934,023	3184	TT13	chr5	5	q11.2	52284325	52287533	3	0	-1.328462	-1.328462	4.737E-15
252,152,934,023	3185	TT13	chr5	5	q11.2	52402997	52407821	3	0	-1.204517	-1.204517	1.518E-17
252,152,934,023	3186	TT13	chr5	5	q11.2	52771441	52780692	5	0	-0.984175	-0.984175	1.137E-16
252,152,934,023	3187	TT13	chr5	5	q11.2	53603703	53607314	3	0	-1.113785	-1.113785	1.996E-15
252,152,934,023	3188	TT13	chr5	5	q11.2	54156688	54185805	9	0	-0.726553	-0.726553	8.809E-18
252,152,934,023	3189	TT13	chr5	5	q11.2	54468349	54473374	8	0	-2.201685	-2.201685	3.946E-77
252,152,934,023	3190	TT13	chr5	5	q11.2	54518317	54530295	6	0	-1.359954	-1.359954	3.295E-34
252,152,934,023	3191	TT13	chr5	5	q11.2	54826874	54832069	4	0	-1.676823	-1.676823	2.473E-32
252,152,934,023	3192	TT13	chr5	5	q11.2	54989547	54998572	4	0	-1.144679	-1.144679	4.555E-19
252,152,934,023	3193	TT13	chr5	5	q11.2	55115282	55119370	3	0	-1.625002	-1.625002	1.897E-25
252,152,934,023	3194	TT13	chr5	5	q11.2	55284032	55341020	29	0	-0.632886	-0.632886	1.007E-38
252,152,934,023	3196	TT13	chr5	5	q11.2	56109178	56117003	5	0	-1.337477	-1.337477	1.046E-31
252,152,934,023	3198	TT13	chr5	5	q11.2	56241580	56255219	7	0	-0.931798	-0.931798	2.574E-23
252,152,934,023	3203	TT13	chr5	5	q11.2	58328982	58338989	6	0	-1.109573	-1.109573	2.984E-28
252,152,934,023	3204	TT13	chr5	5	q12.1	59186383	59192548	5	0	-1.280938	-1.280938	1.818E-25
252,152,934,023	3205	TT13	chr5	5	q12.1	59705578	59732388	11	0	-0.717573	-0.717573	2.598E-22
252,152,934,023	3206	TT13	chr5	5	q12.1	59822722	59831693	4	0	-0.973989	-0.973989	2.06E-15
252,152,934,023	3207	TT13	chr5	5	q12.1	59989932	60002098	8	0	-0.955665	-0.955665	2.004E-27
252,152,934,023	3221	TT13	chr5	5	q12.3	65215015	65275451	29	0	-0.820173	-0.820173	1.176E-68
252,152,934,023	3222	TT13	chr5	5	q12.3	65435553	65448895	6	0	-0.710117	-0.710117	4.151E-12
252,152,934,023	3223	TT13	chr5	5	q12.3	65796963	65803497	3	0	-1.285657	-1.285657	6.534E-19
252,152,934,023	3224	TT13	chr5	5	q12.3	65889921	65894819	3	0	-1.677922	-1.677922	1.939E-23
252,152,934,023	3225	TT13	chr5	5	q12.3	66081490	66087967	4	0	-1.301693	-1.301693	2.163E-25
252,152,934,023	3227	TT13	chr5	5	q12.3	66456289	66462002	4	0	-1.314562	-1.314562	3.62E-21
252,152,934,023	3228	TT13	chr5	5	q13.1	67508101	67514146	4	0	-1.729604	-1.729604	2.519E-34
252,152,934,023	3238	TT13	chr5	5	q13.2	71398860	71408976	6	0	-1.107027	-1.107027	6.522E-28
252,152,934,023	3239	TT13	chr5	5	q13.2	72111010	72302432	91	0	-0.381859	-0.381859	1.395E-39
252,152,934,023	3244	TT13	chr5	5	q13.2	72704649	72750671	18	0	-1.108729	-1.108729	1.647E-71
252,152,934,023	3245	TT13	chr5	5	q13.2	72732276	72745282	8	0	-1.737316	-1.737316	4.394E-10
252,152,934,023	3262	TT13	chr5	5	q13.3	76323382	76383268	29	0	-0.760166	-0.760166	1.978E-57
252,152,934,023	3263	TT13	chr5	5	q13.3	76335447	76340614	3	0	-1.664371	-1.664371	3.537E-10
252,152,934,023	3265	TT13	chr5	5	q13.3	76784355	76796661	5	0	-1.183234	-1.183234	2.443E-26
252,152,934,023	3266	TT13	chr5	5	q14.1	76921797	76944403	13	0	-1.670964	-1.670964	2.267E-96
252,152,934,023	3267	TT13	chr5	5	q14.1	77066978	77093892	13	0	-0.831181	-0.831181	2.201E-33
252,152,934,023	3270	TT13	chr5	5	q14.1	77653821	77659710	4	0	-1.201697	-1.201697	7.674E-22
252,152,934,023	3290	TT13	chr5	5	q14.1	80724381	80734537	7	0	-1.084673	-1.084673	2.5E-30
252,152,934,023	3293	TT13	chr5	5	q14.2	81434496	81439585	4	0	-1.233625	-1.233625	5.679E-20
252,152,934,023	3294	TT13	chr5	5	q14.2	81570282	81573741	4	0	-1.939833	-1.939833	1.198E-37
252,152,934,023	3295	TT13	chr5	5	q14.2	82769093	82773306	4	0	-1.539059	-1.539059	5.058E-30
252,152,934,023	3296	TT13	chr5	5	q14.3	83016598	83020999	3	0	-1.711711	-1.711711	6.723E-26
252,152,934,023	3297	TT13	chr5	5	q14.3	83602324	83610188	5	0	-1.147926	-1.147926	1.389E-24
252,152,934,023	3298	TT13	chr5	5	q14.3	83677904	83682232	3	0	-1.338945	-1.338945	8.871E-15
252,152,934,023	3300	TT13	chr5	5	q14.3	87954205	87978953	32	0	-1.299719	-1.299719	2.215E-157
252,152,934,023	3301	TT13	chr5	5	q14.3	87960448	87966164	9	0	-0.728044	-0.728044	1.335E-14
252,152,934,023	3303	TT13	chr5	5	q14.3	88178587	88180991	3	0	-1.916825	-1.916825	4.688E-32
252,152,934,023	3304	TT13	chr5	5	q14.3	89767092	89771977	4	0	-0.920551	-0.920551	2.962E-11
252,152,934,023	3305	TT13	chr5	5	q14.3	89819691	89900716	34	0	-0.534635	-0.534635	1.483E-33
252,152,934,023	3306	TT13	chr5	5	q14.3	90140821	90145569	3	0	-1.559928	-1.559928	1.588E-25
252,152,934,023	3307	TT13	chr5	5	q14.3	90574111	90577846	3	0	-1.260622	-1.260622	8.011E-16
252,152,934,023	3308	TT13	chr5	5	q14.3	90675696	90679698	4	0	-2.168576	-2.168576	5.721E-46
252,152,934,023	3309	TT13	chr5	5	q14.3	91707899	91715997	4	0	-1.143801	-1.143801	1.331E-20
252,152,934,023	3310	TT13	chr5	5	q15	92905359	92959492	30	0	-1.076982	-1.076982	9.987E-102
252,152,934,023	3311	TT13	chr5	5	q15	92913742	92925352	7	0	-1.879098	-1.879098	9.677E-10
252,152,934,023	3318	TT13	chr5	5	q15	96141284	96145530	4	0	-1.42775	-1.42775	8.058E-28
252,152,934,023	3321	TT13	chr5	5	q15	98102948	98112155	4	0	-1.755298	-1.755298	6.549E-37
252,152,934,023	3322	TT13	chr5	5	q21.1	98262022	98266696	3	0	-1.256177	-1.256177	2.318E-17
252,152,934,023	3324	TT13	chr5	5	q21.1	101489151	101496527	3	0	-1.093484	-1.093484	2.554E-14
252,152,934,023	3326	TT13	chr5	5	q21.1	101824563	101837571	6	0	-1.425783	-1.425783	7.533E-41
252,152,934,023	3331	TT13	chr5	5	q21.3	106826545	106833144	4	0	-1.203785	-1.203785	1.98E-21
252,152,934,023	3332	TT13	chr5	5	q21.3	107002449	107010185	6	0	-1.426094	-1.426094	1.625E-33
252,152,934,023	3333	TT13	chr5	5	q21.3	107712622	107719303	4	0	-1.217557	-1.217557	6.631E-23
252,152,934,023	3335	TT13	chr5	5	q21.3	108081802	108087145	4	0	-1.483528	-1.483528	4.995E-30
252,152,934,023	3344	TT13	chr5	5	q22.2	111753035	111756788	4	0	-1.910525	-1.910525	4.331E-40
252,152,934,023	3350	TT13	chr5	5	q22.3	114504015	114518134	7	0	-1.503699	-1.503699	6.602E-52
252,152,934,023	3360	TT13	chr5	5	q23.1	118404167	118409182	4	0	-1.541205	-1.541205	2.759E-32
252,152,934,023	3361	TT13	chr5	5	q23.1	118601048	118607119	5	0	-1.157899	-1.157899	1.516E-25
252,152,934,023	3362	TT13	chr5	5	q23.1	118690066	118693894	4	0	-1.573886	-1.573886	2.596E-30
252,152,934,023	3364	TT13	chr5	5	q23.1	119797027	119804374	6	0	-1.201923	-1.201923	7.115E-27
252,152,934,023	3365	TT13	chr5	5	q23.1	121185238	121190551	4	0	-1.336263	-1.336263	5.446E-27
252,152,934,023	3367	TT13	chr5	5	q23.2	121646056	121650689	3	0	-1.388142	-1.388142	4.312E-21
252,152,934,023	3368	TT13	chr5	5	q23.2	122108822	122112664	3	0	-1.608259	-1.608259	3.113E-25
252,152,934,023	3369	TT13	chr5	5	q23.2	122178937	122182302	3	0	-1.713195	-1.713195	5.58E-27
252,152,934,023	3371	TT13	chr5	5	q23.2	122420289	122437526	10	0	-1.74001	-1.74001	1.645E-77
252,152,934,023	3372	TT13	chr5	5	q23.2	122758145	122767701	7	0	-2.105738	-2.105738	4.847E-76
252,152,934,023	3373	TT13	chr5	5	q23.2	122845059	122853746	6	0	-1.049532	-1.049532	1.294E-23
252,152,934,023	3374	TT13	chr5	5	q23.2	123851541	123861065	3	0	-0.949498	-0.949498	4.653E-14
252,152,934,023	3376	TT13	chr5	5	q23.2	124069806	124073184	3	0	-2.070215	-2.070215	2.333E-36
252,152,934,023	3407	TT13	chr5	5	q31.1	132147370	132170187	13	0	-1.194127	-1.194127	3.936E-55

252,152,934,023	3408	TT13	chr5	5	q31.1	132284418	132322633	14	0	-0.782201	-0.782201	2.717E-29
252,152,934,023	3409	TT13	chr5	5	q31.1	132380188	132386778	4	0	-1.30383	-1.30383	3.57E-25
252,152,934,023	3418	TT13	chr5	5	q31.1	133746271	133748572	3	0	-1.691442	-1.691442	3.938E-26
252,152,934,023	3423	TT13	chr5	5	q31.1	134092375	134102497	6	0	-1.219469	-1.219469	5.925E-30
252,152,934,023	3426	TT13	chr5	5	q31.1	134332032	134357107	11	0.396915	0	0.396915	3.175E-12
252,152,934,023	3427	TT13	chr5	5	q31.1	134361149	134387783	14	0	-1.050588	-1.050588	9.301E-43
252,152,934,023	3428	TT13	chr5	5	q31.1	134525111	134531284	3	0	-1.126665	-1.126665	1.825E-15
252,152,934,023	3430	TT13	chr5	5	q31.1	134731456	134747062	7	0	-1.170129	-1.170129	1.221E-30
252,152,934,023	3432	TT13	chr5	5	q31.1	134869450	134880854	8	0	-1.533546	-1.533546	1.763E-51
252,152,934,023	3444	TT13	chr5	5	q31.2	137576373	137612604	18	0	-0.845191	-0.845191	9.695E-40
252,152,934,023	3455	TT13	chr5	5	q31.2	138922857	138944681	9	0	-1.269395	-1.269395	2.034E-48
252,152,934,023	3456	TT13	chr5	5	q31.2	139012803	139096755	42	0	-0.753955	-0.753955	2.015E-68
252,152,934,023	3463	TT13	chr5	5	q31.3	139777944	139783535	4	0	-1.778079	-1.778079	3.181E-12
252,152,934,023	3464	TT13	chr5	5	q31.3	139777944	139813589	16	0	-0.850771	-0.850771	1.092E-40
252,152,934,023	3466	TT13	chr5	5	q31.3	140050234	140055459	4	0	-0.906815	-0.906815	5.413E-13
252,152,934,023	3467	TT13	chr5	5	q31.3	140143663	140824865	299	0	-0.896503	-0.896503	4.900e-324
252,152,934,023	3468	TT13	chr5	5	q31.3	140166702	140264429	45	0	-1.888945	-1.888945	1.576E-123
252,152,934,023	3469	TT13	chr5	5	q31.3	140190316	140200930	4	0	-1.072772	-1.072772	4.885E-12
252,152,934,023	3474	TT13	chr5	5	q31.3	140553272	140573327	11	0	-2.364084	-2.364084	2.368E-10
252,152,934,023	3475	TT13	chr5	5	q31.3	140553272	140627824	38	0	-1.788485	-1.788485	6.074E-90
252,152,934,023	3476	TT13	chr5	5	q31.3	140597126	140611804	9	0	-1.250801	-1.250801	9.952E-12
252,152,934,023	3477	TT13	chr5	5	q31.3	140632537	140707362	29	0	-0.341139	-0.341139	7.016E-40
252,152,934,023	3478	TT13	chr5	5	q31.3	140681132	140685717	3	0	-1.492401	-1.492401	9.821E-16
252,152,934,023	3479	TT13	chr5	5	q31.3	140711111	140812764	52	0	-1.560569	-1.560569	1.824E-72
252,152,934,023	3480	TT13	chr5	5	q31.3	140759191	140764891	4	0	-0.654481	-0.654481	1.461E-15
252,152,934,023	3481	TT13	chr5	5	q31.3	140986416	141505819	185	0	-0.279676	-0.279676	8.987E-61
252,152,934,023	3482	TT13	chr5	5	q31.3	140995463	141001091	4	0	-1.481625	-1.481625	1.966E-20
252,152,934,023	3487	TT13	chr5	5	q31.3	141691775	141740296	22	0	-0.517805	-0.517805	9.945E-27
252,152,934,023	3488	TT13	chr5	5	q31.3	142146025	142155561	6	0	-0.799444	-0.799444	5.232E-17
252,152,934,023	3489	TT13	chr5	5	q31.3	142778175	142787306	6	0	-0.909555	-0.909555	9.229E-22
252,152,934,023	3490	TT13	chr5	5	q31.3	143579139	143590259	8	0	-0.707895	-0.707895	4.786E-18
252,152,934,023	3492	TT13	chr5	5	q32	145580013	145586562	5	0	-1.207319	-1.207319	4.861E-29
252,152,934,023	3494	TT13	chr5	5	q32	145823219	145839235	7	0	-1.241531	-1.241531	2.724E-43
252,152,934,023	3495	TT13	chr5	5	q32	146253107	146261539	6	0	-0.898622	-0.898622	8.197E-20
252,152,934,023	3496	TT13	chr5	5	q32	146830689	146837048	5	0	-1.216329	-1.216329	5.592E-29
252,152,934,023	3497	TT13	chr5	5	q32	146885602	146890520	3	0	-1.545238	-1.545238	1.476E-25
252,152,934,023	3498	TT13	chr5	5	q32	148029931	148038066	5	0	-0.997972	-0.997972	3.662E-21
252,152,934,023	3499	TT13	chr5	5	q32	148203639	148211839	5	0	-0.791757	-0.791757	7.254E-15
252,152,934,023	3502	TT13	chr5	5	q32	148734148	148762497	16	0	-0.877412	-0.877412	5.481E-47
252,152,934,023	3516	TT13	chr5	5	q33.1	150631614	150637137	5	0	-1.3054	-1.3054	1.958E-32
252,152,934,023	3519	TT13	chr5	5	q33.2	154060945	154072250	11	0	-1.437447	-1.437447	7.653E-68
252,152,934,023	3523	TT13	chr5	5	q33.3	156689725	156696416	5	0	-0.943994	-0.943994	5.963E-18
252,152,934,023	3525	TT13	chr5	5	q33.3	156972464	157174629	75	0	-0.293099	-0.293099	2.742E-29
252,152,934,023	3526	TT13	chr5	5	q33.3	157077065	157080778	3	0	-1.586498	-1.586498	8.92E-17
252,152,934,023	3527	TT13	chr5	5	q33.3	157282247	157288741	5	0	-1.372375	-1.372375	1.601E-35
252,152,934,023	3529	TT13	chr5	5	q33.3	158520795	158547506	14	0	-1.002543	-1.002543	3.013E-53
252,152,934,023	3535	TT13	chr5	5	q33.3	159617126	159626310	5	0	-1.805212	-1.805212	3.408E-44
252,152,934,023	3536	TT13	chr5	5	q33.3	159736292	159741542	3	0	-1.288727	-1.288727	3.592E-21
252,152,934,023	3537	TT13	chr5	5	q33.3	159796576	159800239	3	0	-1.349669	-1.349669	1.296E-21
252,152,934,023	3538	TT13	chr5	5	q34	160973377	160979408	4	0	-1.186521	-1.186521	1.212E-21
252,152,934,023	3539	TT13	chr5	5	q34	162929946	162936163	5	0	-1.261901	-1.261901	1.427E-31
252,152,934,023	3540	TT13	chr5	5	q34	167283031	167288784	3	0	-1.551143	-1.551143	1.477E-23
252,152,934,023	3541	TT13	chr5	5	q34	167714644	167720463	5	0	-1.126873	-1.126873	1.803E-24
252,152,934,023	3545	TT13	chr5	5	q34	168267264	168280096	8	0	-0.786479	-0.786479	5.229E-28
252,152,934,023	3546	TT13	chr5	5	q35.1	168726663	168729665	3	0	-1.668467	-1.668467	3.383E-30
252,152,934,023	3547	TT13	chr5	5	q35.1	169062968	169068518	4	0	-1.197173	-1.197173	4.291E-23
252,152,934,023	3548	TT13	chr5	5	q35.1	169529354	169536555	5	0	-1.134542	-1.134542	1.492E-24
252,152,934,023	3549	TT13	chr5	5	q35.1	169928027	169932472	4	0	-1.136936	-1.136936	2.212E-24
252,152,934,023	3553	TT13	chr5	5	q35.1	170827317	170849587	13	0	-0.917998	-0.917998	1.454E-44
252,152,934,023	3554	TT13	chr5	5	q35.1	170874809	170881185	3	0	-1.156035	-1.156035	2.87E-16
252,152,934,023	3555	TT13	chr5	5	q35.1	171429007	171437569	6	0	-0.86402	-0.86402	5.268E-20
252,152,934,023	3559	TT13	chr5	5	q35.1	172067705	172071517	3	0	-1.426026	-1.426026	2.332E-21
252,152,934,023	3566	TT13	chr5	5	q35.1	172637519	172673853	17	0	-1.122917	-1.122917	5.251E-74
252,152,934,023	3567	TT13	chr5	5	q35.1	172645734	172654497	4	0	-0.28007	-0.28007	4.191E-14
252,152,934,023	3569	TT13	chr5	5	q35.1	172709192	172712912	3	0	-1.440112	-1.440112	6.912E-23
252,152,934,023	3570	TT13	chr5	5	q35.1	172752327	172759356	5	0	-1.4521	-1.4521	1.013E-30
252,152,934,023	3571	TT13	chr5	5	q35.2	173041667	173046464	4	0	-1.463982	-1.463982	4.619E-30
252,152,934,023	3573	TT13	chr5	5	q35.2	174149493	174179874	13	0	-0.926554	-0.926554	3.748E-44
252,152,934,023	3575	TT13	chr5	5	q35.2	174903214	174912194	6	0	-1.2582	-1.2582	8.738E-37
252,152,934,023	3576	TT13	chr5	5	q35.2	174957670	174964835	4	0	-0.723366	-0.723366	4.514E-11
252,152,934,023	3577	TT13	chr5	5	q35.2	175081324	175088639	6	0	-0.870532	-0.870532	5.889E-20
252,152,934,023	3578	TT13	chr5	5	q35.2	175223346	175227194	4	0	-1.462802	-1.462802	6.792E-29
252,152,934,023	3580	TT13	chr5	5	q35.2	175295735	175301386	4	0	-0.929121	-0.929121	2.836E-16
252,152,934,023	3588	TT13	chr5	5	q35.3	176729171	176740259	7	0	-1.632725	-1.632725	6.848E-20
252,152,934,023	3589	TT13	chr5	5	q35.3	176729171	176946852	92	0	-0.60686	-0.60686	4.389E-47
252,152,934,023	3590	TT13	chr5	5	q35.3	176784162	176796389	6	0	-1.317704	-1.317704	7.81E-11
252,152,934,023	3615	TT13	chr5	5	q35.3	179222229	179250066	24	0	-1.295075	-1.295075	6.612E-64
252,152,934,023	3616	TT13	chr5	5	q35.3	179228181	179235502	8	0	-2.188509	-2.188509	2.156E-10
252,152,934,023	3642	TT13	chr6	6	p25.3	1309409	1318307	4	0	-2.029681	-2.029681	1.263E-40
252,152,934,023	3643	TT13	chr6	6	p25.3	1376203	1395689	9	0	-1.842636	-1.842636	6.142E-65
252,152,934,023	3646	TT13	chr6	6	p25.3	1593227	1626781	17	0	-1.956163	-1.956163	1.093E-135
252,152,934,023	3647	TT13	chr6	6	p25.3	2243559	2246781	3	0	-1.805552	-1.805552	7.569E-29
252,152,934,023	3648	TT13	chr6	6	p25.2	2761146	2768246	5	0	-1.706367	-1.706367	5.615E-42
252,152,934,023	3649	TT13	chr6	6	p25.2	2827403	3294532	197	0	-0.43226	-0.43226	6.176E-107
252,152,934,023	3650	TT13	chr6	6	p25.2	2869134	2877040	4	0	-2.252084	-2.252084	5.08E-25
252,152,934,023	3662	TT13	chr6	6	p25.2	3719574	3724097	4	0	-1.577206	-1.577206	2.625E-29
252,152,934,023	3663	TT13	chr6	6	p25.2	3749197	3773709	11	0	-1.459023	-1.459023	4.869E-69
252,152,934,023	3664	TT13	chr6	6	p25.2	3844229	3854540	6	0	-0.844145	-0.844145	5.558E-16
252,152,934,023	3665	TT13	chr6	6	p25.2	4012440	4025678	7	0	-0.827056	-0.827056	1.18E-18
252,152,934,023	3666	TT13	chr6	6	p25.2	4077154	4091980	9	0	-1.30636	-1.30636	1.961E-51
252,152,934,023	3672	TT13	chr6	6	p25.1	5000154	5006098	4	0	-1.564039	-1.564039	1.581E-30
252,152,934,023	3673	TT13	chr6	6	p25.1	5084065	5089074	3	0	-1.398635	-1.398635	8.642E-20
252,152,934,023	3674	TT13	chr6	6	p25.1	5258871	5267370	6	0	-0.834681	-0.834681	9.649E-16
252,152,934,023	3675	TT13	chr6	6	p25.1	5834384	5856894	8	0	-0.598089	-0.598089	9.215E-12
252,152,934,023	3676	TT13	chr6	6	p25.1	5999056	6010839	6	0	-1.862571	-1.862571	1.371E-51
252,152,934,023	3677	TT13	chr6	6	p25.1	6543291	6547684	3	0	-0.982831	-0.982831	5.464E-12

252,152,934,023	3678	TT13	chr6	6	p25.1	6603577	6618597	6	0	-1.103791	-1.103791	1.645E-26
252,152,934,023	3680	TT13	chr6	6	p25.1	6937176	6954569	8	0	-1.144751	-1.144751	1.152E-36
252,152,934,023	3681	TT13	chr6	6	p24.3	7137753	7145902	7	0	-1.197362	-1.197362	4.833E-33
252,152,934,023	3682	TT13	chr6	6	p24.3	7226973	7250541	13	0	-0.848815	-0.848815	8.449E-33
252,152,934,023	3683	TT13	chr6	6	p24.3	7311785	7319306	4	0	-2.024266	-2.024266	6.225E-41
252,152,934,023	3684	TT13	chr6	6	p24.3	7340915	7347265	5	0	-1.174786	-1.174786	4.574E-25
252,152,934,023	3686	TT13	chr6	6	p24.3	7540382	7545765	3	0	-1.567773	-1.567773	5.377E-23
252,152,934,023	3690	TT13	chr6	6	p24.3	9935592	9950687	8	0	-0.941178	-0.941178	1.839E-26
252,152,934,023	3691	TT13	chr6	6	p24.3	10109484	10118378	4	0	-0.996833	-0.996833	9.742E-17
252,152,934,023	3692	TT13	chr6	6	p24.3	10169133	10174690	3	0	-1.570925	-1.570925	5.978E-24
252,152,934,023	3693	TT13	chr6	6	p24.3	10381379	10428877	25	0	-1.41798	-1.41798	8.843E-152
252,152,934,023	3694	TT13	chr6	6	p24.3	10389311	10395914	5	0	-0.574721	-0.574721	1.402E-17
252,152,934,023	3695	TT13	chr6	6	p24.3	10479260	10496579	8	0	-1.510491	-1.510491	3.512E-57
252,152,934,023	3696	TT13	chr6	6	p24.2	10615262	10621005	3	0	-1.139402	-1.139402	8.012E-15
252,152,934,023	3698	TT13	chr6	6	p24.2	10835904	10841550	4	0	-1.172512	-1.172512	7.165E-21
252,152,934,023	3699	TT13	chr6	6	p24.2	11039564	11047118	5	0	-1.242835	-1.242835	5.203E-28
252,152,934,023	3700	TT13	chr6	6	p24.2	11086580	11096250	6	0	-1.785447	-1.785447	1.082E-52
252,152,934,023	3703	TT13	chr6	6	p24.2	11227831	11244604	10	0	-0.719327	-0.719327	1.061E-19
252,152,934,023	3704	TT13	chr6	6	p24.2	11399095	11418814	5	0	-1.073734	-1.073734	3.331E-21
252,152,934,023	3705	TT13	chr6	6	p24.1	12008097	12020230	7	0	-1.708931	-1.708931	7.299E-50
252,152,934,023	3720	TT13	chr6	6	p22.3	15243182	15250079	5	0	-1.888581	-1.888581	3.51E-49
252,152,934,023	3724	TT13	chr6	6	p22.3	16128411	16130868	3	0	-1.936474	-1.936474	2.188E-31
252,152,934,023	3725	TT13	chr6	6	p22.3	16177435	16240985	25	0	-0.780608	-0.780608	2.352E-53
252,152,934,023	3734	TT13	chr6	6	p22.3	17700778	17747748	21	0	-0.790013	-0.790013	4.157E-46
252,152,934,023	3735	TT13	chr6	6	p22.3	17728000	17730704	3	0	-1.944255	-1.944255	2.107E-13
252,152,934,023	3736	TT13	chr6	6	p22.3	17972335	18022746	22	0	-0.73629	-0.73629	5.254E-42
252,152,934,023	3737	TT13	chr6	6	p22.3	18118646	18124936	4	0	-1.228686	-1.228686	7.419E-23
252,152,934,023	3738	TT13	chr6	6	p22.3	18152599	18158636	4	0	-1.138835	-1.138835	3.912E-20
252,152,934,023	3739	TT13	chr6	6	p22.3	18260047	18281241	10	0	-1.02834	-1.02834	1.435E-35
252,152,934,023	3740	TT13	chr6	6	p22.3	19803745	19865573	26	0	-0.725477	-0.725477	2.627E-46
252,152,934,023	3741	TT13	chr6	6	p22.3	19836692	19840729	4	0	-1.695757	-1.695757	1.97E-11
252,152,934,023	3745	TT13	chr6	6	p22.3	21593054	21610977	10	0	-1.069456	-1.069456	2.673E-39
252,152,934,023	3755	TT13	chr6	6	p22.3	24765004	24780990	8	0	-1.113741	-1.113741	2.048E-37
252,152,934,023	3775	TT13	chr6	6	p22.1	28916592	28945079	11	0	-1.322078	-1.322078	5.795E-61
252,152,934,023	3776	TT13	chr6	6	p22.1	28980549	28985257	4	0	-1.563879	-1.563879	1.896E-31
252,152,934,023	3777	TT13	chr6	6	p22.1	29126369	29133378	4	0	-1.563057	-1.563057	3.16E-31
252,152,934,023	3778	TT13	chr6	6	p22.1	29519822	29523529	3	0	-1.525216	-1.525216	3.881E-23
252,152,934,023	3779	TT13	chr6	6	p22.1	29596182	29601945	4	0	-1.973106	-1.973106	6.397E-39
252,152,934,023	3792	TT13	chr6	6	p21.33	30771930	30784960	7	0	-1.212987	-1.212987	9.366E-36
252,152,934,023	3795	TT13	chr6	6	p21.33	30958537	30994799	15	0	-0.926755	-0.926755	2.694E-45
252,152,934,023	3812	TT13	chr6	6	p21.32	33159066	33179886	23	0	-1.262115	-1.262115	1.322E-98
252,152,934,023	3857	TT13	chr6	6	p21.2	38605327	38609213	3	0	-1.733697	-1.733697	2.888E-30
252,152,934,023	3858	TT13	chr6	6	p21.2	38670045	38686549	9	0	-0.884123	-0.884123	4.1E-31
252,152,934,023	3859	TT13	chr6	6	p21.2	38929229	38933631	3	0	-1.197056	-1.197056	1.299E-19
252,152,934,023	3860	TT13	chr6	6	p21.2	39012019	39020559	4	0	-0.729158	-0.729158	2.881E-11
252,152,934,023	3861	TT13	chr6	6	p21.2	39079444	39085234	4	0	-1.325158	-1.325158	5.736E-28
252,152,934,023	3864	TT13	chr6	6	p21.2	39685661	39766336	32	0	-0.415246	-0.415246	2.375E-26
252,152,934,023	3882	TT13	chr6	6	p21.1	43193423	43254357	30	0	-0.789253	-0.789253	9.274E-56
252,152,934,023	3885	TT13	chr6	6	p21.1	43540869	43552038	6	0	-1.538048	-1.538048	2.686E-42
252,152,934,023	3887	TT13	chr6	6	p21.1	43965513	43972062	5	0	-1.991275	-1.991275	2.597E-42
252,152,934,023	3890	TT13	chr6	6	p21.1	44182812	44283814	48	0	-0.850998	-0.850998	1.15E-109
252,152,934,023	3891	TT13	chr6	6	p21.1	44692262	44710945	4	0	-0.825554	-0.825554	6.876E-12
252,152,934,023	3893	TT13	chr6	6	p21.1	45383847	45397167	7	0	-0.76514	-0.76514	6.248E-16
252,152,934,023	3894	TT13	chr6	6	p21.1	45605214	45610115	4	0	-1.07074	-1.07074	1.076E-16
252,152,934,023	3895	TT13	chr6	6	p21.1	46094041	46101642	6	0	-1.052412	-1.052412	5.367E-24
252,152,934,023	3896	TT13	chr6	6	p12.3	46372141	46376959	3	0	-1.742516	-1.742516	6.667E-27
252,152,934,023	3897	TT13	chr6	6	p12.3	46456278	46460312	3	0	-1.407501	-1.407501	3.104E-21
252,152,934,023	3898	TT13	chr6	6	p12.3	46619593	46623860	4	0	-1.727095	-1.727095	1.405E-36
252,152,934,023	3900	TT13	chr6	6	p12.3	46700352	46704335	3	0	-1.606358	-1.606358	1.1E-25
252,152,934,023	3901	TT13	chr6	6	p12.3	46739142	46745795	4	0	-1.066506	-1.066506	1.982E-18
252,152,934,023	3902	TT13	chr6	6	p12.3	47273494	47279760	4	0	-1.334061	-1.334061	3.534E-26
252,152,934,023	3903	TT13	chr6	6	p12.3	47442966	47447906	3	0	-1.564442	-1.564442	6.382E-22
252,152,934,023	3905	TT13	chr6	6	p12.3	48033661	48038052	3	0	-1.426657	-1.426657	2.125E-22
252,152,934,023	3906	TT13	chr6	6	p12.3	49446569	49456151	5	0	-1.009559	-1.009559	6.095E-20
252,152,934,023	3910	TT13	chr6	6	p12.3	50787061	50794244	5	0	-1.593457	-1.593457	7.436E-40
252,152,934,023	3911	TT13	chr6	6	p12.3	50814914	50820850	5	0	-1.685404	-1.685404	3.642E-42
252,152,934,023	3912	TT13	chr6	6	p12.3	51270746	51276875	5	0	-1.210934	-1.210934	3.281E-27
252,152,934,023	3913	TT13	chr6	6	p12.2	51841829	51848807	5	0	-1.049631	-1.049631	1.29E-21
252,152,934,023	3914	TT13	chr6	6	p12.2	52146753	52150279	3	0	-1.60192	-1.60192	9.999E-25
252,152,934,023	3915	TT13	chr6	6	p12.2	52263833	52274020	7	0	-0.708941	-0.708941	3.756E-14
252,152,934,023	3916	TT13	chr6	6	p12.2	52517805	52540472	12	0	-0.693632	-0.693632	1.676E-22
252,152,934,023	3919	TT13	chr6	6	p12.1	53211616	53229201	8	0	-1.411654	-1.411654	1.718E-51
252,152,934,023	3920	TT13	chr6	6	p12.1	53408502	53412457	3	0	-2.111742	-2.111742	7.071E-31
252,152,934,023	3921	TT13	chr6	6	p12.1	53509943	53524384	9	0	-1.005619	-1.005619	1.99E-34
252,152,934,023	3922	TT13	chr6	6	p12.1	53657785	53662780	3	0	-1.549387	-1.549387	1.407E-24
252,152,934,023	3923	TT13	chr6	6	p12.1	54708719	54713729	3	0	-1.10324	-1.10324	5.221E-14
252,152,934,023	3924	TT13	chr6	6	p12.1	55440569	55444992	3	0	-1.381148	-1.381148	1.078E-21
252,152,934,023	3925	TT13	chr6	6	p12.1	56584355	56589411	3	0	-1.226997	-1.226997	3.97E-17
252,152,934,023	3926	TT13	chr6	6	p12.1	56682173	56712619	15	0	-0.78215	-0.78215	4.473E-33
252,152,934,023	3928	TT13	chr6	6	p11.2	57085694	57088346	3	0	-1.855056	-1.855056	1.605E-29
252,152,934,023	3929	TT13	chr6	6	p11.2	57171457	57180547	4	0	-0.984368	-0.984368	2.454E-14
252,152,934,023	3930	TT13	chr6	6	q11.1	62992663	62997061	3	0	-1.525667	-1.525667	5.079E-25
252,152,934,023	3931	TT13	chr6	6	q12	63919328	63926079	4	0	-1.203367	-1.203367	8.291E-22
252,152,934,023	3932	TT13	chr6	6	q12	63981651	63986080	3	0	-1.255003	-1.255003	3.386E-17
252,152,934,023	3933	TT13	chr6	6	q12	64151606	64157918	3	0	-1.358058	-1.358058	7.771E-21
252,152,934,023	3934	TT13	chr6	6	q12	64279006	64287393	5	0	-1.172108	-1.172108	7.442E-27
252,152,934,023	3936	TT13	chr6	6	q12	66336013	66342052	4	0	-1.122509	-1.122509	5.759E-20
252,152,934,023	3937	TT13	chr6	6	q12	66496293	66499214	3	0	-1.636553	-1.636553	8.521E-28
252,152,934,023	3941	TT13	chr6	6	q13	70672246	70681613	6	0	-1.056541	-1.056541	2.51E-26
252,152,934,023	3942	TT13	chr6	6	q13	71118736	71129800	6	0	-0.901434	-0.901434	2.951E-20
252,152,934,023	3943	TT13	chr6	6	q13	71275026	71280725	4	0	-1.119238	-1.119238	2.715E-18
252,152,934,023	3944	TT13	chr6	6	q13	71660089	71669680	5	0	-0.86028	-0.86028	1.373E-15
252,152,934,023	3945	TT13	chr6	6	q13	71870221	71879888	7	0	-1.025014	-1.025014	7.684E-26
252,152,934,023	3946	TT13	chr6	6	q13	71995521	72003317	5	0	-1.12856	-1.12856	1.438E-22
252,152,934,023	3947	TT13	chr6	6	q13	72124863	72133545	9	0	-0.93898	-0.93898	8.775E-32
252,152,934,023	3948	TT13	chr6	6	q13	72288721	72306024	11	0	-0.479353	-0.479353	1.52E-10

252,152,934,023	3963	TT13	chr6	6	q14.1	75989139	75998023	5	0	-1.05707	-1.05707	2.064E-22
252,152,934,023	3965	TT13	chr6	6	q14.1	76306956	76314033	5	0	-1.1798	-1.1798	1.024E-25
252,152,934,023	3966	TT13	chr6	6	q14.1	76454309	76465418	7	0	-0.874838	-0.874838	1.043E-19
252,152,934,023	3968	TT13	chr6	6	q14.1	79784507	79789852	5	0	-1.594615	-1.594615	1.77E-37
252,152,934,023	3970	TT13	chr6	6	q14.1	80654044	80662540	6	0	-1.082048	-1.082048	3.892E-26
252,152,934,023	3972	TT13	chr6	6	q14.1	80814160	80818803	4	0	-1.381122	-1.381122	9.679E-27
252,152,934,023	3973	TT13	chr6	6	q14.1	82454105	82467986	7	0	-0.72358	-0.72358	7.583E-14
252,152,934,023	3974	TT13	chr6	6	q14.1	82948801	82961233	8	0	-0.934754	-0.934754	1.514E-24
252,152,934,023	3975	TT13	chr6	6	q14.1	83067768	83079036	6	0	-0.829418	-0.829418	9.264E-17
252,152,934,023	3977	TT13	chr6	6	q14.2	83901016	83905955	5	0	-1.32538	-1.32538	1.341E-28
252,152,934,023	3981	TT13	chr6	6	q14.2	84727412	84749374	12	0	-1.054731	-1.054731	4.96E-45
252,152,934,023	3982	TT13	chr6	6	q14.2 - q14.3	84894927	84903375	5	0	-1.005366	-1.005366	1.426E-20
252,152,934,023	3983	TT13	chr6	6	q14.3	84949748	84956140	3	0	-1.340993	-1.340993	2.3E-20
252,152,934,023	3984	TT13	chr6	6	q14.3	85470190	85486043	9	0	-1.123703	-1.123703	4.631E-32
252,152,934,023	3985	TT13	chr6	6	q14.3	86157622	86161134	3	0	-1.623733	-1.623733	3.092E-25
252,152,934,023	3989	TT13	chr6	6	q14.3	87644714	87649744	4	0	-1.336935	-1.336935	5.148E-25
252,152,934,023	3990	TT13	chr6	6	q14.3	87717828	87722792	4	0	-1.619314	-1.619314	6.468E-35
252,152,934,023	3991	TT13	chr6	6	q14.3	87765346	87771355	3	0	-1.194253	-1.194253	2.261E-17
252,152,934,023	3994	TT13	chr6	6	q15	88032021	88032868	3	0	-2.202677	-2.202677	2.74E-35
252,152,934,023	3996	TT13	chr6	6	q15	88179229	88185429	5	0	-1.333571	-1.333571	2.066E-31
252,152,934,023	3997	TT13	chr6	6	q15	88443474	88462126	7	0	-1.042068	-1.042068	2.211E-27
252,152,934,023	4000	TT13	chr6	6	q15	89770002	89868366	46	0	-0.446005	-0.446005	4.81E-31
252,152,934,023	4001	TT13	chr6	6	q15	89789679	89793594	3	0	-1.385548	-1.385548	6.391E-10
252,152,934,023	4005	TT13	chr6	6	q15	91294141	91324449	12	0	-0.925907	-0.925907	7.687E-38
252,152,934,023	4006	TT13	chr6	6	q15	92718656	92723830	4	0	-1.565362	-1.565362	2.331E-29
252,152,934,023	4007	TT13	chr6	6	q16.1	93990143	93995371	4	0	-1.54371	-1.54371	4.551E-30
252,152,934,023	4008	TT13	chr6	6	q16.1	94119841	94133758	7	0	-0.838624	-0.838624	7.503E-16
252,152,934,023	4009	TT13	chr6	6	q16.1	95943457	95948275	3	0	-1.228763	-1.228763	4.164E-19
252,152,934,023	4010	TT13	chr6	6	q16.1	96022834	96026439	3	0	-2.107442	-2.107442	1.898E-35
252,152,934,023	4011	TT13	chr6	6	q16.1	96457284	96467103	6	0	-0.949881	-0.949881	4.418E-22
252,152,934,023	4012	TT13	chr6	6	q16.1	96966148	96973705	5	0	-1.031273	-1.031273	5.212E-20
252,152,934,023	4013	TT13	chr6	6	q16.1	97282228	97286727	3	0	-1.290739	-1.290739	8.721E-20
252,152,934,023	4014	TT13	chr6	6	q16.1	97367158	97378952	6	0	-0.997818	-0.997818	5.614E-24
252,152,934,023	4015	TT13	chr6	6	q16.1	99274167	99297379	13	0	-1.406589	-1.406589	2.025E-75
252,152,934,023	4016	TT13	chr6	6	q16.1	99388702	99400404	6	0	-1.046466	-1.046466	1.742E-24
252,152,934,023	4017	TT13	chr6	6	q16.2	99796128	99802228	4	0	-1.632752	-1.632752	1.333E-29
252,152,934,023	4018	TT13	chr6	6	q16.2	99961506	99969711	4	0	-1.465981	-1.465981	1.237E-27
252,152,934,023	4019	TT13	chr6	6	q16.2	100037677	100069854	18	0	-1.46654	-1.46654	1.196E-108
252,152,934,023	4021	TT13	chr6	6	q16.2	100440591	100445685	4	0	-1.279544	-1.279544	9.897E-24
252,152,934,023	4022	TT13	chr6	6	q16.3	100908500	100917925	5	0	-1.343292	-1.343292	5.175E-31
252,152,934,023	4023	TT13	chr6	6	q16.3	101274930	101279651	3	0	-1.391727	-1.391727	3.217E-23
252,152,934,023	4024	TT13	chr6	6	q16.3	101326372	101331667	4	0	-1.654653	-1.654653	5.565E-35
252,152,934,023	4025	TT13	chr6	6	q16.3	101840425	101852695	8	0	-1.413382	-1.413382	1.57E-46
252,152,934,023	4026	TT13	chr6	6	q16.3	105303592	105310155	4	0	-1.386824	-1.386824	2.192E-26
252,152,934,023	4027	TT13	chr6	6	q21	105581288	105585788	4	0	-1.695927	-1.695927	4.986E-33
252,152,934,023	4029	TT13	chr6	6	q21	105848758	105853164	4	0	-1.65615	-1.65615	1.577E-34
252,152,934,023	4030	TT13	chr6	6	q21	106531659	106540741	7	0	-1.213833	-1.213833	9.858E-37
252,152,934,023	4038	TT13	chr6	6	q21	108253406	108283857	13	0	-0.9659	-0.9659	5.534E-42
252,152,934,023	4039	TT13	chr6	6	q21	108274071	108277645	3	0	-2.341603	-2.341603	1.874E-15
252,152,934,023	4040	TT13	chr6	6	q21	108393327	108397712	4	0	-1.46128	-1.46128	3.254E-27
252,152,934,023	4041	TT13	chr6	6	q21	108440407	108458713	6	0	-1.016186	-1.016186	1.478E-19
252,152,934,023	4042	TT13	chr6	6	q21	108475675	108499843	14	0	-1.487278	-1.487278	7.192E-93
252,152,934,023	4043	TT13	chr6	6	q21	108580268	108593535	7	0	-1.268799	-1.268799	4.667E-40
252,152,934,023	4044	TT13	chr6	6	q21	108878143	108886264	5	0	-1.705705	-1.705705	7.941E-43
252,152,934,023	4052	TT13	chr6	6	q21	109801874	109806229	4	0	-1.844302	-1.844302	2.925E-36
252,152,934,023	4053	TT13	chr6	6	q21	110010382	110013683	3	0	-0.970332	-0.970332	4.561E-12
252,152,934,023	4054	TT13	chr6	6	q21	110296068	110303198	6	0	-1.276142	-1.276142	4.38E-33
252,152,934,023	4055	TT13	chr6	6	q21	110496968	110503833	4	0	-1.148112	-1.148112	5.135E-21
252,152,934,023	4056	TT13	chr6	6	q21	110677214	110681221	4	0	-1.601449	-1.601449	1.046E-31
252,152,934,023	4068	TT13	chr6	6	q21	114174928	114183824	5	0	-1.409938	-1.409938	9.847E-32
252,152,934,023	4074	TT13	chr6	6	q22.1	116887846	116895564	5	0	-1.419778	-1.419778	2.976E-35
252,152,934,023	4080	TT13	chr6	6	q22.1	117802742	117806552	3	0	-1.383176	-1.383176	1.845E-20
252,152,934,023	4084	TT13	chr6	6	q22.31	119332365	119341115	5	0	-1.401187	-1.401187	2.496E-34
252,152,934,023	4085	TT13	chr6	6	q22.31	119392084	119401674	12	0	-0.700238	-0.700238	2.726E-22
252,152,934,023	4086	TT13	chr6	6	q22.31	119666268	119673761	5	0	-1.25864	-1.25864	4.996E-26
252,152,934,023	4087	TT13	chr6	6	q22.31	121724698	121733343	5	0	-1.029947	-1.029947	4.482E-19
252,152,934,023	4088	TT13	chr6	6	q22.31	122002043	122009663	5	0	-1.813659	-1.813659	4.208E-46
252,152,934,023	4089	TT13	chr6	6	q22.31	122715070	122723660	5	0	-1.093496	-1.093496	5.307E-23
252,152,934,023	4090	TT13	chr6	6	q22.31	122927982	122932983	4	0	-1.591975	-1.591975	3.518E-34
252,152,934,023	4093	TT13	chr6	6	q22.31	123314848	123322181	5	0	-1.252554	-1.252554	2.025E-28
252,152,934,023	4094	TT13	chr6	6	q22.31	124123115	124129366	4	0	-1.361652	-1.361652	8.066E-27
252,152,934,023	4095	TT13	chr6	6	q22.31	125281287	125288781	4	0	-0.962784	-0.962784	2.34E-14
252,152,934,023	4096	TT13	chr6	6	q22.31	125416542	125479480	20	0	-0.575417	-0.575417	3.001E-24
252,152,934,023	4105	TT13	chr6	6	q23.1	130683103	130692188	6	0	-1.27728	-1.27728	1.441E-33
252,152,934,023	4107	TT13	chr6	6	q23.2	132125744	132133594	5	0	-0.960333	-0.960333	1.03E-18
252,152,934,023	4108	TT13	chr6	6	q23.2	132269578	132275422	5	0	-1.390717	-1.390717	1.58E-32
252,152,934,023	4109	TT13	chr6	6	q23.2	132718075	132728087	6	0	-1.183379	-1.183379	1.309E-32
252,152,934,023	4110	TT13	chr6	6	q23.2	132832594	132836565	3	0	-1.437014	-1.437014	1.386E-22
252,152,934,023	4113	TT13	chr6	6	q23.2	134270746	134279853	6	0	-1.308887	-1.308887	1.929E-34
252,152,934,023	4114	TT13	chr6	6	q23.2	134494062	134500954	4	0	-1.410209	-1.410209	8.327E-26
252,152,934,023	4115	TT13	chr6	6	q23.2	134951578	134956061	3	0	-1.800491	-1.800491	6.957E-29
252,152,934,023	4119	TT13	chr6	6	q23.3	137110478	137116149	5	0	-1.58443	-1.58443	7.801E-36
252,152,934,023	4120	TT13	chr6	6	q23.3	137140652	137147511	5	0	-1.089225	-1.089225	1.577E-20
252,152,934,023	4121	TT13	chr6	6	q23.3	137241454	137246597	3	0	-1.276641	-1.276641	3.024E-19
252,152,934,023	4123	TT13	chr6	6	q23.3	137537872	137543874	4	0	-1.23518	-1.23518	2.594E-22
252,152,934,023	4124	TT13	chr6	6	q23.3	137809685	137819741	7	0	-2.03686	-2.03686	1.888E-71
252,152,934,023	4125	TT13	chr6	6	q23.3	138183902	138195131	5	0	-0.873191	-0.873191	1.042E-15
252,152,934,023	4126	TT13	chr6	6	q23.3	138425846	138430669	4	0	-1.502948	-1.502948	1.684E-30
252,152,934,023	4127	TT13	chr6	6	q23.3	138478462	138485245	4	0	-1.278122	-1.278122	2.351E-22
252,152,934,023	4128	TT13	chr6	6	q23.3	138610900	138616120	4	0	-1.406956	-1.406956	1.285E-27
252,152,934,023	4129	TT13	chr6	6	q23.3	138720617	138750198	15	0	-0.686363	-0.686363	2.742E-26
252,152,934,023	4138	TT13	chr6	6	q24.2	143378370	143384299	4	0	-1.282658	-1.282658	2.132E-24
252,152,934,023	4139	TT13	chr6	6	q24.2	143827114	143862362	13	0	-0.582782	-0.582782	8.918E-17
252,152,934,023	4140	TT13	chr6	6	q24.2	143996893	144001210	4	0	-1.446081	-1.446081	1.599E-25
252,152,934,023	4146	TT13	chr6	6	q24.2	144605257	144609613	4	0	-2.461498	-2.461498	8.132E-39
252,152,934,023	4147	TT13	chr6	6	q24.2	144747588	144831498	37	0	-0.469196	-0.469196	6.062E-29

252,152,934,023	4148	TT13	chr6	6	q24.3	146053443	146060599	4	0	-0.820356	-0.820356	1.103E-11
252,152,934,023	4149	TT13	chr6	6	q24.3	146132701	146139092	4	0	-1.227482	-1.227482	1.141E-22
252,152,934,023	4151	TT13	chr6	6	q24.3	146862087	146868353	5	0	-1.536172	-1.536172	7.974E-34
252,152,934,023	4154	TT13	chr6	6	q24.3	147519679	147529115	5	0	-1.181242	-1.181242	4.481E-27
252,152,934,023	4155	TT13	chr6	6	q24.3	147827753	147836008	5	0	-1.10686	-1.10686	5.221E-20
252,152,934,023	4156	TT13	chr6	6	q24.3	148660510	148667897	6	0	-1.205415	-1.205415	1.548E-30
252,152,934,023	4158	TT13	chr6	6	q25.1	149635429	149644075	4	0	-1.247077	-1.247077	2.655E-23
252,152,934,023	4179	TT13	chr6	6	q25.2	153280142	153327840	20	0	-0.718804	-0.718804	2.907E-38
252,152,934,023	4180	TT13	chr6	6	q25.2	153445515	153458190	8	0	-1.164352	-1.164352	1.962E-33
252,152,934,023	4181	TT13	chr6	6	q25.2	155052410	155055710	3	0	-1.602036	-1.602036	3.56E-24
252,152,934,023	4182	TT13	chr6	6	q25.2	155284219	155290565	3	0	-1.238339	-1.238339	1.676E-17
252,152,934,023	4183	TT13	chr6	6	q25.2	155312312	155317754	3	0	-1.117438	-1.117438	7.095E-15
252,152,934,023	4184	TT13	chr6	6	q25.3	155565879	155572066	5	0	-1.346825	-1.346825	2.997E-31
252,152,934,023	4186	TT13	chr6	6	q25.3	157096950	157102992	3	0	-1.655362	-1.655362	3.234E-26
252,152,934,023	4187	TT13	chr6	6	q25.3	157280637	157284425	3	0	-0.994295	-0.994295	3.864E-13
252,152,934,023	4188	TT13	chr6	6	q25.3	157341859	157346532	3	0	-1.386912	-1.386912	1.183E-20
252,152,934,023	4192	TT13	chr6	6	q25.3	158243414	158247658	3	0	-2.084408	-2.084408	8.193E-31
252,152,934,023	4194	TT13	chr6	6	q25.3	158626509	158663116	16	0	-0.827335	-0.827335	7.065E-39
252,152,934,023	4195	TT13	chr6	6	q25.3	158652327	158663116	4	0	-1.676557	-1.676557	8.177E-11
252,152,934,023	4198	TT13	chr6	6	q25.3	158917600	158982966	31	0	-0.579285	-0.579285	1.098E-36
252,152,934,023	4205	TT13	chr6	6	q25.3	160110563	160241723	59	0	-0.510893	-0.510893	2.298E-52
252,152,934,023	4206	TT13	chr6	6	q25.3	160206093	160238849	14	0	-0.932653	-0.932653	9.641E-12
252,152,934,023	4211	TT13	chr6	6	q25.3	160762944	160786683	14	0	-0.749527	-0.749527	2.083E-28
252,152,934,023	4225	TT13	chr6	6	q27	166569642	166584897	10	0	-1.253666	-1.253666	1.603E-48
252,152,934,023	4228	TT13	chr6	6	q27	166791465	166827829	19	0	-0.857796	-0.857796	6.381E-47
252,152,934,023	4237	TT13	chr6	6	q27	168360547	170494645	731	0	-0.252333	-0.252333	2.472E-117
252,152,934,023	4238	TT13	chr6	6	q27	168362833	168399337	16	0	-1.122865	-1.122865	6.557E-41
252,152,934,023	4251	TT13	chr6	6	q27	170059093	170065867	5	0	-2.093068	-2.093068	5.388E-44
252,152,934,023	4252	TT13	chr6	6	q27	170101094	170156621	25	0	-0.697119	-0.697119	4.407E-22
252,152,934,023	4254	TT13	chr6	6	q27	170552583	170618912	30	0	-1.419716	-1.419716	3.709E-164
252,152,934,023	4255	TT13	chr6	6	q27	170568349	170572927	3	0	-0.640122	-0.640122	8.375E-10
252,152,934,023	4257	TT13	chr7	7	p22.3	115719	2758322	864	0	-0.608376	-0.608376	4.900e-324
252,152,934,023	4258	TT13	chr7	7	p22.3	149637	678273	47	0	-0.983734	-0.983734	6.419E-22
252,152,934,023	4259	TT13	chr7	7	p22.3	714595	718428	4	0	-1.877958	-1.877958	8.148E-20
252,152,934,023	4261	TT13	chr7	7	p22.3	878759	1151720	131	0	-1.231833	-1.231833	1.334E-145
252,152,934,023	4262	TT13	chr7	7	p22.3	930542	935972	4	0	-2.487433	-2.487433	3.607E-12
252,152,934,023	4274	TT13	chr7	7	p22.3	2009855	2060371	23	0	-1.006494	-1.006494	1.578E-34
252,152,934,023	4275	TT13	chr7	7	p22.3	2025544	2029605	3	0	-2.549312	-2.549312	2.623E-10
252,152,934,023	4276	TT13	chr7	7	p22.3	2194358	2202627	4	0	-1.710553	-1.710553	1.474E-25
252,152,934,023	4278	TT13	chr7	7	p22.3	2340652	2397612	14	0	-0.884838	-0.884838	3.928E-17
252,152,934,023	4281	TT13	chr7	7	p22.3 - p22.2	2799343	2804766	4	0	-1.282967	-1.282967	1.487E-24
252,152,934,023	4282	TT13	chr7	7	p22.2	2880577	2884553	4	0	-0.976267	-0.976267	3.432E-17
252,152,934,023	4283	TT13	chr7	7	p22.2	2948295	2967584	10	0	-1.001308	-1.001308	1.449E-37
252,152,934,023	4285	TT13	chr7	7	p22.2	3078424	3087195	6	0	-0.660284	-0.660284	4.272E-11
252,152,934,023	4286	TT13	chr7	7	p22.2	3338276	3343750	4	0	-1.181049	-1.181049	2.456E-18
252,152,934,023	4287	TT13	chr7	7	p22.2	3987792	3993253	4	0	-0.865177	-0.865177	1.721E-14
252,152,934,023	4288	TT13	chr7	7	p22.2	4253449	4260145	4	0	-0.930748	-0.930748	1.28E-15
252,152,934,023	4290	TT13	chr7	7	p22.1	4787672	7287080	752	0	-0.291188	-0.291188	3.072E-255
252,152,934,023	4291	TT13	chr7	7	p22.1	4793247	4925415	61	0	-0.930453	-0.930453	4.148E-83
252,152,934,023	4292	TT13	chr7	7	p22.1	4796578	4802318	4	0	-2.108167	-2.108167	2.357E-13
252,152,934,023	4293	TT13	chr7	7	p22.1	4916252	4924181	5	0	-2.108763	-2.108763	5.817E-19
252,152,934,023	4295	TT13	chr7	7	p22.1	5370746	5469241	42	0	-0.749581	-0.749581	3.084E-30
252,152,934,023	4296	TT13	chr7	7	p22.1	5769203	5831239	26	0	-0.440675	-0.440675	7.93E-25
252,152,934,023	4297	TT13	chr7	7	p22.1	6191649	6214734	12	0	-1.351205	-1.351205	4.31E-44
252,152,934,023	4298	TT13	chr7	7	p22.1	6261608	6265699	3	0	-1.618492	-1.618492	3.366E-19
252,152,934,023	4301	TT13	chr7	7	p22.1	7219792	7223898	3	0	-1.65191	-1.65191	2.75E-19
252,152,934,023	4302	TT13	chr7	7	p21.3	7516435	7520987	3	0	-1.692186	-1.692186	9.542E-29
252,152,934,023	4303	TT13	chr7	7	p21.3	7603962	7608665	4	0	-1.467434	-1.467434	2.173E-25
252,152,934,023	4305	TT13	chr7	7	p21.3	8300578	8303681	3	0	-1.615759	-1.615759	4.386E-26
252,152,934,023	4307	TT13	chr7	7	p21.3	9659770	9663274	3	0	-1.805037	-1.805037	5.436E-28
252,152,934,023	4308	TT13	chr7	7	p21.3	9763073	9769966	4	0	-1.203354	-1.203354	4.762E-18
252,152,934,023	4309	TT13	chr7	7	p21.3	10502601	10508845	4	0	-1.195381	-1.195381	3.277E-22
252,152,934,023	4310	TT13	chr7	7	p21.3	10972891	11038382	29	0	-0.753313	-0.753313	8.893E-56
252,152,934,023	4311	TT13	chr7	7	p21.3	10977960	10982038	4	0	-1.614901	-1.614901	1.154E-10
252,152,934,023	4312	TT13	chr7	7	p21.3	12248605	12254599	5	0	-1.265368	-1.265368	9.471E-29
252,152,934,023	4313	TT13	chr7	7	p21.3	12441987	12449804	4	0	-0.81083	-0.81083	1.79E-11
252,152,934,023	4314	TT13	chr7	7	p21.3	12506408	12514126	6	0	-1.134401	-1.134401	1.387E-28
252,152,934,023	4315	TT13	chr7	7	p21.3	12725067	12728910	3	0	-1.669385	-1.669385	5.095E-27
252,152,934,023	4316	TT13	chr7	7	p21.2	15434649	15440570	5	0	-1.372495	-1.372495	7.843E-33
252,152,934,023	4317	TT13	chr7	7	p21.2	16207949	16215716	5	0	-0.921616	-0.921616	4.631E-17
252,152,934,023	4318	TT13	chr7	7	p21.2	16455659	16464336	5	0	-1.067165	-1.067165	1.238E-21
252,152,934,023	4321	TT13	chr7	7	p21.1	16789236	16833492	23	0	-0.560145	-0.560145	2.976E-25
252,152,934,023	4324	TT13	chr7	7	p21.1	19153985	19160370	5	0	-1.496392	-1.496392	3.697E-34
252,152,934,023	4325	TT13	chr7	7	p21.1	19729083	19733488	3	0	-1.036652	-1.036652	4.089E-14
252,152,934,023	4326	TT13	chr7	7	p21.1	20365758	20375122	6	0	-0.875308	-0.875308	7.413E-18
252,152,934,023	4327	TT13	chr7	7	p21.1	20706449	20710933	4	0	-1.336337	-1.336337	3.44E-26
252,152,934,023	4329	TT13	chr7	7	p15.3	21463320	21471553	4	0	-1.027678	-1.027678	1.667E-17
252,152,934,023	4330	TT13	chr7	7	p15.3	21497626	21506279	10	0	-1.055801	-1.055801	2.116E-39
252,152,934,023	4331	TT13	chr7	7	p15.3	21578888	21584008	4	0	-1.708165	-1.708165	4.16E-37
252,152,934,023	4332	TT13	chr7	7	p15.3	21982146	21987701	5	0	-1.366299	-1.366299	1.515E-31
252,152,934,023	4333	TT13	chr7	7	p15.3	22394702	22400560	4	0	-1.380396	-1.380396	7.398E-26
252,152,934,023	4338	TT13	chr7	7	p15.3	23220285	23250146	16	0	-0.932163	-0.932163	7.537E-51
252,152,934,023	4339	TT13	chr7	7	p15.3	23285378	23288193	3	0	-1.544178	-1.544178	8.351E-23
252,152,934,023	4341	TT13	chr7	7	p15.3	23504485	23532939	14	0	-1.065538	-1.065538	5.168E-52
252,152,934,023	4342	TT13	chr7	7	p15.3	23510578	23514511	3	0	-2.589485	-2.589485	1.594E-16
252,152,934,023	4353	TT13	chr7	7	p15.2	26409579	26444081	19	0	-0.750893	-0.750893	1.917E-36
252,152,934,023	4360	TT13	chr7	7	p15.1	28216387	28222380	4	0	-1.479474	-1.479474	2.662E-30
252,152,934,023	4362	TT13	chr7	7	p15.1	28597586	28602437	4	0	-1.611379	-1.611379	2.322E-35
252,152,934,023	4363	TT13	chr7	7	p14.3	28874234	28895111	10	0	-0.945239	-0.945239	1.236E-36
252,152,934,023	4364	TT13	chr7	7	p14.3	28990715	29005053	7	0	-0.926202	-0.926202	8.222E-26
252,152,934,023	4365	TT13	chr7	7	p14.3	29228996	29238943	6	0	-1.004462	-1.004462	6.818E-26
252,152,934,023	4366	TT13	chr7	7	p14.3	29295639	29309686	9	0	-0.752231	-0.752231	6.02E-22
252,152,934,023	4367	TT13	chr7	7	p14.3	29601521	29610794	7	0	-1.185834	-1.185834	5.031E-37
252,152,934,023	4368	TT13	chr7	7	p14.3	29686018	29726655	10	0	-0.812214	-0.812214	1.129E-28
252,152,934,023	4369	TT13	chr7	7	p14.3	29922449	29934205	8	0	-1.369034	-1.369034	1.903E-48
252,152,934,023	4392	TT13	chr7	7	p14.2	35069089	35303151	19	0	-0.75731	-0.75731	2.911E-42

252,152,934,023	4393	TT13	chr7	7	p14.2	35295505	35298265	3	0	-1.98147	-1.98147	3.512E-12
252,152,934,023	4396	TT13	chr7	7	p14.2	35835121	35845360	7	0	-0.907415	-0.907415	1.952E-26
252,152,934,023	4397	TT13	chr7	7	p14.2	36004359	36026319	4	0	-1.079528	-1.079528	1.504E-20
252,152,934,023	4399	TT13	chr7	7	p14.2	36234169	36240122	3	0	-0.971436	-0.971436	2.055E-13
252,152,934,023	4401	TT13	chr7	7	p14.2	36401971	36440710	16	0	-0.736537	-0.736537	1.141E-37
252,152,934,023	4402	TT13	chr7	7	p14.2	37009061	37017974	5	0	-1.002218	-1.002218	4.637E-22
252,152,934,023	4403	TT13	chr7	7	p14.1	37329456	37337889	4	0	-0.96436	-0.96436	4.294E-17
252,152,934,023	4404	TT13	chr7	7	p14.1	37486923	37491867	3	0	-1.466051	-1.466051	7.965E-24
252,152,934,023	4405	TT13	chr7	7	p14.1	37955396	37962766	5	0	-1.921299	-1.921299	3.874E-51
252,152,934,023	4406	TT13	chr7	7	p14.1	38216982	38219911	4	0	-1.824336	-1.824336	3.441E-42
252,152,934,023	4408	TT13	chr7	7	p14.1	38664550	38675161	6	0	-0.782831	-0.782831	1.93E-17
252,152,934,023	4409	TT13	chr7	7	p14.1	39013642	39019610	5	0	-1.367827	-1.367827	3.045E-35
252,152,934,023	4410	TT13	chr7	7	p14.1	39375303	39383606	7	0	-0.903571	-0.903571	4.197E-26
252,152,934,023	4412	TT13	chr7	7	p14.1	39599871	39667891	35	0	-0.581303	-0.581303	6.766E-49
252,152,934,023	4413	TT13	chr7	7	p14.1	39648608	39665796	9	0	-1.115309	-1.115309	3.204E-11
252,152,934,023	4415	TT13	chr7	7	p14.1	40169755	40178591	7	0	-1.079564	-1.079564	8.242E-32
252,152,934,023	4416	TT13	chr7	7	p14.1	42001870	42009427	5	0	-1.306244	-1.306244	5.512E-32
252,152,934,023	4417	TT13	chr7	7	p14.1	42265337	42279753	8	0	-1.429615	-1.429615	6.924E-59
252,152,934,023	4418	TT13	chr7	7	p14.1	42944511	42957675	8	0	-0.890983	-0.890983	4.502E-27
252,152,934,023	4419	TT13	chr7	7	p14.1	43149761	43153705	3	0	-1.726197	-1.726197	1.859E-30
252,152,934,023	4421	TT13	chr7	7	p13	43620995	43626154	5	0	-0.999888	-0.999888	2.905E-21
252,152,934,023	4422	TT13	chr7	7	p13	43796266	43801304	4	0	-1.453191	-1.453191	2.096E-30
252,152,934,023	4433	TT13	chr7	7	p13	44885763	44927821	23	0	-0.719643	-0.719643	4.371E-48
252,152,934,023	4435	TT13	chr7	7	p13	45025335	45040773	8	0	-1.618744	-1.618744	2.175E-68
252,152,934,023	4442	TT13	chr7	7	p12.3	47618471	47624157	4	0	-1.166401	-1.166401	4.665E-22
252,152,934,023	4444	TT13	chr7	7	p12.3	48072776	48077592	4	0	-1.516678	-1.516678	8.251E-34
252,152,934,023	4445	TT13	chr7	7	p12.3	48240144	48244713	3	0	-1.20151	-1.20151	4.657E-18
252,152,934,023	4446	TT13	chr7	7	p12.3	48489541	48499552	6	0	-1.000805	-1.000805	2.603E-23
252,152,934,023	4447	TT13	chr7	7	p12.2	49811104	49817512	5	0	-1.492465	-1.492465	1.06E-31
252,152,934,023	4448	TT13	chr7	7	p12.2	50124204	50138025	7	0	-0.905623	-0.905623	7.157E-26
252,152,934,023	4453	TT13	chr7	7	p12.1	50515986	50529817	6	0	-1.323896	-1.323896	2.324E-37
252,152,934,023	4454	TT13	chr7	7	p12.1	50846702	50870917	10	0	-0.762355	-0.762355	1.683E-24
252,152,934,023	4455	TT13	chr7	7	p12.1	51224195	51229224	4	0	-1.318901	-1.318901	1.752E-26
252,152,934,023	4457	TT13	chr7	7	p12.1	52338110	52343453	4	0	-1.475829	-1.475829	1.056E-26
252,152,934,023	4458	TT13	chr7	7	p12.1	53100317	53108866	6	0	-1.10312	-1.10312	2.766E-25
252,152,934,023	4464	TT13	chr7	7	p11.2	55411557	55436359	11	0	-1.072101	-1.072101	4.097E-37
252,152,934,023	4475	TT13	chr7	7	q11.21	64695012	64720967	13	0	-1.073919	-1.073919	8.605E-37
252,152,934,023	4477	TT13	chr7	7	q11.21	65667379	65672228	3	0	-1.327127	-1.327127	4.861E-16
252,152,934,023	4479	TT13	chr7	7	q11.21	66384498	66389102	3	0	-1.191004	-1.191004	8.198E-14
252,152,934,023	4480	TT13	chr7	7	q11.22	67545998	67558429	6	0	-1.340873	-1.340873	2.994E-40
252,152,934,023	4481	TT13	chr7	7	q11.22	69057753	69068374	5	0	-1.105747	-1.105747	1.084E-22
252,152,934,023	4482	TT13	chr7	7	q11.22	70059059	70063474	4	0	-1.439306	-1.439306	8.002E-27
252,152,934,023	4483	TT13	chr7	7	q11.22	70155360	70161546	4	0	-1.507371	-1.507371	2.547E-31
252,152,934,023	4484	TT13	chr7	7	q11.22	70249870	70257794	4	0	-1.186283	-1.186283	1.67E-23
252,152,934,023	4485	TT13	chr7	7	q11.22	71195656	71217971	9	0	-0.886538	-0.886538	2.142E-29
252,152,934,023	4486	TT13	chr7	7	q11.22	71798436	71803630	3	0	-1.23225	-1.23225	7.962E-19
252,152,934,023	4492	TT13	chr7	7	q11.23	73437895	73449843	7	0	-1.261161	-1.261161	1.121E-23
252,152,934,023	4494	TT13	chr7	7	q11.23	73587101	73590414	4	0	-1.751223	-1.751223	3.199E-30
252,152,934,023	4510	TT13	chr7	7	q11.23	76022217	76030630	5	0	-2.481249	-2.481249	1.902E-38
252,152,934,023	4515	TT13	chr7	7	q21.11	79760667	79767666	4	0	-1.274966	-1.274966	3.023E-25
252,152,934,023	4517	TT13	chr7	7	q21.11	82070173	82075513	3	0	-1.193693	-1.193693	7.875E-18
252,152,934,023	4518	TT13	chr7	7	q21.11	82789641	82795021	4	0	-1.465971	-1.465971	1.254E-29
252,152,934,023	4519	TT13	chr7	7	q21.11	83295506	83307014	4	0	-0.875353	-0.875353	1.355E-14
252,152,934,023	4520	TT13	chr7	7	q21.11	84505821	84512668	4	0	-1.282229	-1.282229	7.804E-24
252,152,934,023	4521	TT13	chr7	7	q21.12	86687534	86691295	3	0	-1.692301	-1.692301	6.767E-28
252,152,934,023	4522	TT13	chr7	7	q21.12	86781230	86783593	3	0	-2.080356	-2.080356	7.687E-34
252,152,934,023	4523	TT13	chr7	7	q21.12	86846419	86853927	6	0	-0.987642	-0.987642	6.852E-19
252,152,934,023	4524	TT13	chr7	7	q21.12	87100948	87108002	5	0	-0.937338	-0.937338	3.578E-18
252,152,934,023	4525	TT13	chr7	7	q21.12	87255102	87262741	4	0	-1.136233	-1.136233	4.744E-19
252,152,934,023	4527	TT13	chr7	7	q21.12	87562208	87569096	6	0	-1.155285	-1.155285	4.063E-30
252,152,934,023	4532	TT13	chr7	7	q21.13	89950062	89962227	7	0	-1.129867	-1.129867	9.334E-31
252,152,934,023	4534	TT13	chr7	7	q21.13	90370668	90378462	5	0	-1.264997	-1.264997	5.011E-29
252,152,934,023	4535	TT13	chr7	7	q21.13	90891383	90898203	4	0	-1.373057	-1.373057	6.845E-27
252,152,934,023	4538	TT13	chr7	7	q21.2	91654072	91658501	3	0	-1.670462	-1.670462	9.951E-28
252,152,934,023	4539	TT13	chr7	7	q21.2	91762030	91775520	6	0	-1.448384	-1.448384	3.381E-41
252,152,934,023	4540	TT13	chr7	7	q21.2	91806991	91810954	4	0	-1.52419	-1.52419	3.364E-29
252,152,934,023	4541	TT13	chr7	7	q21.2	91871379	91879865	5	0	-1.095906	-1.095906	7.581E-24
252,152,934,023	4542	TT13	chr7	7	q21.2	92075605	92079552	3	0	-1.185126	-1.185126	7.27E-15
252,152,934,023	4543	TT13	chr7	7	q21.2	92151435	92242253	42	0	-0.432403	-0.432403	1.023E-26
252,152,934,023	4544	TT13	chr7	7	q21.2	92458309	92468386	6	0	-1.317899	-1.317899	9.108E-31
252,152,934,023	4545	TT13	chr7	7	q21.3	93201559	93211439	6	0	-1.165762	-1.165762	2.677E-31
252,152,934,023	4552	TT13	chr7	7	q21.3	94533676	94543981	8	0	-1.162824	-1.162824	1.748E-38
252,152,934,023	4554	TT13	chr7	7	q21.3	95021504	95029425	4	0	-1.083621	-1.083621	2.3E-19
252,152,934,023	4555	TT13	chr7	7	q21.3	95062048	95067182	3	0	-1.424301	-1.424301	5.595E-21
252,152,934,023	4556	TT13	chr7	7	q21.3	95179368	95185093	4	0	-1.28161	-1.28161	3.358E-24
252,152,934,023	4557	TT13	chr7	7	q21.3	95222795	95237299	7	0	-1.062617	-1.062617	4.709E-30
252,152,934,023	4558	TT13	chr7	7	q21.3	95399344	95404902	4	0	-1.163099	-1.163099	2.344E-20
252,152,934,023	4559	TT13	chr7	7	q21.3	95851186	95863771	13	0	-0.767576	-0.767576	7.276E-29
252,152,934,023	4560	TT13	chr7	7	q21.3	95948037	95953772	4	0	-1.372954	-1.372954	5.463E-27
252,152,934,023	4561	TT13	chr7	7	q21.3	96631188	96670770	20	0	-0.80271	-0.80271	2.119E-46
252,152,934,023	4563	TT13	chr7	7	q21.3	97360668	97366305	4	0	-1.840406	-1.840406	9.07E-38
252,152,934,023	4566	TT13	chr7	7	q21.3	97832763	97844684	6	0	-1.500458	-1.500458	1.049E-39
252,152,934,023	4568	TT13	chr7	7	q22.1	98464260	98479533	7	0	-1.086568	-1.086568	2.328E-30
252,152,934,023	4570	TT13	chr7	7	q22.1	98963933	99039836	36	0	-0.5373	-0.5373	3.059E-33
252,152,934,023	4579	TT13	chr7	7	q22.1	99755365	99761053	4	0	-1.360534	-1.360534	6.332E-14
252,152,934,023	4580	TT13	chr7	7	q22.1	99974712	99983182	5	0	-0.895238	-0.895238	1.477E-21
252,152,934,023	4583	TT13	chr7	7	q22.1	100199857	100211455	6	0	-1.548314	-1.548314	2.541E-11
252,152,934,023	4584	TT13	chr7	7	q22.1	100199857	100304901	47	0	-0.758144	-0.758144	2.001E-34
252,152,934,023	4586	TT13	chr7	7	q22.1	100449705	100496262	23	0	-1.176428	-1.176428	5.851E-56
252,152,934,023	4587	TT13	chr7	7	q22.1	100454918	100458920	3	0	-0.371436	-0.371436	5.589E-10
252,152,934,023	4588	TT13	chr7	7	q22.1	100730280	100737545	5	0	-2.150619	-2.150619	9.937E-58
252,152,934,023	4589	TT13	chr7	7	q22.1	100795313	100825751	16	0	-1.181298	-1.181298	6.745E-46
252,152,934,023	4591	TT13	chr7	7	q22.1	100941667	100965945	11	0	-1.009502	-1.009502	1.553E-21
252,152,934,023	4593	TT13	chr7	7	q22.1	101455968	101462497	5	0	-1.735067	-1.735067	7.722E-35
252,152,934,023	4594	TT13	chr7	7	q22.1	101576300	101581247	4	0	-0.903759	-0.903759	7.542E-13
252,152,934,023	4595	TT13	chr7	7	q22.1	101836646	101846894	7	0	-1.166174	-1.166174	1.366E-32

252,152,934,023	4598	TT13	chr7	7	q22.1	102071880	102075405	3	0	-1.287554	-1.287554	6.87E-15
252,152,934,023	4599	TT13	chr7	7	q22.1	102095825	102332688	12	0	-1.282703	-1.282703	4.349E-59
252,152,934,023	4600	TT13	chr7	7	q22.1	102788003	102790521	3	0	-1.842355	-1.842355	5.457E-31
252,152,934,023	4609	TT13	chr7	7	q22.3	105026344	105030370	3	0	-1.842515	-1.842515	1.939E-29
252,152,934,023	4616	TT13	chr7	7	q22.3	105921597	105929388	5	0	-1.36255	-1.36255	1.204E-32
252,152,934,023	4617	TT13	chr7	7	q22.3	106294540	106304742	7	0	-1.029284	-1.029284	6.016E-29
252,152,934,023	4618	TT13	chr7	7	q22.3	106505940	106511905	5	0	-1.527945	-1.527945	8.854E-36
252,152,934,023	4619	TT13	chr7	7	q22.3	106680103	106687644	4	0	-1.525496	-1.525496	4.107E-29
252,152,934,023	4621	TT13	chr7	7	q22.3	107293710	107306417	7	0	-0.650732	-0.650732	5.666E-12
252,152,934,023	4623	TT13	chr7	7	q31.1	107485828	107493457	5	0	-1.363195	-1.363195	8.05E-33
252,152,934,023	4624	TT13	chr7	7	q31.1	107641369	107645565	3	0	-1.533325	-1.533325	5.182E-22
252,152,934,023	4626	TT13	chr7	7	q31.1	108292579	108309071	9	0	-0.802232	-0.802232	1.282E-22
252,152,934,023	4627	TT13	chr7	7	q31.1	111196626	111251515	20	0	-0.717075	-0.717075	9.152E-37
252,152,934,023	4634	TT13	chr7	7	q31.1	112655127	112659489	4	0	-1.457771	-1.457771	1.266E-30
252,152,934,023	4635	TT13	chr7	7	q31.1	112721585	112729222	6	0	-1.12313	-1.12313	8.777E-27
252,152,934,023	4636	TT13	chr7	7	q31.1	113715020	113730005	7	0	-1.641433	-1.641433	2.057E-48
252,152,934,023	4637	TT13	chr7	7	q31.1	114557354	114566274	5	0	-0.810123	-0.810123	2.324E-13
252,152,934,023	4638	TT13	chr7	7	q31.2	115113319	115121632	6	0	-0.879947	-0.879947	1.802E-17
252,152,934,023	4639	TT13	chr7	7	q31.2	115429088	115431931	3	0	-2.171062	-2.171062	3.481E-33
252,152,934,023	4640	TT13	chr7	7	q31.2	115818265	115852700	16	0	-0.587782	-0.587782	2.624E-20
252,152,934,023	4641	TT13	chr7	7	q31.2	116134200	116170141	20	0	-0.623692	-0.623692	1.242E-27
252,152,934,023	4642	TT13	chr7	7	q31.2	116276183	116279668	3	0	-1.371728	-1.371728	1.962E-21
252,152,934,023	4643	TT13	chr7	7	q31.2	116308977	116317177	7	0	-0.91776	-0.91776	6.869E-23
252,152,934,023	4644	TT13	chr7	7	q31.2	116498278	116505598	5	0	-1.203349	-1.203349	1.347E-24
252,152,934,023	4645	TT13	chr7	7	q31.2	116591420	116597335	4	0	-1.199045	-1.199045	3.447E-21
252,152,934,023	4647	TT13	chr7	7	q31.2	116959157	116968443	7	0	-1.215486	-1.215486	2.127E-33
252,152,934,023	4648	TT13	chr7	7	q31.2	117063404	117070679	5	0	-1.363309	-1.363309	4.765E-31
252,152,934,023	4649	TT13	chr7	7	q31.2	117232144	117240806	5	0	-1.324134	-1.324134	2.721E-31
252,152,934,023	4650	TT13	chr7	7	q31.31	117820867	117828852	7	0	-1.054931	-1.054931	3.354E-29
252,152,934,023	4651	TT13	chr7	7	q31.31	118496618	118502220	3	0	-1.284158	-1.284158	7.254E-19
252,152,934,023	4652	TT13	chr7	7	q31.31	119046346	119077309	10	0	-0.66739	-0.66739	1.279E-17
252,152,934,023	4653	TT13	chr7	7	q31.31	119590243	119594297	3	0	-1.929252	-1.929252	1.029E-32
252,152,934,023	4654	TT13	chr7	7	q31.31	119911666	119914266	3	0	-2.11044	-2.11044	2.036E-35
252,152,934,023	4658	TT13	chr7	7	q31.31	120692267	120704361	6	0	-0.810084	-0.810084	5.888E-16
252,152,934,023	4660	TT13	chr7	7	q31.32	121508967	121516569	5	0	-1.191916	-1.191916	1.041E-25
252,152,934,023	4662	TT13	chr7	7	q31.32	121938571	121958454	12	0	-1.761492	-1.761492	4.43E-97
252,152,934,023	4663	TT13	chr7	7	q31.32	122522790	122529674	5	0	-1.321275	-1.321275	2.284E-29
252,152,934,023	4664	TT13	chr7	7	q31.32	123384451	123409948	13	0	-0.85374	-0.85374	7.149E-35
252,152,934,023	4665	TT13	chr7	7	q31.32	123667122	123676967	6	0	-1.160419	-1.160419	3.479E-29
252,152,934,023	4666	TT13	chr7	7	q31.33	124401780	124411604	7	0	-1.033803	-1.033803	8.363E-26
252,152,934,023	4667	TT13	chr7	7	q31.33	126441363	126445036	4	0	-0.999721	-0.999721	1.343E-16
252,152,934,023	4668	TT13	chr7	7	q31.33	126593925	126603020	5	0	-0.708485	-0.708485	4.263E-11
252,152,934,023	4669	TT13	chr7	7	q31.33	126886752	126897610	6	0	-0.98881	-0.98881	5.356E-19
252,152,934,023	4670	TT13	chr7	7	q31.33	126982867	126992781	6	0	-1.224636	-1.224636	4.478E-32
252,152,934,023	4671	TT13	chr7	7	q31.33	127030294	127035994	4	0	-1.246385	-1.246385	3.331E-22
252,152,934,023	4672	TT13	chr7	7	q32.1	127224628	127230346	3	0	-1.589296	-1.589296	2.144E-23
252,152,934,023	4673	TT13	chr7	7	q32.1	127289875	127295375	4	0	-1.433239	-1.433239	5.232E-24
252,152,934,023	4687	TT13	chr7	7	q32.1	128762715	128769917	5	0	-1.125992	-1.125992	1.307E-15
252,152,934,023	4700	TT13	chr7	7	q32.2	130125921	130135743	13	0	-1.378272	-1.378272	5.222E-71
252,152,934,023	4701	TT13	chr7	7	q32.2	130352477	130355822	3	0	-1.79563	-1.79563	2.65E-29
252,152,934,023	4706	TT13	chr7	7	q32.3	131009737	131016541	5	0	-1.229574	-1.229574	7.667E-29
252,152,934,023	4707	TT13	chr7	7	q32.3	131237966	131245047	5	0	-0.846979	-0.846979	1.742E-16
252,152,934,023	4708	TT13	chr7	7	q32.3	131589070	131597623	6	0	-0.981476	-0.981476	9.268E-22
252,152,934,023	4710	TT13	chr7	7	q32.3	132298434	132302283	4	0	-1.357256	-1.357256	1.472E-25
252,152,934,023	4714	TT13	chr7	7	q33	133106010	133114120	6	0	-1.061159	-1.061159	9.288E-28
252,152,934,023	4715	TT13	chr7	7	q33	133997030	134002732	4	0	-1.421605	-1.421605	5.047E-28
252,152,934,023	4716	TT13	chr7	7	q33	134142351	134146993	3	0	-1.226246	-1.226246	9.286E-20
252,152,934,023	4718	TT13	chr7	7	q33	134928580	134935240	5	0	-1.146305	-1.146305	2.643E-25
252,152,934,023	4719	TT13	chr7	7	q33	135187187	135207894	11	0	-0.550286	-0.550286	1.986E-16
252,152,934,023	4720	TT13	chr7	7	q33	135342444	135350139	5	0	-0.878719	-0.878719	1.335E-17
252,152,934,023	4721	TT13	chr7	7	q33	135409471	135414341	4	0	-0.81402	-0.81402	6.839E-13
252,152,934,023	4722	TT13	chr7	7	q33	136551599	136563088	9	0	-0.767969	-0.767969	1.2E-21
252,152,934,023	4723	TT13	chr7	7	q33	137527137	137537400	5	0	-0.826349	-0.826349	8.334E-17
252,152,934,023	4724	TT13	chr7	7	q33	137802013	137837714	17	0	-0.7158	-0.7158	8.12E-38
252,152,934,023	4727	TT13	chr7	7	q34	138663129	138669417	4	0	-1.347872	-1.347872	5.966E-28
252,152,934,023	4728	TT13	chr7	7	q34	138715761	138725712	7	0	-0.755925	-0.755925	9.521E-18
252,152,934,023	4729	TT13	chr7	7	q34	138784854	138795965	5	0	-1.358921	-1.358921	5.638E-37
252,152,934,023	4730	TT13	chr7	7	q34	138908654	138918894	4	0	-1.647546	-1.647546	3.067E-38
252,152,934,023	4743	TT13	chr7	7	q34	140337142	140343239	4	0	-1.38664	-1.38664	1.857E-28
252,152,934,023	4744	TT13	chr7	7	q34	140370122	140379100	6	0	-1.1724	-1.1724	3.095E-31
252,152,934,023	4757	TT13	chr7	7	q35	144098121	144114023	10	0	-1.028395	-1.028395	2.94E-42
252,152,934,023	4758	TT13	chr7	7	q35	144343073	144353775	6	0	-0.857838	-0.857838	2.835E-21
252,152,934,023	4759	TT13	chr7	7	q35	144530418	144537505	4	0	-1.131969	-1.131969	2.863E-18
252,152,934,023	4760	TT13	chr7	7	q35	145047537	145066141	9	0	-0.472659	-0.472659	1.123E-10
252,152,934,023	4761	TT13	chr7	7	q35	145393053	145397672	4	0	-1.278461	-1.278461	4.524E-26
252,152,934,023	4762	TT13	chr7	7	q35	145811624	145815546	3	0	-1.466877	-1.466877	8.995E-25
252,152,934,023	4764	TT13	chr7	7	q36.1	148057076	148064774	6	0	-1.091883	-1.091883	5.665E-28
252,152,934,023	4765	TT13	chr7	7	q36.1	148119250	148149741	13	0	-0.643776	-0.643776	1.222E-24
252,152,934,023	4766	TT13	chr7	7	q36.1	148394712	148400324	4	0	-1.225807	-1.225807	1.817E-18
252,152,934,023	4783	TT13	chr7	7	q36.1	150199447	150212781	8	0	-1.059472	-1.059472	1.42E-36
252,152,934,023	4791	TT13	chr7	7	q36.1	150863253	150877386	7	0	-1.975651	-1.975651	1.791E-33
252,152,934,023	4802	TT13	chr7	7	q36.1	151566488	151576308	6	0	-1.52603	-1.52603	1.181E-43
252,152,934,023	4805	TT13	chr7	7	q36.1 - q36.2	152364002	152629830	72	0	-0.33595	-0.33595	2.362E-34
252,152,934,023	4806	TT13	chr7	7	q36.1	152370166	152375249	5	0	-1.343578	-1.343578	7.6E-20
252,152,934,023	4809	TT13	chr7	7	q36.2	153581689	153590171	6	0	-1.300405	-1.300405	8.65E-37
252,152,934,023	4810	TT13	chr7	7	q36.2	153998331	154006584	6	0	-1.069232	-1.069232	3.186E-24
252,152,934,023	4811	TT13	chr7	7	q36.2	154414974	154422121	3	0	-0.712507	-0.712507	5.206E-10
252,152,934,023	4812	TT13	chr7	7	q36.2	154583747	154588141	4	0	-1.146988	-1.146988	7.615E-20
252,152,934,023	4817	TT13	chr7	7	q36.3	155129714	155176063	22	0	-1.57027	-1.57027	4.098E-111
252,152,934,023	4818	TT13	chr7	7	q36.3	155143541	155156535	8	0	-1.011491	-1.011491	9.825E-11
252,152,934,023	4821	TT13	chr7	7	q36.3	155241210	155262168	11	0	-1.252108	-1.252108	4.481E-34
252,152,934,023	4823	TT13	chr7	7	q36.3	155434904	155440625	4	0	-1.640826	-1.640826	9.187E-30
252,152,934,023	4824	TT13	chr7	7	q36.3	155528794	155536185	6	0	-0.958933	-0.958933	1.677E-16
252,152,934,023	4825	TT13	chr7	7	q36.3	155577275	155603747	15	0	-1.464182	-1.464182	6.753E-53
252,152,934,023	4833	TT13	chr7	7	q36.3	156791205	156816588	12	0	-1.599922	-1.599922	2.019E-57
252,152,934,023	4835	TT13	chr7	7	q36.3	157125472	157133356	5	0	-1.026207	-1.026207	5.934E-15

252,152,934,023	4836	TT13	chr7	7	q36.3	157192682	158384574	617	0	-0.423905	-0.423905	4.466E-128
252,152,934,023	4837	TT13	chr7	7	q36.3	157197628	157220103	15	0	-1.284064	-1.284064	7.321E-36
252,152,934,023	4842	TT13	chr7	7	q36.3	157367248	157383037	19	0	-1.48791	-1.48791	1.715E-63
252,152,934,023	4843	TT13	chr7	7	q36.3	157407155	157410619	3	0	-2.453867	-2.453867	1.75E-27
252,152,934,023	4844	TT13	chr7	7	q36.3	157445508	157455033	6	0	-1.953362	-1.953362	7.322E-29
252,152,934,023	4859	TT13	chr7	7	q36.3	158276385	158303453	18	0	-1.217814	-1.217814	2.123E-37
252,152,934,023	4860	TT13	chr7	7	q36.3	158286800	158290277	3	0	-0.259291	-0.259291	8.158E-13
252,152,934,023	4861	TT13	chr7	7	q36.3	158342546	158379295	23	0	-0.822362	-0.822362	1.57E-15
252,152,934,023	4872	TT13	chr8	8	p23.3	485022	497628	6	0	-1.144225	-1.144225	1.035E-26
252,152,934,023	4873	TT13	chr8	8	p23.3	586338	1976636	516	0	-0.335581	-0.335581	7.424E-234
252,152,934,023	4874	TT13	chr8	8	p23.3	623287	655907	14	0	-1.007456	-1.007456	4.668E-24
252,152,934,023	4875	TT13	chr8	8	p23.3	686538	704962	9	0	-2.050316	-2.050316	5.817E-67
252,152,934,023	4880	TT13	chr8	8	p23.3	1298169	1322779	8	0	-1.445606	-1.445606	1.131E-32
252,152,934,023	4881	TT13	chr8	8	p23.3	1364248	1401604	12	0	-1.012285	-1.012285	4.08E-22
252,152,934,023	4885	TT13	chr8	8	p23.3	1770502	1802602	23	0	-1.478708	-1.478708	5.732E-89
252,152,934,023	4887	TT13	chr8	8	p23.3	2071278	2078719	5	0	-1.260777	-1.260777	2.15E-29
252,152,934,023	4888	TT13	chr8	8	p23.2	2239287	2244456	3	0	-0.937451	-0.937451	1.054E-12
252,152,934,023	4889	TT13	chr8	8	p23.2	4848712	4852686	3	0	-2.803122	-2.803122	9.558E-34
252,152,934,023	4890	TT13	chr8	8	p23.2	4854425	4858690	4	0	-0.756421	-0.756421	6.118E-10
252,152,934,023	4891	TT13	chr8	8	p23.1	6261022	6267159	4	0	-1.207223	-1.207223	1.313E-21
252,152,934,023	4892	TT13	chr8	8	p23.1	6394197	6405494	6	0	-0.95735	-0.95735	2.45E-22
252,152,934,023	4893	TT13	chr8	8	p23.1	8173844	8179070	5	0	-1.316925	-1.316925	3.312E-29
252,152,934,023	4894	TT13	chr8	8	p23.1	8237302	8247721	5	0	-1.111752	-1.111752	1.412E-22
252,152,934,023	4895	TT13	chr8	8	p23.1	8553614	8582387	14	0	-0.64318	-0.64318	6.762E-23
252,152,934,023	4899	TT13	chr8	8	p23.1	9220909	9226839	3	0	-1.193645	-1.193645	1.129E-16
252,152,934,023	4900	TT13	chr8	8	p23.1	9410458	9417866	5	0	-1.203511	-1.203511	4.036E-29
252,152,934,023	4902	TT13	chr8	8	p23.1	9910815	9914928	3	0	-1.54986	-1.54986	2.448E-25
252,152,934,023	4903	TT13	chr8	8	p23.1	10186342	10198552	8	0	-0.742688	-0.742688	1.958E-18
252,152,934,023	4904	TT13	chr8	8	p23.1	10580900	10595443	11	0	-1.440226	-1.440226	8.296E-68
252,152,934,023	4905	TT13	chr8	8	p23.1	10693804	10699685	8	0	-1.201116	-1.201116	1.398E-42
252,152,934,023	4906	TT13	chr8	8	p23.1	10871069	10876145	5	0	-1.110542	-1.110542	3.214E-20
252,152,934,023	4908	TT13	chr8	8	p23.1	11053719	11064282	7	0	-1.024211	-1.024211	7.325E-29
252,152,934,023	4909	TT13	chr8	8	p23.1	11141188	11145066	3	0	-1.169119	-1.169119	3.099E-16
252,152,934,023	4912	TT13	chr8	8	p23.1	11417938	11426839	5	0	-0.773708	-0.773708	1.239E-11
252,152,934,023	4913	TT13	chr8	8	p23.1	11536598	11567555	16	0	-1.391842	-1.391842	1.907E-83
252,152,934,023	4914	TT13	chr8	8	p23.1	11539201	11547429	5	0	-0.715481	-0.715481	6.151E-12
252,152,934,023	4915	TT13	chr8	8	p23.1	11648361	11668219	11	0	-1.643968	-1.643968	1.018E-89
252,152,934,023	4919	TT13	chr8	8	p22	12786927	12812396	13	0	-0.989727	-0.989727	2.853E-43
252,152,934,023	4920	TT13	chr8	8	p22	12795008	12803013	5	0	-0.350324	-0.350324	2.466E-10
252,152,934,023	4922	TT13	chr8	8	p22	12985674	13015678	15	0	-0.650584	-0.650584	3.057E-24
252,152,934,023	4923	TT13	chr8	8	p22	13129537	13138565	6	0	-1.088111	-1.088111	5.304E-27
252,152,934,023	4924	TT13	chr8	8	p22	14419478	14429315	6	0	-1.042926	-1.042926	1.995E-26
252,152,934,023	4925	TT13	chr8	8	p22	15092029	15097276	4	0	-1.395436	-1.395436	4.713E-27
252,152,934,023	4926	TT13	chr8	8	p22	15395070	15400507	3	0	-1.17432	-1.17432	3.22E-17
252,152,934,023	4928	TT13	chr8	8	p22	16854413	16901098	21	0	-0.850673	-0.850673	1.272E-56
252,152,934,023	4929	TT13	chr8	8	p22	16883661	16888055	3	0	-1.863316	-1.863316	2.231E-11
252,152,934,023	4948	TT13	chr8	8	p21.3	21901426	22036147	66	0	-0.678358	-0.678358	1.565E-83
252,152,934,023	4952	TT13	chr8	8	p21.3	22406971	22481245	37	0	-0.984419	-0.984419	3.18E-105
252,152,934,023	4967	TT13	chr8	8	p21.2	24770040	24774606	3	0	-1.269192	-1.269192	2.46E-18
252,152,934,023	4968	TT13	chr8	8	p21.2	24810716	24815861	4	0	-1.152768	-1.152768	2.138E-21
252,152,934,023	4969	TT13	chr8	8	p21.2	25019612	25048603	14	0	-0.661618	-0.661618	5.113E-24
252,152,934,023	4970	TT13	chr8	8	p21.2	25314671	25318025	3	0	-1.835842	-1.835842	2.837E-26
252,152,934,023	4971	TT13	chr8	8	p21.2	25525483	25529679	3	0	-1.383459	-1.383459	2.353E-20
252,152,934,023	4972	TT13	chr8	8	p21.2	25856558	25863854	6	0	-1.225032	-1.225032	4.895E-34
252,152,934,023	4973	TT13	chr8	8	p21.2	25902343	25908297	4	0	-1.603607	-1.603607	5.225E-29
252,152,934,023	4974	TT13	chr8	8	p21.2	26144516	26150312	3	0	-1.207849	-1.207849	1.391E-17
252,152,934,023	4978	TT13	chr8	8	p21.2	26716353	26729991	8	0	-0.772559	-0.772559	1.067E-21
252,152,934,023	4979	TT13	chr8	8	p21.2	27140185	27173129	15	0	-0.647791	-0.647791	4.748E-34
252,152,934,023	4980	TT13	chr8	8	p21.2	27344784	27349578	5	0	-1.189493	-1.189493	1.491E-28
252,152,934,023	4981	TT13	chr8	8	p21.1	27487862	27499756	7	0	-0.519875	-0.519875	4.029E-11
252,152,934,023	4982	TT13	chr8	8	p21.1	27777670	27781563	3	0	-1.234793	-1.234793	6.593E-21
252,152,934,023	4983	TT13	chr8	8	p21.1	28239796	28273346	17	0	-0.844277	-0.844277	1.59E-45
252,152,934,023	4985	TT13	chr8	8	p21.1	28733604	28750128	9	0	-0.774692	-0.774692	7.934E-21
252,152,934,023	4986	TT13	chr8	8	p12	28924978	28932632	5	0	-1.065873	-1.065873	1.436E-18
252,152,934,023	4987	TT13	chr8	8	p12	29116730	29123416	4	0	-1.123435	-1.123435	2.904E-18
252,152,934,023	4988	TT13	chr8	8	p12	29190763	29213589	12	0	-0.89418	-0.89418	3.587E-32
252,152,934,023	4989	TT13	chr8	8	p12	29938907	29954567	7	0	-1.371478	-1.371478	6.425E-42
252,152,934,023	4991	TT13	chr8	8	p12	30099552	30108695	4	0	-0.815552	-0.815552	2.795E-12
252,152,934,023	4992	TT13	chr8	8	p12	30239046	30244016	3	0	-1.484058	-1.484058	3.864E-24
252,152,934,023	4993	TT13	chr8	8	p12	30511086	30518129	6	0	-1.372795	-1.372795	5.072E-39
252,152,934,023	4995	TT13	chr8	8	p12	30886622	30892125	4	0	-1.335854	-1.335854	1.236E-26
252,152,934,023	4997	TT13	chr8	8	p12	32404251	32409136	3	0	-1.543735	-1.543735	9.883E-24
252,152,934,023	5001	TT13	chr8	8	p12	33578148	33586602	3	0	-1.020994	-1.020994	8.616E-14
252,152,934,023	5011	TT13	chr8	8	p11.23	38232915	38248784	7	0	-1.189349	-1.189349	9.203E-36
252,152,934,023	5016	TT13	chr8	8	p11.22	38823746	38861270	20	0	-0.670959	-0.670959	1.005E-32
252,152,934,023	5018	TT13	chr8	8	p11.22	39378357	39385234	4	0	-1.785048	-1.785048	2.574E-34
252,152,934,023	5023	TT13	chr8	8	p11.21	41475883	41513334	24	0	-0.816707	-0.816707	2.539E-49
252,152,934,023	5024	TT13	chr8	8	p11.21	41508316	41512329	4	0	-2.139401	-2.139401	1.651E-15
252,152,934,023	5025	TT13	chr8	8	p11.21	41551241	41556129	3	0	-1.099647	-1.099647	6.651E-14
252,152,934,023	5026	TT13	chr8	8	p11.21	41580502	41585225	4	0	-1.319007	-1.319007	8.264E-24
252,152,934,023	5039	TT13	chr8	8	p11.1	43125662	43148965	12	0	-1.113063	-1.113063	2.649E-27
252,152,934,023	5047	TT13	chr8	8	q11.21	49617399	49651550	15	0	-0.959378	-0.959378	2.573E-46
252,152,934,023	5048	TT13	chr8	8	q11.21	49635141	49641497	4	0	-0.281501	-0.281501	6.193E-10
252,152,934,023	5054	TT13	chr8	8	q11.22	52318787	52322743	3	0	-2.51312	-2.51312	4.833E-41
252,152,934,023	5055	TT13	chr8	8	q11.22	52442864	52455456	6	0	-1.086114	-1.086114	6.348E-27
252,152,934,023	5056	TT13	chr8	8	q11.23	52808033	52814362	4	0	-1.253781	-1.253781	1.666E-21
252,152,934,023	5058	TT13	chr8	8	q11.23	53477427	53487201	4	0	-1.804531	-1.804531	7.519E-29
252,152,934,023	5060	TT13	chr8	8	q11.23	53848366	53884039	12	0	-1.123541	-1.123541	2.232E-52
252,152,934,023	5063	TT13	chr8	8	q11.23	54789131	54795621	5	0	-2.186746	-2.186746	2.191E-37
252,152,934,023	5067	TT13	chr8	8	q11.23	54995799	55048867	18	0	-0.935999	-0.935999	5.682E-55
252,152,934,023	5068	TT13	chr8	8	q11.23	55363955	55383329	9	0	-1.475087	-1.475087	9.935E-52
252,152,934,023	5069	TT13	chr8	8	q12.1	55530523	55538079	5	0	-1.223362	-1.223362	1.841E-28
252,152,934,023	5070	TT13	chr8	8	q12.1	56012260	56017767	5	0	-1.381062	-1.381062	3.921E-23
252,152,934,023	5071	TT13	chr8	8	q12.1	56682642	56688441	4	0	-1.289466	-1.289466	1.613E-22
252,152,934,023	5072	TT13	chr8	8	q12.1	56790942	56796645	4	0	-1.377487	-1.377487	3.071E-25
252,152,934,023	5073	TT13	chr8	8	q12.1	57013893	57032778	9	0	-1.186056	-1.186056	1.315E-45

252,152,934,023	5088	TT13	chr8	8	q12.1	61588520	61593702	3	0	-1.651208	-1.651208	1.569E-26
252,152,934,023	5089	TT13	chr8	8	q12.2	61623073	61629596	5	0	-1.159295	-1.159295	1.314E-24
252,152,934,023	5091	TT13	chr8	8	q12.3	63156756	63166711	5	0	-1.148525	-1.148525	1.924E-24
252,152,934,023	5097	TT13	chr8	8	q12.3	65280685	65290129	12	0	-1.205511	-1.205511	1.385E-53
252,152,934,023	5109	TT13	chr8	8	q13.1	67684168	67689711	5	0	-1.5064	-1.5064	2.028E-35
252,152,934,023	5119	TT13	chr8	8	q13.3	70742470	70749418	5	0	-1.471182	-1.471182	3.612E-34
252,152,934,023	5120	TT13	chr8	8	q13.3	70980737	70985412	3	0	-1.803511	-1.803511	1.842E-27
252,152,934,023	5121	TT13	chr8	8	q13.3	71309017	71320250	7	0	-1.09472	-1.09472	7.961E-31
252,152,934,023	5122	TT13	chr8	8	q13.3	71576227	71586987	5	0	-0.955903	-0.955903	3.18E-18
252,152,934,023	5123	TT13	chr8	8	q13.3	72271816	72275362	3	0	-1.067282	-1.067282	1.424E-14
252,152,934,023	5124	TT13	chr8	8	q13.3	72455961	72471656	5	0	-1.393668	-1.393668	1.468E-32
252,152,934,023	5130	TT13	chr8	8	q21.11	74197122	74209228	6	0	-1.588684	-1.588684	1.386E-46
252,152,934,023	5131	TT13	chr8	8	q21.11	74787392	74792841	4	0	-1.372411	-1.372411	5.654E-28
252,152,934,023	5132	TT13	chr8	8	q21.11	74887278	74891044	3	0	-1.546632	-1.546632	5.599E-22
252,152,934,023	5133	TT13	chr8	8	q21.11	75222746	75236394	7	0	-1.240606	-1.240606	8.71E-35
252,152,934,023	5135	TT13	chr8	8	q21.11	77586735	77598066	6	0	-1.758306	-1.758306	9.231E-49
252,152,934,023	5142	TT13	chr8	8	q21.13	81396247	81402832	4	0	-1.297539	-1.297539	8.892E-24
252,152,934,023	5144	TT13	chr8	8	q21.13	81784315	81789677	3	0	-1.443316	-1.443316	3.826E-20
252,152,934,023	5145	TT13	chr8	8	q21.13	82431666	82439088	5	0	-1.395663	-1.395663	8.191E-31
252,152,934,023	5146	TT13	chr8	8	q21.13	82630359	82646435	8	0	-0.974925	-0.974925	2.389E-30
252,152,934,023	5148	TT13	chr8	8	q21.2	85093859	85098303	3	0	-2.051191	-2.051191	4.052E-33
252,152,934,023	5149	TT13	chr8	8	q21.2	86018738	86021757	3	0	-1.109328	-1.109328	6.361E-15
252,152,934,023	5150	TT13	chr8	8	q21.2	86086087	86091715	4	0	-1.71277	-1.71277	1.942E-35
252,152,934,023	5154	TT13	chr8	8	q21.3	87078226	87084919	5	0	-1.304818	-1.304818	1.995E-30
252,152,934,023	5155	TT13	chr8	8	q21.3	87353171	87357427	4	0	-1.638917	-1.638917	4.447E-19
252,152,934,023	5156	TT13	chr8	8	q21.3	87353171	87447987	48	0	-0.485859	-0.485859	4.992E-38
252,152,934,023	5157	TT13	chr8	8	q21.3	87399572	87404756	4	0	-1.479923	-1.479923	4.169E-16
252,152,934,023	5163	TT13	chr8	8	q21.3	90992941	90999106	4	0	-1.40407	-1.40407	6.834E-28
252,152,934,023	5164	TT13	chr8	8	q21.3	91608726	91664687	24	0	-0.559657	-0.559657	9.006E-27
252,152,934,023	5177	TT13	chr8	8	q22.1	97152788	97177902	14	0	-0.865661	-0.865661	5.174E-33
252,152,934,023	5178	TT13	chr8	8	q22.1	97271621	97277370	5	0	-1.446138	-1.446138	4.736E-29
252,152,934,023	5179	TT13	chr8	8	q22.1	97500171	97510244	6	0	-0.969045	-0.969045	6.219E-21
252,152,934,023	5180	TT13	chr8	8	q22.1	97542191	97553101	6	0	-0.851162	-0.851162	1.539E-17
252,152,934,023	5181	TT13	chr8	8	q22.1	97655452	97658719	3	0	-1.862291	-1.862291	8.013E-31
252,152,934,023	5182	TT13	chr8	8	q22.1	98283968	98292297	5	0	-1.052008	-1.052008	1.902E-19
252,152,934,023	5187	TT13	chr8	8	q22.2	99061346	99080725	10	0	-1.083129	-1.083129	3.28E-42
252,152,934,023	5196	TT13	chr8	8	q22.2	101155484	101174677	10	0	-1.263248	-1.263248	2.626E-53
252,152,934,023	5219	TT13	chr8	8	q22.3	105477570	105479839	3	0	-2.186842	-2.186842	1.429E-34
252,152,934,023	5220	TT13	chr8	8	q22.3	105594397	105604913	6	0	-0.987837	-0.987837	2.954E-23
252,152,934,023	5221	TT13	chr8	8	q23.1	106331591	106335008	3	0	-1.860943	-1.860943	1.503E-27
252,152,934,023	5222	TT13	chr8	8	q23.1	106396205	106403256	5	0	-1.215502	-1.215502	1.757E-25
252,152,934,023	5223	TT13	chr8	8	q23.1	107280540	107284366	4	0	-1.427765	-1.427765	4.534E-28
252,152,934,023	5224	TT13	chr8	8	q23.1	107668097	107676376	5	0	-1.018008	-1.018008	4.724E-19
252,152,934,023	5225	TT13	chr8	8	q23.1	109091820	109099704	6	0	-0.867988	-0.867988	2.603E-17
252,152,934,023	5226	TT13	chr8	8	q23.1	109796016	109803032	5	0	-1.019095	-1.019095	9.69E-18
252,152,934,023	5227	TT13	chr8	8	q23.2	110549771	110555691	5	0	-1.537411	-1.537411	5.915E-40
252,152,934,023	5228	TT13	chr8	8	q23.2	110651702	110660826	6	0	-1.007725	-1.007725	1.008E-24
252,152,934,023	5229	TT13	chr8	8	q23.2	110697087	110707538	7	0	-1.082453	-1.082453	1.272E-29
252,152,934,023	5230	TT13	chr8	8	q23.2	110984176	110989973	4	0	-1.087876	-1.087876	1.839E-18
252,152,934,023	5231	TT13	chr8	8	q23.3	114384276	114394843	7	0	-1.182327	-1.182327	1.125E-35
252,152,934,023	5232	TT13	chr8	8	q23.3	116657756	116684743	15	0	-0.842772	-0.842772	2.482E-39
252,152,934,023	5233	TT13	chr8	8	q23.3	117308897	117313643	3	0	-1.313957	-1.313957	1.758E-19
252,152,934,023	5234	TT13	chr8	8	q23.3	117685121	117694251	5	0	-1.117649	-1.117649	1.019E-23
252,152,934,023	5237	TT13	chr8	8	q24.11	118528015	118540684	5	0	-0.744454	-0.744454	1.309E-13
252,152,934,023	5238	TT13	chr8	8	q24.11	119084816	119089742	4	0	-1.458664	-1.458664	1.069E-31
252,152,934,023	5239	TT13	chr8	8	q24.11	119120552	119125752	3	0	-1.140624	-1.140624	6.894E-16
252,152,934,023	5240	TT13	chr8	8	q24.12	120219767	120228381	5	0	-0.962986	-0.962986	1.473E-20
252,152,934,023	5241	TT13	chr8	8	q24.12	120427379	120432364	4	0	-1.133645	-1.133645	1.04E-21
252,152,934,023	5242	TT13	chr8	8	q24.12	120862782	120893922	17	0	-0.729385	-0.729385	6.884E-39
252,152,934,023	5243	TT13	chr8	8	q24.12	121819387	121826895	5	0	-1.12555	-1.12555	6.695E-24
252,152,934,023	5244	TT13	chr8	8	q24.13	122649044	122684694	13	0	-0.880328	-0.880328	3.963E-43
252,152,934,023	5245	TT13	chr8	8	q24.13	123791277	123796116	4	0	-1.391549	-1.391549	1.191E-23
252,152,934,023	5246	TT13	chr8	8	q24.13	124083184	124089416	5	0	-1.384023	-1.384023	1.048E-36
252,152,934,023	5252	TT13	chr8	8	q24.13	124427780	124431770	3	0	-1.639016	-1.639016	2.285E-18
252,152,934,023	5254	TT13	chr8	8	q24.13	124778948	124783326	3	0	-1.71736	-1.71736	5.729E-31
252,152,934,023	5258	TT13	chr8	8	q24.13	126098059	126110098	8	0	-0.906166	-0.906166	8.214E-31
252,152,934,023	5263	TT13	chr8	8	q24.21	129832907	129842186	6	0	-1.177486	-1.177486	2.675E-35
252,152,934,023	5264	TT13	chr8	8	q24.21	130992197	130997839	4	0	-1.23064	-1.23064	8.96E-26
252,152,934,023	5265	TT13	chr8	8	q24.21	131025093	131029820	3	0	-1.175138	-1.175138	2.969E-18
252,152,934,023	5266	TT13	chr8	8	q24.21	131366679	131374048	4	0	-1.127464	-1.127464	8.371E-23
252,152,934,023	5267	TT13	chr8	8	q24.22	132047991	132061191	8	0	-0.909546	-0.909546	1.888E-27
252,152,934,023	5269	TT13	chr8	8	q24.22	133257265	133264227	5	0	-1.361083	-1.361083	1.083E-35
252,152,934,023	5270	TT13	chr8	8	q24.22	133486414	133497404	5	0	-0.795989	-0.795989	1.717E-16
252,152,934,023	5271	TT13	chr8	8	q24.22	133688275	133691180	3	0	-1.029791	-1.029791	3.928E-16
252,152,934,023	5272	TT13	chr8	8	q24.22	133782374	133792128	6	0	-0.878384	-0.878384	5.683E-22
252,152,934,023	5273	TT13	chr8	8	q24.22	134228521	134255245	15	0	-0.596845	-0.596845	1.816E-26
252,152,934,023	5274	TT13	chr8	8	q24.22	134764544	134777476	7	0	-0.82063	-0.82063	1.071E-23
252,152,934,023	5275	TT13	chr8	8	q24.22	135721867	135729524	5	0	-1.081272	-1.081272	5.667E-25
252,152,934,023	5276	TT13	chr8	8	q24.22	135839104	135851593	7	0	-1.07638	-1.07638	3.622E-36
252,152,934,023	5280	TT13	chr8	8	q24.23	139505652	139512552	5	0	-1.209612	-1.209612	2.202E-30
252,152,934,023	5281	TT13	chr8	8	q24.23	139889627	139893144	3	0	-1.445048	-1.445048	3.468E-19
252,152,934,023	5282	TT13	chr8	8	q24.3	139924022	139928769	4	0	-0.730995	-0.730995	5.665E-12
252,152,934,023	5283	TT13	chr8	8	q24.3	140638231	140644369	4	0	-0.764531	-0.764531	5.878E-13
252,152,934,023	5284	TT13	chr8	8	q24.3	140712187	140750530	22	0	-0.410028	-0.410028	1.245E-18
252,152,934,023	5287	TT13	chr8	8	q24.3	141461824	141530438	28	0	-0.636991	-0.636991	1.703E-47
252,152,934,023	5288	TT13	chr8	8	q24.3	141466604	141476942	5	0	-1.525407	-1.525407	1.672E-14
252,152,934,023	5293	TT13	chr8	8	q24.3	142204597	142484760	110	0	-0.516651	-0.516651	8.741E-108
252,152,934,023	5294	TT13	chr8	8	q24.3	142215121	142243427	16	0	-1.446751	-1.446751	2.788E-40
252,152,934,023	5295	TT13	chr8	8	q24.3	142285947	142294684	4	0	-1.406707	-1.406707	1.039E-11
252,152,934,023	5296	TT13	chr8	8	q24.3	142420401	142441579	8	0	-1.459221	-1.459221	1.633E-19
252,152,934,023	5299	TT13	chr8	8	q24.3	143314534	143922629	230	0	-0.368246	-0.368246	7.33E-110
252,152,934,023	5300	TT13	chr8	8	q24.3	143427853	143432613	3	0	-2.461424	-2.461424	1.397E-28
252,152,934,023	5301	TT13	chr8	8	q24.3	143780930	143785049	3	0	-1.736928	-1.736928	9.612E-19
252,152,934,023	5316	TT13	chr8	8	q24.3	145255770	145262644	5	0	-0.924496	-0.924496	7.2E-10
252,152,934,023	5317	TT13	chr8	8	q24.3	145502945	145516146	7	0	-2.297775	-2.297775	8.938E-39
252,152,934,023	5318	TT13	chr8	8	q24.3	145631418	145675373	20	0	-1.099885	-1.099885	4.005E-11

252,152,934,023	5327	TT13	chr9	9	p24.3	970432	978104	5	0	-2.117088	-2.117088	4.696E-48
252,152,934,023	5332	TT13	chr9	9	p24.3	2045009	2048624	3	0	-1.808196	-1.808196	2.822E-13
252,152,934,023	5333	TT13	chr9	9	p24.2	2620066	2625282	3	0	-1.296764	-1.296764	2.562E-16
252,152,934,023	5335	TT13	chr9	9	p24.2	2929119	2938331	5	0	-0.944004	-0.944004	1.717E-19
252,152,934,023	5336	TT13	chr9	9	p24.2	3519377	3529354	6	0	-0.928906	-0.928906	5.396E-23
252,152,934,023	5337	TT13	chr9	9	p24.2	3729564	3738475	4	0	-0.961936	-0.961936	2.967E-16
252,152,934,023	5339	TT13	chr9	9	p24.2	4296652	4300987	3	0	-2.079122	-2.079122	3.194E-34
252,152,934,023	5340	TT13	chr9	9	p24.2	4487597	4492250	3	0	-1.239529	-1.239529	1.228E-17
252,152,934,023	5342	TT13	chr9	9	p24.1	4739106	4743687	3	0	-1.358219	-1.358219	8.61E-19
252,152,934,023	5343	TT13	chr9	9	p24.1	4791853	4808850	9	0	-1.059203	-1.059203	1.867E-34
252,152,934,023	5344	TT13	chr9	9	p24.1	4977083	5192042	73	0	-0.484152	-0.484152	8.786E-56
252,152,934,023	5345	TT13	chr9	9	p24.1	4983600	4988005	3	0	-1.674544	-1.674544	6.505E-15
252,152,934,023	5349	TT13	chr9	9	p24.1	5430769	5455434	12	0	-1.086518	-1.086518	9.613E-50
252,152,934,023	5350	TT13	chr9	9	p24.1	5432421	5438240	3	0	-2.343244	-2.343244	9.987E-13
252,152,934,023	5353	TT13	chr9	9	p24.1	6618048	6650002	16	0	-0.735514	-0.735514	2.07E-31
252,152,934,023	5355	TT13	chr9	9	p24.1	6946042	6951762	4	0	-1.577509	-1.577509	4.8E-34
252,152,934,023	5356	TT13	chr9	9	p24.1	8855658	8860210	4	0	-1.458282	-1.458282	1.256E-31
252,152,934,023	5357	TT13	chr9	9	p23	10446984	10451012	3	0	-1.29459	-1.29459	1.646E-19
252,152,934,023	5358	TT13	chr9	9	p23	10610765	10616408	3	0	-1.361385	-1.361385	1.267E-22
252,152,934,023	5359	TT13	chr9	9	p23	10831676	10840093	5	0	-0.974443	-0.974443	3.321E-21
252,152,934,023	5361	TT13	chr9	9	p22.3	14311332	14323744	6	0	-2.111454	-2.111454	2.467E-63
252,152,934,023	5362	TT13	chr9	9	p22.3	14691082	14697187	5	0	-1.28715	-1.28715	1.286E-29
252,152,934,023	5364	TT13	chr9	9	p22.3	15403983	15448258	17	0	-0.723533	-0.723533	6.602E-32
252,152,934,023	5365	TT13	chr9	9	p22.3	15505449	15555541	25	0	-0.735346	-0.735346	1.432E-46
252,152,934,023	5366	TT13	chr9	9	p22.3	15507965	15512130	3	0	-1.647075	-1.647075	6.528E-10
252,152,934,023	5367	TT13	chr9	9	p22.3	15809225	15812314	3	0	-1.847869	-1.847869	5.674E-31
252,152,934,023	5372	TT13	chr9	9	p22.2	17133390	17137839	3	0	-1.456652	-1.456652	4.777E-18
252,152,934,023	5373	TT13	chr9	9	p22.2	17295644	17297547	3	0	-1.617523	-1.617523	2.774E-20
252,152,934,023	5376	TT13	chr9	9	p22.1	19028558	19052754	11	0	-0.762196	-0.762196	5.458E-24
252,152,934,023	5380	TT13	chr9	9	p22.1	19785974	19791545	4	0	-1.428898	-1.428898	6.484E-29
252,152,934,023	5387	TT13	chr9	9	p21.3	21954646	22011741	34	0	-1.091326	-1.091326	6.879E-124
252,152,934,023	5388	TT13	chr9	9	p21.3	21957735	21961821	4	0	-2.248739	-2.248739	5.192E-15
252,152,934,023	5389	TT13	chr9	9	p21.3	22004984	22008226	3	0	-2.316734	-2.316734	5.894E-12
252,152,934,023	5405	TT13	chr9	9	p21.1	33020467	33030968	6	0	-1.362792	-1.362792	1.358E-37
252,152,934,023	5419	TT13	chr9	9	p13.3	34934330	34962640	14	0	-0.844724	-0.844724	2.706E-22
252,152,934,023	5420	TT13	chr9	9	p13.3	35069957	35073894	3	0	-1.612778	-1.612778	8.327E-20
252,152,934,023	5423	TT13	chr9	9	p13.3	35489657	35492529	3	0	-1.456565	-1.456565	1.331E-18
252,152,934,023	5424	TT13	chr9	9	p13.3	35602918	35616410	9	0	-1.104738	-1.104738	7.356E-21
252,152,934,023	5425	TT13	chr9	9	p13.3	35644670	35691600	28	0	-0.945671	-0.945671	1.165E-49
252,152,934,023	5430	TT13	chr9	9	p13.3	36163040	36195314	12	0	-0.946444	-0.946444	1.225E-35
252,152,934,023	5431	TT13	chr9	9	p13.3	36251581	36262270	6	0	-0.73113	-0.73113	1.028E-11
252,152,934,023	5436	TT13	chr9	9	p13.2	36983817	36987957	3	0	-1.753628	-1.753628	1.464E-10
252,152,934,023	5437	TT13	chr9	9	p13.2	36983817	37040069	29	0	-0.640872	-0.640872	4.527E-39
252,152,934,023	5442	TT13	chr9	9	p13.2	37573876	37582591	6	0	-1.158267	-1.158267	4.467E-29
252,152,934,023	5444	TT13	chr9	9	p13.2	37781956	37803716	12	0	-1.180796	-1.180796	1.209E-53
252,152,934,023	5445	TT13	chr9	9	p13.2	37889150	37905988	9	0	-1.198468	-1.198468	9.05E-43
252,152,934,023	5446	TT13	chr9	9	p13.2	38066163	38079534	5	0	-0.944959	-0.944959	1.027E-17
252,152,934,023	5447	TT13	chr9	9	p13.2	38375232	38394815	11	0	-0.898816	-0.898816	9.831E-37
252,152,934,023	5453	TT13	chr9	9	q21.11	71623658	71655249	17	0	-0.61604	-0.61604	1.032E-23
252,152,934,023	5454	TT13	chr9	9	q21.11	71786564	71791557	4	0	-1.699181	-1.699181	6.656E-31
252,152,934,023	5455	TT13	chr9	9	q21.11	71937907	71942782	4	0	-1.608688	-1.608688	3.233E-32
252,152,934,023	5456	TT13	chr9	9	q21.11	72128514	72133993	4	0	-1.643947	-1.643947	5.536E-33
252,152,934,023	5458	TT13	chr9	9	q21.12	72371066	72377352	4	0	-1.506414	-1.506414	7.01E-29
252,152,934,023	5459	TT13	chr9	9	q21.12	72658291	72660838	3	0	-1.163408	-1.163408	1.796E-15
252,152,934,023	5460	TT13	chr9	9	q21.12	72869164	72878485	6	0	-1.042018	-1.042018	2.389E-24
252,152,934,023	5461	TT13	chr9	9	q21.12	73026563	73033741	4	0	-1.891887	-1.891887	9.404E-41
252,152,934,023	5462	TT13	chr9	9	q21.13	74058483	74067521	5	0	-1.079422	-1.079422	4.567E-23
252,152,934,023	5464	TT13	chr9	9	q21.13	74523511	74526990	3	0	-1.878366	-1.878366	5.115E-31
252,152,934,023	5466	TT13	chr9	9	q21.13	74760714	74767246	5	0	-1.131196	-1.131196	1.016E-23
252,152,934,023	5467	TT13	chr9	9	q21.13	74976791	74982048	3	0	-1.419806	-1.419806	3.495E-21
252,152,934,023	5468	TT13	chr9	9	q21.13	75091304	75096406	3	0	-1.188694	-1.188694	7.143E-17
252,152,934,023	5469	TT13	chr9	9	q21.13	75454139	75467343	4	0	-1.674451	-1.674451	1.663E-35
252,152,934,023	5474	TT13	chr9	9	q21.13	78501765	78508622	5	0	-1.197008	-1.197008	8.741E-27
252,152,934,023	5475	TT13	chr9	9	q21.13	78672175	78684062	7	0	-0.699096	-0.699096	3.919E-14
252,152,934,023	5476	TT13	chr9	9	q21.13	79005855	79010332	3	0	-1.215533	-1.215533	1.039E-17
252,152,934,023	5477	TT13	chr9	9	q21.13	79070918	79077046	4	0	-1.280474	-1.280474	1.551E-23
252,152,934,023	5478	TT13	chr9	9	q21.13	79136670	79145572	6	0	-1.88856	-1.88856	5.121E-56
252,152,934,023	5481	TT13	chr9	9	q21.2	79629435	79640217	6	0	-1.687973	-1.687973	9.085E-42
252,152,934,023	5482	TT13	chr9	9	q21.2	79790140	79797656	3	0	-1.271723	-1.271723	3.428E-18
252,152,934,023	5483	TT13	chr9	9	q21.2	80102496	80107615	3	0	-1.027448	-1.027448	5.841E-14
252,152,934,023	5484	TT13	chr9	9	q21.2	80261645	80264786	3	0	-1.155462	-1.155462	5.818E-15
252,152,934,023	5487	TT13	chr9	9	q21.2	80848919	80854092	4	0	-1.329191	-1.329191	2.038E-26
252,152,934,023	5489	TT13	chr9	9	q21.31	82004557	82008678	3	0	-1.007442	-1.007442	3.976E-13
252,152,934,023	5490	TT13	chr9	9	q21.31	82187027	82190691	3	0	-1.528596	-1.528596	4.601E-23
252,152,934,023	5492	TT13	chr9	9	q21.32	84300213	84308713	5	0	-1.287282	-1.287282	1.523E-30
252,152,934,023	5493	TT13	chr9	9	q21.32	84589561	84595992	5	0	-1.115097	-1.115097	1.156E-22
252,152,934,023	5494	TT13	chr9	9	q21.32	84662701	84668029	3	0	-0.938795	-0.938795	8.395E-12
252,152,934,023	5502	TT13	chr9	9	q21.33	87006706	87026758	6	0	-0.827192	-0.827192	8.768E-17
252,152,934,023	5503	TT13	chr9	9	q21.33	87282139	87286592	3	0	-2.033561	-2.033561	2.674E-34
252,152,934,023	5523	TT13	chr9	9	q22.2	91922590	91939512	9	0	-1.325178	-1.325178	3.163E-48
252,152,934,023	5524	TT13	chr9	9	q22.2	92078508	92111604	15	0	-0.767897	-0.767897	7.388E-32
252,152,934,023	5529	TT13	chr9	9	q22.31	94165574	94187906	10	0	-1.390319	-1.390319	8.206E-56
252,152,934,023	5533	TT13	chr9	9	q22.31	94988415	94991899	3	0	-1.460207	-1.460207	1.986E-22
252,152,934,023	5534	TT13	chr9	9	q22.31	95084195	95091440	5	0	-1.197521	-1.197521	3.55E-26
252,152,934,023	5542	TT13	chr9	9	q22.31	96010177	96018246	5	0	-2.105261	-2.105261	1.402E-17
252,152,934,023	5543	TT13	chr9	9	q22.31	96010177	96080532	32	0	-0.909966	-0.909966	1.092E-77
252,152,934,023	5546	TT13	chr9	9	q22.31	96328612	96341179	8	0	-0.963266	-0.963266	7.293E-25
252,152,934,023	5550	TT13	chr9	9	q22.32	96926852	96934945	8	0	-1.1146	-1.1146	4.227E-36
252,152,934,023	5551	TT13	chr9	9	q22.32	97399440	97403884	4	0	-1.127358	-1.127358	1.196E-15
252,152,934,023	5555	TT13	chr9	9	q22.32	97860162	97864899	6	0	-2.064707	-2.064707	2.688E-60
252,152,934,023	5556	TT13	chr9	9	q22.32	98052971	98058562	3	0	-0.961932	-0.961932	2.83E-12
252,152,934,023	5557	TT13	chr9	9	q22.32	98078300	98081531	3	0	-1.927378	-1.927378	2.59E-32
252,152,934,023	5559	TT13	chr9	9	q22.32	98253397	98280517	15	0	-1.342228	-1.342228	8.964E-77
252,152,934,023	5562	TT13	chr9	9	q22.32	98760080	98792062	15	0	-0.872282	-0.872282	4.035E-37
252,152,934,023	5563	TT13	chr9	9	q22.32	98786613	98790524	3	0	-2.205664	-2.205664	4.217E-14
252,152,934,023	5571	TT13	chr9	9	q22.33	99448387	99483928	10	0	-1.46604	-1.46604	3.944E-65

252,152,934,023	5575	TT13	chr9	9	q22.33	100258515	100265778	5	0	-1.909938	-1.909938	1.175E-46
252,152,934,023	5581	TT13	chr9	9	q22.33	100879432	100883527	4	0	-1.463897	-1.463897	3.866E-27
252,152,934,023	5583	TT13	chr9	9	q22.33	101217475	101237975	10	0	-0.348324	-0.348324	2.843E-12
252,152,934,023	5584	TT13	chr9	9	q22.33	101467897	101472314	3	0	-1.431563	-1.431563	1.236E-15
252,152,934,023	5585	TT13	chr9	9	q22.33	101550148	101573553	13	0	-1.144934	-1.144934	1.624E-55
252,152,934,023	5588	TT13	chr9	9	q22.33	102055528	102060019	3	0	-1.560607	-1.560607	6.104E-24
252,152,934,023	5589	TT13	chr9	9	q22.33	102580589	102593896	7	0	-1.805762	-1.805762	1.239E-61
252,152,934,023	5597	TT13	chr9	9	q31.1	104245794	104252214	4	0	-1.408103	-1.408103	3.176E-28
252,152,934,023	5598	TT13	chr9	9	q31.1	104480536	104504065	11	0	-0.932541	-0.932541	1.794E-36
252,152,934,023	5603	TT13	chr9	9	q31.1	107507403	107528732	11	0	-0.954093	-0.954093	1.346E-36
252,152,934,023	5628	TT13	chr9	9	q31.3	114360123	114429342	35	0	-0.855693	-0.855693	9.366E-91
252,152,934,023	5629	TT13	chr9	9	q31.3	114392312	114405579	7	0	-1.421704	-1.421704	4.752E-10
252,152,934,023	5630	TT13	chr9	9	q31.3	114654696	114661591	3	0	-1.260469	-1.260469	1.037E-18
252,152,934,023	5632	TT13	chr9	9	q32	115242307	115252623	6	0	-1.315512	-1.315512	6.656E-35
252,152,934,023	5633	TT13	chr9	9	q32	115510485	115515536	4	0	-1.296642	-1.296642	2.2E-21
252,152,934,023	5635	TT13	chr9	9	q32	115648438	115655749	5	0	-1.213595	-1.213595	4.793E-26
252,152,934,023	5637	TT13	chr9	9	q32	116097894	116174885	35	0	-0.605313	-0.605313	2.53E-44
252,152,934,023	5638	TT13	chr9	9	q32	116102819	116113138	6	0	-1.41989	-1.41989	4.328E-15
252,152,934,023	5642	TT13	chr9	9	q32	116607623	116642488	16	0	-0.617102	-0.617102	1.202E-22
252,152,934,023	5645	TT13	chr9	9	q32	116912867	116932991	10	0	-0.960701	-0.960701	1.663E-31
252,152,934,023	5650	TT13	chr9	9	q33.1	118912806	118920303	5	0	-1.284355	-1.284355	3.31E-31
252,152,934,023	5651	TT13	chr9	9	q33.1	119447778	119452882	4	0	-1.402047	-1.402047	1.916E-29
252,152,934,023	5652	TT13	chr9	9	q33.1	119597370	119603895	4	0	-1.061643	-1.061643	2.65E-20
252,152,934,023	5654	TT13	chr9	9	q33.1	122124690	122133782	6	0	-0.932995	-0.932995	3.012E-23
252,152,934,023	5656	TT13	chr9	9	q33.2	123474921	123478784	3	0	-1.629801	-1.629801	7.897E-25
252,152,934,023	5659	TT13	chr9	9	q33.2	123628684	123659184	16	0	-0.858386	-0.858386	2.07E-39
252,152,934,023	5662	TT13	chr9	9	q33.2	123959840	123966332	4	0	-1.47933	-1.47933	9.908E-29
252,152,934,023	5664	TT13	chr9	9	q33.2	124260000	124262871	3	0	-1.399903	-1.399903	9.967E-20
252,152,934,023	5669	TT13	chr9	9	q33.2	124973814	124992222	10	0	-1.033022	-1.033022	2.848E-30
252,152,934,023	5671	TT13	chr9	9	q33.2	125097489	125110235	6	0	-1.332264	-1.332264	2.067E-36
252,152,934,023	5673	TT13	chr9	9	q33.2	125663023	125670460	5	0	-0.993965	-0.993965	3.757E-20
252,152,934,023	5676	TT13	chr9	9	q33.3	126117303	126146504	16	0	-0.867683	-0.867683	1.236E-29
252,152,934,023	5677	TT13	chr9	9	q33.3	126758344	126810130	26	0	-1.103344	-1.103344	6.868E-89
252,152,934,023	5678	TT13	chr9	9	q33.3	126769022	126780439	7	0	-2.218071	-2.218071	3.411E-17
252,152,934,023	5684	TT13	chr9	9	q33.3	127359334	127364589	4	0	-1.433422	-1.433422	3.679E-29
252,152,934,023	5685	TT13	chr9	9	q33.3	127533747	127538325	4	0	-1.762616	-1.762616	5.123E-32
252,152,934,023	5686	TT13	chr9	9	q33.3	127597888	127632867	18	0	-1.010947	-1.010947	2.579E-60
252,152,934,023	5692	TT13	chr9	9	q33.3	128088724	128091579	3	0	-1.936738	-1.936738	3.356E-31
252,152,934,023	5699	TT13	chr9	9	q33.3	128649033	128654591	5	0	-1.5925	-1.5925	6.916E-44
252,152,934,023	5700	TT13	chr9	9	q33.3	129086622	129101516	8	0	-1.250112	-1.250112	1.526E-39
252,152,934,023	5701	TT13	chr9	9	q33.3	129222299	129227389	3	0	-1.223206	-1.223206	4.187E-16
252,152,934,023	5702	TT13	chr9	9	q33.3	129261711	129279860	10	0	-1.078836	-1.078836	1.973E-31
252,152,934,023	5706	TT13	chr9	9	q33.3	129674755	129680510	4	0	-1.512671	-1.512671	2.011E-29
252,152,934,023	5707	TT13	chr9	9	q33.3	129886162	129891193	4	0	-0.81813	-0.81813	1.751E-14
252,152,934,023	5708	TT13	chr9	9	q33.3	129982994	129989493	4	0	-1.246464	-1.246464	3.403E-27
252,152,934,023	5709	TT13	chr9	9	q33.3	130155498	130169494	8	0	-0.932157	-0.932157	5.63E-25
252,152,934,023	5711	TT13	chr9	9	q34.11	130370207	130376065	4	0	-2.159336	-2.159336	1.028E-45
252,152,934,023	5712	TT13	chr9	9	q34.11	130472585	130593174	57	0	-0.740067	-0.740067	1.042E-61
252,152,934,023	5713	TT13	chr9	9	q34.11	130587204	130591481	3	0	-2.334106	-2.334106	3.249E-17
252,152,934,023	5716	TT13	chr9	9	q34.11	130950687	130967546	7	0	-1.144219	-1.144219	2.956E-25
252,152,934,023	5719	TT13	chr9	9	q34.11	131101096	131103605	3	0	-1.9105	-1.9105	4.571E-26
252,152,934,023	5730	TT13	chr9	9	q34.11	132076259	132407173	117	0	-0.44429	-0.44429	1.869E-32
252,152,934,023	5731	TT13	chr9	9	q34.11	132142499	132147859	5	0	-1.232064	-1.232064	2.103E-12
252,152,934,023	5744	TT13	chr9	9	q34.12	133783418	133813049	13	0	-0.93154	-0.93154	4.228E-25
252,152,934,023	5746	TT13	chr9	9	q34.12 - q34.13	133969501	134003945	17	0	-0.630519	-0.630519	1.7E-15
252,152,934,023	5772	TT13	chr9	9	q34.2	137215352	137359668	59	0	-0.642375	-0.642375	8.267E-22
252,152,934,023	5773	TT13	chr9	9	q34.2	137249610	137255076	4	0	-1.863801	-1.863801	2.703E-13
252,152,934,023	5782	TT13	chr9	9	q34.3	138369004	138395147	13	0	-1.127983	-1.127983	7.423E-46
252,152,934,023	5783	TT13	chr9	9	q34.3	138374663	138380766	3	0	-2.351041	-2.351041	2.714E-12
252,152,934,023	5795	TT13	chr9	9	q34.3	139711416	139719136	4	0	-2.648245	-2.648245	1.935E-30
252,152,934,023	5812	TT13	chr10	10	p15.3	178045	185314	4	0	-1.193972	-1.193972	3.073E-24
252,152,934,023	5813	TT13	chr10	10	p15.3	338219	1419818	456	0	-0.261763	-0.261763	3.133E-130
252,152,934,023	5814	TT13	chr10	10	p15.3	344839	358626	6	0	-1.390909	-1.390909	1.217E-28
252,152,934,023	5818	TT13	chr10	10	p15.3	677484	688807	8	0	-2.268088	-2.268088	2.564E-75
252,152,934,023	5825	TT13	chr10	10	p15.3	1776762	1781779	4	0	-1.253445	-1.253445	1.716E-25
252,152,934,023	5830	TT13	chr10	10	p15.1	3823236	3830679	4	0	-1.0942	-1.0942	2.266E-19
252,152,934,023	5832	TT13	chr10	10	p15.1	5075300	5076628	3	0	-1.409188	-1.409188	5.744E-22
252,152,934,023	5837	TT13	chr10	10	p15.1	5695350	5736758	19	0	-1.045063	-1.045063	3.6E-79
252,152,934,023	5838	TT13	chr10	10	p15.1	5727751	5734344	4	0	-1.865044	-1.865044	7.386E-10
252,152,934,023	5839	TT13	chr10	10	p15.1	5849516	5857171	5	0	-1.353026	-1.353026	2.855E-34
252,152,934,023	5840	TT13	chr10	10	p15.1	5929273	5935863	4	0	-0.991173	-0.991173	3.69E-17
252,152,934,023	5843	TT13	chr10	10	p15.1	6181567	6208739	12	0	-0.659272	-0.659272	1.284E-22
252,152,934,023	5845	TT13	chr10	10	p14	6619639	6623812	3	0	-1.30046	-1.30046	2.346E-20
252,152,934,023	5846	TT13	chr10	10	p14	7211838	7216515	4	0	-1.284164	-1.284164	1.68E-23
252,152,934,023	5847	TT13	chr10	10	p14	7452187	7458916	5	0	-1.496194	-1.496194	2.352E-37
252,152,934,023	5852	TT13	chr10	10	p14	8045265	8101963	31	0	-0.556774	-0.556774	3.117E-35
252,152,934,023	5854	TT13	chr10	10	p14	11057430	11062483	4	0	-1.517939	-1.517939	6.067E-33
252,152,934,023	5855	TT13	chr10	10	p14	11203097	11210469	4	0	-0.771279	-0.771279	2.513E-12
252,152,934,023	5856	TT13	chr10	10	p14	11340878	11347514	5	0	-1.660021	-1.660021	7.873E-43
252,152,934,023	5857	TT13	chr10	10	p14	11384273	11389101	4	0	-1.474258	-1.474258	8.691E-30
252,152,934,023	5871	TT13	chr10	10	p13	13198469	13205451	5	0	-1.692936	-1.692936	7.6E-37
252,152,934,023	5880	TT13	chr10	10	p13	15128527	15142134	8	0	-1.189365	-1.189365	1.148E-42
252,152,934,023	5881	TT13	chr10	10	p13	15207953	15216968	6	0	-0.883196	-0.883196	3.648E-21
252,152,934,023	5882	TT13	chr10	10	p13	15407939	15418293	7	0	-1.026454	-1.026454	6.695E-30
252,152,934,023	5883	TT13	chr10	10	p13	15573574	15580931	5	0	-1.18938	-1.18938	1.157E-27
252,152,934,023	5884	TT13	chr10	10	p13	15758353	15763098	3	0	-1.456074	-1.456074	6.578E-24
252,152,934,023	5885	TT13	chr10	10	p13	16557584	16565830	6	0	-1.122311	-1.122311	4.657E-26
252,152,934,023	5886	TT13	chr10	10	p13	17238016	17279962	23	0	-0.529831	-0.529831	1.135E-29
252,152,934,023	5888	TT13	chr10	10	p12.33	17655390	17676173	10	0	-0.99782	-0.99782	3.058E-40
252,152,934,023	5890	TT13	chr10	10	p12.31	18944851	18951329	4	0	-1.043766	-1.043766	4.568E-20
252,152,934,023	5891	TT13	chr10	10	p12.31	19239339	19245564	3	0	-1.288643	-1.288643	1.09E-20
252,152,934,023	5892	TT13	chr10	10	p12.31	20100464	20107688	6	0	-1.126017	-1.126017	2.339E-30
252,152,934,023	5893	TT13	chr10	10	p12.31	21459641	21465684	4	0	-1.40799	-1.40799	4.539E-30
252,152,934,023	5894	TT13	chr10	10	p12.31	21781656	21826911	43	0	-1.350473	-1.350473	5.461E-241
252,152,934,023	5898	TT13	chr10	10	p12.2	22603928	22635726	18	0	-1.879586	-1.879586	6.882E-170
252,152,934,023	5899	TT13	chr10	10	p12.2	22998933	23006417	5	0	-1.177276	-1.177276	1.168E-27

252,152,934,023	5900	TT13	chr10	10	p12.2	23213472	23220958	6	0	-0.689206	-0.689206	2.527E-14
252,152,934,023	5901	TT13	chr10	10	p12.2	23377491	23389814	6	0	-0.653113	-0.653113	5.928E-12
252,152,934,023	5903	TT13	chr10	10	p12.2	23479832	23489189	6	0	-2.144943	-2.144943	1.249E-60
252,152,934,023	5906	TT13	chr10	10	p12.2	23982077	23988976	4	0	-1.388053	-1.388053	2.861E-23
252,152,934,023	5908	TT13	chr10	10	p12.1	25009566	25017285	4	0	-1.154787	-1.154787	7.783E-20
252,152,934,023	5909	TT13	chr10	10	p12.1	25302955	25309417	4	0	-1.380645	-1.380645	3.034E-30
252,152,934,023	5911	TT13	chr10	10	p12.1	26218844	26228242	5	0	-1.160079	-1.160079	4.366E-28
252,152,934,023	5914	TT13	chr10	10	p12.1	26854436	26858737	4	0	-1.548193	-1.548193	3.579E-33
252,152,934,023	5917	TT13	chr10	10	p12.1	27524276	27640283	44	0	-0.740181	-0.740181	2.503E-93
252,152,934,023	5918	TT13	chr10	10	p12.1	27541926	27547510	4	0	-2.845548	-2.845548	1.249E-31
252,152,934,023	5921	TT13	chr10	10	p12.1	28027940	28036032	4	0	-1.749079	-1.749079	2.53E-36
252,152,934,023	5924	TT13	chr10	10	p12.1	28954565	28970024	9	0	-1.340177	-1.340177	1.573E-53
252,152,934,023	5940	TT13	chr10	10	p11.22	33292828	33301620	5	0	-1.475831	-1.475831	6.159E-34
252,152,934,023	5941	TT13	chr10	10	p11.22	33332598	33344749	6	0	-0.822324	-0.822324	8.049E-14
252,152,934,023	5942	TT13	chr10	10	p11.22	33619794	33629695	5	0	-1.209338	-1.209338	5.799E-25
252,152,934,023	5943	TT13	chr10	10	p11.21	34407663	34413384	4	0	-0.956778	-0.956778	3.465E-17
252,152,934,023	5944	TT13	chr10	10	p11.21	34630743	34646055	8	0	-0.936797	-0.936797	5.39E-30
252,152,934,023	5950	TT13	chr10	10	p11.21	35894893	35898383	3	0	-1.52685	-1.52685	2.349E-23
252,152,934,023	5951	TT13	chr10	10	p11.21	35924660	35937962	6	0	-0.846373	-0.846373	2.948E-17
252,152,934,023	5952	TT13	chr10	10	p11.21	37276960	37280422	3	0	-1.105896	-1.105896	3.227E-17
252,152,934,023	5953	TT13	chr10	10	p11.1	38143970	38147661	3	0	-1.258648	-1.258648	1.122E-18
252,152,934,023	5954	TT13	chr10	10	p11.1	38261574	38306544	14	0	-0.646054	-0.646054	7.474E-26
252,152,934,023	5955	TT13	chr10	10	q11.21	42965018	42977009	6	0	-0.667103	-0.667103	3.15E-13
252,152,934,023	5956	TT13	chr10	10	q11.21	43595760	43604955	5	0	-0.915148	-0.915148	1.73E-14
252,152,934,023	5957	TT13	chr10	10	q11.21	43632389	43636004	3	0	-1.642272	-1.642272	2.011E-26
252,152,934,023	5961	TT13	chr10	10	q11.21	43890103	43957769	29	0	-1.036258	-1.036258	5.847E-100
252,152,934,023	5963	TT13	chr10	10	q11.21	44318638	44324499	4	0	-1.101088	-1.101088	1.392E-19
252,152,934,023	5964	TT13	chr10	10	q11.21	44787591	44810197	7	0	-0.790789	-0.790789	1.137E-16
252,152,934,023	5965	TT13	chr10	10	q11.21	44878967	44884552	3	0	-1.40461	-1.40461	9.087E-17
252,152,934,023	5971	TT13	chr10	10	q11.21	46087456	46098932	6	0	-1.48529	-1.48529	4.596E-34
252,152,934,023	5975	TT13	chr10	10	q11.22	48426220	48439737	7	0	-1.361706	-1.361706	6.548E-40
252,152,934,023	5976	TT13	chr10	10	q11.22	49514027	49517737	3	0	-1.734878	-1.734878	3.004E-28
252,152,934,023	5978	TT13	chr10	10	q11.22	49727041	49735835	4	0	-0.943771	-0.943771	1.371E-14
252,152,934,023	5979	TT13	chr10	10	q11.22	49861012	49881348	7	0	-0.832381	-0.832381	2.82E-19
252,152,934,023	5980	TT13	chr10	10	q11.23	50532143	50536919	4	0	-1.141938	-1.141938	1.522E-16
252,152,934,023	5981	TT13	chr10	10	q11.23	50600628	50608345	5	0	-1.534413	-1.534413	7.077E-38
252,152,934,023	5984	TT13	chr10	10	q11.23	50968591	50978529	5	0	-1.796283	-1.796283	2.808E-41
252,152,934,023	5985	TT13	chr10	10	q11.23	51562356	51574215	7	0	-1.568772	-1.568772	3.346E-54
252,152,934,023	5986	TT13	chr10	10	q11.23	52173815	52183990	6	0	-1.022306	-1.022306	2.8E-25
252,152,934,023	5987	TT13	chr10	10	q11.23	52380281	52394263	7	0	-1.428881	-1.428881	5.15E-47
252,152,934,023	5988	TT13	chr10	10	q11.23	52746381	52754159	5	0	-1.195192	-1.195192	1.083E-26
252,152,934,023	5989	TT13	chr10	10	q11.23	52830820	52837886	4	0	-1.444669	-1.444669	4.429E-29
252,152,934,023	5990	TT13	chr10	10	q21.1	53148868	53155203	5	0	-1.365565	-1.365565	3.936E-33
252,152,934,023	5991	TT13	chr10	10	q21.1	54167481	54172872	4	0	-1.444624	-1.444624	1.554E-30
252,152,934,023	5993	TT13	chr10	10	q21.1	55677277	55690813	7	0	-0.82223	-0.82223	6.395E-20
252,152,934,023	5994	TT13	chr10	10	q21.1	55745569	55754373	5	0	-1.046692	-1.046692	3.355E-22
252,152,934,023	5995	TT13	chr10	10	q21.1	57389273	57394691	3	0	-1.235199	-1.235199	5.595E-19
252,152,934,023	5996	TT13	chr10	10	q21.1	60024166	60030270	4	0	-1.332601	-1.332601	2.303E-25
252,152,934,023	5997	TT13	chr10	10	q21.1	60081105	60098638	10	0	-1.070115	-1.070115	2.232E-43
252,152,934,023	6004	TT13	chr10	10	q21.2	61663550	61670355	4	0	-1.311041	-1.311041	1.512E-25
252,152,934,023	6005	TT13	chr10	10	q21.2	62701487	62705499	3	0	-1.455603	-1.455603	4.409E-22
252,152,934,023	6006	TT13	chr10	10	q21.2	63419923	63425764	4	0	-1.556074	-1.556074	1.452E-32
252,152,934,023	6007	TT13	chr10	10	q21.2	63661199	63666429	5	0	-1.284728	-1.284728	1.158E-25
252,152,934,023	6008	TT13	chr10	10	q21.2	64024177	64041735	9	0	-1.129812	-1.129812	6.397E-43
252,152,934,023	6009	TT13	chr10	10	q21.2	64131921	64137778	4	0	-1.445351	-1.445351	2.717E-29
252,152,934,023	6010	TT13	chr10	10	q21.3	64564361	64583449	10	0	-1.471611	-1.471611	5.888E-64
252,152,934,023	6016	TT13	chr10	10	q21.3	69829268	69839999	6	0	-1.089114	-1.089114	1.876E-27
252,152,934,023	6017	TT13	chr10	10	q21.3	70035847	70040742	3	0	-1.122556	-1.122556	7.169E-16
252,152,934,023	6018	TT13	chr10	10	q21.3	70164514	70167485	3	0	-2.08644	-2.08644	3.206E-34
252,152,934,023	6030	TT13	chr10	10	q22.1	71886544	72239788	160	0	-0.358215	-0.358215	8.243E-66
252,152,934,023	6031	TT13	chr10	10	q22.1	71889268	71932870	19	0	-0.823888	-0.823888	2.529E-18
252,152,934,023	6062	TT13	chr10	10	q22.2	75755092	75759863	4	0	-1.383352	-1.383352	1.48E-23
252,152,934,023	6063	TT13	chr10	10	q22.2	75896367	75939822	23	0	-0.655399	-0.655399	5.974E-37
252,152,934,023	6064	TT13	chr10	10	q22.2	76574556	76588748	7	0	-1.182228	-1.182228	2.628E-36
252,152,934,023	6068	TT13	chr10	10	q22.2	77151923	77194620	20	0	-0.781357	-0.781357	1.136E-35
252,152,934,023	6069	TT13	chr10	10	q22.2	77158059	77167022	5	0	-1.816017	-1.816017	6.297E-10
252,152,934,023	6070	TT13	chr10	10	q22.2	77507218	77512870	3	0	-1.259734	-1.259734	6.018E-21
252,152,934,023	6071	TT13	chr10	10	q22.3	79394923	79400335	4	0	-1.430001	-1.430001	9.97E-25
252,152,934,023	6072	TT13	chr10	10	q22.3	79684879	79689762	3	0	-1.358662	-1.358662	2.92E-23
252,152,934,023	6075	TT13	chr10	10	q22.3	80721958	80736291	7	0	-0.877647	-0.877647	2.632E-24
252,152,934,023	6076	TT13	chr10	10	q22.3	81031473	81061673	15	0	-0.678687	-0.678687	4.08E-23
252,152,934,023	6081	TT13	chr10	10	q23.1	82165967	82169772	3	0	-1.119652	-1.119652	4.687E-15
252,152,934,023	6082	TT13	chr10	10	q23.1	82292848	82304288	6	0	-1.210478	-1.210478	8.782E-30
252,152,934,023	6083	TT13	chr10	10	q23.1	83623490	83639866	9	0	-0.977149	-0.977149	5.384E-33
252,152,934,023	6084	TT13	chr10	10	q23.1	85894680	85902810	4	0	-1.128125	-1.128125	3.615E-21
252,152,934,023	6085	TT13	chr10	10	q23.1	85996544	86000148	3	0	-1.308673	-1.308673	8.159E-17
252,152,934,023	6086	TT13	chr10	10	q23.1	86085731	86110744	13	0	-0.850611	-0.850611	5.174E-34
252,152,934,023	6088	TT13	chr10	10	q23.2	88128555	88161905	11	0	-1.069572	-1.069572	2.319E-42
252,152,934,023	6096	TT13	chr10	10	q23.2	89416904	89424056	5	0	-1.200718	-1.200718	8.43E-27
252,152,934,023	6117	TT13	chr10	10	q23.33	94435866	94457619	10	0	-1.3794	-1.3794	7.17E-54
252,152,934,023	6118	TT13	chr10	10	q23.33	94604788	94610667	5	0	-1.426283	-1.426283	1.664E-36
252,152,934,023	6120	TT13	chr10	10	q23.33	94818006	94835618	9	0	-1.68198	-1.68198	1.519E-54
252,152,934,023	6124	TT13	chr10	10	q23.33	95458100	95463303	4	0	-1.514175	-1.514175	5.889E-32
252,152,934,023	6125	TT13	chr10	10	q23.33	95649745	95657211	5	0	-1.169836	-1.169836	1.331E-26
252,152,934,023	6129	TT13	chr10	10	q24.1	97412505	97421156	7	0	-1.166447	-1.166447	3.649E-35
252,152,934,023	6148	TT13	chr10	10	q24.2	99891787	99922820	14	0	-0.735883	-0.735883	5.048E-30
252,152,934,023	6149	TT13	chr10	10	q24.2	99911230	99914897	3	0	-1.634794	-1.634794	4.355E-10
252,152,934,023	6150	TT13	chr10	10	q24.2	100025737	100034435	6	0	-0.719107	-0.719107	2.026E-10
252,152,934,023	6151	TT13	chr10	10	q24.2	100200499	100234840	15	0	-0.631968	-0.631968	1.198E-22
252,152,934,023	6152	TT13	chr10	10	q24.2	100989787	100998313	6	0	-1.232911	-1.232911	8.123E-33
252,152,934,023	6153	TT13	chr10	10	q24.2	101075430	101093756	9	0	-0.864474	-0.864474	1.455E-26
252,152,934,023	6154	TT13	chr10	10	q24.2	101284199	101298352	7	0	-1.734237	-1.734237	1.031E-54
252,152,934,023	6156	TT13	chr10	10	q24.2	101417265	101421210	4	0	-1.604486	-1.604486	7.593E-34
252,152,934,023	6164	TT13	chr10	10	q24.31	102034430	102048000	8	0	-1.432017	-1.432017	2.273E-45
252,152,934,023	6168	TT13	chr10	10	q24.31	102471517	102507331	14	0	-1.516569	-1.516569	1.808E-70
252,152,934,023	6170	TT13	chr10	10	q24.31	102725976	102728342	4	0	-1.102209	-1.102209	5.957E-13

252,152,934,023	6178	TT13	chr10	10	q24.32	103529574	103541147	5	0	-1.376333	-1.376333	1.111E-21
252,152,934,023	6179	TT13	chr10	10	q24.32	103574969	103604715	16	0	-1.054763	-1.054763	2.57E-42
252,152,934,023	6181	TT13	chr10	10	q24.32	103814176	103829156	9	0	-0.911655	-0.911655	2.615E-21
252,152,934,023	6182	TT13	chr10	10	q24.32	103872818	103894850	9	0	-1.156301	-1.156301	4.044E-29
252,152,934,023	6183	TT13	chr10	10	q24.32	103988889	104003157	8	0	-0.984786	-0.984786	6.455E-20
252,152,934,023	6184	TT13	chr10	10	q24.32	104058032	104066885	4	0	-1.125471	-1.125471	1.331E-15
252,152,934,023	6185	TT13	chr10	10	q24.32	104153596	104182994	23	0	-1.252896	-1.252896	6.85E-71
252,152,934,023	6186	TT13	chr10	10	q24.32	104205719	104232024	20	0	-0.942019	-0.942019	1.334E-43
252,152,934,023	6187	TT13	chr10	10	q24.32	104261646	104268127	4	0	-1.014069	-1.014069	3.339E-13
252,152,934,023	6188	TT13	chr10	10	q24.32	104399806	104419090	12	0	-0.93065	-0.93065	1.536E-27
252,152,934,023	6189	TT13	chr10	10	q24.32	104470304	104477485	4	0	-1.041289	-1.041289	9.943E-15
252,152,934,023	6190	TT13	chr10	10	q24.32	104623492	104630134	4	0	-1.307243	-1.307243	1.422E-20
252,152,934,023	6191	TT13	chr10	10	q24.32	104674452	104681246	4	0	-1.210252	-1.210252	5.346E-15
252,152,934,023	6192	TT13	chr10	10	q24.32	104829572	104838942	6	0	-1.40668	-1.40668	3.935E-33
252,152,934,023	6193	TT13	chr10	10	q24.32	104886986	104891087	3	0	-2.053614	-2.053614	7.621E-31
252,152,934,023	6194	TT13	chr10	10	q24.33	105035441	105039703	3	0	-1.454141	-1.454141	8.209E-19
252,152,934,023	6195	TT13	chr10	10	q24.33	105107293	105128605	10	0	-1.114477	-1.114477	1.444E-33
252,152,934,023	6202	TT13	chr10	10	q24.33	105611469	105616505	3	0	-1.358673	-1.358673	1.525E-18
252,152,934,023	6203	TT13	chr10	10	q24.33	105674463	105682526	6	0	-0.991705	-0.991705	7.775E-23
252,152,934,023	6206	TT13	chr10	10	q25.1	105988725	106017608	18	0	-1.107654	-1.107654	1.235E-75
252,152,934,023	6209	TT13	chr10	10	q25.1	106541444	106547265	5	0	-1.391111	-1.391111	2.278E-34
252,152,934,023	6210	TT13	chr10	10	q25.1	108685261	108690775	4	0	-1.441352	-1.441352	2.353E-28
252,152,934,023	6211	TT13	chr10	10	q25.1	108918794	108930187	6	0	-0.942651	-0.942651	1.275E-21
252,152,934,023	6212	TT13	chr10	10	q25.1	111680203	111685021	3	0	-1.409456	-1.409456	1.228E-20
252,152,934,023	6213	TT13	chr10	10	q25.1	111765668	111777140	7	0	-0.700229	-0.700229	3.39E-14
252,152,934,023	6214	TT13	chr10	10	q25.2	111964959	111990093	12	0	-1.037521	-1.037521	5.045E-43
252,152,934,023	6232	TT13	chr10	10	q25.3	116518044	116585884	25	0	-0.623328	-0.623328	2.945E-36
252,152,934,023	6233	TT13	chr10	10	q25.3	116579263	116584435	4	0	-1.653519	-1.653519	6.041E-16
252,152,934,023	6234	TT13	chr10	10	q25.3	116851374	116856352	3	0	-1.504003	-1.504003	1.741E-24
252,152,934,023	6235	TT13	chr10	10	q25.3	118029152	118034765	3	0	-1.561838	-1.561838	1.269E-22
252,152,934,023	6236	TT13	chr10	10	q25.3	118141819	118157646	6	0	-0.719898	-0.719898	1.851E-13
252,152,934,023	6239	TT13	chr10	10	q25.3	118425239	118439274	7	0	-0.802035	-0.802035	2.565E-16
252,152,934,023	6240	TT13	chr10	10	q25.3	118500387	118505077	3	0	-1.60492	-1.60492	1.541E-17
252,152,934,023	6242	TT13	chr10	10	q25.3	118762186	118767938	4	0	-1.452566	-1.452566	1.537E-30
252,152,934,023	6243	TT13	chr10	10	q25.3	118882121	118930983	23	0	-0.960538	-0.960538	1.33E-72
252,152,934,023	6244	TT13	chr10	10	q25.3	118906065	118918993	7	0	-0.305755	-0.305755	4.019E-15
252,152,934,023	6245	TT13	chr10	10	q25.3	118921274	118929096	4	0	-1.820694	-1.820694	1.074E-10
252,152,934,023	6246	TT13	chr10	10	q25.3	118973554	118977252	3	0	-1.271851	-1.271851	1.582E-17
252,152,934,023	6248	TT13	chr10	10	q26.11	119291707	119313735	12	0	-1.652622	-1.652622	1.291E-78
252,152,934,023	6250	TT13	chr10	10	q26.11	120512571	120523404	5	0	-1.554259	-1.554259	2.596E-40
252,152,934,023	6251	TT13	chr10	10	q26.11	120838595	120842645	3	0	-1.535932	-1.535932	6.937E-24
252,152,934,023	6253	TT13	chr10	10	q26.11	120923670	120946458	11	0	-0.917973	-0.917973	1.982E-33
252,152,934,023	6269	TT13	chr10	10	q26.13	123353203	123370216	8	0	-1.117709	-1.117709	4.185E-35
252,152,934,023	6270	TT13	chr10	10	q26.13	123683710	123690568	5	0	-1.305092	-1.305092	4.182E-31
252,152,934,023	6271	TT13	chr10	10	q26.13	123730621	123740904	5	0	-1.235426	-1.235426	3.125E-27
252,152,934,023	6276	TT13	chr10	10	q26.13	124636450	124640852	4	0	-1.27289	-1.27289	7.733E-25
252,152,934,023	6277	TT13	chr10	10	q26.13	124709988	124776610	30	0	-0.610512	-0.610512	2.337E-41
252,152,934,023	6278	TT13	chr10	10	q26.13	124766646	124774182	4	0	-1.538238	-1.538238	1.282E-13
252,152,934,023	6279	TT13	chr10	10	q26.13	124893503	124917504	14	0	-1.588074	-1.588074	1.564E-90
252,152,934,023	6287	TT13	chr10	10	q26.13	126079329	126316032	109	0	-0.387397	-0.387397	6.823E-52
252,152,934,023	6288	TT13	chr10	10	q26.13	126105636	126110157	3	0	-1.575312	-1.575312	2.116E-15
252,152,934,023	6291	TT13	chr10	10	q26.13	126476585	126492618	8	0	-1.043881	-1.043881	3.309E-31
252,152,934,023	6292	TT13	chr10	10	q26.13	126710852	126716425	3	0	-1.808447	-1.808447	2.613E-25
252,152,934,023	6293	TT13	chr10	10	q26.13	126838833	126847075	5	0	-1.712845	-1.712845	3.131E-39
252,152,934,023	6294	TT13	chr10	10	q26.13	127458901	127465132	3	0	-1.204696	-1.204696	1.892E-16
252,152,934,023	6295	TT13	chr10	10	q26.2	127508542	127515025	4	0	-1.22504	-1.22504	1.034E-24
252,152,934,023	6296	TT13	chr10	10	q26.2	127656436	127661280	4	0	-1.769794	-1.769794	8.604E-41
252,152,934,023	6297	TT13	chr10	10	q26.2	128075388	128079014	3	0	-1.608851	-1.608851	1.872E-22
252,152,934,023	6298	TT13	chr10	10	q26.2	128591794	128600405	5	0	-0.712291	-0.712291	5.907E-13
252,152,934,023	6299	TT13	chr10	10	q26.2	128790748	128795090	3	0	-1.378855	-1.378855	8.331E-23
252,152,934,023	6300	TT13	chr10	10	q26.2	128990450	128998111	4	0	-1.05832	-1.05832	4.548E-20
252,152,934,023	6303	TT13	chr10	10	q26.2	129918836	129929609	6	0	-1.048334	-1.048334	9.493E-28
252,152,934,023	6311	TT13	chr10	10	q26.3	131691440	131710765	10	0	-1.142417	-1.142417	1.942E-48
252,152,934,023	6312	TT13	chr10	10	q26.3	131748905	131772350	13	0	-1.640801	-1.640801	2.803E-90
252,152,934,023	6313	TT13	chr10	10	q26.3	131898456	131938654	18	0	-1.010023	-1.010023	9.458E-71
252,152,934,023	6355	TT13	chr11	11	p15.5	870664	879751	5	0.306678	0	0.306678	1.83E-12
252,152,934,023	6363	TT13	chr11	11	p15.5	1704417	1715980	6	0	-1.526947	-1.526947	5.541E-21
252,152,934,023	6366	TT13	chr11	11	p15.5	2051498	2106979	15	0.301921	0	0.301921	6.226E-36
252,152,934,023	6367	TT13	chr11	11	p15.5	2162582	2166327	6	0	-2.147238	-2.147238	1.983E-33
252,152,934,023	6368	TT13	chr11	11	p15.5	2399787	2442877	21	0	-1.030066	-1.030066	2.227E-16
252,152,934,023	6371	TT13	chr11	11	p15.5 - p15.4	2799036	2831914	14	0	-1.095746	-1.095746	1.745E-18
252,152,934,023	6378	TT13	chr11	11	p15.4	3660627	3692438	15	0	-0.863525	-0.863525	5.184E-38
252,152,934,023	6379	TT13	chr11	11	p15.4	3815442	3879297	36	0	-0.635163	-0.635163	5.697E-53
252,152,934,023	6380	TT13	chr11	11	p15.4	3817650	3820836	3	0	-1.630098	-1.630098	1.418E-10
252,152,934,023	6382	TT13	chr11	11	p15.4	4156274	4160221	4	0	-1.835547	-1.835547	4.476E-39
252,152,934,023	6383	TT13	chr11	11	p15.4	5159768	5168451	5	0	-0.915376	-0.915376	6.332E-18
252,152,934,023	6384	TT13	chr11	11	p15.4	5312429	5316920	3	0	-1.668532	-1.668532	2.224E-26
252,152,934,023	6386	TT13	chr11	11	p15.4	6247451	6499209	114	0	-0.293642	-0.293642	6.927E-33
252,152,934,023	6387	TT13	chr11	11	p15.4	6253299	6260624	5	0	-1.241459	-1.241459	3.473E-16
252,152,934,023	6393	TT13	chr11	11	p15.4	7108849	7114226	4	0	-1.481218	-1.481218	2.727E-28
252,152,934,023	6394	TT13	chr11	11	p15.4	7270427	7278884	8	0	-1.18194	-1.18194	6.242E-41
252,152,934,023	6397	TT13	chr11	11	p15.4	8005448	8056498	24	0	-0.524521	-0.524521	1.506E-23
252,152,934,023	6405	TT13	chr11	11	p15.4	8980510	9029834	24	0	-0.695341	-0.695341	2.513E-42
252,152,934,023	6407	TT13	chr11	11	p15.4	9101045	9115885	9	0	-0.98597	-0.98597	4.991E-31
252,152,934,023	6409	TT13	chr11	11	p15.4	9333556	9338441	4	0	-1.299911	-1.299911	1.645E-25
252,152,934,023	6410	TT13	chr11	11	p15.4	9404568	9408705	4	0	-1.615358	-1.615358	1.921E-32
252,152,934,023	6416	TT13	chr11	11	p15.4	10314779	10334418	10	0	-0.994915	-0.994915	2.575E-33
252,152,934,023	6434	TT13	chr11	11	p15.2	14364038	14407587	19	0	-0.601389	-0.601389	1.639E-26
252,152,934,023	6435	TT13	chr11	11	p15.2	14663817	14668634	3	0	-1.753336	-1.753336	2.453E-29
252,152,934,023	6436	TT13	chr11	11	p15.2	14908713	14929081	12	0	-0.957851	-0.957851	1.074E-41
252,152,934,023	6438	TT13	chr11	11	p15.1	16626299	16630210	3	0	-2.406869	-2.406869	2.782E-39
252,152,934,023	6439	TT13	chr11	11	p15.1	16905745	16952160	23	0	-0.66365	-0.66365	2.049E-38
252,152,934,023	6443	TT13	chr11	11	p15.1	17372183	17376047	3	0	-1.738043	-1.738043	7.734E-28
252,152,934,023	6448	TT13	chr11	11	p15.1	17737036	17759540	11	0	-0.811094	-0.811094	1.195E-24
252,152,934,023	6457	TT13	chr11	11	p15.1	19136731	19140291	6	0	-1.422061	-1.422061	4.229E-38
252,152,934,023	6458	TT13	chr11	11	p15.1	19365914	19370491	3	0	-1.359516	-1.359516	1.299E-19

252,152,934,023	6459	TT13	chr11	11	p15.1	19730580	19738105	5	0	-1.120834	-1.120834	2.581E-26
252,152,934,023	6460	TT13	chr11	11	p15.1	19796446	19801655	4	0	-1.244875	-1.244875	3.495E-27
252,152,934,023	6461	TT13	chr11	11	p15.1	19878211	19883393	3	0	-1.205262	-1.205262	2.689E-19
252,152,934,023	6462	TT13	chr11	11	p15.1	20176715	20183826	5	0	-1.759928	-1.759928	1.139E-43
252,152,934,023	6463	TT13	chr11	11	p15.1	20384491	20416861	21	0	-0.637247	-0.637247	2.258E-32
252,152,934,023	6466	TT13	chr11	11	p15.1	20881109	20889247	5	0	-0.995892	-0.995892	8.415E-21
252,152,934,023	6467	TT13	chr11	11	p14.3	22211779	22218779	5	0	-0.857019	-0.857019	1.357E-14
252,152,934,023	6468	TT13	chr11	11	p14.3	22683695	22691259	5	0	-1.37063	-1.37063	5.698E-35
252,152,934,023	6469	TT13	chr11	11	p14.3	22848709	22853716	4	0	-1.425665	-1.425665	2.337E-27
252,152,934,023	6470	TT13	chr11	11	p14.3	24516632	24523214	5	0	-1.181455	-1.181455	3.132E-26
252,152,934,023	6471	TT13	chr11	11	p14.3	24915066	24921572	4	0	-1.209049	-1.209049	1.869E-24
252,152,934,023	6472	TT13	chr11	11	p14.1	27382917	27388218	3	0	-1.337759	-1.337759	5.082E-20
252,152,934,023	6473	TT13	chr11	11	p14.1	27486957	27501753	7	0	-0.759901	-0.759901	4.087E-17
252,152,934,023	6474	TT13	chr11	11	p14.1	27717104	27746606	18	0	-0.981774	-0.981774	8.75E-59
252,152,934,023	6475	TT13	chr11	11	p14.1	27726105	27736144	6	0	-0.391566	-0.391566	5.115E-11
252,152,934,023	6478	TT13	chr11	11	p14.1	29731611	29736053	3	0	-1.076507	-1.076507	9.08E-16
252,152,934,023	6479	TT13	chr11	11	p14.1	30034682	30040913	5	0	-1.199258	-1.199258	2.468E-27
252,152,934,023	6480	TT13	chr11	11	p14.1	30604821	30611804	4	0	-1.414873	-1.414873	4.234E-27
252,152,934,023	6481	TT13	chr11	11	p13	31818255	31852078	15	0	-1.217165	-1.217165	4.527E-59
252,152,934,023	6482	TT13	chr11	11	p13	32109790	32116617	4	0	-1.274906	-1.274906	4.651E-23
252,152,934,023	6483	TT13	chr11	11	p13	32449179	32459180	7	0	-1.206596	-1.206596	1.806E-31
252,152,934,023	6486	TT13	chr11	11	p13	32908435	32918561	5	0	-1.6235	-1.6235	1.199E-39
252,152,934,023	6487	TT13	chr11	11	p13	33032652	33069045	18	0	-0.643859	-0.643859	1.992E-29
252,152,934,023	6488	TT13	chr11	11	p13	33263667	33284108	9	0	-1.106029	-1.106029	7.702E-41
252,152,934,023	6489	TT13	chr11	11	p13	33660814	33895328	97	0	-0.282972	-0.282972	2.806E-26
252,152,934,023	6490	TT13	chr11	11	p13	33719857	33724957	3	0	-1.485467	-1.485467	8.093E-17
252,152,934,023	6498	TT13	chr11	11	p13	35439046	35443362	3	0	-1.372768	-1.372768	1.028E-18
252,152,934,023	6499	TT13	chr11	11	p13	35637057	35644045	5	0	-1.129686	-1.129686	5.62E-23
252,152,934,023	6508	TT13	chr11	11	p11.2	43595385	43602965	9	0	-1.615872	-1.615872	2.114E-51
252,152,934,023	6509	TT13	chr11	11	p11.2	43944214	43948890	4	0	-1.151481	-1.151481	4.62E-20
252,152,934,023	6511	TT13	chr11	11	p11.2	44116607	44119706	3	0	-1.439651	-1.439651	2.222E-22
252,152,934,023	6512	TT13	chr11	11	p11.2	44328213	44338734	6	0	-1.605319	-1.605319	1.384E-38
252,152,934,023	6518	TT13	chr11	11	p11.2	45227244	45238305	9	0	-1.129409	-1.129409	1.448E-36
252,152,934,023	6521	TT13	chr11	11	p11.2	45904761	45946787	22	0	-0.729376	-0.729376	8.467E-36
252,152,934,023	6522	TT13	chr11	11	p11.2	46136248	46147283	7	0	-1.118652	-1.118652	1.029E-31
252,152,934,023	6523	TT13	chr11	11	p11.2	46251855	46416933	74	0	-0.40444	-0.40444	6.457E-38
252,152,934,023	6524	TT13	chr11	11	p11.2	46258402	46264128	3	0	-1.728618	-1.728618	9.959E-17
252,152,934,023	6525	TT13	chr11	11	p11.2	46405288	46415124	5	0	-1.349553	-1.349553	2.481E-11
252,152,934,023	6531	TT13	chr11	11	p11.2	47116672	47122954	4	0	-1.459124	-1.459124	4.539E-31
252,152,934,023	6532	TT13	chr11	11	p11.2	47194776	47212123	11	0	-0.944245	-0.944245	2.195E-34
252,152,934,023	6534	TT13	chr11	11	p11.2	47414042	47430799	10	0	-1.026265	-1.026265	4.394E-32
252,152,934,023	6535	TT13	chr11	11	p11.2	47568799	47620670	26	0	-0.797117	-0.797117	3.337E-59
252,152,934,023	6536	TT13	chr11	11	p11.2	47786209	47790012	3	0	-1.590722	-1.590722	6.717E-24
252,152,934,023	6537	TT13	chr11	11	p11.2	48000790	48005637	3	0	-1.400374	-1.400374	2.212E-23
252,152,934,023	6539	TT13	chr11	11	q12.1	55910143	55914165	3	0	-1.875248	-1.875248	9.916E-31
252,152,934,023	6549	TT13	chr11	11	q12.1	57705351	57713337	3	0	-0.861044	-0.861044	2.791E-11
252,152,934,023	6550	TT13	chr11	11	q12.1	58340765	58354022	9	0	-0.890225	-0.890225	2.208E-29
252,152,934,023	6551	TT13	chr11	11	q12.1	58909710	58942042	15	0	-0.696309	-0.696309	2.163E-29
252,152,934,023	6555	TT13	chr11	11	q12.1	59663297	59671141	6	0	-1.001119	-1.001119	1.083E-21
252,152,934,023	6556	TT13	chr11	11	q12.1	59837689	59843561	4	0	-1.259136	-1.259136	7.036E-23
252,152,934,023	6559	TT13	chr11	11	q12.2	60377746	60416381	16	0	-1.036	-1.036	1.177E-55
252,152,934,023	6561	TT13	chr11	11	q12.2	60581667	60585476	3	0	-1.482796	-1.482796	2.891E-21
252,152,934,023	6564	TT13	chr11	11	q12.2	60669438	60719900	24	0	-1.085099	-1.085099	1.108E-79
252,152,934,023	6574	TT13	chr11	11	q12.2	61303739	61356517	25	0	-0.79983	-0.79983	5.306E-40
252,152,934,023	6578	TT13	chr11	11	q12.2	61579557	61599978	20	0	-0.833469	-0.833469	2.318E-40
252,152,934,023	6580	TT13	chr11	11	q12.3	61720684	61738716	10	0	-0.779587	-0.779587	8.41E-20
252,152,934,023	6582	TT13	chr11	11	q12.3	62102564	62124627	6	0	-1.212305	-1.212305	2.845E-30
252,152,934,023	6583	TT13	chr11	11	q12.3	62312437	62316295	4	0	-1.424959	-1.424959	2.541E-15
252,152,934,023	6584	TT13	chr11	11	q12.3	62366474	62499137	64	0	-0.429607	-0.429607	3.158E-29
252,152,934,023	6590	TT13	chr11	11	q13.1 - q13.3	63434251	68928165	2272	0	-0.296575	-0.296575	4.900e-324
252,152,934,023	6591	TT13	chr11	11	q13.1	63437832	63451323	8	0	-1.473352	-1.473352	1.872E-39
252,152,934,023	6604	TT13	chr11	11	q13.1	64467351	64696757	129	0	-0.656397	-0.656397	1.138E-58
252,152,934,023	6605	TT13	chr11	11	q13.1	64644515	64647643	4	0	-1.764212	-1.764212	1.121E-14
252,152,934,023	6612	TT13	chr11	11	q13.1	65309389	65431718	58	0	-0.92603	-0.92603	7.216E-70
252,152,934,023	6621	TT13	chr11	11	q13.1	65807239	65842381	19	0	-0.913755	-0.913755	8.613E-28
252,152,934,023	6622	TT13	chr11	11	q13.1	65823398	65831005	5	0	-0.279197	-0.279197	1.377E-10
252,152,934,023	6631	TT13	chr11	11	q13.2	66608193	66611764	3	0	-1.577861	-1.577861	4.894E-18
252,152,934,023	6637	TT13	chr11	11	q13.2	67051748	67087111	14	0	-0.883063	-0.883063	1.426E-16
252,152,934,023	6638	TT13	chr11	11	q13.2	67161345	67294515	59	0	-0.827637	-0.827637	1.021E-51
252,152,934,023	6640	TT13	chr11	11	q13.2	67574343	67818566	26	0	-0.943065	-0.943065	3.31E-33
252,152,934,023	6641	TT13	chr11	11	q13.2	67886087	67896664	7	0	-1.367148	-1.367148	5.09E-25
252,152,934,023	6645	TT13	chr11	11	q13.2	68191411	68207577	10	0	-0.962697	-0.962697	5.837E-17
252,152,934,023	6647	TT13	chr11	11	q13.3	68432948	68458288	12	0	-0.695865	-0.695865	1.154E-23
252,152,934,023	6648	TT13	chr11	11	q13.3	68513511	68522318	5	0	-0.871629	-0.871629	5.796E-17
252,152,934,023	6650	TT13	chr11	11	q13.3	68812002	68826488	7	0	-0.884538	-0.884538	1.689E-10
252,152,934,023	6652	TT13	chr11	11	q13.3	69449751	69501368	24	0	-1.274115	-1.274115	6.319E-113
252,152,934,023	6656	TT13	chr11	11	q13.3	70112043	70147881	33	0	-0.476706	-0.476706	4.162E-28
252,152,934,023	6657	TT13	chr11	11	q13.3	70195647	70201726	4	0	-1.158641	-1.158641	3.121E-21
252,152,934,023	6659	TT13	chr11	11	q13.3	70302169	70308262	4	0	-1.67599	-1.67599	2.535E-35
252,152,934,023	6661	TT13	chr11	11	q13.4	70505060	70517728	6	0	-1.122241	-1.122241	1.398E-24
252,152,934,023	6664	TT13	chr11	11	q13.4	71157788	71166146	5	0	-1.65261	-1.65261	1.702E-42
252,152,934,023	6677	TT13	chr11	11	q13.4	73280098	73286040	4	0	-1.405839	-1.405839	2.217E-28
252,152,934,023	6678	TT13	chr11	11	q13.4	73306697	73310951	4	0	-1.07494	-1.07494	6.598E-16
252,152,934,023	6679	TT13	chr11	11	q13.4	73468798	73487451	11	0	-0.927299	-0.927299	1.03E-35
252,152,934,023	6681	TT13	chr11	11	q13.4	73691098	73698179	5	0	-0.799851	-0.799851	6.281E-13
252,152,934,023	6682	TT13	chr11	11	q13.4	73835993	73849979	6	0	-0.637727	-0.637727	2.772E-11
252,152,934,023	6683	TT13	chr11	11	q13.4	74017371	74115087	44	0	-0.540877	-0.540877	6.929E-48
252,152,934,023	6691	TT13	chr11	11	q13.5	75270381	75297561	12	0	-0.966472	-0.966472	1.372E-35
252,152,934,023	6703	TT13	chr11	11	q13.5	76750433	76756760	5	0	-1.874125	-1.874125	8.245E-40
252,152,934,023	6704	TT13	chr11	11	q13.5	76848437	76862747	7	0	-0.660365	-0.660365	4.965E-12
252,152,934,023	6705	TT13	chr11	11	q14.1	77181269	77204942	9	0	-0.95499	-0.95499	6.763E-32
252,152,934,023	6708	TT13	chr11	11	q14.1	77898052	77910028	7	0	-1.272685	-1.272685	1.202E-39
252,152,934,023	6713	TT13	chr11	11	q14.1	78584670	78617579	20	0	-0.607202	-0.607202	1.148E-28
252,152,934,023	6715	TT13	chr11	11	q14.1	79146004	79153538	6	0	-1.727021	-1.727021	1.153E-44
252,152,934,023	6721	TT13	chr11	11	q14.1	83903383	83909103	4	0	-1.424802	-1.424802	2.346E-30
252,152,934,023	6722	TT13	chr11	11	q14.1	84013584	84022116	5	0	-1.037869	-1.037869	6.762E-20

252,152,934,023	6724	TT13	chr11	11	q14.2	85769301	85829457	24	0	-0.545601	-0.545601	2.749E-28
252,152,934,023	6725	TT13	chr11	11	q14.2	85955110	85958793	3	0	-1.654703	-1.654703	1.174E-28
252,152,934,023	6726	TT13	chr11	11	q14.2	86141566	86146534	4	0	-1.835666	-1.835666	5.706E-34
252,152,934,023	6733	TT13	chr11	11	q14.2	86993913	86999144	4	0	-1.267296	-1.267296	1.058E-23
252,152,934,023	6734	TT13	chr11	11	q14.2	88239415	88245280	4	0	-1.641472	-1.641472	1.622E-34
252,152,934,023	6736	TT13	chr11	11	q14.3	89218485	89227408	6	0	-1.112582	-1.112582	2.736E-28
252,152,934,023	6741	TT13	chr11	11	q14.3	92700099	92706410	4	0	-1.320843	-1.320843	5.302E-25
252,152,934,023	6749	TT13	chr11	11	q21	94130874	94139009	6	0	-1.13588	-1.13588	8.369E-29
252,152,934,023	6750	TT13	chr11	11	q21	94237793	94303240	31	0	-0.550918	-0.550918	4.419E-35
252,152,934,023	6751	TT13	chr11	11	q21	94243686	94246411	3	0	-1.66091	-1.66091	3.111E-13
252,152,934,023	6754	TT13	chr11	11	q21	94767201	94829645	27	0	-0.615672	-0.615672	1.316E-38
252,152,934,023	6755	TT13	chr11	11	q21	94961093	94968667	5	0	-1.297423	-1.297423	1.066E-31
252,152,934,023	6762	TT13	chr11	11	q22.1	100994153	101003165	9	0	-1.077562	-1.077562	1.462E-35
252,152,934,023	6763	TT13	chr11	11	q22.1	101452901	101459930	4	0	-1.076127	-1.076127	1.514E-15
252,152,934,023	6764	TT13	chr11	11	q22.1	101976251	101989130	7	0	-0.852127	-0.852127	9.113E-21
252,152,934,023	6765	TT13	chr11	11	q22.2	102216571	102220390	3	0	-1.618553	-1.618553	1.625E-27
252,152,934,023	6767	TT13	chr11	11	q22.3	102953909	103076284	62	0	-0.301265	-0.301265	1.569E-20
252,152,934,023	6768	TT13	chr11	11	q22.3	103903695	103909613	4	0	-1.014152	-1.014152	9.32E-18
252,152,934,023	6804	TT13	chr11	11	q23.3	116638333	116664870	17	0	-0.936474	-0.936474	6.784E-53
252,152,934,023	6805	TT13	chr11	11	q23.3	116657948	116662010	4	0	-1.872625	-1.872625	1.213E-10
252,152,934,023	6810	TT13	chr11	11	q23.3	117296313	117302780	4	0	-0.872654	-0.872654	4.807E-12
252,152,934,023	6812	TT13	chr11	11	q23.3	117746224	117749034	3	0	-1.595647	-1.595647	2.859E-25
252,152,934,023	6813	TT13	chr11	11	q23.3	117846567	117860560	9	0	-1.288424	-1.288424	7.185E-50
252,152,934,023	6814	TT13	chr11	11	q23.3	118014122	118026311	9	0	-1.255768	-1.255768	5.141E-43
252,152,934,023	6815	TT13	chr11	11	q23.3	118303478	118311331	5	0	-1.059032	-1.059032	7.938E-21
252,152,934,023	6816	TT13	chr11	11	q23.3	118475268	118506831	16	0	-0.870197	-0.870197	2.103E-40
252,152,934,023	6817	TT13	chr11	11	q23.3	118660474	118665812	5	0	-1.07968	-1.07968	3.056E-19
252,152,934,023	6825	TT13	chr11	11	q23.3	119225829	119237202	7	0	-1.34316	-1.34316	4.136E-25
252,152,934,023	6827	TT13	chr11	11	q23.3	119595335	119618860	11	0	-0.746219	-0.746219	7.728E-24
252,152,934,023	6831	TT13	chr11	11	q23.3	120194236	120210904	10	0	-1.185994	-1.185994	4.878E-50
252,152,934,023	6833	TT13	chr11	11	q23.3	120433865	120438533	4	0	-1.526857	-1.526857	8.203E-30
252,152,934,023	6840	TT13	chr11	11	q24.1	122748165	122758834	5	0	-0.798787	-0.798787	4.803E-14
252,152,934,023	6841	TT13	chr11	11	q24.1	122846045	122857207	6	0	-1.385578	-1.385578	8.904E-41
252,152,934,023	6842	TT13	chr11	11	q24.1	123062012	123069918	5	0	-1.128736	-1.128736	2.606E-21
252,152,934,023	6847	TT13	chr11	11	q24.2	124272171	124275707	3	0	-1.194149	-1.194149	5.408E-16
252,152,934,023	6849	TT13	chr11	11	q24.2	124608870	124634483	16	0	-1.515054	-1.515054	8.146E-97
252,152,934,023	6853	TT13	chr11	11	q24.2	124930946	124936382	4	0	-1.277432	-1.277432	3.742E-23
252,152,934,023	6854	TT13	chr11	11	q24.2	124959076	124975549	9	0	-0.871627	-0.871627	1.167E-26
252,152,934,023	6859	TT13	chr11	11	q24.2	126136004	126176743	22	0	-0.729537	-0.729537	1.926E-44
252,152,934,023	6860	TT13	chr11	11	q24.2	126223710	126227552	3	0	-1.536469	-1.536469	4.161E-19
252,152,934,023	6863	TT13	chr11	11	q24.2	126872555	126875921	3	0	-1.424801	-1.424801	3.185E-22
252,152,934,023	6877	TT13	chr11	11	q24.3	130056825	130068655	7	0	-1.488892	-1.488892	1.032E-21
252,152,934,023	6878	TT13	chr11	11	q24.3	130182493	130186508	4	0	-1.592109	-1.592109	2.162E-31
252,152,934,023	6883	TT13	chr11	11	q24.3	130781203	130797336	7	0	-0.732855	-0.732855	2.184E-17
252,152,934,023	6884	TT13	chr11	11	q25	130949738	130957068	3	0	-0.87951	-0.87951	4.286E-12
252,152,934,023	6885	TT13	chr11	11	q25	131556686	131560194	3	0	-1.753816	-1.753816	1.088E-26
252,152,934,023	6886	TT13	chr11	11	q25	131778700	131784074	4	0	-1.335873	-1.335873	6.857E-27
252,152,934,023	6887	TT13	chr11	11	q25	132949848	132954250	3	0	-1.375643	-1.375643	6.083E-21
252,152,934,023	6890	TT13	chr11	11	q25	133791772	133841143	25	0	-0.840314	-0.840314	4.883E-22
252,152,934,023	6891	TT13	chr11	11	q25	133791772	134215782	202	0	-0.355436	-0.355436	2.229E-105
252,152,934,023	6892	TT13	chr11	11	q25	133905271	133921481	10	0	-0.959407	-0.959407	9.971E-15
252,152,934,023	6902	TT13	chr12	12	p13.33	230421	314207	44	0	-0.550621	-0.550621	6.135E-51
252,152,934,023	6904	TT13	chr12	12	p13.33	675545	758647	42	0	-0.413688	-0.413688	2.603E-30
252,152,934,023	6905	TT13	chr12	12	p13.33	680835	684180	3	0	-1.494202	-1.494202	4.128E-13
252,152,934,023	6906	TT13	chr12	12	p13.33	716094	720255	3	0	-1.518877	-1.518877	2.3E-14
252,152,934,023	6909	TT13	chr12	12	p13.33	1095928	1103372	5	0	-1.176913	-1.176913	1.949E-28
252,152,934,023	6910	TT13	chr12	12	p13.33	1739965	1756693	11	0	-1.406585	-1.406585	1.569E-49
252,152,934,023	6922	TT13	chr12	12	p13.33	3178420	3207808	16	0	-0.784196	-0.784196	7.818E-41
252,152,934,023	6931	TT13	chr12	12	p13.32	5152613	5155716	3	0	-1.742342	-1.742342	4.071E-29
252,152,934,023	6932	TT13	chr12	12	p13.31	5535744	5547660	7	0	-0.612691	-0.612691	9.721E-12
252,152,934,023	6933	TT13	chr12	12	p13.31	5996726	6000292	3	0	-1.974228	-1.974228	1.264E-33
252,152,934,023	6934	TT13	chr12	12	p13.31	6051625	6056490	4	0	-1.512203	-1.512203	1.776E-31
252,152,934,023	6940	TT13	chr12	12	p13.31	6577916	7049790	232	0	-0.402703	-0.402703	1.175E-151
252,152,934,023	6941	TT13	chr12	12	p13.31	6581556	6589045	4	0	-1.461775	-1.461775	6.844E-17
252,152,934,023	6960	TT13	chr12	12	p13.31	8775453	8782521	4	0	-1.055199	-1.055199	4.225E-18
252,152,934,023	6961	TT13	chr12	12	p13.31	8832266	8855207	12	0	-0.756846	-0.756846	3.189E-26
252,152,934,023	6962	TT13	chr12	12	p13.31	9062802	9070712	5	0	-0.992134	-0.992134	4.129E-20
252,152,934,023	6963	TT13	chr12	12	p13.31	9213539	9223334	5	0	-0.927408	-0.927408	2.36E-17
252,152,934,023	6968	TT13	chr12	12	p13.2	10869583	10877763	6	0	-1.052713	-1.052713	2.245E-25
252,152,934,023	6970	TT13	chr12	12	p13.2	11800304	11805269	4	0	-1.516945	-1.516945	9.406E-25
252,152,934,023	6971	TT13	chr12	12	p13.2	12417837	12422830	4	0	-1.451734	-1.451734	2.907E-28
252,152,934,023	6972	TT13	chr12	12	p13.2	12502215	12511974	6	0	-1.823108	-1.823108	1.273E-58
252,152,934,023	6973	TT13	chr12	12	p13.2	12599418	12722679	56	0	-0.489197	-0.489197	1.301E-47
252,152,934,023	6974	TT13	chr12	12	p13.2	12603013	12606432	3	0	-1.387585	-1.387585	4.331E-11
252,152,934,023	6975	TT13	chr12	12	p13.2	12621251	12632327	7	0	-1.017231	-1.017231	9.084E-10
252,152,934,023	6977	TT13	chr12	12	p13.1	12867075	12881712	9	0	-1.34785	-1.34785	1.488E-48
252,152,934,023	6978	TT13	chr12	12	p13.1	12937478	12942691	5	0	-1.399238	-1.399238	9.575E-33
252,152,934,023	6979	TT13	chr12	12	p13.1	13042053	13047196	6	0	-1.354298	-1.354298	2.131E-35
252,152,934,023	6981	TT13	chr12	12	p13.1	13196732	13200527	3	0	-1.73877	-1.73877	5.476E-28
252,152,934,023	6982	TT13	chr12	12	p13.1	13249490	13259721	6	0	-0.826036	-0.826036	1.18E-16
252,152,934,023	6983	TT13	chr12	12	p13.1	14131575	14136336	4	0	-1.342361	-1.342361	1.011E-22
252,152,934,023	6984	TT13	chr12	12	p13.1	14509789	14521169	8	0	-1.071118	-1.071118	6.851E-34
252,152,934,023	6985	TT13	chr12	12	p13.1	14717811	14722600	4	0	-1.206212	-1.206212	2.748E-22
252,152,934,023	6986	TT13	chr12	12	p12.3	15473350	15478658	5	0	-1.506736	-1.506736	2.141E-38
252,152,934,023	6988	TT13	chr12	12	p12.3	16061029	16065936	3	0	-1.32191	-1.32191	2.329E-21
252,152,934,023	6989	TT13	chr12	12	p12.3	18647619	18657193	6	0	-0.925891	-0.925891	2.212E-21
252,152,934,023	6990	TT13	chr12	12	p12.3	19282053	19285386	3	0	-1.780874	-1.780874	5.037E-30
252,152,934,023	6992	TT13	chr12	12	p12.3	19489411	19497187	6	0	-1.324017	-1.324017	6.446E-35
252,152,934,023	6993	TT13	chr12	12	p12.3	19590680	19595967	4	0	-1.616992	-1.616992	3.441E-30
252,152,934,023	6996	TT13	chr12	12	p12.2	20961362	20965985	4	0	-1.365932	-1.365932	1.883E-27
252,152,934,023	6997	TT13	chr12	12	p12.1	21678913	21682538	3	0	-1.400456	-1.400456	2.78E-21
252,152,934,023	6998	TT13	chr12	12	p12.1	21811496	21832929	11	0	-1.126395	-1.126395	7.427E-49
252,152,934,023	7003	TT13	chr12	12	p12.1	25015703	25107159	46	0	-0.503822	-0.503822	1.129E-42
252,152,934,023	7004	TT13	chr12	12	p12.1	25017254	25021595	3	0	-1.48679	-1.48679	8.432E-12
252,152,934,023	7005	TT13	chr12	12	p12.1	25400422	25407415	5	0	-1.372389	-1.372389	2.125E-32
252,152,934,023	7006	TT13	chr12	12	p12.1	25517037	25549568	26	0	-0.767177	-0.767177	9.793E-54

252,152,934,023	7007	TT13	chr12	12	p12.1	25538002	25541573	4	0	-2.069683	-2.069683	3.538E-20
252,152,934,023	7008	TT13	chr12	12	p12.1	26107686	26117732	6	0	-0.970702	-0.970702	3.409E-22
252,152,934,023	7009	TT13	chr12	12	p12.1	26266480	26280157	9	0	-1.682809	-1.682809	3.737E-71
252,152,934,023	7010	TT13	chr12	12	p12.1	26344725	26352451	5	0	-1.314964	-1.314964	2.71E-30
252,152,934,023	7011	TT13	chr12	12	p11.23	26935726	26939602	3	0	-1.738413	-1.738413	2.588E-27
252,152,934,023	7012	TT13	chr12	12	p11.23	26984458	26994117	5	0	-1.804619	-1.804619	1.066E-49
252,152,934,023	7013	TT13	chr12	12	p11.23	27087501	27095511	5	0	-0.89267	-0.89267	2.587E-17
252,152,934,023	7014	TT13	chr12	12	p11.23	27395930	27399439	3	0	-1.636675	-1.636675	1.588E-27
252,152,934,023	7018	TT13	chr12	12	p11.22	28340896	28358370	6	0	-1.08885	-1.08885	3.85E-29
252,152,934,023	7019	TT13	chr12	12	p11.22	29300917	29307172	3	0	-1.112452	-1.112452	2.073E-15
252,152,934,023	7020	TT13	chr12	12	p11.22	29406639	29419794	5	0	-0.921445	-0.921445	3.012E-17
252,152,934,023	7021	TT13	chr12	12	p11.22	29540336	29542222	3	0	-2.255846	-2.255846	4.493E-32
252,152,934,023	7033	TT13	chr12	12	p11.21	32540560	32555670	8	0	-1.432851	-1.432851	2.792E-52
252,152,934,023	7034	TT13	chr12	12	p11.21	32674474	32683485	7	0	-0.809587	-0.809587	2.445E-19
252,152,934,023	7035	TT13	chr12	12	p11.21	32712627	32720999	10	0	-1.116084	-1.116084	8.667E-47
252,152,934,023	7041	TT13	chr12	12	q12	40493401	40505788	6	0	-0.826445	-0.826445	7.363E-17
252,152,934,023	7042	TT13	chr12	12	q12	40615702	40619978	3	0	-1.773	-1.773	7.432E-28
252,152,934,023	7043	TT13	chr12	12	q12	40743740	40748357	3	0	-1.535807	-1.535807	1.161E-22
252,152,934,023	7045	TT13	chr12	12	q12	42531728	42540492	5	0	-1.018174	-1.018174	1.063E-20
252,152,934,023	7046	TT13	chr12	12	q12	42617907	42634368	7	0	-1.589339	-1.589339	1.587E-55
252,152,934,023	7047	TT13	chr12	12	q12	42664771	42671152	4	0	-1.188387	-1.188387	6.579E-18
252,152,934,023	7048	TT13	chr12	12	q12	42738999	42748613	4	0	-0.935843	-0.935843	4.501E-15
252,152,934,023	7050	TT13	chr12	12	q12	42979841	43007262	14	0	-0.800923	-0.800923	3.403E-32
252,152,934,023	7051	TT13	chr12	12	q12	43941792	43969324	14	0	-0.85131	-0.85131	3.917E-36
252,152,934,023	7054	TT13	chr12	12	q12	45442232	45446268	4	0	-1.606482	-1.606482	6.288E-32
252,152,934,023	7055	TT13	chr12	12	q12	45566682	45570550	3	0	-1.568444	-1.568444	1.462E-21
252,152,934,023	7056	TT13	chr12	12	q12	45607228	45611829	4	0	-1.331482	-1.331482	1.117E-20
252,152,934,023	7057	TT13	chr12	12	q12	46120090	46125125	3	0	-1.664859	-1.664859	2.789E-26
252,152,934,023	7058	TT13	chr12	12	q12	46381079	46396788	8	0	-1.220726	-1.220726	7.358E-43
252,152,934,023	7060	TT13	chr12	12	q13.11	46762961	46779659	11	0	-1.352391	-1.352391	1.865E-61
252,152,934,023	7061	TT13	chr12	12	q13.11	47216556	47228816	8	0	-0.639846	-0.639846	1.578E-13
252,152,934,023	7062	TT13	chr12	12	q13.11	47470238	47476740	4	0	-1.186919	-1.186919	8.282E-22
252,152,934,023	7063	TT13	chr12	12	q13.11	47563336	47566856	3	0	-0.875834	-0.875834	4.825E-10
252,152,934,023	7064	TT13	chr12	12	q13.11	47577443	47632930	26	0.460979	0	0.460979	1.661E-33
252,152,934,023	7067	TT13	chr12	12	q13.11	48204884	48215823	8	0	-0.874071	-0.874071	8.319E-23
252,152,934,023	7072	TT13	chr12	12	q13.11 - q13.12	48719959	49836462	482	0	-0.28043	-0.28043	1.648E-93
252,152,934,023	7073	TT13	chr12	12	q13.11	48722841	48728516	4	0	-2.750872	-2.750872	8.032E-51
252,152,934,023	7074	TT13	chr12	12	q13.11	48890654	48925336	13	0	-1.227465	-1.227465	3.415E-46
252,152,934,023	7075	TT13	chr12	12	q13.11	49032351	49038827	7	0	-1.466657	-1.466657	1.019E-36
252,152,934,023	7076	TT13	chr12	12	q13.12	49175272	49184851	10	0	-1.127882	-1.127882	3.751E-23
252,152,934,023	7078	TT13	chr12	12	q13.12	49304300	49319940	8	0	-1.039551	-1.039551	1.445E-18
252,152,934,023	7080	TT13	chr12	12	q13.12	49481052	49490960	6	0	-1.219949	-1.219949	1.034E-18
252,152,934,023	7108	TT13	chr12	12	q13.13	52222241	52235712	7	0.320164	0	0.320164	1.99E-13
252,152,934,023	7111	TT13	chr12	12	q13.13	52442652	52474270	17	0	-0.868364	-0.868364	4.681E-14
252,152,934,023	7115	TT13	chr12	12	q13.13	52991064	52998518	4	0	-0.894852	-0.894852	8.369E-14
252,152,934,023	7116	TT13	chr12	12	q13.13	53062213	53088375	13	0	-0.893527	-0.893527	2.379E-34
252,152,934,023	7131	TT13	chr12	12	q13.13	54140742	54149430	4	0	-1.290326	-1.290326	1.966E-21
252,152,934,023	7137	TT13	chr12	12	q13.13	54611250	54619571	6	0	-0.519483	-0.519483	8.568E-14
252,152,934,023	7138	TT13	chr12	12	q13.13	54761095	54786694	13	0	-0.912238	-0.912238	3.744E-32
252,152,934,023	7142	TT13	chr12	12	q13.2	56099636	56102952	3	0	-1.292691	-1.292691	1.609E-15
252,152,934,023	7145	TT13	chr12	12	q13.2	56395540	56404692	6	0	-1.452754	-1.452754	2.021E-40
252,152,934,023	7150	TT13	chr12	12	q13.3	56649876	56662701	7	0	-1.319195	-1.319195	5.765E-35
252,152,934,023	7151	TT13	chr12	12	q13.3	56690275	56698163	5	0	-1.027225	-1.027225	9.679E-20
252,152,934,023	7152	TT13	chr12	12	q13.3	56881124	56889887	4	0	-1.368981	-1.368981	4.565E-26
252,152,934,023	7156	TT13	chr12	12	q13.3	57175974	57186362	5	0	-1.738144	-1.738144	4.389E-49
252,152,934,023	7157	TT13	chr12	12	q13.3	57395971	57403889	6	0	-0.847332	-0.847332	1.036E-16
252,152,934,023	7158	TT13	chr12	12	q13.3	57480585	57485731	3	0	-1.381237	-1.381237	1.878E-19
252,152,934,023	7163	TT13	chr12	12	q13.3	57939182	57944711	5	0	-1.972863	-1.972863	3.561E-30
252,152,934,023	7164	TT13	chr12	12	q13.3	57995799	58027260	20	0	-1.493503	-1.493503	1.362E-56
252,152,934,023	7168	TT13	chr12	12	q14.1	59988376	59991613	3	0	-1.550332	-1.550332	5.818E-24
252,152,934,023	7171	TT13	chr12	12	q14.1	62992307	63004042	16	0	-1.127193	-1.127193	1.392E-71
252,152,934,023	7266	TT13	chr12	12	q23.1	100949725	100970644	12	0	-1.171845	-1.171845	1.347E-56
252,152,934,023	7267	TT13	chr12	12	q23.1	101109078	101123425	3	0	-0.960915	-0.960915	8.604E-12
252,152,934,023	7268	TT13	chr12	12	q23.2	102090024	102094256	3	0	-1.497662	-1.497662	2.908E-23
252,152,934,023	7271	TT13	chr12	12	q23.2	103349683	103353153	3	0	-2.180827	-2.180827	5.688E-36
252,152,934,023	7272	TT13	chr12	12	q23.3	103886177	103891964	4	0	-1.277972	-1.277972	3.864E-23
252,152,934,023	7273	TT13	chr12	12	q23.3	104034879	104040137	4	0	-1.242313	-1.242313	7.154E-22
252,152,934,023	7274	TT13	chr12	12	q23.3	104233414	104238255	4	0	-1.220173	-1.220173	3.979E-17
252,152,934,023	7291	TT13	chr12	12	q23.3	106974605	106981968	5	0	-1.934738	-1.934738	3.968E-34
252,152,934,023	7292	TT13	chr12	12	q23.3	107166250	107171271	4	0	-1.146293	-1.146293	8.352E-21
252,152,934,023	7293	TT13	chr12	12	q23.3	107346618	107351649	4	0	-1.707308	-1.707308	6.374E-36
252,152,934,023	7294	TT13	chr12	12	q23.3	107482477	107489356	3	0	-0.919307	-0.919307	5.331E-11
252,152,934,023	7297	TT13	chr12	12	q23.3	108150388	108174688	13	0	-0.983584	-0.983584	5.485E-44
252,152,934,023	7336	TT13	chr12	12	q24.13	113492289	113627111	60	0	-0.634808	-0.634808	4.499E-73
252,152,934,023	7337	TT13	chr12	12	q24.13	113590755	113597478	4	0	-2.01599	-2.01599	3.084E-17
252,152,934,023	7338	TT13	chr12	12	q24.13	113768359	113774529	4	0	-1.361598	-1.361598	2.155E-24
252,152,934,023	7340	TT13	chr12	12	q24.21	114832611	114853108	10	0	-1.429568	-1.429568	8.673E-64
252,152,934,023	7341	TT13	chr12	12	q24.21	115109251	115135453	12	0	-1.304271	-1.304271	2.598E-60
252,152,934,023	7342	TT13	chr12	12	q24.21	116711535	116717834	4	0	-1.319053	-1.319053	6.61E-26
252,152,934,023	7343	TT13	chr12	12	q24.22	117170809	117190337	11	0	-0.986014	-0.986014	3.54E-37
252,152,934,023	7347	TT13	chr12	12	q24.22	117445947	117450521	4	0	-1.250728	-1.250728	1.549E-23
252,152,934,023	7360	TT13	chr12	12	q24.23	120125540	120131593	7	0	-1.210089	-1.210089	5.933E-36
252,152,934,023	7383	TT13	chr12	12	q24.31	122229528	122271171	20	0	-1.39962	-1.39962	1.123E-93
252,152,934,023	7396	TT13	chr12	12	q24.31	123319418	123355438	18	0	-1.083937	-1.083937	1.983E-56
252,152,934,023	7402	TT13	chr12	12	q24.31	123846339	123875180	13	0	-1.394916	-1.394916	5.83E-76
252,152,934,023	7408	TT13	chr12	12	q24.31	124419194	124434666	10	0	-1.038253	-1.038253	9.204E-35
252,152,934,023	7409	TT13	chr12	12	q24.31	124455811	124462550	3	0	-1.129329	-1.129329	1.164E-15
252,152,934,023	7410	TT13	chr12	12	q24.31	124763456	124931849	84	0	-0.654301	-0.654301	1.316E-98
252,152,934,023	7411	TT13	chr12	12	q24.31	124820914	124830160	7	0	-1.83361	-1.83361	2.407E-24
252,152,934,023	7415	TT13	chr12	12	q24.31	125433500	125442007	5	0	-0.724172	-0.724172	8.173E-11
252,152,934,023	7416	TT13	chr12	12	q24.31	125464683	125484712	10	0	-0.91861	-0.91861	1.991E-29
252,152,934,023	7417	TT13	chr12	12	q24.31	125535008	125552032	8	0	-1.111297	-1.111297	1.46E-34
252,152,934,023	7418	TT13	chr12	12	q24.31	125593112	125600621	4	0	-1.04189	-1.04189	1.324E-16
252,152,934,023	7419	TT13	chr12	12	q24.32	127208385	127212723	3	0	-1.26414	-1.26414	3.171E-17
252,152,934,023	7420	TT13	chr12	12	q24.32	127629887	127653849	9	0	-0.933278	-0.933278	2.722E-28
252,152,934,023	7423	TT13	chr12	12	q24.33	129302665	129339492	14	0	-0.761216	-0.761216	1.653E-33

252,152,934,023	7424	TT13	chr12	12	q24.33	129416379	129434016	10	0	-0.790216	-0.790216	1.462E-27
252,152,934,023	7425	TT13	chr12	12	q24.33	130180064	130190314	6	0	-0.825199	-0.825199	3.444E-19
252,152,934,023	7426	TT13	chr12	12	q24.33	130384657	130390490	4	0	-1.412812	-1.412812	4.991E-28
252,152,934,023	7427	TT13	chr12	12	q24.33	130493287	130532086	19	0	-0.589994	-0.589994	1.723E-29
252,152,934,023	7428	TT13	chr12	12	q24.33	130644434	130648915	3	0	-1.868173	-1.868173	1.378E-28
252,152,934,023	7431	TT13	chr12	12	q24.33	130905840	130926198	11	0	-0.814111	-0.814111	3.769E-28
252,152,934,023	7441	TT13	chr12	12	q24.33	132184085	132196884	7	0	-1.09585	-1.09585	1.193E-32
252,152,934,023	7456	TT13	chr12	12	q24.33	133262369	133268428	4	0	-1.600148	-1.600148	1.36E-11
252,152,934,023	7462	TT13	chr13	13	q12.11	20691070	20772374	42	0	-0.77199	-0.77199	4.135E-61
252,152,934,023	7464	TT13	chr13	13	q12.11	20961973	21013860	25	0	-0.735747	-0.735747	4.563E-34
252,152,934,023	7465	TT13	chr13	13	q12.11	21097911	21100927	3	0	-1.63686	-1.63686	8.247E-21
252,152,934,023	7467	TT13	chr13	13	q12.11	21275506	21353149	33	0	-0.789637	-0.789637	9.973E-51
252,152,934,023	7476	TT13	chr13	13	q12.11	22243051	22250288	6	0	-2.239165	-2.239165	4.589E-58
252,152,934,023	7477	TT13	chr13	13	q12.11	22389899	22398078	3	0	-0.823003	-0.823003	1.822E-11
252,152,934,023	7478	TT13	chr13	13	q12.11	23267118	23273897	5	0	-1.37387	-1.37387	9.522E-28
252,152,934,023	7479	TT13	chr13	13	q12.12	23409089	23437045	12	0	-1.130478	-1.130478	1.413E-43
252,152,934,023	7482	TT13	chr13	13	q12.12	24150165	24158075	6	0	-1.293748	-1.293748	1.534E-29
252,152,934,023	7483	TT13	chr13	13	q12.12	24248411	24270793	11	0	-0.969501	-0.969501	2.542E-28
252,152,934,023	7484	TT13	chr13	13	q12.12	24462132	24482636	11	0	-0.964288	-0.964288	4.075E-28
252,152,934,023	7485	TT13	chr13	13	q12.12	24545805	24556108	4	0	-1.344332	-1.344332	1.402E-22
252,152,934,023	7489	TT13	chr13	13	q12.12	24878333	24915426	11	0	-0.756861	-0.756861	9.44E-18
252,152,934,023	7490	TT13	chr13	13	q12.12	25079941	25087350	4	0	-2.419275	-2.419275	1.205E-48
252,152,934,023	7495	TT13	chr13	13	q12.13	25741819	25747508	6	0	-1.418265	-1.418265	4.704E-34
252,152,934,023	7496	TT13	chr13	13	q12.13	25859411	25878454	12	0	-0.878498	-0.878498	1.728E-27
252,152,934,023	7497	TT13	chr13	13	q12.13	25940349	25949161	6	0	-1.26956	-1.26956	9.61E-25
252,152,934,023	7498	TT13	chr13	13	q12.13	26039313	26056496	8	0	-1.120236	-1.120236	1.151E-27
252,152,934,023	7499	TT13	chr13	13	q12.13	26081219	26089969	5	0	-1.182169	-1.182169	2.961E-23
252,152,934,023	7500	TT13	chr13	13	q12.13	26618772	26628790	6	0	-1.064452	-1.064452	1.393E-21
252,152,934,023	7504	TT13	chr13	13	q12.13	27130704	27135716	3	0	-1.217579	-1.217579	7.334E-18
252,152,934,023	7505	TT13	chr13	13	q12.13	27331624	27339320	6	0	-0.992369	-0.992369	3.93E-21
252,152,934,023	7506	TT13	chr13	13	q12.13	27740903	27747665	5	0	-1.41386	-1.41386	5.819E-33
252,152,934,023	7511	TT13	chr13	13	q12.2	28525529	28553990	17	0	-1.773221	-1.773221	4.43E-127
252,152,934,023	7514	TT13	chr13	13	q12.3	29067457	29070258	3	0	-2.709136	-2.709136	1.269E-39
252,152,934,023	7515	TT13	chr13	13	q12.3	29230689	29238675	6	0	-1.133131	-1.133131	1.276E-28
252,152,934,023	7516	TT13	chr13	13	q12.3	29292004	29294476	3	0	-1.769717	-1.769717	4.725E-23
252,152,934,023	7517	TT13	chr13	13	q12.3	30163544	30172791	6	0	-0.931701	-0.931701	2.56E-17
252,152,934,023	7518	TT13	chr13	13	q12.3	30422675	30426835	4	0	-1.763101	-1.763101	7.031E-34
252,152,934,023	7519	TT13	chr13	13	q12.3	30840880	30888045	21	0	-0.728241	-0.728241	1.455E-40
252,152,934,023	7520	TT13	chr13	13	q12.3	30880669	30883393	3	0	-1.644441	-1.644441	8.726E-10
252,152,934,023	7521	TT13	chr13	13	q12.3	30980115	31044591	37	0	-0.640243	-0.640243	1.821E-53
252,152,934,023	7522	TT13	chr13	13	q12.3	31035934	31041052	3	0	-1.513831	-1.513831	3.703E-10
252,152,934,023	7523	TT13	chr13	13	q12.3	31189193	31195289	5	0	-1.580425	-1.580425	5.739E-41
252,152,934,023	7526	TT13	chr13	13	q12.3	31714543	31781196	32	0	-0.564036	-0.564036	7.495E-36
252,152,934,023	7529	TT13	chr13	13	q13.1	32882699	32893200	6	0	-1.357997	-1.357997	2.212E-35
252,152,934,023	7530	TT13	chr13	13	q13.1	32998986	33004703	4	0	-1.235952	-1.235952	7.663E-22
252,152,934,023	7531	TT13	chr13	13	q13.1	33285440	33297966	6	0	-1.336693	-1.336693	3.888E-38
252,152,934,023	7533	TT13	chr13	13	q13.1	33918736	33934739	7	0	-1.287141	-1.287141	1.187E-39
252,152,934,023	7534	TT13	chr13	13	q13.3	35513053	35520298	5	0	-1.534143	-1.534143	3.48E-41
252,152,934,023	7542	TT13	chr13	13	q13.3	37572650	37576752	3	0	-1.809705	-1.809705	7.472E-28
252,152,934,023	7543	TT13	chr13	13	q13.3	37631471	37646294	7	0	-1.434374	-1.434374	1.772E-42
252,152,934,023	7544	TT13	chr13	13	q13.3	38932912	38943274	7	0	-1.129118	-1.129118	2.598E-33
252,152,934,023	7546	TT13	chr13	13	q13.3	39610059	39616403	5	0	-1.712972	-1.712972	4.2E-44
252,152,934,023	7547	TT13	chr13	13	q14.11	40175506	40180664	4	0	-1.251466	-1.251466	1.287E-21
252,152,934,023	7548	TT13	chr13	13	q14.11	40228973	40231658	3	0	-1.975879	-1.975879	6.744E-33
252,152,934,023	7549	TT13	chr13	13	q14.11	41234789	41245263	7	0	-0.878324	-0.878324	4.003E-19
252,152,934,023	7551	TT13	chr13	13	q14.11	41528223	41533050	3	0	-1.242756	-1.242756	4.071E-18
252,152,934,023	7552	TT13	chr13	13	q14.11	41632038	41639215	6	0	-1.332658	-1.332658	2.555E-37
252,152,934,023	7553	TT13	chr13	13	q14.11	41881169	41891113	8	0	-1.092667	-1.092667	5.118E-35
252,152,934,023	7554	TT13	chr13	13	q14.11	42143683	42149929	4	0	-0.966873	-0.966873	1.818E-15
252,152,934,023	7555	TT13	chr13	13	q14.11	42452757	42477371	12	0	-0.872358	-0.872358	1.9E-35
252,152,934,023	7556	TT13	chr13	13	q14.11	42532854	42535746	3	0	-1.898563	-1.898563	4.491E-32
252,152,934,023	7557	TT13	chr13	13	q14.11	42611231	42626378	8	0	-1.465865	-1.465865	1.147E-54
252,152,934,023	7558	TT13	chr13	13	q14.11	42843286	42850169	5	0	-1.390671	-1.390671	5.879E-32
252,152,934,023	7559	TT13	chr13	13	q14.11	43128106	43154034	13	0	-0.905361	-0.905361	1.294E-36
252,152,934,023	7560	TT13	chr13	13	q14.11	43987176	43993314	4	0	-1.299404	-1.299404	1.852E-25
252,152,934,023	7561	TT13	chr13	13	q14.11	44356729	44365756	6	0	-1.300142	-1.300142	1.493E-32
252,152,934,023	7562	TT13	chr13	13	q14.11	44449103	44457931	6	0	-0.839043	-0.839043	8.49E-18
252,152,934,023	7563	TT13	chr13	13	q14.11	44712828	44720039	4	0	-1.223114	-1.223114	2.619E-22
252,152,934,023	7564	TT13	chr13	13	q14.11	44946588	44951139	4	0	-1.389332	-1.389332	8.274E-20
252,152,934,023	7565	TT13	chr13	13	q14.11	44984558	44992048	6	0	-0.871489	-0.871489	8.726E-18
252,152,934,023	7567	TT13	chr13	13	q14.11	45147566	45171293	12	0	-0.915742	-0.915742	2.053E-38
252,152,934,023	7568	TT13	chr13	13	q14.12	45253190	45263063	5	0	-1.082826	-1.082826	4.432E-22
252,152,934,023	7569	TT13	chr13	13	q14.13	45883229	45887765	4	0	-1.585666	-1.585666	1.265E-32
252,152,934,023	7584	TT13	chr13	13	q14.2	48876536	48897894	11	0	-1.250296	-1.250296	6.324E-58
252,152,934,023	7585	TT13	chr13	13	q14.2	49104734	49108938	4	0	-1.457355	-1.457355	1.845E-24
252,152,934,023	7586	TT13	chr13	13	q14.2	49548240	49552156	3	0	-1.470773	-1.470773	5.081E-22
252,152,934,023	7587	TT13	chr13	13	q14.2	49793390	49800535	4	0	-1.136363	-1.136363	1.378E-18
252,152,934,023	7590	TT13	chr13	13	q14.2	50137868	50140498	3	0	-1.851856	-1.851856	1.635E-11
252,152,934,023	7591	TT13	chr13	13	q14.2	50137868	50164153	23	0	-0.822803	-0.822803	2.638E-29
252,152,934,023	7592	TT13	chr13	13	q14.2	50250202	50267758	11	0	-1.182295	-1.182295	4.337E-34
252,152,934,023	7594	TT13	chr13	13	q14.2	50508295	50511952	3	0	-1.609332	-1.609332	2.317E-18
252,152,934,023	7596	TT13	chr13	13	q14.2	50647274	50659403	11	0	-1.103194	-1.103194	1.892E-31
252,152,934,023	7597	TT13	chr13	13	q14.2	50697822	50708236	5	0	-2.211754	-2.211754	1.129E-44
252,152,934,023	7599	TT13	chr13	13	q14.3	51481542	51486874	3	0	-1.085077	-1.085077	4.383E-15
252,152,934,023	7600	TT13	chr13	13	q14.3	51793637	51800613	5	0	-1.050282	-1.050282	2.429E-21
252,152,934,023	7603	TT13	chr13	13	q14.3	52157656	52160490	3	0	-1.778257	-1.778257	3.876E-21
252,152,934,023	7611	TT13	chr13	13	q14.3	53020529	53034388	9	0	-1.190363	-1.190363	1.538E-42
252,152,934,023	7613	TT13	chr13	13	q14.3	53385536	53430507	40	0	-0.817113	-0.817113	3.051E-88
252,152,934,023	7614	TT13	chr13	13	q14.3	53387468	53401978	11	0	-1.333651	-1.333651	1.86E-12
252,152,934,023	7615	TT13	chr13	13	q14.3	53422873	53426456	4	0	-2.050765	-2.050765	8.231E-13
252,152,934,023	7616	TT13	chr13	13	q14.3	53771960	53779892	4	0	-1.22057	-1.22057	1.072E-23
252,152,934,023	7617	TT13	chr13	13	q14.3	54013191	54028076	3	0	-1.190569	-1.190569	7.631E-16
252,152,934,023	7620	TT13	chr13	13	q21.2	60968878	60972718	3	0	-1.570849	-1.570849	3.197E-25
252,152,934,023	7621	TT13	chr13	13	q21.32	67131860	67137011	4	0	-1.367113	-1.367113	1.387E-25
252,152,934,023	7622	TT13	chr13	13	q21.32	67194886	67198295	3	0	-1.692792	-1.692792	4.705E-27
252,152,934,023	7623	TT13	chr13	13	q21.32	67800816	67809104	5	0	-1.014289	-1.014289	1.289E-20

252,152,934,023	7624	TT13	chr13	13	q21.33	69558681	69561448	3	0	-1.844733	-1.844733	1.949E-27
252,152,934,023	7626	TT13	chr13	13	q21.33	72436388	72442284	4	0	-1.39008	-1.39008	1.103E-22
252,152,934,023	7627	TT13	chr13	13	q21.33 - q22.1	73298447	73307382	7	0	-1.121205	-1.121205	2.52E-33
252,152,934,023	7629	TT13	chr13	13	q22.1	73630549	73637982	5	0	-1.234825	-1.234825	1.424E-28
252,152,934,023	7633	TT13	chr13	13	q22.2	76207504	76213253	5	0	-1.203782	-1.203782	1.313E-20
252,152,934,023	7635	TT13	chr13	13	q22.3	77456449	77465373	7	0	-1.115329	-1.115329	5.658E-31
252,152,934,023	7636	TT13	chr13	13	q22.3	77549217	77603971	31	0	-0.62772	-0.62772	3.111E-43
252,152,934,023	7637	TT13	chr13	13	q22.3	77564739	77567927	3	0	-1.795159	-1.795159	4.528E-14
252,152,934,023	7638	TT13	chr13	13	q22.3	77598987	77602912	3	0	-1.538845	-1.538845	1.858E-10
252,152,934,023	7639	TT13	chr13	13	q22.3	77896921	77902530	3	0	-1.211268	-1.211268	4.826E-18
252,152,934,023	7640	TT13	chr13	13	q22.3	78045567	78053361	4	0	-0.903894	-0.903894	3.177E-14
252,152,934,023	7642	TT13	chr13	13	q31.1	79168919	79178668	6	0	-1.49607	-1.49607	8.147E-38
252,152,934,023	7646	TT13	chr13	13	q31.1	80910339	80932365	15	0	-1.003876	-1.003876	5.533E-49
252,152,934,023	7647	TT13	chr13	13	q31.1	81221625	81231551	7	0	-1.119887	-1.119887	2.697E-33
252,152,934,023	7652	TT13	chr13	13	q31.2	88317963	88331657	7	0	-1.091008	-1.091008	4.082E-31
252,152,934,023	7653	TT13	chr13	13	q31.3	90012370	90018429	4	0	-1.300428	-1.300428	1.235E-25
252,152,934,023	7654	TT13	chr13	13	q31.3	91996408	92005613	12	0	-1.371599	-1.371599	2.59E-70
252,152,934,023	7655	TT13	chr13	13	q31.3	92048327	92054518	5	0	-1.393844	-1.393844	1.346E-33
252,152,934,023	7656	TT13	chr13	13	q31.3	92941000	92942569	3	0	-1.339232	-1.339232	1.595E-20
252,152,934,023	7657	TT13	chr13	13	q31.3	93878059	93881663	3	0	-1.424778	-1.424778	2.107E-22
252,152,934,023	7658	TT13	chr13	13	q31.3	94103533	94111797	5	0	-1.132982	-1.132982	9.253E-28
252,152,934,023	7659	TT13	chr13	13	q32.1	95250354	95258947	6	0	-1.254497	-1.254497	6.197E-32
252,152,934,023	7660	TT13	chr13	13	q32.1	95358636	95367832	7	0	-1.450872	-1.450872	2.781E-44
252,152,934,023	7666	TT13	chr13	13	q32.1	96328214	96331854	3	0	-1.788082	-1.788082	1.342E-11
252,152,934,023	7667	TT13	chr13	13	q32.1	96576483	96592322	6	0	-1.013896	-1.013896	2.137E-23
252,152,934,023	7668	TT13	chr13	13	q32.1	96704741	96709374	4	0	-1.301091	-1.301091	2.047E-24
252,152,934,023	7669	TT13	chr13	13	q32.1	96738891	96748283	7	0	-1.05335	-1.05335	1.74E-29
252,152,934,023	7670	TT13	chr13	13	q32.1	97643260	97649927	4	0	-1.322988	-1.322988	9.935E-28
252,152,934,023	7671	TT13	chr13	13	q32.1	97997265	97999896	3	0	-2.208947	-2.208947	5.141E-38
252,152,934,023	7672	TT13	chr13	13	q32.1	98083941	98090381	4	0	-1.107142	-1.107142	2.024E-21
252,152,934,023	7673	TT13	chr13	13	q32.2	98625939	98629748	3	0	-1.6222	-1.6222	3.431E-28
252,152,934,023	7675	TT13	chr13	13	q32.2	98790645	98859536	37	0	-0.440845	-0.440845	4.082E-31
252,152,934,023	7676	TT13	chr13	13	q32.2	98794159	98797701	3	0	-1.502455	-1.502455	9.196E-13
252,152,934,023	7682	TT13	chr13	13	q32.3	100544845	100551177	4	0	-1.331607	-1.331607	6.643E-27
252,152,934,023	7683	TT13	chr13	13	q32.3	100609077	100652618	24	0	-1.462803	-1.462803	2.423E-134
252,152,934,023	7684	TT13	chr13	13	q32.3	100640496	100645522	4	0	-0.554758	-0.554758	1.623E-14
252,152,934,023	7685	TT13	chr13	13	q32.3	100726406	100742027	6	0	-1.573074	-1.573074	6.025E-47
252,152,934,023	7686	TT13	chr13	13	q32.3	100871566	100880125	6	0	-1.127265	-1.127265	6.409E-32
252,152,934,023	7688	TT13	chr13	13	q32.3	101178155	101189558	7	0	-0.96594	-0.96594	8.456E-27
252,152,934,023	7692	TT13	chr13	13	q33.1	102061286	102111391	27	0	-0.547765	-0.547765	5.705E-36
252,152,934,023	7693	TT13	chr13	13	q33.1	102066579	102071567	3	0	-1.424752	-1.424752	1.794E-10
252,152,934,023	7694	TT13	chr13	13	q33.1	102563975	102571548	5	0	-0.984913	-0.984913	1.277E-18
252,152,934,023	7695	TT13	chr13	13	q33.1	102714806	102726820	7	0	-0.993414	-0.993414	7.132E-31
252,152,934,023	7697	TT13	chr13	13	q33.1	103248526	103251698	3	0	-1.59689	-1.59689	2.037E-27
252,152,934,023	7698	TT13	chr13	13	q33.1	103421350	103457724	19	0	-0.735093	-0.735093	6.974E-42
252,152,934,023	7699	TT13	chr13	13	q33.3	107180744	107223312	24	0	-0.684767	-0.684767	1.688E-44
252,152,934,023	7700	TT13	chr13	13	q33.3	107184767	107190156	5	0	-1.669512	-1.669512	1.009E-13
252,152,934,023	7704	TT13	chr13	13	q33.3	108868860	108872912	4	0	-2.102932	-2.102932	2.564E-45
252,152,934,023	7705	TT13	chr13	13	q33.3	109144668	109152015	4	0	-1.071669	-1.071669	3.746E-19
252,152,934,023	7706	TT13	chr13	13	q33.3	109791724	109796247	3	0	-1.816979	-1.816979	4.516E-30
252,152,934,023	7712	TT13	chr13	13	q34	111181035	111184420	3	0	-1.218785	-1.218785	1.435E-11
252,152,934,023	7713	TT13	chr13	13	q34	111181035	111810666	265	0	-0.292458	-0.292458	2.635E-95
252,152,934,023	7714	TT13	chr13	13	q34	111211736	111216375	4	0	-1.314651	-1.314651	8.796E-16
252,152,934,023	7715	TT13	chr13	13	q34	111283865	111298630	8	0	-1.294025	-1.294025	8.456E-26
252,152,934,023	7716	TT13	chr13	13	q34	111357935	111374509	10	0	-1.789634	-1.789634	3.021E-58
252,152,934,023	7724	TT13	chr13	13	q34	112687262	115086913	991	0	-0.419202	-0.419202	4.900e-324
252,152,934,023	7725	TT13	chr13	13	q34	112707545	112730077	12	0	-2.062667	-2.062667	1.053E-55
252,152,934,023	7726	TT13	chr13	13	q34	112861856	112875692	6	0	-1.066724	-1.066724	3.735E-11
252,152,934,023	7735	TT13	chr13	13	q34	113620493	113813242	102	0	-0.898087	-0.898087	2.023E-80
252,152,934,023	7736	TT13	chr13	13	q34	113701133	113704453	3	0	-2.055787	-2.055787	2.569E-11
252,152,934,023	7739	TT13	chr13	13	q34	113860859	113864725	3	0	-1.710183	-1.710183	1.096E-29
252,152,934,023	7741	TT13	chr13	13	q34	114046284	114077003	14	0	-0.962308	-0.962308	4.89E-15
252,152,934,023	7746	TT13	chr13	13	q34	114502688	114517464	9	0	-1.181134	-1.181134	1.575E-12
252,152,934,023	7751	TT13	chr13	13	q34	114803512	114843971	23	0	-1.713943	-1.713943	1.656E-101
252,152,934,023	7752	TT13	chr13	13	q34	114810347	114817543	5	0	-2.655611	-2.655611	4.251E-10
252,152,934,023	7765	TT13	chr14	14	q11.2	21540231	21569461	16	0	-1.622275	-1.622275	2.938E-116
252,152,934,023	7768	TT13	chr14	14	q11.2	22595057	22962593	188	0	-0.816383	-0.816383	5.819E-274
252,152,934,023	7769	TT13	chr14	14	q11.2	22782629	22832572	23	0	-1.513822	-1.513822	5.015E-21
252,152,934,023	7772	TT13	chr14	14	q11.2	23300862	23359151	31	0	-0.743652	-0.743652	2.095E-53
252,152,934,023	7773	TT13	chr14	14	q11.2	23419374	23580140	95	0	-0.348334	-0.348334	7.051E-34
252,152,934,023	7774	TT13	chr14	14	q11.2	23446892	23450306	3	0	-1.342111	-1.342111	8.376E-11
252,152,934,023	7781	TT13	chr14	14	q11.2	23886941	23892560	8	0	-1.293831	-1.293831	1.975E-42
252,152,934,023	7783	TT13	chr14	14	q11.2	24043186	24058150	7	0	-1.304757	-1.304757	2.211E-34
252,152,934,023	7784	TT13	chr14	14	q11.2	24362332	24369414	3	0	-1.359365	-1.359365	2.417E-20
252,152,934,023	7787	TT13	chr14	14	q12	24661789	24667051	4	0	-1.111307	-1.111307	1.594E-18
252,152,934,023	7790	TT13	chr14	14	q12	24777360	24788020	7	0	-1.595925	-1.595925	5.955E-53
252,152,934,023	7793	TT13	chr14	14	q12	25517001	25522121	3	0	-1.299778	-1.299778	1.013E-21
252,152,934,023	7794	TT13	chr14	14	q12	27063534	27070881	5	0	-1.157807	-1.157807	3.356E-22
252,152,934,023	7795	TT13	chr14	14	q12	29231513	29256588	15	0	-0.759822	-0.759822	1.951E-30
252,152,934,023	7796	TT13	chr14	14	q12	30369545	30403885	20	0	-0.788009	-0.788009	2.461E-42
252,152,934,023	7797	TT13	chr14	14	q12	31339379	31348376	6	0	-1.05289	-1.05289	1.948E-22
252,152,934,023	7798	TT13	chr14	14	q12	31491683	31499141	9	0	-0.952484	-0.952484	9.943E-30
252,152,934,023	7799	TT13	chr14	14	q12	31671062	31681453	8	0	-1.02694	-1.02694	4.317E-31
252,152,934,023	7800	TT13	chr14	14	q12	31880644	31928659	26	0	-0.778944	-0.778944	2.24E-54
252,152,934,023	7801	TT13	chr14	14	q12	31887749	31890058	3	0	-1.97627	-1.97627	2.062E-11
252,152,934,023	7803	TT13	chr14	14	q12	32167696	32184239	6	0	-1.181842	-1.181842	5.143E-30
252,152,934,023	7804	TT13	chr14	14	q12	32544653	32549978	4	0	-1.620112	-1.620112	4.36E-32
252,152,934,023	7805	TT13	chr14	14	q12	32592535	32598829	4	0	-1.4605	-1.4605	9.388E-29
252,152,934,023	7806	TT13	chr14	14	q12	32668214	32678318	7	0	-1.017236	-1.017236	9.188E-28
252,152,934,023	7807	TT13	chr14	14	q13.1	33401486	33412363	6	0	-1.520408	-1.520408	1.412E-41
252,152,934,023	7809	TT13	chr14	14	q13.1	34268466	34272471	3	0	-1.520978	-1.520978	5.841E-24
252,152,934,023	7810	TT13	chr14	14	q13.1	34417757	34423166	5	0	-1.411054	-1.411054	1.907E-33
252,152,934,023	7812	TT13	chr14	14	q13.1	34929695	34950748	11	0	-0.893587	-0.893587	2.12E-30
252,152,934,023	7813	TT13	chr14	14	q13.1	35017199	35024144	3	0	-1.123847	-1.123847	4.404E-15
252,152,934,023	7814	TT13	chr14	14	q13.1	35095504	35104365	6	0	-0.920087	-0.920087	3.249E-18
252,152,934,023	7815	TT13	chr14	14	q13.1	35179148	35184872	4	0	-1.417987	-1.417987	1.188E-27

252,152,934,023	7816	TT13	chr14	14	q13.2	35341299	35347502	5	0	-1.397552	-1.397552	4.179E-28
252,152,934,023	7817	TT13	chr14	14	q13.2	35510609	35519181	5	0	-1.229233	-1.229233	4.383E-28
252,152,934,023	7818	TT13	chr14	14	q13.2	35619702	35625099	4	0	-1.426305	-1.426305	9.773E-29
252,152,934,023	7819	TT13	chr14	14	q13.2	35869847	35875663	5	0	-1.256267	-1.256267	1.356E-28
252,152,934,023	7820	TT13	chr14	14	q13.2	36000420	36007524	4	0	-1.262025	-1.262025	2.093E-23
252,152,934,023	7821	TT13	chr14	14	q13.2	36275623	36302047	14	0	-1.151656	-1.151656	1.354E-61
252,152,934,023	7823	TT13	chr14	14	q13.3	37048038	37055678	9	0	-1.148946	-1.148946	1.452E-31
252,152,934,023	7824	TT13	chr14	14	q13.3	37114400	37141112	16	0	-0.994258	-0.994258	9.917E-48
252,152,934,023	7825	TT13	chr14	14	q13.3	37133259	37137583	4	0	-2.10976	-2.10976	8.524E-13
252,152,934,023	7828	TT13	chr14	14	q21.1	38049086	38092245	22	0	-1.123564	-1.123564	2.946E-89
252,152,934,023	7829	TT13	chr14	14	q21.1	38052340	38062732	6	0	-1.933704	-1.933704	1.576E-13
252,152,934,023	7832	TT13	chr14	14	q21.1	38723471	38728331	3	0	-1.255727	-1.255727	3.661E-18
252,152,934,023	7834	TT13	chr14	14	q21.1	39733757	39760647	11	0	-0.804048	-0.804048	1.51E-26
252,152,934,023	7835	TT13	chr14	14	q21.1	39895195	39906306	8	0	-0.757374	-0.757374	1.854E-17
252,152,934,023	7836	TT13	chr14	14	q21.1	42073262	42081942	5	0	-1.336655	-1.336655	3.07E-28
252,152,934,023	7837	TT13	chr14	14	q21.1	42139845	42146342	4	0	-1.347451	-1.347451	6.257E-27
252,152,934,023	7838	TT13	chr14	14	q21.2	45363730	45389300	17	0	-0.94349	-0.94349	1.565E-54
252,152,934,023	7839	TT13	chr14	14	q21.2	45548554	45554035	4	0	-2.402319	-2.402319	5.653E-53
252,152,934,023	7840	TT13	chr14	14	q21.2	45597639	45610642	9	0	-0.705489	-0.705489	1.296E-17
252,152,934,023	7841	TT13	chr14	14	q21.2	45721093	45725129	4	0	-1.164619	-1.164619	1.094E-20
252,152,934,023	7842	TT13	chr14	14	q21.3	47287784	47294086	4	0	-1.323632	-1.323632	6.016E-26
252,152,934,023	7843	TT13	chr14	14	q21.3	47708985	47713593	3	0	-1.692507	-1.692507	8.376E-28
252,152,934,023	7844	TT13	chr14	14	q21.3	48093914	48097812	3	0	-1.852661	-1.852661	2.715E-29
252,152,934,023	7852	TT13	chr14	14	q21.3	50580656	50587033	6	0	-0.987039	-0.987039	9.633E-23
252,152,934,023	7853	TT13	chr14	14	q21.3	50692419	50705498	8	0	-0.775729	-0.775729	8.163E-19
252,152,934,023	7854	TT13	chr14	14	q21.3	50826798	50830174	3	0	-1.925089	-1.925089	1.52E-32
252,152,934,023	7855	TT13	chr14	14	q21.3	50859769	50866533	5	0	-1.111594	-1.111594	3.765E-21
252,152,934,023	7856	TT13	chr14	14	q22.1	50995494	51030867	13	0	-0.881123	-0.881123	3.98E-35
252,152,934,023	7860	TT13	chr14	14	q22.1	51406333	51426877	13	0	-1.026179	-1.026179	5.795E-43
252,152,934,023	7862	TT13	chr14	14	q22.1	52114439	52123564	8	0	-1.110515	-1.110515	1.292E-31
252,152,934,023	7863	TT13	chr14	14	q22.1	52454453	52459307	4	0	-1.669418	-1.669418	1.102E-35
252,152,934,023	7871	TT13	chr14	14	q22.1	53416428	53420475	3	0	-1.708857	-1.708857	2.081E-28
252,152,934,023	7872	TT13	chr14	14	q22.1	53612268	53622857	7	0	-0.989203	-0.989203	8.835E-26
252,152,934,023	7873	TT13	chr14	14	q22.2	54411087	54424898	8	0	-1.659465	-1.659465	8.321E-63
252,152,934,023	7875	TT13	chr14	14	q22.2	54903077	54913742	6	0	-1.319214	-1.319214	1.833E-35
252,152,934,023	7876	TT13	chr14	14	q22.2	54954898	54956753	3	0	-1.962741	-1.962741	3.341E-32
252,152,934,023	7877	TT13	chr14	14	q22.2	55223771	55229554	4	0	-1.14228	-1.14228	1.464E-17
252,152,934,023	7878	TT13	chr14	14	q22.2	55367380	55373191	4	0	-1.336636	-1.336636	5.889E-24
252,152,934,023	7879	TT13	chr14	14	q22.2 - q22.3	55492935	55523171	20	0	-0.576624	-0.576624	8.665E-23
252,152,934,023	7881	TT13	chr14	14	q22.3	55697604	55770779	38	0	-0.532396	-0.532396	2.78E-36
252,152,934,023	7882	TT13	chr14	14	q22.3	55706361	55710718	3	0	-1.534102	-1.534102	3.132E-12
252,152,934,023	7883	TT13	chr14	14	q22.3	55735855	55739136	3	0	-1.747111	-1.747111	4.144E-15
252,152,934,023	7885	TT13	chr14	14	q22.3	55902772	55925038	13	0	-0.76989	-0.76989	1.387E-28
252,152,934,023	7886	TT13	chr14	14	q22.3	56044103	56049680	3	0	-1.148861	-1.148861	2.225E-14
252,152,934,023	7889	TT13	chr14	14	q22.3	57258647	57285751	20	0	-1.62631	-1.62631	8.995E-136
252,152,934,023	7890	TT13	chr14	14	q22.3	57274211	57279754	5	0	-2.854137	-2.854137	2.187E-13
252,152,934,023	7892	TT13	chr14	14	q22.3	57733332	57736474	3	0	-1.921349	-1.921349	9.352E-32
252,152,934,023	7893	TT13	chr14	14	q22.3	57854489	57863559	6	0	-1.182948	-1.182948	5.444E-30
252,152,934,023	7907	TT13	chr14	14	q23.1	61103389	61125553	11	0	-1.805964	-1.805964	3.467E-89
252,152,934,023	7915	TT13	chr14	14	q23.2	62276772	62281091	3	0	-1.620247	-1.620247	1.504E-25
252,152,934,023	7916	TT13	chr14	14	q23.2	62325083	62334178	5	0	-0.877388	-0.877388	6.217E-16
252,152,934,023	7917	TT13	chr14	14	q23.2	62521748	62527224	3	0	-1.509254	-1.509254	5.072E-24
252,152,934,023	7918	TT13	chr14	14	q23.2	63510029	63515707	4	0	-1.249117	-1.249117	4.055E-24
252,152,934,023	7919	TT13	chr14	14	q23.2	63983211	64018079	21	0	-0.64146	-0.64146	2.466E-30
252,152,934,023	7921	TT13	chr14	14	q23.2	64058913	64065392	4	0	-0.964487	-0.964487	3.678E-15
252,152,934,023	7922	TT13	chr14	14	q23.2	64189947	64229278	18	0	-0.809404	-0.809404	1.23E-40
252,152,934,023	7923	TT13	chr14	14	q23.2	64198227	64212469	8	0	-0.316722	-0.316722	2.112E-10
252,152,934,023	7928	TT13	chr14	14	q23.3	64929644	64933895	3	0	-1.321703	-1.321703	1.29E-13
252,152,934,023	7929	TT13	chr14	14	q23.3	64929644	65219434	131	0	-0.293328	-0.293328	2.054E-30
252,152,934,023	7930	TT13	chr14	14	q23.3	64968282	64974456	5	0	-1.301508	-1.301508	2.728E-17
252,152,934,023	7933	TT13	chr14	14	q23.3	65437559	65443488	4	0	-1.078468	-1.078468	2.468E-21
252,152,934,023	7934	TT13	chr14	14	q23.3	65566737	65571629	4	0	-1.3085	-1.3085	1.826E-24
252,152,934,023	7935	TT13	chr14	14	q23.3	65874310	65884593	6	0	-0.947713	-0.947713	6.717E-21
252,152,934,023	7936	TT13	chr14	14	q23.3	66096291	66105585	5	0	-0.875633	-0.875633	5.545E-16
252,152,934,023	7937	TT13	chr14	14	q23.3	66965552	67015740	26	0	-0.622229	-0.622229	7.998E-35
252,152,934,023	7938	TT13	chr14	14	q23.3	67524565	67529326	4	0	-1.185737	-1.185737	4.132E-22
252,152,934,023	7939	TT13	chr14	14	q23.3	67705678	67710796	4	0	-1.36948	-1.36948	1.756E-21
252,152,934,023	7941	TT13	chr14	14	q23.3	67876171	67881516	3	0	-1.1665	-1.1665	5.04E-16
252,152,934,023	7943	TT13	chr14	14	q24.1	67979793	68003191	13	0	-0.808426	-0.808426	9.63E-28
252,152,934,023	7944	TT13	chr14	14	q24.1	68062764	68094260	15	0	-0.867618	-0.867618	1.722E-39
252,152,934,023	7945	TT13	chr14	14	q24.1	68135099	68146540	7	0	-0.861809	-0.861809	5.062E-18
252,152,934,023	7947	TT13	chr14	14	q24.1	69092689	69097471	5	0	-0.988186	-0.988186	4.474E-21
252,152,934,023	7949	TT13	chr14	14	q24.1	69338297	69341337	3	0	-1.219625	-1.219625	2.54E-16
252,152,934,023	7953	TT13	chr14	14	q24.1	69723949	69730950	4	0	-1.027167	-1.027167	8.749E-19
252,152,934,023	7955	TT13	chr14	14	q24.1	70034649	70042358	5	0	-1.015639	-1.015639	1.527E-21
252,152,934,023	7956	TT13	chr14	14	q24.1	70072935	70085555	9	0	-0.786392	-0.786392	3.494E-24
252,152,934,023	7957	TT13	chr14	14	q24.1	70191512	70195074	3	0	-1.615472	-1.615472	4.121E-27
252,152,934,023	7958	TT13	chr14	14	q24.2	70341794	70376683	20	0	-0.613333	-0.613333	6.642E-32
252,152,934,023	7960	TT13	chr14	14	q24.2	70697769	70725454	14	0	-0.889754	-0.889754	6.943E-44
252,152,934,023	7962	TT13	chr14	14	q24.2	71107328	71113019	4	0	-1.106559	-1.106559	8.796E-20
252,152,934,023	7963	TT13	chr14	14	q24.2	71268978	71291932	14	0	-0.810798	-0.810798	3.934E-36
252,152,934,023	7964	TT13	chr14	14	q24.2	71372349	71377831	3	0	-1.53661	-1.53661	2.099E-24
252,152,934,023	7965	TT13	chr14	14	q24.2	72395288	72402393	7	0	-1.379266	-1.379266	7.824E-46
252,152,934,023	7966	TT13	chr14	14	q24.2	73353906	73403890	26	0	-0.563486	-0.563486	3.24E-33
252,152,934,023	7967	TT13	chr14	14	q24.2	73491346	73496885	4	0	-1.420334	-1.420334	1.112E-27
252,152,934,023	7968	TT13	chr14	14	q24.2	73600748	73603956	3	0	-1.756855	-1.756855	1.131E-29
252,152,934,023	7973	TT13	chr14	14	q24.3	74001651	74005806	3	0	-1.260404	-1.260404	6.808E-15
252,152,934,023	7974	TT13	chr14	14	q24.3	74031574	74109768	28	0	-0.729137	-0.729137	1.193E-54
252,152,934,023	7984	TT13	chr14	14	q24.3	75344405	75352510	6	0	-1.199054	-1.199054	3.291E-32
252,152,934,023	7987	TT13	chr14	14	q24.3	75514538	75538180	12	0	-1.020853	-1.020853	3.245E-44
252,152,934,023	7988	TT13	chr14	14	q24.3	75522292	75531992	4	0	-0.262981	-0.262981	5.436E-12
252,152,934,023	7989	TT13	chr14	14	q24.3	75591111	75596561	4	0	-1.281543	-1.281543	1.408E-26
252,152,934,023	7990	TT13	chr14	14	q24.3	75642039	75645060	3	0	-1.570539	-1.570539	4.819E-26
252,152,934,023	7995	TT13	chr14	14	q24.3	76446901	76454189	5	0	-1.389905	-1.389905	2.957E-29
252,152,934,023	7996	TT13	chr14	14	q24.3	76841741	76845772	3	0	-1.326522	-1.326522	4.387E-19
252,152,934,023	7999	TT13	chr14	14	q24.3	77168143	77292707	53	0	-0.60379	-0.60379	6.489E-76

252,152,934,023	8000	TT13	chr14	14	q24.3	77225464	77230131	4	0	-1.508361	-1.508361	6.611E-13
252,152,934,023	8001	TT13	chr14	14	q24.3	77277307	77279940	3	0	-1.888247	-1.888247	4.508E-16
252,152,934,023	8016	TT13	chr14	14	q24.3	78431866	78485146	10	0	-0.69555	-0.69555	2.526E-25
252,152,934,023	8017	TT13	chr14	14	q31.1	80095314	80101764	5	0	-1.218427	-1.218427	3.946E-30
252,152,934,023	8018	TT13	chr14	14	q31.1	80749088	80757522	4	0	-1.067751	-1.067751	8.917E-20
252,152,934,023	8019	TT13	chr14	14	q31.1	81685966	81705406	9	0	-0.897935	-0.897935	4.804E-29
252,152,934,023	8020	TT13	chr14	14	q31.1	81783830	81792748	6	0	-0.873186	-0.873186	3.698E-20
252,152,934,023	8022	TT13	chr14	14	q31.3	85997344	86004728	6	0	-1.286813	-1.286813	6.847E-32
252,152,934,023	8023	TT13	chr14	14	q31.3	87367755	87375723	3	0	-0.844048	-0.844048	9.049E-11
252,152,934,023	8024	TT13	chr14	14	q31.3	88455287	88463306	6	0	-1.118175	-1.118175	2.867E-30
252,152,934,023	8026	TT13	chr14	14	q31.3	88942231	88949636	5	0	-1.303072	-1.303072	2.447E-30
252,152,934,023	8027	TT13	chr14	14	q31.3	89017312	89033968	10	0	-1.415557	-1.415557	2.006E-62
252,152,934,023	8028	TT13	chr14	14	q31.3	89253600	89266208	7	0	-0.827825	-0.827825	3.43E-19
252,152,934,023	8029	TT13	chr14	14	q32.11	89879335	89889042	7	0	-0.870583	-0.870583	6.574E-22
252,152,934,023	8030	TT13	chr14	14	q32.11	89969280	89973879	3	0	-1.553932	-1.553932	8.617E-25
252,152,934,023	8034	TT13	chr14	14	q32.11	90858478	90867813	5	0	-1.124768	-1.124768	1.123E-25
252,152,934,023	8040	TT13	chr14	14	q32.11	91523957	91531647	6	0	-1.072448	-1.072448	1.587E-25
252,152,934,023	8042	TT13	chr14	14	q32.11	91716455	91743077	14	0	-1.100258	-1.100258	8.126E-60
252,152,934,023	8045	TT13	chr14	14	q32.12	92036746	92052798	9	0	-1.092605	-1.092605	6.882E-40
252,152,934,023	8046	TT13	chr14	14	q32.12	92300396	92305166	4	0	-1.566036	-1.566036	2.835E-31
252,152,934,023	8056	TT13	chr14	14	q32.12	93373238	93418924	25	0	-0.963632	-0.963632	7.019E-76
252,152,934,023	8060	TT13	chr14	14	q32.12	93633600	93678883	24	0	-0.606956	-0.606956	6.642E-37
252,152,934,023	8061	TT13	chr14	14	q32.12	93797160	93818518	8	0	-1.001245	-1.001245	1.402E-32
252,152,934,023	8063	TT13	chr14	14	q32.12	94389092	94407867	10	0	-0.863086	-0.863086	5.61E-27
252,152,934,023	8065	TT13	chr14	14	q32.12	94490233	94494759	3	0	-1.37902	-1.37902	3.515E-21
252,152,934,023	8066	TT13	chr14	14	q32.12	94637875	94645107	5	0	-1.045961	-1.045961	6.612E-21
252,152,934,023	8067	TT13	chr14	14	q32.13	95121273	95126687	3	0	-1.263535	-1.263535	3.75E-19
252,152,934,023	8068	TT13	chr14	14	q32.13	95619912	95625546	5	0	-1.487419	-1.487419	7.511E-41
252,152,934,023	8071	TT13	chr14	14	q32.13	95977673	96008059	17	0	-0.690681	-0.690681	4.472E-33
252,152,934,023	8072	TT13	chr14	14	q32.13	96148293	96154804	5	0	-1.301632	-1.301632	1.624E-30
252,152,934,023	8074	TT13	chr14	14	q32.2	96337894	96346134	3	0	-0.867716	-0.867716	8.614E-11
252,152,934,023	8078	TT13	chr14	14	q32.2	97261721	97267291	5	0	-1.501198	-1.501198	1.925E-39
252,152,934,023	8089	TT13	chr14	14	q32.2	100437239	100440767	3	0	-1.561107	-1.561107	2.606E-21
252,152,934,023	8091	TT13	chr14	14	q32.2	100610264	100815211	107	0	-0.611728	-0.611728	3.432E-119
252,152,934,023	8092	TT13	chr14	14	q32.2	100624062	100660902	12	0	-1.155504	-1.155504	9.201E-14
252,152,934,023	8101	TT13	chr14	14	q32.2	101369432	101373577	7	0	-1.253861	-1.253861	3.897E-35
252,152,934,023	8104	TT13	chr14	14	q32.31	102023622	102171935	42	0	-0.763586	-0.763586	4.896E-76
252,152,934,023	8105	TT13	chr14	14	q32.31	102028739	102039274	11	0	-1.368954	-1.368954	2.189E-13
252,152,934,023	8115	TT13	chr14	14	q32.31	102780475	102787102	6	0	-1.572418	-1.572418	1.525E-41
252,152,934,023	8121	TT13	chr14	14	q32.31	103140741	103150914	6	0	-1.624221	-1.624221	1.076E-50
252,152,934,023	8123	TT13	chr14	14	q32.32	103241059	103247059	5	0	-1.153339	-1.153339	3.125E-21
252,152,934,023	8128	TT13	chr14	14	q32.32	103429470	103442047	11	0	-1.311374	-1.311374	2.037E-35
252,152,934,023	8129	TT13	chr14	14	q32.32	103520907	103700268	67	0	-0.664734	-0.664734	2.841E-24
252,152,934,023	8130	TT13	chr14	14	q32.32	103715850	103726022	5	0.265256	0	0.265256	9.888E-10
252,152,934,023	8136	TT13	chr14	14	q32.33	104155516	104207012	26	0	-1.082096	-1.082096	8.52E-78
252,152,934,023	8137	TT13	chr14	14	q32.33	104387280	104396392	6	0	-1.460708	-1.460708	4.499E-33
252,152,934,023	8138	TT13	chr14	14	q32.33	104601088	104641150	20	0	-1.19292	-1.19292	1.301E-28
252,152,934,023	8139	TT13	chr14	14	q32.33	105041783	105379080	154	0	-0.611418	-0.611418	1.493E-34
252,152,934,023	8140	TT13	chr14	14	q32.33	105046926	105060451	9	0	-1.467986	-1.467986	1.625E-11
252,152,934,023	8150	TT13	chr14	14	q32.33	106326756	106334966	5	0	-1.487739	-1.487739	9.151E-32
252,152,934,023	8151	TT13	chr14	14	q32.33	106741758	106747304	3	0	-1.265653	-1.265653	1.748E-18
252,152,934,023	8152	TT13	chr14	14	q32.33	107218078	107229116	4	0	-1.019382	-1.019382	2.594E-19
252,152,934,023	8154	TT13	chr15	15	q11.2	23031729	23036761	4	0	-1.459379	-1.459379	3.139E-28
252,152,934,023	8158	TT13	chr15	15	q11.2	23929562	23933678	3	0	-1.618346	-1.618346	3.719E-25
252,152,934,023	8162	TT13	chr15	15	q11.2	25197592	25202344	5	0	-1.076807	-1.076807	8.664E-23
252,152,934,023	8163	TT13	chr15	15	q11.2	25496757	25499318	3	0	-2.207673	-2.207673	8.3E-36
252,152,934,023	8172	TT13	chr15	15	q12	27108247	27249917	65	0	-0.721921	-0.721921	2.929E-112
252,152,934,023	8173	TT13	chr15	15	q12	27126550	27142232	21	0	-1.247927	-1.247927	1.411E-21
252,152,934,023	8178	TT13	chr15	15	q13.1	28321191	28370366	20	0	-1.160549	-1.160549	8.431E-84
252,152,934,023	8189	TT13	chr15	15	q13.3	33004222	33015714	8	0	-1.195217	-1.195217	1.198E-38
252,152,934,023	8190	TT13	chr15	15	q13.3	33308657	33320827	8	0	-0.862313	-0.862313	1.59E-23
252,152,934,023	8191	TT13	chr15	15	q13.3 - q14	33599209	33608980	7	0	-0.773667	-0.773667	6.394E-17
252,152,934,023	8192	TT13	chr15	15	q14	34328703	34333852	4	0	-1.408849	-1.408849	7.011E-26
252,152,934,023	8193	TT13	chr15	15	q14	34500217	34503577	3	0	-1.476233	-1.476233	5.741E-20
252,152,934,023	8204	TT13	chr15	15	q14	35834701	35839986	5	0	-1.355386	-1.355386	3.859E-31
252,152,934,023	8205	TT13	chr15	15	q14	35942073	35951735	5	0	-1.251677	-1.251677	7.229E-28
252,152,934,023	8206	TT13	chr15	15	q14	37108184	37112209	4	0	-1.77924	-1.77924	1.423E-37
252,152,934,023	8207	TT13	chr15	15	q14	37389105	37397581	6	0	-1.146815	-1.146815	6.642E-26
252,152,934,023	8208	TT13	chr15	15	q14	38361211	38373257	8	0	-0.630538	-0.630538	3.683E-12
252,152,934,023	8210	TT13	chr15	15	q14	38853585	38859762	5	0	-1.224733	-1.224733	1.983E-25
252,152,934,023	8211	TT13	chr15	15	q14	39868783	39876886	5	0	-1.146797	-1.146797	9.636E-23
252,152,934,023	8216	TT13	chr15	15	q15.1	40394780	40404771	7	0	-1.593753	-1.593753	2.752E-36
252,152,934,023	8217	TT13	chr15	15	q15.1	40527554	40585630	33	0	-0.784851	-0.784851	3.361E-42
252,152,934,023	8218	TT13	chr15	15	q15.1	40612530	40646388	21	0	-0.556152	-0.556152	3.842E-13
252,152,934,023	8219	TT13	chr15	15	q15.1	40648032	40651644	3	0	-2.246748	-2.246748	3.563E-29
252,152,934,023	8229	TT13	chr15	15	q15.1	41216801	41258794	21	0	-0.966134	-0.966134	5.843E-43
252,152,934,023	8238	TT13	chr15	15	q15.1	42062528	42069931	5	0	-0.695306	-0.695306	1.76E-12
252,152,934,023	8240	TT13	chr15	15	q15.1	42253300	42265426	7	0	-1.582012	-1.582012	1.188E-48
252,152,934,023	8244	TT13	chr15	15	q15.2	42839654	42899364	35	0	-0.638916	-0.638916	2.22E-49
252,152,934,023	8245	TT13	chr15	15	q15.2	42867144	42870817	3	0	-2.077796	-2.077796	1.389E-16
252,152,934,023	8247	TT13	chr15	15	q15.2	43026114	43032525	5	0	-1.214288	-1.214288	7.024E-26
252,152,934,023	8248	TT13	chr15	15	q15.2	43208959	43211553	3	0	-0.99589	-0.99589	3.798E-13
252,152,934,023	8249	TT13	chr15	15	q15.2	43294807	43311110	8	0	-1.399384	-1.399384	5.039E-53
252,152,934,023	8259	TT13	chr15	15	q15.3	44115984	44121541	5	0	-0.820133	-0.820133	1.983E-14
252,152,934,023	8260	TT13	chr15	15	q15.3	44484701	44490216	5	0	-1.267117	-1.267117	2.176E-27
252,152,934,023	8261	TT13	chr15	15	q15.3	44578368	44584260	4	0	-1.24295	-1.24295	7.092E-24
252,152,934,023	8262	TT13	chr15	15	q21.1	44826572	44833518	4	0	-1.254684	-1.254684	2.829E-20
252,152,934,023	8263	TT13	chr15	15	q21.1	44950592	44959775	7	0	-1.011397	-1.011397	2.566E-26
252,152,934,023	8264	TT13	chr15	15	q21.1	44963801	45067770	47	0.28616	0	0.28616	1.094E-25
252,152,934,023	8273	TT13	chr15	15	q21.1	45721409	45724484	5	0	-1.761065	-1.761065	5.939E-23
252,152,934,023	8277	TT13	chr15	15	q21.1	47475463	47480231	4	0	-1.479675	-1.479675	3.374E-29
252,152,934,023	8278	TT13	chr15	15	q21.1	48006696	48013919	5	0	-1.198832	-1.198832	1.465E-26
252,152,934,023	8279	TT13	chr15	15	q21.1	48467898	48471352	3	0	-1.480195	-1.480195	5.098E-23
252,152,934,023	8280	TT13	chr15	15	q21.1	48619956	48627009	5	0	-1.317343	-1.317343	1.814E-27
252,152,934,023	8281	TT13	chr15	15	q21.1	48931938	48941122	6	0	-1.138965	-1.138965	1.017E-25
252,152,934,023	8282	TT13	chr15	15	q21.1	49266014	49270441	4	0	-1.489424	-1.489424	2.622E-28

252,152,934,023	8285	TT13	chr15	15	q21.2	50468785	50477510	7	0	-1.328691	-1.328691	3.483E-44
252,152,934,023	8291	TT13	chr15	15	q21.2	51631638	51636940	5	0	-1.21092	-1.21092	6.368E-26
252,152,934,023	8292	TT13	chr15	15	q21.2	51909761	51918862	6	0	-0.881822	-0.881822	1.094E-18
252,152,934,023	8293	TT13	chr15	15	q21.2	52027853	52046582	8	0	-1.298331	-1.298331	1.603E-47
252,152,934,023	8299	TT13	chr15	15	q21.2	52577201	52590077	14	0	-1.27859	-1.27859	1.388E-70
252,152,934,023	8300	TT13	chr15	15	q21.2	52818232	52822942	4	0	-1.532378	-1.532378	7.819E-28
252,152,934,023	8301	TT13	chr15	15	q21.2	52858999	52863301	3	0	-1.098459	-1.098459	3.261E-15
252,152,934,023	8302	TT13	chr15	15	q21.3	52967715	52977509	8	0	-1.016843	-1.016843	1.479E-29
252,152,934,023	8303	TT13	chr15	15	q21.3	53072784	53098895	15	0	-1.133431	-1.133431	2.727E-53
252,152,934,023	8304	TT13	chr15	15	q21.3	54046835	54054134	4	0	-1.030667	-1.030667	7.783E-16
252,152,934,023	8305	TT13	chr15	15	q21.3	54753187	54756516	3	0	-1.816697	-1.816697	1.049E-27
252,152,934,023	8306	TT13	chr15	15	q21.3	55579566	55593587	6	0	-1.361483	-1.361483	1.445E-37
252,152,934,023	8307	TT13	chr15	15	q21.3	55697912	55703332	5	0	-1.442557	-1.442557	4.286E-33
252,152,934,023	8316	TT13	chr15	15	q21.3	57667528	57671393	3	0	-1.364375	-1.364375	2.547E-20
252,152,934,023	8317	TT13	chr15	15	q21.3	58348474	58366003	10	0	-0.664471	-0.664471	1.947E-23
252,152,934,023	8318	TT13	chr15	15	q21.3	59036772	59067093	16	0	-0.814894	-0.814894	1.319E-38
252,152,934,023	8320	TT13	chr15	15	q22.1	59223714	59226879	3	0	-2.029361	-2.029361	3.377E-34
252,152,934,023	8323	TT13	chr15	15	q22.2	59940232	59986376	28	0	-0.587859	-0.587859	1.56E-34
252,152,934,023	8324	TT13	chr15	15	q22.2	59980202	59983189	3	0	-1.748996	-1.748996	2.578E-14
252,152,934,023	8325	TT13	chr15	15	q22.2	60286854	60300438	9	0	-1.311361	-1.311361	9E-46
252,152,934,023	8329	TT13	chr15	15	q22.2	60879106	60891848	7	0	-1.018307	-1.018307	3.656E-28
252,152,934,023	8330	TT13	chr15	15	q22.2	61235189	61242042	9	0	-1.209277	-1.209277	4.943E-46
252,152,934,023	8331	TT13	chr15	15	q22.2	61515965	61526899	6	0	-0.792324	-0.792324	1.387E-18
252,152,934,023	8332	TT13	chr15	15	q22.2	62350092	62364547	10	0	-1.337255	-1.337255	1.975E-59
252,152,934,023	8333	TT13	chr15	15	q22.2	62449514	62519780	22	0	-0.904663	-0.904663	3.607E-61
252,152,934,023	8337	TT13	chr15	15	q22.2	63333471	63343178	6	0	-1.752329	-1.752329	3.458E-50
252,152,934,023	8341	TT13	chr15	15	q22.2	63568659	63573844	5	0	-1.147654	-1.147654	6.315E-24
252,152,934,023	8347	TT13	chr15	15	q22.31	64332144	64359243	16	0	-0.811297	-0.811297	5.17E-39
252,152,934,023	8348	TT13	chr15	15	q22.31	64437030	64459458	14	0	-0.821691	-0.821691	5.962E-33
252,152,934,023	8349	TT13	chr15	15	q22.31	64751278	64756864	4	0	-1.348207	-1.348207	6.004E-25
252,152,934,023	8353	TT13	chr15	15	q22.31	65319367	65324327	4	0	-1.560766	-1.560766	3.828E-30
252,152,934,023	8359	TT13	chr15	15	q22.31	65808013	65826911	7	0	-1.008211	-1.008211	2.028E-27
252,152,934,023	8360	TT13	chr15	15	q22.31	66082061	66085464	3	0	-1.720482	-1.720482	6.2E-28
252,152,934,023	8362	TT13	chr15	15	q22.31	66272213	66278837	4	0	-1.118128	-1.118128	2.786E-18
252,152,934,023	8363	TT13	chr15	15	q22.31	66541108	66550046	7	0	-0.914364	-0.914364	1.183E-19
252,152,934,023	8364	TT13	chr15	15	q22.31	66583837	66587334	3	0	-1.770572	-1.770572	8.277E-27
252,152,934,023	8366	TT13	chr15	15	q22.31	66992462	66999839	4	0	-1.600835	-1.600835	2.895E-23
252,152,934,023	8369	TT13	chr15	15	q22.33	67321980	67328556	5	0	-1.012066	-1.012066	3.481E-16
252,152,934,023	8370	TT13	chr15	15	q22.33	67357060	67360534	3	0	-1.723641	-1.723641	4.391E-25
252,152,934,023	8371	TT13	chr15	15	q23	67544603	67549766	4	0	-1.310875	-1.310875	4.299E-25
252,152,934,023	8372	TT13	chr15	15	q23	67810023	67843677	18	0	-0.666465	-0.666465	3.355E-29
252,152,934,023	8374	TT13	chr15	15	q23	68346196	68350562	4	0	-1.225947	-1.225947	1.628E-21
252,152,934,023	8376	TT13	chr15	15	q23	68507514	68576842	32	0	-0.752631	-0.752631	1.861E-60
252,152,934,023	8379	TT13	chr15	15	q23	69218967	69272569	21	0	-0.765808	-0.765808	1.074E-46
252,152,934,023	8381	TT13	chr15	15	q23	69364251	69370061	4	0	-1.105866	-1.105866	7.938E-19
252,152,934,023	8382	TT13	chr15	15	q23	69450959	69455870	4	0	-1.426242	-1.426242	1.967E-28
252,152,934,023	8383	TT13	chr15	15	q23	69704215	69709886	4	0	-1.358837	-1.358837	3.505E-28
252,152,934,023	8384	TT13	chr15	15	q23	69743923	69747755	4	0	-1.65342	-1.65342	3.552E-32
252,152,934,023	8385	TT13	chr15	15	q23	70102596	70108550	3	0	-0.893244	-0.893244	8.651E-16
252,152,934,023	8387	TT13	chr15	15	q23	70381876	70395711	15	0	-0.946594	-0.946594	4.258E-41
252,152,934,023	8388	TT13	chr15	15	q23	71050426	71059156	5	0	-1.078426	-1.078426	1.864E-22
252,152,934,023	8389	TT13	chr15	15	q23	71141150	71190376	26	0	-0.72147	-0.72147	3.18E-48
252,152,934,023	8390	TT13	chr15	15	q23	71407084	71410596	3	0	-1.520287	-1.520287	2.233E-23
252,152,934,023	8391	TT13	chr15	15	q23	71502879	71510937	5	0	-1.167312	-1.167312	4.133E-29
252,152,934,023	8392	TT13	chr15	15	q23	72058993	72063846	3	0	-1.352344	-1.352344	4.871E-21
252,152,934,023	8393	TT13	chr15	15	q23	72385471	72416740	16	0	-0.838351	-0.838351	4.428E-43
252,152,934,023	8394	TT13	chr15	15	q23	72477304	72492559	10	0	-0.992675	-0.992675	3.086E-32
252,152,934,023	8395	TT13	chr15	15	q23	72519530	72525446	3	0	-0.998818	-0.998818	5.18E-11
252,152,934,023	8407	TT13	chr15	15	q24.1	74311708	74433358	31	0	-0.690939	-0.690939	1.964E-46
252,152,934,023	8408	TT13	chr15	15	q24.1	74313955	74316829	3	0	-1.736382	-1.736382	7.861E-12
252,152,934,023	8409	TT13	chr15	15	q24.1	74534995	74541097	4	0	-1.081145	-1.081145	5.03E-23
252,152,934,023	8410	TT13	chr15	15	q24.1	74657037	74667685	8	0	-1.255885	-1.255885	1.862E-41
252,152,934,023	8412	TT13	chr15	15	q24.1	74722617	74729227	5	0	-0.979437	-0.979437	2.449E-18
252,152,934,023	8431	TT13	chr15	15	q24.2	76350018	76354556	3	0	-1.760967	-1.760967	9.927E-30
252,152,934,023	8434	TT13	chr15	15	q24.3	76628429	76640635	8	0	-1.816394	-1.816394	4.157E-53
252,152,934,023	8437	TT13	chr15	15	q24.3	77709817	77712954	3	0	-1.994758	-1.994758	7.62E-33
252,152,934,023	8447	TT13	chr15	15	q25.1	78796442	79173518	140	0	-0.400411	-0.400411	3.015E-70
252,152,934,023	8448	TT13	chr15	15	q25.1	78829756	78836382	7	0	-1.202919	-1.202919	2.94E-20
252,152,934,023	8455	TT13	chr15	15	q25.1	79721552	79726706	4	0	-1.084049	-1.084049	6.322E-19
252,152,934,023	8456	TT13	chr15	15	q25.1	80186288	80192880	4	0	-1.252316	-1.252316	3.491E-23
252,152,934,023	8457	TT13	chr15	15	q25.1	80209582	80220172	5	0	-1.580767	-1.580767	1.207E-38
252,152,934,023	8462	TT13	chr15	15	q25.1	81277856	81299708	12	0	-0.844894	-0.844894	1.026E-31
252,152,934,023	8463	TT13	chr15	15	q25.1	81450154	81454339	3	0	-1.562802	-1.562802	8.889E-24
252,152,934,023	8464	TT13	chr15	15	q25.2	82332581	82344411	7	0	-1.197267	-1.197267	2.081E-31
252,152,934,023	8467	TT13	chr15	15	q25.2	83310700	83318650	4	0	-1.061109	-1.061109	7.071E-18
252,152,934,023	8475	TT13	chr15	15	q25.2	84113502	84119451	4	0	-1.113482	-1.113482	5.276E-18
252,152,934,023	8476	TT13	chr15	15	q25.2	84317728	84325634	4	0	-0.738529	-0.738529	4.55E-10
252,152,934,023	8477	TT13	chr15	15	q25.2	84488135	84494799	4	0	-0.964839	-0.964839	4.59E-15
252,152,934,023	8478	TT13	chr15	15	q25.2	85141413	85147052	3	0	-1.156094	-1.156094	2.628E-16
252,152,934,023	8479	TT13	chr15	15	q25.2	85175886	85181737	4	0	-1.094755	-1.094755	5.58E-19
252,152,934,023	8480	TT13	chr15	15	q25.2 - q25.3	85194774	85220594	15	0	-0.893928	-0.893928	1.966E-41
252,152,934,023	8481	TT13	chr15	15	q25.3	85290642	85294318	3	0	-1.368255	-1.368255	4.464E-20
252,152,934,023	8482	TT13	chr15	15	q25.3	85358111	85363391	5	0	-1.184052	-1.184052	1.109E-21
252,152,934,023	8483	TT13	chr15	15	q25.3	85521610	85527948	4	0	-1.506143	-1.506143	8.34E-30
252,152,934,023	8484	TT13	chr15	15	q25.3	85921568	85927078	3	0	-1.484256	-1.484256	1.548E-22
252,152,934,023	8485	TT13	chr15	15	q25.3	86300612	86303772	5	0	-0.807658	-0.807658	4.879E-12
252,152,934,023	8486	TT13	chr15	15	q25.3	86336512	86340444	4	0	-1.353114	-1.353114	3.263E-20
252,152,934,023	8487	TT13	chr15	15	q25.3	88794816	88806403	6	0	-0.878249	-0.878249	6.142E-20
252,152,934,023	8496	TT13	chr15	15	q26.1	89900747	89923923	28	0	-1.316551	-1.316551	1.186E-118
252,152,934,023	8498	TT13	chr15	15	q26.1	90030714	90046075	10	0	-0.594627	-0.594627	2.909E-12
252,152,934,023	8499	TT13	chr15	15	q26.1	90117093	90123950	5	0	-0.962529	-0.962529	1.826E-15
252,152,934,023	8500	TT13	chr15	15	q26.1	90168909	90209748	29	0	-1.005336	-1.005336	4.463E-81
252,152,934,023	8501	TT13	chr15	15	q26.1	90191005	90197599	6	0	-1.813011	-1.813011	3.303E-12
252,152,934,023	8512	TT13	chr15	15	q26.1	90806006	90822507	9	0	-1.213982	-1.213982	1.38E-46
252,152,934,023	8514	TT13	chr15	15	q26.1	91051213	91076777	14	0	-0.722124	-0.722124	6.036E-26
252,152,934,023	8515	TT13	chr15	15	q26.1	91366136	91370728	3	0	-1.120907	-1.120907	8.225E-15

252,152,934,023	8516	TT13	chr15	15	q26.1	91411246	91542086	70	0	-0.561688	-0.561688	7.717E-68
252,152,934,023	8517	TT13	chr15	15	q26.1	91414203	91433790	11	0	-1.483079	-1.483079	3.996E-24
252,152,934,023	8526	TT13	chr15	15	q26.1	93573047	93633535	32	0	-0.894894	-0.894894	7.682E-78
252,152,934,023	8528	TT13	chr15	15	q26.2	94768959	94780542	8	0	-1.075767	-1.075767	9.537E-35
252,152,934,023	8529	TT13	chr15	15	q26.2	95386703	95402240	7	0	-1.458542	-1.458542	1.224E-45
252,152,934,023	8530	TT13	chr15	15	q26.2	96862755	96907628	47	0	-1.334844	-1.334844	1.595E-221
252,152,934,023	8531	TT13	chr15	15	q26.2	96896823	96900752	4	0	-2.53111	-2.53111	3.266E-10
252,152,934,023	8534	TT13	chr15	15	q26.2	97299599	97311573	8	0	-1.490754	-1.490754	3.421E-55
252,152,934,023	8536	TT13	chr15	15	q26.3	98501801	98507009	4	0	-1.339223	-1.339223	2.039E-25
252,152,934,023	8537	TT13	chr15	15	q26.3	98628330	98650685	6	0	-0.976227	-0.976227	5.622E-21
252,152,934,023	8538	TT13	chr15	15	q26.3	98832984	98839269	4	0	-1.228807	-1.228807	5.706E-22
252,152,934,023	8539	TT13	chr15	15	q26.3	98966382	98975511	6	0	-0.760654	-0.760654	3.221E-14
252,152,934,023	8540	TT13	chr15	15	q26.3	99086246	99096391	6	0	-0.817304	-0.817304	2.017E-14
252,152,934,023	8541	TT13	chr15	15	q26.3	99187191	99197341	6	0	-0.898021	-0.898021	6.876E-17
252,152,934,023	8542	TT13	chr15	15	q26.3	99390845	99412322	14	0	-0.705564	-0.705564	4.927E-27
252,152,934,023	8543	TT13	chr15	15	q26.3	99546039	99559239	6	0	-2.004315	-2.004315	7.869E-61
252,152,934,023	8544	TT13	chr15	15	q26.3	99635690	99648593	8	0	-1.127538	-1.127538	2.524E-34
252,152,934,023	8545	TT13	chr15	15	q26.3	99788925	99794518	4	0	-1.241549	-1.241549	1.961E-22
252,152,934,023	8546	TT13	chr15	15	q26.3	100103171	100111083	6	0	-1.316173	-1.316173	5.461E-31
252,152,934,023	8547	TT13	chr15	15	q26.3	100269849	100277224	6	0	-1.031009	-1.031009	3.975E-23
252,152,934,023	8549	TT13	chr15	15	q26.3	101083535	101086353	3	0	-2.136239	-2.136239	9.257E-36
252,152,934,023	8555	TT13	chr15	15	q26.3	101512959	101515926	4	0	-1.852153	-1.852153	6.835E-34
252,152,934,023	8565	TT13	chr16	16	p13.3	407830	420900	6	0	-1.518582	-1.518582	2.558E-11
252,152,934,023	8592	TT13	chr16	16	p13.3	2801591	2807527	5	0	-1.986684	-1.986684	3.605E-24
252,152,934,023	8611	TT13	chr16	16	p13.3	4523488	4526026	3	0	-2.411689	-2.411689	8.312E-32
252,152,934,023	8620	TT13	chr16	16	p13.3	6067553	6071360	3	0	-1.431542	-1.431542	2.226E-23
252,152,934,023	8621	TT13	chr16	16	p13.3	6530097	6537346	4	0	-1.105417	-1.105417	1.896E-21
252,152,934,023	8622	TT13	chr16	16	p13.3	7702926	7705547	3	0	-1.686553	-1.686553	1.739E-28
252,152,934,023	8623	TT13	chr16	16	p13.2	8763992	8772656	5	0	-0.81079	-0.81079	5.366E-16
252,152,934,023	8624	TT13	chr16	16	p13.2	8822143	8832909	4	0	-0.896971	-0.896971	7.083E-14
252,152,934,023	8625	TT13	chr16	16	p13.2	8960262	8963418	4	0	-1.777738	-1.777738	7.475E-27
252,152,934,023	8627	TT13	chr16	16	p13.2	9183714	9188059	4	0	-1.960201	-1.960201	6.193E-41
252,152,934,023	8630	TT13	chr16	16	p13.13	10852378	10859619	5	0	-1.177574	-1.177574	9.803E-26
252,152,934,023	8632	TT13	chr16	16	p13.13	11342920	11352749	6	0	-1.444457	-1.444457	1.406E-35
252,152,934,023	8633	TT13	chr16	16	p13.13	11425689	11444765	13	0	-0.906612	-0.906612	7.863E-43
252,152,934,023	8638	TT13	chr16	16	p13.13	12008151	12012499	3	0	-2.023568	-2.023568	1.579E-26
252,152,934,023	8639	TT13	chr16	16	p13.13	12068400	12076188	4	0	-1.016447	-1.016447	1.937E-18
252,152,934,023	8640	TT13	chr16	16	p13.12	12658099	12671612	7	0	-0.551719	-0.551719	3.205E-15
252,152,934,023	8641	TT13	chr16	16	p13.12	12892587	12904770	6	0	-0.761314	-0.761314	1.534E-20
252,152,934,023	8643	TT13	chr16	16	p13.12	14367771	14400156	27	0	-0.60992	-0.60992	3.53E-40
252,152,934,023	8644	TT13	chr16	16	p13.12	14377515	14380375	3	0	-1.83438	-1.83438	1.349E-13
252,152,934,023	8648	TT13	chr16	16	p13.11	15142157	15534187	35	0	-0.421273	-0.421273	3.202E-27
252,152,934,023	8649	TT13	chr16	16	p13.11	15526707	15529678	3	0	-1.351505	-1.351505	1.841E-11
252,152,934,023	8650	TT13	chr16	16	p13.11	15732078	15747215	19	0	-1.109369	-1.109369	4.867E-88
252,152,934,023	8651	TT13	chr16	16	p13.11	15949527	15956209	5	0	-1.394093	-1.394093	4.316E-34
252,152,934,023	8655	TT13	chr16	16	p12.3	18994598	19015542	7	0	-1.493455	-1.493455	5.17E-51
252,152,934,023	8656	TT13	chr16	16	p12.3	19073585	19130354	25	0	-0.428121	-0.428121	2.285E-21
252,152,934,023	8659	TT13	chr16	16	p12.3	19526960	19540587	10	0	-0.683867	-0.683867	4.592E-22
252,152,934,023	8660	TT13	chr16	16	p12.3	19725084	19733288	6	0	-0.871095	-0.871095	8.382E-19
252,152,934,023	8661	TT13	chr16	16	p12.3	19880827	19897618	11	0	-0.792641	-0.792641	7.507E-29
252,152,934,023	8662	TT13	chr16	16	p12.3	20081799	20088177	5	0	-0.987252	-0.987252	1.474E-19
252,152,934,023	8663	TT13	chr16	16	p12.3	20358903	20365944	5	0	-1.043477	-1.043477	2.089E-23
252,152,934,023	8664	TT13	chr16	16	p12.3	20910139	20916949	4	0	-1.15652	-1.15652	2.599E-22
252,152,934,023	8665	TT13	chr16	16	p12.3	21162998	21172618	4	0	-1.68518	-1.68518	1.792E-37
252,152,934,023	8666	TT13	chr16	16	p12.2	21289986	21325311	15	0	-1.043296	-1.043296	2.125E-63
252,152,934,023	8678	TT13	chr16	16	p12.2	24116302	24126000	5	0	-0.867859	-0.867859	1.128E-17
252,152,934,023	8679	TT13	chr16	16	p12.1	24548742	24592793	21	0	-0.628899	-0.628899	6.515E-36
252,152,934,023	8681	TT13	chr16	16	p12.1	25023826	25029119	3	0	-1.411431	-1.411431	3.618E-23
252,152,934,023	8683	TT13	chr16	16	p12.1	25700803	25704988	3	0	-1.475992	-1.475992	4.28E-24
252,152,934,023	8685	TT13	chr16	16	p12.1	27558886	27562647	3	0	-1.553055	-1.553055	2.332E-28
252,152,934,023	8701	TT13	chr16	16	p11.2	30755576	31244505	230	0	-0.647561	-0.647561	3.118E-77
252,152,934,023	8702	TT13	chr16	16	p11.2	30758794	30763132	5	0	-1.408363	-1.408363	1.204E-11
252,152,934,023	8709	TT13	chr16	16	p11.2	31377267	31382396	3	0	-0.808392	-0.808392	1.832E-11
252,152,934,023	8710	TT13	chr16	16	p11.2	31438471	31487258	23	0	-1.236578	-1.236578	4.763E-57
252,152,934,023	8711	TT13	chr16	16	p11.2	31472225	31478492	4	0	-2.458045	-2.458045	3.381E-12
252,152,934,023	8713	TT13	chr16	16	p11.2	31708285	31714658	4	0	-0.915595	-0.915595	6.263E-10
252,152,934,023	8714	TT13	chr16	16	p11.2	31723992	31727460	3	0	-1.375691	-1.375691	1.014E-16
252,152,934,023	8715	TT13	chr16	16	p11.2	31883199	31888038	4	0	-1.413899	-1.413899	3.181E-22
252,152,934,023	8716	TT13	chr16	16	p11.2	34207619	34210370	3	0	-1.671952	-1.671952	3.682E-21
252,152,934,023	8719	TT13	chr16	16	p11.1	34774258	34789035	7	0	-1.112246	-1.112246	1.838E-16
252,152,934,023	8722	TT13	chr16	16	q11.2	46719156	46729920	11	0	-1.520831	-1.520831	8.302E-81
252,152,934,023	8723	TT13	chr16	16	q11.2	46862311	46877829	6	0	-1.542063	-1.542063	4.845E-46
252,152,934,023	8725	TT13	chr16	16	q12.1	47002617	47050082	16	0	-0.741364	-0.741364	2.36E-37
252,152,934,023	8726	TT13	chr16	16	q12.1	47005160	47008695	3	0	-1.737712	-1.737712	2.384E-11
252,152,934,023	8729	TT13	chr16	16	q12.1	48277949	48281051	3	0	-1.624884	-1.624884	2.807E-26
252,152,934,023	8730	TT13	chr16	16	q12.1	48391952	48456514	30	0	-0.483722	-0.483722	9.672E-32
252,152,934,023	8731	TT13	chr16	16	q12.1	48513092	48546076	17	0	-0.867166	-0.867166	2.057E-52
252,152,934,023	8732	TT13	chr16	16	q12.1	48640247	48644631	3	0	-1.65755	-1.65755	1.124E-27
252,152,934,023	8733	TT13	chr16	16	q12.1	49308114	49319655	6	0	-1.395374	-1.395374	2.338E-41
252,152,934,023	8734	TT13	chr16	16	q12.1	49516165	49528919	9	0	-1.03519	-1.03519	1.311E-35
252,152,934,023	8735	TT13	chr16	16	q12.1	49697118	49700354	3	0	-1.046525	-1.046525	3.284E-14
252,152,934,023	8745	TT13	chr16	16	q12.1	51162967	51193705	17	0	-0.898596	-0.898596	5.668E-53
252,152,934,023	8746	TT13	chr16	16	q12.1	52575553	52584146	5	0	-1.105797	-1.105797	2.423E-25
252,152,934,023	8749	TT13	chr16	16	q12.2	53534729	53543912	8	0	-0.873758	-0.873758	1.028E-23
252,152,934,023	8750	TT13	chr16	16	q12.2	53571050	53578120	7	0	-1.111535	-1.111535	9.152E-36
252,152,934,023	8751	TT13	chr16	16	q12.2	53655367	53660404	4	0	-1.233076	-1.233076	1.008E-24
252,152,934,023	8754	TT13	chr16	16	q12.2	54962090	54965732	3	0	-3.270091	-3.270091	6.913E-38
252,152,934,023	8755	TT13	chr16	16	q12.2	55351930	55364089	6	0	-0.744421	-0.744421	4.209E-15
252,152,934,023	8756	TT13	chr16	16	q12.2	55504943	55546758	21	0	-0.560342	-0.560342	1.623E-28
252,152,934,023	8757	TT13	chr16	16	q12.2	55687352	55691482	3	0	-1.333742	-1.333742	3.79E-21
252,152,934,023	8762	TT13	chr16	16	q12.2 - q13	56640465	56719464	38	0	-1.18709	-1.18709	1.344E-190
252,152,934,023	8763	TT13	chr16	16	q12.2	56665576	56668077	3	0	-2.442965	-2.442965	1.338E-10
252,152,934,023	8764	TT13	chr16	16	q13	56764964	56778340	8	0	-0.893995	-0.893995	1.534E-27
252,152,934,023	8766	TT13	chr16	16	q13	57018131	57035191	8	0	-0.587802	-0.587802	2.06E-21
252,152,934,023	8771	TT13	chr16	16	q21	57479063	57571441	45	0	-0.693245	-0.693245	2.869E-74
252,152,934,023	8772	TT13	chr16	16	q21	57553714	57571441	11	0	-1.434823	-1.434823	2.161E-18

252,152,934,023	8776	TT13	chr16	16	q21	58016960	58036819	13	0	-1.179127	-1.179127	1.99E-56
252,152,934,023	8783	TT13	chr16	16	q21	65154321	65158495	3	0	-1.752888	-1.752888	2.755E-27
252,152,934,023	8784	TT13	chr16	16	q21 - q22.1	66428657	68320477	899	0	-0.260721	-0.260721	5.023E-245
252,152,934,023	8785	TT13	chr16	16	q21	66503091	66515048	7	0	-0.914012	-0.914012	6.38E-12
252,152,934,023	8794	TT13	chr16	16	q22.1	67183753	67235342	35	0	-1.301195	-1.301195	4.654E-100
252,152,934,023	8799	TT13	chr16	16	q22.1	67684888	67689798	3	0	-1.691472	-1.691472	9.192E-18
252,152,934,023	8800	TT13	chr16	16	q22.1	67744581	67754542	6	0	-1.248043	-1.248043	9.247E-24
252,152,934,023	8802	TT13	chr16	16	q22.1	67866783	67933130	30	0	-0.777051	-0.777051	3.089E-32
252,152,934,023	8803	TT13	chr16	16	q22.1	67875432	67880102	3	0	-1.902001	-1.902001	2.663E-12
252,152,934,023	8804	TT13	chr16	16	q22.1	67997365	68034655	20	0	-1.003347	-1.003347	5.15E-37
252,152,934,023	8806	TT13	chr16	16	q22.1	68265291	68279598	9	0	-1.201128	-1.201128	2.451E-25
252,152,934,023	8807	TT13	chr16	16	q22.1	68295054	68315795	11	0	-0.809048	-0.809048	4.035E-15
252,152,934,023	8809	TT13	chr16	16	q22.1	68476460	68486446	7	0	-0.892074	-0.892074	2.845E-23
252,152,934,023	8810	TT13	chr16	16	q22.1	68559978	68575601	8	0	-1.444622	-1.444622	3.043E-58
252,152,934,023	8812	TT13	chr16	16	q22.1	68768913	68776713	5	0	-1.104137	-1.104137	1.979E-25
252,152,934,023	8813	TT13	chr16	16	q22.1	68873949	68878863	3	0	-0.900417	-0.900417	4.408E-12
252,152,934,023	8814	TT13	chr16	16	q22.1	69136200	69173835	21	0	-0.586949	-0.586949	1.527E-30
252,152,934,023	8815	TT13	chr16	16	q22.1	69220360	69223845	3	0	-1.624815	-1.624815	2.08E-28
252,152,934,023	8819	TT13	chr16	16	q22.1	69596037	69604594	11	0	-1.145065	-1.145065	1.092E-49
252,152,934,023	8820	TT13	chr16	16	q22.1	69793911	69799216	4	0	-1.145442	-1.145442	1.83E-21
252,152,934,023	8822	TT13	chr16	16	q22.1	70470744	70490442	8	0	-1.125579	-1.125579	2.446E-38
252,152,934,023	8831	TT13	chr16	16	q22.2	71619334	71627397	4	0	-0.990193	-0.990193	9.517E-18
252,152,934,023	8832	TT13	chr16	16	q22.2	71657621	71663171	4	0	-0.807261	-0.807261	6.094E-10
252,152,934,023	8833	TT13	chr16	16	q22.2	71754421	71760699	4	0	-1.174633	-1.174633	7.771E-24
252,152,934,023	8834	TT13	chr16	16	q22.2	71876194	71933449	30	0	-0.543906	-0.543906	2.323E-38
252,152,934,023	8839	TT13	chr16	16	q22.3	73078930	73101861	12	0	-1.345605	-1.345605	3.317E-67
252,152,934,023	8840	TT13	chr16	16	q22.3	73091270	73097792	4	0	-2.45791	-2.45791	3.113E-10
252,152,934,023	8841	TT13	chr16	16	q23.1	74635539	74644661	6	0	-0.955843	-0.955843	2.724E-22
252,152,934,023	8842	TT13	chr16	16	q23.1	74694612	74706277	7	0	-0.890319	-0.890319	6.528E-25
252,152,934,023	8847	TT13	chr16	16	q23.1	75255184	75286897	15	0	-1.57177	-1.57177	8.134E-85
252,152,934,023	8848	TT13	chr16	16	q23.1	75465555	75604732	64	0	-0.659231	-0.659231	5.031E-112
252,152,934,023	8849	TT13	chr16	16	q23.1	75495683	75514089	9	0	-1.209656	-1.209656	7.514E-12
252,152,934,023	8851	TT13	chr16	16	q23.1	75680919	75688197	4	0	-1.25655	-1.25655	1.676E-25
252,152,934,023	8852	TT13	chr16	16	q23.1	76532473	76539889	4	0	-1.266892	-1.266892	3.628E-21
252,152,934,023	8853	TT13	chr16	16	q23.1	77225113	77250412	13	0	-0.563831	-0.563831	1.601E-18
252,152,934,023	8854	TT13	chr16	16	q23.1	77466760	77470334	3	0	-1.654081	-1.654081	3.74E-27
252,152,934,023	8856	TT13	chr16	16	q23.1	78076677	78084246	4	0	-1.210448	-1.210448	1.679E-24
252,152,934,023	8857	TT13	chr16	16	q23.1	78131499	78134914	3	0	-1.621641	-1.621641	2.69E-26
252,152,934,023	8858	TT13	chr16	16	q23.2	79620939	79636091	10	0	-1.451601	-1.451601	3.928E-73
252,152,934,023	8859	TT13	chr16	16	q23.2	79800827	79809845	3	0	-0.922186	-0.922186	1.371E-12
252,152,934,023	8860	TT13	chr16	16	q23.2	80833452	80843034	5	0	-1.16647	-1.16647	8.621E-29
252,152,934,023	8861	TT13	chr16	16	q23.2	81035492	81073644	20	0	-0.627382	-0.627382	8.311E-34
252,152,934,023	8862	TT13	chr16	16	q23.2	81068752	81072096	3	0	-1.843925	-1.843925	1.123E-14
252,152,934,023	8863	TT13	chr16	16	q23.2	81127047	81131106	3	0	-1.692303	-1.692303	1.862E-27
252,152,934,023	8864	TT13	chr16	16	q23.2	81341164	81356362	9	0	-0.77749	-0.77749	6.204E-23
252,152,934,023	8866	TT13	chr16	16	q23.3	81809379	81817460	6	0	-1.019486	-1.019486	7.028E-23
252,152,934,023	8867	TT13	chr16	16	q23.3	82197554	82209631	8	0	-0.61573	-0.61573	3.705E-17
252,152,934,023	8868	TT13	chr16	16	q23.3	82658024	82664874	5	0	-1.089661	-1.089661	1.082E-28
252,152,934,023	8869	TT13	chr16	16	q23.3	83838927	83845947	6	0	-1.237355	-1.237355	1.854E-36
252,152,934,023	8872	TT13	chr16	16	q24.1	84209504	84257129	21	0	-1.034992	-1.034992	3.7E-78
252,152,934,023	8873	TT13	chr16	16	q24.1	84223890	84227598	3	0	-2.347028	-2.347028	1.055E-12
252,152,934,023	8875	TT13	chr16	16	q24.1	84398842	84403517	3	0	-1.505369	-1.505369	5.11E-25
252,152,934,023	8877	TT13	chr16	16	q24.1	84683455	84697213	9	0	-1.345011	-1.345011	4.512E-55
252,152,934,023	8878	TT13	chr16	16	q24.1	84731632	84738337	4	0	-1.063166	-1.063166	9.98E-18
252,152,934,023	8879	TT13	chr16	16	q24.1	84850607	84857502	5	0	-1.164688	-1.164688	6.906E-26
252,152,934,023	8881	TT13	chr16	16	q24.1	84969114	84981718	6	0	-0.868023	-0.868023	4.453E-17
252,152,934,023	8895	TT13	chr16	16	q24.1	85831290	85843184	7	0	-1.309258	-1.309258	3.414E-46
252,152,934,023	8896	TT13	chr16	16	q24.1	85929385	85955197	15	0	-0.673914	-0.673914	2.622E-28
252,152,934,023	8897	TT13	chr16	16	q24.1	86311167	86342005	14	0	-0.69138	-0.69138	5.747E-28
252,152,934,023	8903	TT13	chr16	16	q24.2	87348454	87384983	19	0	-0.610986	-0.610986	2.785E-29
252,152,934,023	8904	TT13	chr16	16	q24.2	87414417	87453927	23	0	-0.944425	-0.944425	1.773E-73
252,152,934,023	8905	TT13	chr16	16	q24.2	87444579	87452462	5	0	-1.829531	-1.829531	4.617E-12
252,152,934,023	8907	TT13	chr16	16	q24.2 - q24.3	87709952	90118391	913	0	-0.518494	-0.518494	4.900e-324
252,152,934,023	8908	TT13	chr16	16	q24.2	87732880	87760958	15	0	-1.566374	-1.566374	7.669E-42
252,152,934,023	8910	TT13	chr16	16	q24.2	88089171	88092425	3	0	-1.677571	-1.677571	2.09E-12
252,152,934,023	8917	TT13	chr16	16	q24.3	88872123	88879089	4	0	-0.254913	-0.254913	4.329E-11
252,152,934,023	8926	TT13	chr16	16	q24.3	89596883	89789686	85	0	-0.827539	-0.827539	4.424E-29
252,152,934,023	8927	TT13	chr16	16	q24.3	89601973	89608633	4	0	-1.883238	-1.883238	1.688E-12
252,152,934,023	8953	TT13	chr17	17	p13.3	1918261	1952633	27	0	-0.888421	-0.888421	2.753E-47
252,152,934,023	8956	TT13	chr17	17	p13.3	2291738	2306683	8	0	-1.358837	-1.358837	2.338E-35
252,152,934,023	8960	TT13	chr17	17	p13.3	2592003	2619473	16	0	-1.027498	-1.027498	1.733E-35
252,152,934,023	8961	TT13	chr17	17	p13.3	2594489	2598595	3	0	-2.431365	-2.431365	1.102E-11
252,152,934,023	8963	TT13	chr17	17	p13.3	3011851	3018131	4	0	-1.237793	-1.237793	2.207E-27
252,152,934,023	8964	TT13	chr17	17	p13.3	3285826	3291900	5	0	-1.141945	-1.141945	3.638E-16
252,152,934,023	8965	TT13	chr17	17	p13.2	3365791	3377180	6	0	-1.633341	-1.633341	3.362E-42
252,152,934,023	8966	TT13	chr17	17	p13.2	3465801	3477378	7	0	-1.184905	-1.184905	1.045E-22
252,152,934,023	8971	TT13	chr17	17	p13.2	3893839	3911912	9	0	-1.175683	-1.175683	3.219E-33
252,152,934,023	8976	TT13	chr17	17	p13.2	4479428	4501117	11	0	-0.905598	-0.905598	1.124E-21
252,152,934,023	8978	TT13	chr17	17	p13.2	4640914	4649451	6	0	-1.527679	-1.527679	5.281E-35
252,152,934,023	8989	TT13	chr17	17	p13.2	5970918	5987328	9	0	-1.103709	-1.103709	4.175E-41
252,152,934,023	8990	TT13	chr17	17	p13.2	6342802	6361367	9	0	-0.756492	-0.756492	4.041E-20
252,152,934,023	8991	TT13	chr17	17	p13.2	6454725	6463715	6	0	-0.592912	-0.592912	9.619E-10
252,152,934,023	8992	TT13	chr17	17	p13.1	6545397	6557827	8	0	-1.065039	-1.065039	5.597E-38
252,152,934,023	8993	TT13	chr17	17	p13.1	6613032	6621817	5	0	-0.897271	-0.897271	6.498E-19
252,152,934,023	8994	TT13	chr17	17	p13.1	6678819	6683477	4	0	-1.208368	-1.208368	1.338E-23
252,152,934,023	9000	TT13	chr17	17	p13.1	7002202	7006569	3	0	-1.211888	-1.211888	1.704E-13
252,152,934,023	9007	TT13	chr17	17	p13.1	7541707	7556442	8	0	-1.13499	-1.13499	6.957E-27
252,152,934,023	9009	TT13	chr17	17	p13.1	7604068	7622043	10	0	-0.771729	-0.771729	1.328E-13
252,152,934,023	9010	TT13	chr17	17	p13.1	7739535	7757450	11	0	-1.442249	-1.442249	1.178E-45
252,152,934,023	9017	TT13	chr17	17	p13.1	8274643	8297199	13	0	-1.295587	-1.295587	3.266E-57
252,152,934,023	9020	TT13	chr17	17	p13.1	8730159	8738917	6	0	-1.674758	-1.674758	2.117E-39
252,152,934,023	9024	TT13	chr17	17	p13.1	9126149	9149593	12	0	-0.517094	-0.517094	1.358E-13
252,152,934,023	9025	TT13	chr17	17	p13.1	9547123	9551539	4	0	-1.507693	-1.507693	9.811E-25
252,152,934,023	9026	TT13	chr17	17	p13.1	9957388	9963484	4	0	-1.070941	-1.070941	9.303E-19
252,152,934,023	9028	TT13	chr17	17	p13.1	10598679	10602822	3	0	-1.729202	-1.729202	1.087E-29
252,152,934,023	9030	TT13	chr17	17	p12	11498561	11505360	5	0	-1.135589	-1.135589	2.923E-26

252,152,934,023	9031	TT13	chr17	17	p12	11923401	11927378	3	0	-1.779672	-1.779672	3.692E-29
252,152,934,023	9032	TT13	chr17	17	p12	12689787	12697268	6	0	-1.071236	-1.071236	7.891E-28
252,152,934,023	9034	TT13	chr17	17	p12	12917812	12925441	6	0	-1.013931	-1.013931	6.203E-27
252,152,934,023	9035	TT13	chr17	17	p12	13501750	13508264	4	0	-1.361137	-1.361137	5.946E-28
252,152,934,023	9036	TT13	chr17	17	p12	14105350	14114877	6	0	-0.786673	-0.786673	2.136E-17
252,152,934,023	9037	TT13	chr17	17	p12	14198501	14213458	7	0	-2.081828	-2.081828	4.589E-75
252,152,934,023	9038	TT13	chr17	17	p12	15160022	15167661	5	0	-0.784892	-0.784892	1.759E-14
252,152,934,023	9058	TT13	chr17	17	p11.2	17584371	17749395	101	0	-0.588993	-0.588993	9.824E-63
252,152,934,023	9059	TT13	chr17	17	p11.2	17596223	17604860	6	0	-1.300639	-1.300639	4.205E-10
252,152,934,023	9063	TT13	chr17	17	p11.2	18084877	18090030	4	0	-1.299747	-1.299747	5.838E-20
252,152,934,023	9064	TT13	chr17	17	p11.2	18128420	18169106	22	0	-0.96521	-0.96521	4.015E-45
252,152,934,023	9073	TT13	chr17	17	p11.2	19549250	19559044	5	0	-1.586071	-1.586071	1.788E-35
252,152,934,023	9076	TT13	chr17	17	p11.2	19880310	19883904	3	0	-2.294141	-2.294141	2.607E-34
252,152,934,023	9077	TT13	chr17	17	p11.2	19910012	19923614	8	0	-1.442753	-1.442753	6.827E-46
252,152,934,023	9096	TT13	chr17	17	q11.2	26542710	26581726	14	0	-0.69384	-0.69384	7.549E-21
252,152,934,023	9097	TT13	chr17	17	q11.2	26627877	26736072	54	0	-0.676595	-0.676595	8.176E-66
252,152,934,023	9098	TT13	chr17	17	q11.2	26698290	26712983	8	0	-1.404659	-1.404659	3.51E-14
252,152,934,023	9100	TT13	chr17	17	q11.2	26923315	26935361	7	0	-1.148829	-1.148829	8.809E-30
252,152,934,023	9101	TT13	chr17	17	q11.2	26969877	26988624	11	0	-1.068358	-1.068358	4.877E-39
252,152,934,023	9103	TT13	chr17	17	q11.2	27039811	27054363	9	0	-1.33919	-1.33919	3.205E-43
252,152,934,023	9115	TT13	chr17	17	q11.2	27918692	27952794	15	0	-1.047907	-1.047907	8.035E-43
252,152,934,023	9117	TT13	chr17	17	q11.2	28252990	28258120	4	0	-1.180902	-1.180902	6.323E-23
252,152,934,023	9119	TT13	chr17	17	q11.2	28704875	28717772	8	0	-1.539296	-1.539296	2.424E-54
252,152,934,023	9122	TT13	chr17	17	q11.2	29876002	29889772	15	0	-1.220487	-1.220487	1.926E-63
252,152,934,023	9131	TT13	chr17	17	q11.2	31146624	31154762	5	0	-1.252225	-1.252225	1.985E-31
252,152,934,023	9133	TT13	chr17	17	q12	32951805	32965723	9	0	-1.025953	-1.025953	2.718E-33
252,152,934,023	9140	TT13	chr17	17	q12	33814697	33827134	6	0	-1.400579	-1.400579	1.894E-33
252,152,934,023	9141	TT13	chr17	17	q12	33920970	33925687	3	0	-1.719576	-1.719576	2.729E-25
252,152,934,023	9144	TT13	chr17	17	q12	34837938	34843241	4	0	-2.133658	-2.133658	4.967E-37
252,152,934,023	9145	TT13	chr17	17	q12	34889076	34905468	10	0	-1.238908	-1.238908	7.862E-45
252,152,934,023	9147	TT13	chr17	17	q12	35297142	35307769	7	0	-1.99302	-1.99302	1.565E-58
252,152,934,023	9154	TT13	chr17	17	q12	36713116	36737811	14	0	-1.07184	-1.07184	1.549E-35
252,152,934,023	9161	TT13	chr17	17	q12	37355502	37367894	6	0	-1.224514	-1.224514	4.542E-27
252,152,934,023	9163	TT13	chr17	17	q12	37751458	37770902	11	0	-1.457162	-1.457162	1.868E-58
252,152,934,023	9170	TT13	chr17	17	q21.2	38798320	38807177	5	0	-1.142064	-1.142064	4.314E-29
252,152,934,023	9207	TT13	chr17	17	q21.31	42249063	42319056	32	0	-0.784387	-0.784387	4.928E-53
252,152,934,023	9208	TT13	chr17	17	q21.31	42253276	42259488	3	0	-1.965574	-1.965574	1.328E-11
252,152,934,023	9210	TT13	chr17	17	q21.31	42384292	42467605	42	0	-0.542548	-0.542548	2.666E-29
252,152,934,023	9212	TT13	chr17	17	q21.31	42631330	42641887	7	0	-0.99208	-0.99208	6.057E-21
252,152,934,023	9215	TT13	chr17	17	q21.31	43034757	43065023	15	0	-0.894232	-0.894232	1.462E-31
252,152,934,023	9216	TT13	chr17	17	q21.31	43094058	43102699	5	0	-0.940949	-0.940949	4.526E-14
252,152,934,023	9220	TT13	chr17	17	q21.31	43193251	43343314	69	0	-0.404115	-0.404115	2.821E-23
252,152,934,023	9227	TT13	chr17	17	q21.31	44845055	44852174	5	0	-1.048173	-1.048173	3.391E-14
252,152,934,023	9229	TT13	chr17	17	q21.32	44916115	44933016	9	0	-1.121838	-1.121838	8.261E-36
252,152,934,023	9233	TT13	chr17	17	q21.32	45468876	45504099	14	0	-0.689912	-0.689912	6.251E-21
252,152,934,023	9234	TT13	chr17	17	q21.32	45722686	45731475	6	0	-1.08443	-1.08443	9.06E-24
252,152,934,023	9235	TT13	chr17	17	q21.32	45767661	45787523	9	0	-1.073306	-1.073306	2.107E-30
252,152,934,023	9239	TT13	chr17	17	q21.32	46087225	46134253	48	0	-0.78118	-0.78118	7.342E-80
252,152,934,023	9241	TT13	chr17	17	q21.32	46601070	46727291	119	0	-1.252209	-1.252209	4.900e-324
252,152,934,023	9242	TT13	chr17	17	q21.32	46618771	46634145	12	0	-1.861024	-1.861024	7.696E-12
252,152,934,023	9250	TT13	chr17	17	q21.32	46983431	46988852	4	0	-1.151365	-1.151365	1.327E-16
252,152,934,023	9252	TT13	chr17	17	q21.32	47069742	47096758	15	0	-1.389826	-1.389826	1.362E-69
252,152,934,023	9274	TT13	chr17	17	q21.33	49334370	49342429	6	0	-1.227292	-1.227292	1.961E-27
252,152,934,023	9275	TT13	chr17	17	q21.33	49741220	49750443	5	0	-0.936958	-0.936958	1.098E-20
252,152,934,023	9276	TT13	chr17	17	q22	50232184	50239372	6	0	-1.114626	-1.114626	6.23E-27
252,152,934,023	9277	TT13	chr17	17	q22	52973174	52984102	6	0	-0.937439	-0.937439	2.624E-23
252,152,934,023	9279	TT13	chr17	17	q22	53496098	53503296	5	0	-1.189194	-1.189194	1.713E-28
252,152,934,023	9282	TT13	chr17	17	q22	54986328	54995871	6	0	-0.995384	-0.995384	8.929E-25
252,152,934,023	9283	TT13	chr17	17	q22	55038611	55057430	5	0	-1.643305	-1.643305	1.531E-43
252,152,934,023	9286	TT13	chr17	17	q22	55331015	55337404	4	0	-1.21054	-1.21054	4.341E-24
252,152,934,023	9296	TT13	chr17	17	q22	57181848	57187299	5	0	-1.699395	-1.699395	8.595E-44
252,152,934,023	9303	TT13	chr17	17	q23.2	58672176	58695493	10	0	-0.928267	-0.928267	7.344E-31
252,152,934,023	9304	TT13	chr17	17	q23.2	59051584	59058570	3	0	-1.271374	-1.271374	4.023E-17
252,152,934,023	9305	TT13	chr17	17	q23.2	59472649	59542310	29	0	-0.930823	-0.930823	2.15E-65
252,152,934,023	9306	TT13	chr17	17	q23.2	59530332	59534773	3	0	-3.261954	-3.261954	9.073E-23
252,152,934,023	9307	TT13	chr17	17	q23.2	60095607	60101354	4	0	-1.256628	-1.256628	1.767E-22
252,152,934,023	9308	TT13	chr17	17	q23.2	60139533	60150178	6	0	-1.747427	-1.747427	2.761E-45
252,152,934,023	9310	TT13	chr17	17	q23.2	60727052	60732221	5	0	-0.878186	-0.878186	9.702E-13
252,152,934,023	9311	TT13	chr17	17	q23.2	60754217	60783023	14	0	-0.942219	-0.942219	3.017E-38
252,152,934,023	9312	TT13	chr17	17	q23.2	60882468	60888859	4	0	-0.981251	-0.981251	1.543E-14
252,152,934,023	9313	TT13	chr17	17	q23.2	61040408	61045475	4	0	-1.287409	-1.287409	1.697E-23
252,152,934,023	9317	TT13	chr17	17	q23.3	61847713	61854270	5	0	-1.504408	-1.504408	7.826E-35
252,152,934,023	9323	TT13	chr17	17	q24.1	62958203	62974818	8	0	-1.250334	-1.250334	2.278E-48
252,152,934,023	9324	TT13	chr17	17	q24.1	63089611	63137995	18	0	-0.650521	-0.650521	1.675E-32
252,152,934,023	9329	TT13	chr17	17	q24.2	64295954	64300380	3	0	-1.829142	-1.829142	3.742E-30
252,152,934,023	9334	TT13	chr17	17	q24.2	65353809	65379432	13	0	-0.877173	-0.877173	5.233E-41
252,152,934,023	9336	TT13	chr17	17	q24.2	65815844	65827530	5	0	-0.790058	-0.790058	4.447E-15
252,152,934,023	9337	TT13	chr17	17	q24.2	65987167	66257030	45	0	-0.697747	-0.697747	3.874E-81
252,152,934,023	9338	TT13	chr17	17	q24.2	66196359	66203790	4	0	-2.197443	-2.197443	4.057E-18
252,152,934,023	9340	TT13	chr17	17	q24.2	66448337	66513153	27	0	-0.509689	-0.509689	6.352E-30
252,152,934,023	9342	TT13	chr17	17	q24.3	67322130	67329933	5	0	-1.189309	-1.189309	9.771E-28
252,152,934,023	9343	TT13	chr17	17	q24.3	68160468	68169577	5	0	-0.891239	-0.891239	2.018E-18
252,152,934,023	9344	TT13	chr17	17	q24.3	70119330	70122213	3	0	-1.860846	-1.860846	1.421E-32
252,152,934,023	9347	TT13	chr17	17	q24.3	70631748	70645772	9	0	-0.860355	-0.860355	7.068E-27
252,152,934,023	9352	TT13	chr17	17	q25.1	72205984	72211448	4	0	-1.092901	-1.092901	2.522E-20
252,152,934,023	9354	TT13	chr17	17	q25.1	72349871	72355929	4	0	-1.805814	-1.805814	6.83E-32
252,152,934,023	9355	TT13	chr17	17	q25.1	72424496	72437100	9	0	-0.735021	-0.735021	5.137E-20
252,152,934,023	9356	TT13	chr17	17	q25.1	72664246	72671896	5	0	-0.81716	-0.81716	3.507E-16
252,152,934,023	9364	TT13	chr17	17	q25.1	73254784	73270223	8	0	-0.859179	-0.859179	2.556E-27
252,152,934,023	9366	TT13	chr17	17	q25.1	73515494	73522589	4	0	-2.100746	-2.100746	6.872E-28
252,152,934,023	9372	TT13	chr17	17	q25.1	73887398	73915391	15	0	-1.285137	-1.285137	3.69E-46
252,152,934,023	9374	TT13	chr17	17	q25.1	73995712	74016653	11	0	-0.937983	-0.937983	3.277E-19
252,152,934,023	9378	TT13	chr17	17	q25.1	74251888	74270574	9	0	-1.282066	-1.282066	2.037E-28
252,152,934,023	9382	TT13	chr17	17	q25.1	74701184	74737161	32	0	-0.920877	-0.920877	7.38E-52
252,152,934,023	9383	TT13	chr17	17	q25.1	74731135	74734630	4	0	-1.853482	-1.853482	7.54E-11
252,152,934,023	9392	TT13	chr17	17	q25.3	76099391	76116600	8	0	-1.706715	-1.706715	1.831E-66

252,152,934,023	9400	TT13	chr17	17	q25.3	76986374	77123583	60	0	-0.577778	-0.577778	1.172E-68
252,152,934,023	9401	TT13	chr17	17	q25.3	77069479	77089454	11	0	-1.11543	-1.11543	1.818E-12
252,152,934,023	9404	TT13	chr17	17	q25.3	77384568	77390815	5	0	-0.939709	-0.939709	2.897E-19
252,152,934,023	9409	TT13	chr17	17	q25.3	77749226	77790187	21	0	-1.437936	-1.437936	1.282E-48
252,152,934,023	9412	TT13	chr17	17	q25.3	77961839	77975160	7	0	-1.633084	-1.633084	4.018E-30
252,152,934,023	9413	TT13	chr17	17	q25.3	78064623	78096049	16	0	-1.219129	-1.219129	4.496E-28
252,152,934,023	9449	TT13	chr18	18	p11.32	499057	516883	8	0	-1.429307	-1.429307	4.145E-49
252,152,934,023	9450	TT13	chr18	18	p11.32	578396	597813	8	0	-1.352753	-1.352753	6.101E-54
252,152,934,023	9453	TT13	chr18	18	p11.32	808779	813556	3	0	-1.471181	-1.471181	4.145E-25
252,152,934,023	9454	TT13	chr18	18	p11.32	907041	912347	4	0	-1.652268	-1.652268	1.347E-31
252,152,934,023	9455	TT13	chr18	18	p11.32	1095364	1103263	3	0	-1.089128	-1.089128	2.517E-16
252,152,934,023	9456	TT13	chr18	18	p11.32	2652689	2657612	3	0	-1.561478	-1.561478	4.832E-25
252,152,934,023	9457	TT13	chr18	18	p11.32	2843267	2885022	19	0	-0.774178	-0.774178	1.129E-47
252,152,934,023	9459	TT13	chr18	18	p11.31	3245540	3266037	10	0	-1.050857	-1.050857	1.697E-42
252,152,934,023	9462	TT13	chr18	18	p11.31	3495718	3502555	4	0	-1.405098	-1.405098	4.407E-31
252,152,934,023	9465	TT13	chr18	18	p11.31	3876819	3882047	4	0	-1.809552	-1.809552	1.611E-39
252,152,934,023	9471	TT13	chr18	18	p11.31	5542616	5546661	3	0	-1.683281	-1.683281	3.577E-29
252,152,934,023	9472	TT13	chr18	18	p11.31	5886208	5898162	6	0	-1.62746	-1.62746	2.117E-51
252,152,934,023	9473	TT13	chr18	18	p11.31	6281512	6291307	6	0	-0.832251	-0.832251	2.195E-16
252,152,934,023	9474	TT13	chr18	18	p11.31	6413336	6419139	3	0	-1.40033	-1.40033	1.639E-23
252,152,934,023	9475	TT13	chr18	18	p11.31	6822895	6829186	3	0	-1.15972	-1.15972	2.752E-18
252,152,934,023	9476	TT13	chr18	18	p11.31	6918001	6932270	7	0	-1.278096	-1.278096	1.933E-43
252,152,934,023	9484	TT13	chr18	18	p11.22	9473516	9478281	3	0	-1.847226	-1.847226	6.346E-25
252,152,934,023	9490	TT13	chr18	18	p11.22	10591010	10610381	3	0	-1.052832	-1.052832	1.719E-15
252,152,934,023	9491	TT13	chr18	18	p11.22	10720743	10731541	11	0	-0.927928	-0.927928	9.845E-40
252,152,934,023	9494	TT13	chr18	18	p11.21	11748122	11756505	4	0	-1.213945	-1.213945	4.863E-23
252,152,934,023	9495	TT13	chr18	18	p11.21	11818472	11824957	5	0	-1.142642	-1.142642	1.098E-26
252,152,934,023	9496	TT13	chr18	18	p11.21	11897829	13224296	504	0	-0.27806	-0.27806	1.682E-163
252,152,934,023	9497	TT13	chr18	18	p11.21	11906025	11911790	4	0	-1.403468	-1.403468	2.545E-18
252,152,934,023	9509	TT13	chr18	18	p11.21	12977287	12994852	10	0	-1.396191	-1.396191	2.082E-46
252,152,934,023	9512	TT13	chr18	18	p11.21	13378837	13396141	11	0	-1.304796	-1.304796	7.042E-69
252,152,934,023	9518	TT13	chr18	18	q11.1	18818354	18824592	4	0	-1.323498	-1.323498	3.063E-26
252,152,934,023	9521	TT13	chr18	18	q11.2	19282985	19288765	4	0	-1.676876	-1.676876	2.749E-34
252,152,934,023	9522	TT13	chr18	18	q11.2	19319970	19323804	4	0	-1.999811	-1.999811	6.654E-42
252,152,934,023	9523	TT13	chr18	18	q11.2	19744116	19759791	9	0	-1.896151	-1.896151	1.074E-69
252,152,934,023	9529	TT13	chr18	18	q11.2	21155661	21168594	7	0	-1.507546	-1.507546	5.64E-50
252,152,934,023	9530	TT13	chr18	18	q11.2	21197687	21203188	4	0	-1.154785	-1.154785	5.157E-21
252,152,934,023	9534	TT13	chr18	18	q11.2	21953840	22017768	29	0	-0.616858	-0.616858	4.018E-40
252,152,934,023	9535	TT13	chr18	18	q11.2	21976393	21980160	3	0	-1.741597	-1.741597	1.913E-12
252,152,934,023	9536	TT13	chr18	18	q11.2	22928725	22934634	3	0	-1.807167	-1.807167	2.437E-29
252,152,934,023	9538	TT13	chr18	18	q11.2	23802850	23810908	6	0	-1.281225	-1.281225	2.508E-35
252,152,934,023	9540	TT13	chr18	18	q11.2	24440794	24447345	4	0	-1.128394	-1.128394	1.157E-20
252,152,934,023	9541	TT13	chr18	18	q11.2	24762658	24772511	5	0	-0.912096	-0.912096	7.491E-18
252,152,934,023	9542	TT13	chr18	18	q12.1	25754520	25760426	4	0	-1.750228	-1.750228	2.782E-37
252,152,934,023	9543	TT13	chr18	18	q12.1	28619981	28626198	5	0	-1.291131	-1.291131	2.682E-28
252,152,934,023	9544	TT13	chr18	18	q12.1	28674712	28684762	6	0	-1.178885	-1.178885	1.822E-32
252,152,934,023	9545	TT13	chr18	18	q12.1	29077006	29082312	4	0	-0.865533	-0.865533	2.791E-11
252,152,934,023	9551	TT13	chr18	18	q12.1	30724183	30733416	6	0	-1.224023	-1.224023	7.705E-35
252,152,934,023	9558	TT13	chr18	18	q12.2	32845573	32854591	4	0	-1.544998	-1.544998	9.311E-32
252,152,934,023	9561	TT13	chr18	18	q12.2	33154772	33164337	6	0	-1.209898	-1.209898	2.632E-31
252,152,934,023	9562	TT13	chr18	18	q12.2	33643938	33655500	7	0	-1.24107	-1.24107	2.681E-40
252,152,934,023	9600	TT13	chr18	18	q21.1	46972129	47020610	36	0	-0.620205	-0.620205	2.614E-51
252,152,934,023	9601	TT13	chr18	18	q21.1	46981718	46988550	6	0	-1.511082	-1.511082	1.867E-18
252,152,934,023	9602	TT13	chr18	18	q21.1	47012774	47014843	4	0	-1.991031	-1.991031	3.251E-22
252,152,934,023	9603	TT13	chr18	18	q21.1	47100705	47107233	4	0	-1.041048	-1.041048	7.729E-16
252,152,934,023	9604	TT13	chr18	18	q21.1	47323813	47341251	8	0	-1.248365	-1.248365	1.92E-42
252,152,934,023	9606	TT13	chr18	18	q21.1	48130937	48138249	5	0	-1.14898	-1.14898	5.239E-26
252,152,934,023	9609	TT13	chr18	18	q21.2	48635935	48649128	3	0	-1.594061	-1.594061	1.479E-24
252,152,934,023	9610	TT13	chr18	18	q21.2	48720053	48728192	5	0	-0.917737	-0.917737	1.53E-14
252,152,934,023	9611	TT13	chr18	18	q21.2	49386675	49394022	3	0	-0.896059	-0.896059	4.134E-11
252,152,934,023	9612	TT13	chr18	18	q21.2	49890067	49897355	4	0	-1.231676	-1.231676	1.803E-24
252,152,934,023	9617	TT13	chr18	18	q21.2	52623590	52633275	6	0	-0.97782	-0.97782	6.8E-24
252,152,934,023	9618	TT13	chr18	18	q21.2	52983619	52995246	7	0	-1.031615	-1.031615	3.263E-27
252,152,934,023	9619	TT13	chr18	18	q21.2	53251017	53260413	6	0	-0.917692	-0.917692	4.78E-19
252,152,934,023	9620	TT13	chr18	18	q21.31	55097206	55108507	6	0	-1.821678	-1.821678	9.735E-54
252,152,934,023	9621	TT13	chr18	18	q21.31	55250393	55256446	4	0	-1.376132	-1.376132	6.616E-29
252,152,934,023	9622	TT13	chr18	18	q21.31	55287773	55319324	12	0	-1.140165	-1.140165	7.45E-53
252,152,934,023	9623	TT13	chr18	18	q21.31	55311997	55315586	3	0	-2.451065	-2.451065	4.53E-12
252,152,934,023	9626	TT13	chr18	18	q21.32	56336464	56339703	3	0	-1.962807	-1.962807	1.538E-31
252,152,934,023	9663	TT13	chr18	18	q22.3	72110906	72126667	9	0	-1.008014	-1.008014	2.617E-33
252,152,934,023	9664	TT13	chr18	18	q22.3	72162880	72166815	3	0	-1.119296	-1.119296	7.484E-15
252,152,934,023	9666	TT13	chr18	18	q22.3	72914306	72925263	6	0	-1.710586	-1.710586	5.851E-49
252,152,934,023	9669	TT13	chr18	18	q23	74060534	74070045	6	0	-1.248609	-1.248609	7.99E-10
252,152,934,023	9670	TT13	chr18	18	q23	74060534	74211566	69	0	-0.574638	-0.574638	8.63E-80
252,152,934,023	9671	TT13	chr18	18	q23	74090214	74094429	3	0	-1.768872	-1.768872	1.934E-14
252,152,934,023	9686	TT13	chr18	18	q23	76721787	76765386	22	0	-1.308023	-1.308023	1.825E-55
252,152,934,023	9687	TT13	chr18	18	q23	76828454	76835047	5	0	-1.548896	-1.548896	9.904E-21
252,152,934,023	9688	TT13	chr18	18	q23	77003582	77009149	4	0	-0.85884	-0.85884	2.512E-14
252,152,934,023	9690	TT13	chr18	18	q23	77130486	77675197	208	0	-1.030939	-1.030939	4.900e-324
252,152,934,023	9691	TT13	chr18	18	q23	77146135	77246275	46	0	-1.736986	-1.736986	1.706E-54
252,152,934,023	9692	TT13	chr18	18	q23	77229219	77232057	3	0	-0.701795	-0.701795	1.073E-12
252,152,934,023	9693	TT13	chr18	18	q23	77346319	77359204	5	0	-0.327672	-0.327672	2.576E-10
252,152,934,023	9697	TT13	chr18	18	q23	77541120	77570262	10	0	-1.752716	-1.752716	1.556E-14
252,152,934,023	9698	TT13	chr18	18	q23	77607645	77665953	22	0	-1.526106	-1.526106	4.035E-16
252,152,934,023	9712	TT13	chr19	19	p13.3	795608	835675	15	0	-1.607073	-1.607073	1.804E-23
252,152,934,023	9713	TT13	chr19	19	p13.3	886690	905833	10	0	-1.515222	-1.515222	3.045E-13
252,152,934,023	9731	TT13	chr19	19	p13.3	2191183	2241994	40	0	-1.178715	-1.178715	5.179E-14
252,152,934,023	9735	TT13	chr19	19	p13.3	2635316	2642302	5	0	-0.759321	-0.759321	9.066E-15
252,152,934,023	9753	TT13	chr19	19	p13.3	3570099	3831199	115	0	-0.985907	-0.985907	1.293E-65
252,152,934,023	9754	TT13	chr19	19	p13.3	3594732	3669554	35	0	-1.356771	-1.356771	1.928E-14
252,152,934,023	9763	TT13	chr19	19	p13.3	4668463	4682293	8	0	-1.254793	-1.254793	1.879E-12
252,152,934,023	9764	TT13	chr19	19	p13.3	4785024	4791675	6	0	-1.390013	-1.390013	1.581E-24
252,152,934,023	9765	TT13	chr19	19	p13.3	4829302	4833210	3	0	-1.539635	-1.539635	3.367E-15
252,152,934,023	9767	TT13	chr19	19	p13.3	4940287	4973136	18	0	-0.820622	-0.820622	5.225E-20
252,152,934,023	9771	TT13	chr19	19	p13.3	5142757	5149317	4	0	-2.209985	-2.209985	2.961E-20
252,152,934,023	9774	TT13	chr19	19	p13.3	5587025	5595578	5	0	-1.730045	-1.730045	3.57E-32

252,152,934,023	9775	TT13	chr19	19	p13.3	5619990	5625109	4	0	-1.217919	-1.217919	9.835E-18
252,152,934,023	9778	TT13	chr19	19	p13.3	5782690	5803451	9	0	-1.171016	-1.171016	3.873E-27
252,152,934,023	9779	TT13	chr19	19	p13.3	5893739	5918346	14	0	-1.567888	-1.567888	2.583E-72
252,152,934,023	9781	TT13	chr19	19	p13.3	5994427	6010007	9	0	-1.386431	-1.386431	4.29E-45
252,152,934,023	9782	TT13	chr19	19	p13.3	6194932	6240958	29	0	-0.915176	-0.915176	2.188E-53
252,152,934,023	9783	TT13	chr19	19	p13.3	6225984	6238199	9	0	-1.56998	-1.56998	8.695E-12
252,152,934,023	9792	TT13	chr19	19	p13.3	6819835	6825140	4	0	-0.990351	-0.990351	1.714E-18
252,152,934,023	9793	TT13	chr19	19	p13.2	7052997	7105600	21	0	-0.391239	-0.391239	2.219E-18
252,152,934,023	9794	TT13	chr19	19	p13.2	7196559	7201142	3	0	-1.413935	-1.413935	2.678E-23
252,152,934,023	9795	TT13	chr19	19	p13.2	7457177	7461980	4	0	-1.359385	-1.359385	2.923E-22
252,152,934,023	9800	TT13	chr19	19	p13.2	7966891	8010265	26	0	-1.200656	-1.200656	4.364E-33
252,152,934,023	9801	TT13	chr19	19	p13.2	7988098	7997828	6	0	-2.157054	-2.157054	7.093E-10
252,152,934,023	9808	TT13	chr19	19	p13.2	8547954	8593881	27	0	-0.884269	-0.884269	5.265E-16
252,152,934,023	9809	TT13	chr19	19	p13.2	8645122	8653346	5	0	-1.4282	-1.4282	1.938E-14
252,152,934,023	9811	TT13	chr19	19	p13.2	8806229	8812592	5	0	-0.83067	-0.83067	1.335E-10
252,152,934,023	9812	TT13	chr19	19	p13.2	8940531	8944873	3	0	-1.344176	-1.344176	9.957E-18
252,152,934,023	9813	TT13	chr19	19	p13.2	9364953	9400006	16	0	-0.521957	-0.521957	1.437E-10
252,152,934,023	9814	TT13	chr19	19	p13.2	9418155	9434080	8	0	-1.181961	-1.181961	9.022E-30
252,152,934,023	9815	TT13	chr19	19	p13.2	9919720	9964200	24	0	-0.63763	-0.63763	2.224E-23
252,152,934,023	9825	TT13	chr19	19	p13.2	10503158	10683338	107	0	-0.749522	-0.749522	3.078E-76
252,152,934,023	9826	TT13	chr19	19	p13.2	10528033	10542298	11	0	-1.705073	-1.705073	1.44E-25
252,152,934,023	9830	TT13	chr19	19	p13.2	10824363	10830456	6	0	-1.806804	-1.806804	2.928E-32
252,152,934,023	9857	TT13	chr19	19	p13.2	13259858	13273349	6	0	-1.441898	-1.441898	6.199E-23
252,152,934,023	9862	TT13	chr19	19	p13.13 - p13.12	13907861	14272554	209	0	-0.686775	-0.686775	1.843E-108
252,152,934,023	9863	TT13	chr19	19	p13.13	13936943	13961274	27	0	-1.156024	-1.156024	1.423E-17
252,152,934,023	9864	TT13	chr19	19	p13.12	14015566	14016642	3	0	-1.701098	-1.701098	3.723E-11
252,152,934,023	9865	TT13	chr19	19	p13.12	14062599	14090906	17	0	-1.277966	-1.277966	3.141E-18
252,152,934,023	9869	TT13	chr19	19	p13.12	14672582	14678117	3	0	-1.397456	-1.397456	1.397E-19
252,152,934,023	9870	TT13	chr19	19	p13.12	14797551	14802341	3	0	-1.366425	-1.366425	2.493E-23
252,152,934,023	9871	TT13	chr19	19	p13.12	15082943	15092543	7	0	-1.70784	-1.70784	1.041E-39
252,152,934,023	9872	TT13	chr19	19	p13.12	15120620	15135465	9	0	-1.045826	-1.045826	1.337E-20
252,152,934,023	9877	TT13	chr19	19	p13.12	15341672	15349182	5	0	-1.97626	-1.97626	6.19E-17
252,152,934,023	9879	TT13	chr19	19	p13.12	15471986	15582592	69	0	-0.992611	-0.992611	3.772E-105
252,152,934,023	9880	TT13	chr19	19	p13.12	15528981	15548586	16	0	-1.530581	-1.530581	9.912E-15
252,152,934,023	9881	TT13	chr19	19	p13.12	15561784	15565924	6	0	-1.845763	-1.845763	2.067E-11
252,152,934,023	9888	TT13	chr19	19	p13.12	16009655	16025336	7	0	-1.600041	-1.600041	3.733E-55
252,152,934,023	9894	TT13	chr19	19	p13.11	16635689	16654355	9	0	-1.484924	-1.484924	4.039E-52
252,152,934,023	9895	TT13	chr19	19	p13.11	16681497	16688687	5	0	-2.460266	-2.460266	3.095E-59
252,152,934,023	9896	TT13	chr19	19	p13.11	16735999	16741708	4	0	-1.177693	-1.177693	7.37E-22
252,152,934,023	9907	TT13	chr19	19	p13.11	17457976	17489143	15	0.26711	0	0.26711	1.23E-22
252,152,934,023	9922	TT13	chr19	19	p13.11	18646874	18653321	5	0	-1.300907	-1.300907	2.75E-10
252,152,934,023	9923	TT13	chr19	19	p13.11	18646874	18983997	156	0	-0.560496	-0.560496	8.523E-37
252,152,934,023	9924	TT13	chr19	19	p13.11	18699012	18722976	14	0	-1.192879	-1.192879	5.744E-18
252,152,934,023	9929	TT13	chr19	19	p13.11	19141829	19146231	4	0	-1.457968	-1.457968	1.352E-23
252,152,934,023	9939	TT13	chr19	19	p13.11	19611221	19662069	31	0	-0.689682	-0.689682	4.96E-32
252,152,934,023	9940	TT13	chr19	19	p13.11	19727081	19763054	21	0	-1.157103	-1.157103	8.592E-68
252,152,934,023	9952	TT13	chr19	19	p12	22879610	22895377	8	0	-1.021947	-1.021947	1.132E-17
252,152,934,023	9953	TT13	chr19	19	p12	23077296	23086678	3	0	-1.563086	-1.563086	8.138E-18
252,152,934,023	9961	TT13	chr19	19	q12	29699399	29707053	6	0	-1.1536	-1.1536	4.105E-30
252,152,934,023	9963	TT13	chr19	19	q12	29982900	30009505	12	0.424853	0	0.424853	5.691E-11
252,152,934,023	9970	TT13	chr19	19	q12	30861900	30869692	5	0	-1.244591	-1.244591	2.086E-30
252,152,934,023	9982	TT13	chr19	19	q13.11	33862909	33866541	4	0	-1.905157	-1.905157	3.17E-22
252,152,934,023	9986	TT13	chr19	19	q13.11	34283651	34312894	17	0	-1.185405	-1.185405	2.619E-47
252,152,934,023	9987	TT13	chr19	19	q13.11	34285090	34290190	4	0	-2.530963	-2.530963	7.134E-12
252,152,934,023	9988	TT13	chr19	19	q13.11	34390918	34400071	4	0	-1.38089	-1.38089	3.825E-21
252,152,934,023	9989	TT13	chr19	19	q13.11	34568101	34574140	4	0	-1.399109	-1.399109	2.169E-30
252,152,934,023	9991	TT13	chr19	19	q13.11	34849842	34858113	5	0	-1.58956	-1.58956	3.179E-31
252,152,934,023	10001	TT13	chr19	19	q13.12	36046707	36053113	5	0	-1.397017	-1.397017	1.242E-23
252,152,934,023	10002	TT13	chr19	19	q13.12	36119283	36279728	87	0	-0.526214	-0.526214	3.674E-32
252,152,934,023	10003	TT13	chr19	19	q13.12	36122920	36137567	12	0	-1.005518	-1.005518	6.835E-11
252,152,934,023	10017	TT13	chr19	19	q13.12	37548468	37575188	11	0	-0.838084	-0.838084	2.062E-29
252,152,934,023	10018	TT13	chr19	19	q13.12	37857521	37865189	6	0	-1.233861	-1.233861	4.964E-33
252,152,934,023	10022	TT13	chr19	19	q13.13	38396769	38400209	3	0	-1.57373	-1.57373	2.978E-24
252,152,934,023	10030	TT13	chr19	19	q13.2	39086388	39088626	3	0	-1.637304	-1.637304	5.572E-18
252,152,934,023	10041	TT13	chr19	19	q13.2	39797218	39812413	9	0	-1.516835	-1.516835	3.735E-49
252,152,934,023	10043	TT13	chr19	19	q13.2	39892865	39916414	15	0	-1.287193	-1.287193	1.528E-39
252,152,934,023	10044	TT13	chr19	19	q13.2	39990266	39998709	5	0	-2.240112	-2.240112	3.698E-17
252,152,934,023	10045	TT13	chr19	19	q13.2	39990266	40033206	24	0	-1.031946	-1.031946	3.222E-57
252,152,934,023	10046	TT13	chr19	19	q13.2	40021576	40031279	6	0	-1.758789	-1.758789	1.565E-11
252,152,934,023	10047	TT13	chr19	19	q13.2	40314690	40338891	16	0	-1.457983	-1.457983	5.077E-81
252,152,934,023	10048	TT13	chr19	19	q13.2	40421022	40432428	6	0	-1.222555	-1.222555	7.978E-23
252,152,934,023	10053	TT13	chr19	19	q13.2	41012332	41194629	90	0	-0.985419	-0.985419	4.588E-173
252,152,934,023	10054	TT13	chr19	19	q13.2	41018077	41026585	5	0	-1.818451	-1.818451	6.77E-12
252,152,934,023	10060	TT13	chr19	19	q13.2	41830808	41838453	5	0	-2.184941	-2.184941	8.861E-46
252,152,934,023	10063	TT13	chr19	19	q13.2	42068177	42073676	4	0	-1.280737	-1.280737	2.212E-29
252,152,934,023	10065	TT13	chr19	19	q13.2	42388995	42448893	30	0	-1.070786	-1.070786	4.367E-54
252,152,934,023	10066	TT13	chr19	19	q13.2	42430564	42445976	7	0	-1.950838	-1.950838	5.02E-11
252,152,934,023	10071	TT13	chr19	19	q13.2	42578840	42586163	5	0	-1.894872	-1.894872	1.819E-34
252,152,934,023	10072	TT13	chr19	19	q13.2	42598359	42602917	3	0	-1.136247	-1.136247	8.399E-11
252,152,934,023	10073	TT13	chr19	19	q13.2	42712363	42917428	110	0	-0.773298	-0.773298	1.723E-115
252,152,934,023	10074	TT13	chr19	19	q13.2	42713546	42722353	5	0	-1.633742	-1.633742	3.386E-11
252,152,934,023	10077	TT13	chr19	19	q13.2	43110539	43113064	4	0	-0.926253	-0.926253	2.926E-16
252,152,934,023	10078	TT13	chr19	19	q13.2	43139757	43147336	4	0	-0.813908	-0.813908	1.14E-13
252,152,934,023	10079	TT13	chr19	19	q13.31	43908564	43915777	5	0	-1.231	-1.231	1.982E-29
252,152,934,023	10084	TT13	chr19	19	q13.31	44256091	44306013	25	0	-0.609998	-0.609998	1.522E-17
252,152,934,023	10085	TT13	chr19	19	q13.31	44700930	44711528	5	0	-0.997158	-0.997158	2.818E-22
252,152,934,023	10086	TT13	chr19	19	q13.31	44989468	44996783	5	0	-1.048874	-1.048874	1.355E-25
252,152,934,023	10087	TT13	chr19	19	q13.31	45144796	45149168	4	0	-1.628246	-1.628246	5.729E-35
252,152,934,023	10128	TT13	chr19	19	q13.32	47613761	47615975	3	0	-1.430606	-1.430606	3.245E-13
252,152,934,023	10129	TT13	chr19	19	q13.32	47725550	47779333	29	0	-1.174281	-1.174281	5.871E-86
252,152,934,023	10131	TT13	chr19	19	q13.32	47950128	47989264	23	0	-1.130865	-1.130865	2.203E-69
252,152,934,023	10134	TT13	chr19	19	q13.33	48361889	48368743	4	0	-0.96436	-0.96436	1.253E-18
252,152,934,023	10138	TT13	chr19	19	q13.33	48898230	48910171	6	0	-1.325457	-1.325457	1.845E-23
252,152,934,023	10146	TT13	chr19	19	q13.33	49249649	49255565	5	0	-1.087604	-1.087604	7.756E-10
252,152,934,023	10147	TT13	chr19	19	q13.33	49301712	49316280	8	0	-1.049843	-1.049843	2.769E-13
252,152,934,023	10151	TT13	chr19	19	q13.33	49651669	49704206	29	0	-0.794746	-0.794746	3.186E-19

252,152,934,023	10152	TT13	chr19	19	q13.33	49839408	49846292	6	0	-1.036039	-1.036039	1.623E-11
252,152,934,023	10153	TT13	chr19	19	q13.33	49916177	49933373	12	0	-1.262147	-1.262147	1.005E-30
252,152,934,023	10154	TT13	chr19	19	q13.33	50094192	50107039	8	0	-1.953419	-1.953419	3.581E-52
252,152,934,023	10158	TT13	chr19	19	q13.33	50352394	50379251	17	0	-1.19922	-1.19922	2.145E-29
252,152,934,023	10159	TT13	chr19	19	q13.33	50779886	50790062	5	0	-1.784383	-1.784383	3.968E-29
252,152,934,023	10168	TT13	chr19	19	q13.41	51520035	51536185	11	0	-1.231775	-1.231775	3.453E-49
252,152,934,023	10169	TT13	chr19	19	q13.41	51599773	51608914	6	0	-1.626999	-1.626999	1.821E-41
252,152,934,023	10171	TT13	chr19	19	q13.41	51683580	51688329	3	0	-1.304909	-1.304909	2.917E-16
252,152,934,023	10173	TT13	chr19	19	q13.41	52188506	52198677	9	0	-0.789227	-0.789227	2.948E-19
252,152,934,023	10174	TT13	chr19	19	q13.41	52208410	52226930	14	0	-1.30079	-1.30079	3.05E-70
252,152,934,023	10175	TT13	chr19	19	q13.41	52452099	52457801	4	0	-1.151866	-1.151866	8.033E-25
252,152,934,023	10177	TT13	chr19	19	q13.41	52770555	52812245	38	0	-0.525946	-0.525946	2.126E-32
252,152,934,023	10178	TT13	chr19	19	q13.41	52771370	52773046	4	0	-1.566839	-1.566839	2.093E-15
252,152,934,023	10185	TT13	chr19	19	q13.42	53632674	53776701	68	0	-0.456776	-0.456776	2.713E-41
252,152,934,023	10186	TT13	chr19	19	q13.42	53724671	53728199	3	0	-1.914112	-1.914112	1.643E-19
252,152,934,023	10190	TT13	chr19	19	q13.42	54366672	54416537	26	0	-0.660228	-0.660228	1.445E-34
252,152,934,023	10192	TT13	chr19	19	q13.42	54629653	54698414	36	0	-0.743064	-0.743064	3.643E-53
252,152,934,023	10193	TT13	chr19	19	q13.42	54650152	54652739	3	0	-2.230522	-2.230522	3.848E-14
252,152,934,023	10194	TT13	chr19	19	q13.42	54714711	54720826	4	0	-1.088656	-1.088656	6.252E-17
252,152,934,023	10195	TT13	chr19	19	q13.42	54924751	54984817	29	0	-1.108847	-1.108847	4.127E-86
252,152,934,023	10196	TT13	chr19	19	q13.42	54933164	54959268	12	0	-0.630853	-0.630853	4.95E-11
252,152,934,023	10198	TT13	chr19	19	q13.42	55450244	55453197	3	0	-1.387595	-1.387595	2.107E-16
252,152,934,023	10215	TT13	chr19	19	q13.43	56594133	56633700	19	0	-0.99296	-0.99296	3.932E-38
252,152,934,023	10224	TT13	chr19	19	q13.43	57304192	57308885	4	0	-1.698326	-1.698326	1.469E-29
252,152,934,023	10226	TT13	chr19	19	q13.43	57615390	57635382	12	0	-1.077391	-1.077391	5.434E-34
252,152,934,023	10227	TT13	chr19	19	q13.43	57682597	57705764	12	0	-0.828186	-0.828186	1.409E-18
252,152,934,023	10228	TT13	chr19	19	q13.43	57992354	58014686	18	0	-1.028036	-1.028036	1.779E-42
252,152,934,023	10229	TT13	chr19	19	q13.43	58000778	58005761	5	0	-0.251429	-0.251429	1.813E-14
252,152,934,023	10231	TT13	chr19	19	q13.43	58088564	58146492	31	0	-0.727715	-0.727715	3.016E-34
252,152,934,023	10238	TT13	chr19	19	q13.43	58691316	58697978	5	0	-1.138386	-1.138386	2.769E-18
252,152,934,023	10239	TT13	chr19	19	q13.43	58736600	58742040	5	0	-0.887052	-0.887052	9.777E-10
252,152,934,023	10246	TT13	chr20	20	p13	360875	405550	16	0	-0.757263	-0.757263	7.789E-14
252,152,934,023	10247	TT13	chr20	20	p13	441352	445266	3	0	-1.274876	-1.274876	1.553E-18
252,152,934,023	10249	TT13	chr20	20	p13	812017	828202	9	0	-1.435977	-1.435977	1.475E-35
252,152,934,023	10267	TT13	chr20	20	p13	3138994	3156347	10	0	-1.175631	-1.175631	2.73E-30
252,152,934,023	10268	TT13	chr20	20	p13	3180171	3222076	18	0	-0.616652	-0.616652	3.118E-13
252,152,934,023	10270	TT13	chr20	20	p13	3640125	3778956	65	0	-0.563297	-0.563297	1.374E-31
252,152,934,023	10272	TT13	chr20	20	p13	3824462	3829105	3	0	-1.286834	-1.286834	9.8E-15
252,152,934,023	10275	TT13	chr20	20	p13	3993490	3996823	3	0	-1.987494	-1.987494	2.256E-27
252,152,934,023	10280	TT13	chr20	20	p13	4663778	4670476	4	0	-1.377426	-1.377426	1.201E-26
252,152,934,023	10283	TT13	chr20	20	p13 - p12.3	5091437	5109105	7	0	-1.319055	-1.319055	2.826E-50
252,152,934,023	10284	TT13	chr20	20	p12.3	5586470	5595062	4	0	-1.024039	-1.024039	2.265E-19
252,152,934,023	10285	TT13	chr20	20	p12.3	5889767	5893019	3	0	-1.771997	-1.771997	5.282E-36
252,152,934,023	10286	TT13	chr20	20	p12.3	5982898	6036113	24	0	-0.828941	-0.828941	3.565E-67
252,152,934,023	10287	TT13	chr20	20	p12.3	6020972	6034022	6	0	-1.531373	-1.531373	3.384E-11
252,152,934,023	10288	TT13	chr20	20	p12.3	6101588	6111293	5	0	-0.897258	-0.897258	6.124E-19
252,152,934,023	10289	TT13	chr20	20	p12.3	6743214	6752735	6	0	-1.263937	-1.263937	2.538E-34
252,152,934,023	10295	TT13	chr20	20	p12.2	9362201	9373708	6	0	-0.769243	-0.769243	9.13E-17
252,152,934,023	10296	TT13	chr20	20	p12.2	9618348	9628126	5	0	-1.013679	-1.013679	1.175E-22
252,152,934,023	10297	TT13	chr20	20	p12.2	10007619	10021203	7	0	-1.313491	-1.313491	3.336E-43
252,152,934,023	10298	TT13	chr20	20	p12.2	10196626	10202282	3	0	-1.487086	-1.487086	9.563E-24
252,152,934,023	10299	TT13	chr20	20	p12.2	10369042	10382710	5	0	-0.979997	-0.979997	2.421E-21
252,152,934,023	10300	TT13	chr20	20	p12.2	10412303	10418132	4	0	-1.185416	-1.185416	2.154E-22
252,152,934,023	10301	TT13	chr20	20	p12.2	10646897	10656015	6	0	-1.764585	-1.764585	5.971E-52
252,152,934,023	10302	TT13	chr20	20	p12.2	11866450	11876773	6	0	-0.865641	-0.865641	1.367E-20
252,152,934,023	10304	TT13	chr20	20	p12.1	13970542	14034017	28	0	-0.590798	-0.590798	5.425E-42
252,152,934,023	10305	TT13	chr20	20	p12.1	13974982	13978474	3	0	-1.879063	-1.879063	3.49E-16
252,152,934,023	10306	TT13	chr20	20	p12.1	14022921	14028195	3	0	-1.599831	-1.599831	5.951E-12
252,152,934,023	10307	TT13	chr20	20	p12.1	14203607	14208425	3	0	-1.306705	-1.306705	5.71E-21
252,152,934,023	10309	TT13	chr20	20	p12.1	16202576	16211423	5	0	-1.195466	-1.195466	8.405E-26
252,152,934,023	10310	TT13	chr20	20	p12.1	16550058	16558305	6	0	-1.124149	-1.124149	2.814E-31
252,152,934,023	10311	TT13	chr20	20	p12.1	17200870	17213707	8	0	-0.872547	-0.872547	1.475E-26
252,152,934,023	10318	TT13	chr20	20	p11.23	18174411	18178157	3	0	-1.800889	-1.800889	1.874E-23
252,152,934,023	10319	TT13	chr20	20	p11.23	18202152	18212995	6	0	-0.724019	-0.724019	1.024E-15
252,152,934,023	10321	TT13	chr20	20	p11.23	19177065	19196437	8	0	-0.651825	-0.651825	4.197E-15
252,152,934,023	10325	TT13	chr20	20	p11.23	20344619	20351182	5	0	-1.690205	-1.690205	1.145E-37
252,152,934,023	10327	TT13	chr20	20	p11.23	21080612	21112811	16	0	-0.609923	-0.609923	9.862E-26
252,152,934,023	10330	TT13	chr20	20	p11.22	21486084	21501624	8	0	-1.826429	-1.826429	1.151E-54
252,152,934,023	10331	TT13	chr20	20	p11.22	21685654	21697071	6	0	-1.938957	-1.938957	3.521E-50
252,152,934,023	10332	TT13	chr20	20	p11.21	22551231	22568503	9	0	-1.491477	-1.491477	1.874E-56
252,152,934,023	10334	TT13	chr20	20	p11.21	23330322	23347721	9	0	-1.898457	-1.898457	1.561E-86
252,152,934,023	10335	TT13	chr20	20	p11.21	23395306	23406342	5	0	-1.187176	-1.187176	5.479E-28
252,152,934,023	10336	TT13	chr20	20	p11.21	23615548	23622790	4	0	-0.909361	-0.909361	1.515E-15
252,152,934,023	10337	TT13	chr20	20	p11.21	24447185	24454168	5	0	-1.134389	-1.134389	3.997E-24
252,152,934,023	10339	TT13	chr20	20	p11.21	25174620	25179249	4	0	-1.510063	-1.510063	3.526E-25
252,152,934,023	10345	TT13	chr20	20	q11.21	30056766	30075326	9	0	-1.184571	-1.184571	1.035E-33
252,152,934,023	10347	TT13	chr20	20	q11.21	30157286	30229251	32	0	-0.888537	-0.888537	1.064E-71
252,152,934,023	10348	TT13	chr20	20	q11.21	30160533	30167224	4	0	-2.225494	-2.225494	4.433E-18
252,152,934,023	10351	TT13	chr20	20	q11.21	30307817	30313623	4	0	-1.113645	-1.113645	9.323E-18
252,152,934,023	10354	TT13	chr20	20	q11.21	30768995	30801746	18	0	-0.694491	-0.694491	2.739E-26
252,152,934,023	10355	TT13	chr20	20	q11.21	30943377	30947721	3	0	-1.323265	-1.323265	4.948E-18
252,152,934,023	10356	TT13	chr20	20	q11.21	31014722	31073846	26	0	-0.688826	-0.688826	1.049E-35
252,152,934,023	10365	TT13	chr20	20	q11.22	32249319	32292411	22	0	-1.087654	-1.087654	5.867E-72
252,152,934,023	10369	TT13	chr20	20	q11.22	32698471	32712107	7	0	-1.289941	-1.289941	1.769E-35
252,152,934,023	10370	TT13	chr20	20	q11.22	32804760	32810346	4	0	-1.878391	-1.878391	7.059E-38
252,152,934,023	10377	TT13	chr20	20	q11.22	33288695	33300518	7	0	-1.287243	-1.287243	1.153E-33
252,152,934,023	10379	TT13	chr20	20	q11.22	33446355	33465230	10	0	-1.71148	-1.71148	1.064E-75
252,152,934,023	10403	TT13	chr20	20	q11.23	35693844	35818100	57	0	-0.398949	-0.398949	2.779E-22
252,152,934,023	10408	TT13	chr20	20	q11.23	36569424	36573752	3	0	-1.067787	-1.067787	1.511E-16
252,152,934,023	10409	TT13	chr20	20	q11.23	36886761	36892313	4	0	-1.060252	-1.060252	1.092E-20
252,152,934,023	10421	TT13	chr20	20	q12	39308744	39318785	5	0	-1.459599	-1.459599	1.303E-31
252,152,934,023	10422	TT13	chr20	20	q12	39655715	39662835	5	0	-0.894499	-0.894499	4.482E-16
252,152,934,023	10423	TT13	chr20	20	q12	39761340	39772760	5	0	-0.874812	-0.874812	1.166E-15
252,152,934,023	10424	TT13	chr20	20	q12	39943286	39947403	3	0	-1.355657	-1.355657	1.246E-21
252,152,934,023	10426	TT13	chr20	20	q12	40239695	40253727	8	0	-0.65276	-0.65276	5.054E-16
252,152,934,023	10428	TT13	chr20	20	q13.12	42134882	42144533	5	0	-1.706589	-1.706589	1.053E-44

252,152,934,023	10429	TT13	chr20	20	q13.12	42216608	42239044	12	0	-0.745552	-0.745552	3.772E-30
252,152,934,023	10430	TT13	chr20	20	q13.12	42282679	42307139	12	0	-1.125474	-1.125474	1.901E-54
252,152,934,023	10443	TT13	chr20	20	q13.12	43922081	43947175	16	0	-1.473215	-1.473215	3.988E-82
252,152,934,023	10454	TT13	chr20	20	q13.12	44716508	44729506	7	0	-1.594878	-1.594878	2.431E-47
252,152,934,023	10455	TT13	chr20	20	q13.12	44800433	44804064	3	0	-1.208199	-1.208199	7.773E-14
252,152,934,023	10473	TT13	chr20	20	q13.13	48518418	48555976	18	0	-0.937746	-0.937746	8.892E-60
252,152,934,023	10483	TT13	chr20	20	q13.13	49542777	49552600	6	0	-1.156659	-1.156659	4.135E-29
252,152,934,023	10484	TT13	chr20	20	q13.13	49620164	49643017	11	0	-1.012319	-1.012319	1.394E-39
252,152,934,023	10486	TT13	chr20	20	q13.2	50138238	50181919	22	0	-0.602835	-0.602835	3.694E-34
252,152,934,023	10487	TT13	chr20	20	q13.2	50177649	50181919	3	0	-1.503227	-1.503227	6.988E-10
252,152,934,023	10488	TT13	chr20	20	q13.2	50380940	50387615	5	0	-1.251069	-1.251069	1.753E-26
252,152,934,023	10492	TT13	chr20	20	q13.2	52269459	52281217	8	0	-0.736288	-0.736288	3.693E-20
252,152,934,023	10493	TT13	chr20	20	q13.2	52788933	52792350	3	0	-1.839595	-1.839595	1.81E-31
252,152,934,023	10494	TT13	chr20	20	q13.2	52822317	52829088	5	0	-1.210542	-1.210542	3.495E-29
252,152,934,023	10495	TT13	chr20	20	q13.2	53088083	53100497	6	0	-0.752956	-0.752956	7.626E-16
252,152,934,023	10496	TT13	chr20	20	q13.2	54568755	54588533	10	0	-0.489509	-0.489509	4.157E-12
252,152,934,023	10497	TT13	chr20	20	q13.2	54917408	54938678	9	0	-0.829077	-0.829077	1.206E-25
252,152,934,023	10501	TT13	chr20	20	q13.31	55903201	55930958	14	0	-1.027265	-1.027265	8.564E-57
252,152,934,023	10506	TT13	chr20	20	q13.31	56282373	56291458	5	0	-1.048535	-1.048535	1.615E-22
252,152,934,023	10511	TT13	chr20	20	q13.32	57035306	57042967	5	0	-2.211172	-2.211172	1.063E-53
252,152,934,023	10512	TT13	chr20	20	q13.32	57085841	57091582	4	0	-1.081541	-1.081541	5.164E-18
252,152,934,023	10514	TT13	chr20	20	q13.32	57223780	57294857	33	0	-0.468105	-0.468105	1.725E-31
252,152,934,023	10515	TT13	chr20	20	q13.32	57406191	57630503	106	0	-0.361972	-0.361972	8.132E-58
252,152,934,023	10516	TT13	chr20	20	q13.32	57413133	57433564	13	0	-1.106196	-1.106196	1.09E-24
252,152,934,023	10517	TT13	chr20	20	q13.32	57605205	57619173	9	0	-1.318266	-1.318266	5.027E-31
252,152,934,023	10518	TT13	chr20	20	q13.32	57794977	57800766	4	0	-1.243805	-1.243805	4.529E-24
252,152,934,023	10520	TT13	chr20	20	q13.32	58146544	58183500	19	0	-0.499534	-0.499534	1.385E-19
252,152,934,023	10521	TT13	chr20	20	q13.33	58505245	58519072	8	0	-1.347967	-1.347967	1.623E-49
252,152,934,023	10529	TT13	chr20	20	q13.33	60503660	62732642	989	0	-0.56182	-0.56182	4.900e-324
252,152,934,023	10530	TT13	chr20	20	q13.33	60539920	60559120	12	0	-1.311496	-1.311496	1.358E-19
252,152,934,023	10531	TT13	chr20	20	q13.33	60636532	60644631	5	0	-0.849746	-0.849746	2.054E-13
252,152,934,023	10534	TT13	chr20	20	q13.33	60814301	60819769	3	0	-2.42615	-2.42615	5.535E-24
252,152,934,023	10535	TT13	chr20	20	q13.33	60877081	60884184	6	0	-2.487888	-2.487888	2.789E-40
252,152,934,023	10552	TT13	chr20	20	q13.33	62525378	62528129	3	0	-1.899463	-1.899463	7.296E-15
252,152,934,023	10554	TT13	chr20	20	q13.33	62584261	62614580	22	0	-0.987007	-0.987007	9.575E-14
252,152,934,023	10555	TT13	chr20	20	q13.33	62693713	62712215	10	0	-1.251685	-1.251685	5.183E-14
252,152,934,023	10560	TT13	chr21	21	q21.1	16433963	16440059	4	0	-1.695013	-1.695013	2.205E-37
252,152,934,023	10562	TT13	chr21	21	q21.1	18981740	18989268	6	0	-1.244765	-1.244765	6.44E-34
252,152,934,023	10566	TT13	chr21	21	q21.1	21127745	21136875	7	0	-1.259118	-1.259118	2.598E-39
252,152,934,023	10567	TT13	chr21	21	q21.1	22366524	22372677	5	0	-1.283009	-1.283009	3.965E-28
252,152,934,023	10569	TT13	chr21	21	q21.3	27010035	27015933	5	0	-1.123844	-1.123844	2.835E-25
252,152,934,023	10573	TT13	chr21	21	q21.3	27540006	27543635	3	0	-1.736085	-1.736085	1.302E-27
252,152,934,023	10578	TT13	chr21	21	q21.3	30369359	30394548	14	0	-1.024207	-1.024207	6.611E-53
252,152,934,023	10579	TT13	chr21	21	q21.3	30444831	30455803	7	0	-0.945745	-0.945745	1.33E-24
252,152,934,023	10580	TT13	chr21	21	q21.3	30666963	30675823	7	0	-1.085165	-1.085165	1.657E-30
252,152,934,023	10582	TT13	chr21	21	q22.11	32621245	32629427	6	0	-1.016348	-1.016348	1.791E-24
252,152,934,023	10583	TT13	chr21	21	q22.11	32713730	32720512	6	0	-0.686407	-0.686407	8.763E-15
252,152,934,023	10584	TT13	chr21	21	q22.11	32926933	32933343	5	0	-0.967256	-0.967256	4.462E-18
252,152,934,023	10585	TT13	chr21	21	q22.11	33025685	33034851	5	0	-1.544751	-1.544751	4.698E-39
252,152,934,023	10586	TT13	chr21	21	q22.11	33100357	33108427	6	0	-1.127209	-1.127209	1.883E-28
252,152,934,023	10588	TT13	chr21	21	q22.11	33635404	33654376	11	0	-1.218507	-1.218507	1.095E-57
252,152,934,023	10592	TT13	chr21	21	q22.11	33847697	33851370	3	0	-0.969722	-0.969722	4.965E-12
252,152,934,023	10593	TT13	chr21	21	q22.11	34017365	34019925	3	0	-2.027972	-2.027972	1.965E-33
252,152,934,023	10594	TT13	chr21	21	q22.11	34097841	34103780	5	0	-1.300481	-1.300481	2.857E-29
252,152,934,023	10595	TT13	chr21	21	q22.11	34141096	34146718	4	0	-1.312839	-1.312839	1.578E-25
252,152,934,023	10596	TT13	chr21	21	q22.11	34391464	34407144	9	0	-1.549352	-1.549352	2.631E-63
252,152,934,023	10598	TT13	chr21	21	q22.11	34468744	34484438	6	0	-1.052911	-1.052911	5.155E-27
252,152,934,023	10602	TT13	chr21	21	q22.11	34911445	34930743	12	0	-0.990478	-0.990478	6.715E-42
252,152,934,023	10604	TT13	chr21	21	q22.11	35010830	35018245	5	0	-1.18731	-1.18731	4.026E-27
252,152,934,023	10605	TT13	chr21	21	q22.11	35239449	35242940	3	0	-1.623927	-1.623927	3.469E-27
252,152,934,023	10606	TT13	chr21	21	q22.11	35440818	35449032	7	0	-1.117829	-1.117829	3.515E-29
252,152,934,023	10607	TT13	chr21	21	q22.11	35745046	35750513	4	0	-1.183381	-1.183381	5.047E-23
252,152,934,023	10611	TT13	chr21	21	q22.12	35985909	35990224	5	0	-1.831366	-1.831366	5.972E-50
252,152,934,023	10614	TT13	chr21	21	q22.12	36255667	36266336	9	0	-1.215727	-1.215727	3.736E-44
252,152,934,023	10615	TT13	chr21	21	q22.12	37258570	37273814	7	0	-1.17113	-1.17113	1.5E-39
252,152,934,023	10617	TT13	chr21	21	q22.12	37438263	37532081	45	0	-0.510245	-0.510245	1.313E-50
252,152,934,023	10618	TT13	chr21	21	q22.12	37439289	37444330	5	0	-1.191553	-1.191553	1.216E-10
252,152,934,023	10620	TT13	chr21	21	q22.12	37692080	37695114	3	0	-2.137017	-2.137017	9.872E-35
252,152,934,023	10622	TT13	chr21	21	q22.13	37833120	37837736	4	0	-1.098916	-1.098916	7.857E-20
252,152,934,023	10623	TT13	chr21	21	q22.13	38062854	38084862	13	0	-1.353232	-1.353232	5.372E-57
252,152,934,023	10624	TT13	chr21	21	q22.13	38117816	38122231	4	0	-1.441854	-1.441854	2.25E-29
252,152,934,023	10631	TT13	chr21	21	q22.2	40028977	40036864	6	0	-1.278657	-1.278657	1.236E-38
252,152,934,023	10632	TT13	chr21	21	q22.2	40175324	40194594	13	0	-0.696018	-0.696018	1.505E-27
252,152,934,023	10633	TT13	chr21	21	q22.2	40525729	40562120	21	0	-0.67551	-0.67551	9.191E-41
252,152,934,023	10634	TT13	chr21	21	q22.2	40553682	40557131	3	0	-1.934515	-1.934515	8.475E-16
252,152,934,023	10635	TT13	chr21	21	q22.2	40681403	40688465	5	0	-1.259472	-1.259472	5.781E-28
252,152,934,023	10637	TT13	chr21	21	q22.2	40750388	40761938	8	0	-1.377241	-1.377241	8.386E-54
252,152,934,023	10638	TT13	chr21	21	q22.2	40812895	40822326	6	0	-0.933249	-0.933249	5.291E-23
252,152,934,023	10639	TT13	chr21	21	q22.2	40983093	40988857	5	0	-1.216678	-1.216678	8.078E-26
252,152,934,023	10640	TT13	chr21	21	q22.2	42214433	42223228	8	0	-1.042066	-1.042066	2.843E-34
252,152,934,023	10641	TT13	chr21	21	q22.2	42537209	42542691	4	0	-1.274509	-1.274509	1.612E-26
252,152,934,023	10642	TT13	chr21	21	q22.3	42673420	42690823	10	0	-1.040324	-1.040324	4.649E-40
252,152,934,023	10649	TT13	chr21	21	q22.3	43233967	43239515	4	0	-2.805164	-2.805164	5.018E-35
252,152,934,023	10651	TT13	chr21	21	q22.3	43368892	43378056	5	0	-0.902142	-0.902142	1.158E-17
252,152,934,023	10658	TT13	chr21	21	q22.3	44254723	44269392	9	0	-1.286621	-1.286621	7.475E-32
252,152,934,023	10663	TT13	chr21	21	q22.3	44838738	44873526	22	0	-1.594289	-1.594289	1.474E-91
252,152,934,023	10664	TT13	chr21	21	q22.3	45076568	45080822	4	0	-1.628235	-1.628235	8.769E-25
252,152,934,023	10673	TT13	chr21	21	q22.3	45644593	47882721	1041	0	-0.54755	-0.54755	4.900e-324
252,152,934,023	10674	TT13	chr21	21	q22.3	45714507	45732496	12	0	-1.15771	-1.15771	1.686E-11
252,152,934,023	10676	TT13	chr21	21	q22.3	45904024	45922484	9	0	-1.684747	-1.684747	1.487E-34
252,152,934,023	10677	TT13	chr21	21	q22.3	45919188	45922484	3	0	-3.18288	-3.18288	1.261E-11
252,152,934,023	10680	TT13	chr21	21	q22.3	46353338	46451234	38	0	-1.183005	-1.183005	1.125E-45
252,152,934,023	10688	TT13	chr21	21	q22.3	47054701	47064525	5	0	-2.241038	-2.241038	2.825E-31
252,152,934,023	10689	TT13	chr21	21	q22.3	47202903	47206616	3	0	-1.450064	-1.450064	1.72E-20
252,152,934,023	10691	TT13	chr21	21	q22.3	47326397	47335385	8	0	-1.049472	-1.049472	4.821E-16
252,152,934,023	10695	TT13	chr21	21	q22.3	47646642	47654360	5	0	-1.258888	-1.258888	1.691E-26

252,152,934,023	10696	TT13	chr21	21	q22.3	47703447	47708092	5	0	-1.640592	-1.640592	3.944E-18
252,152,934,023	10700	TT13	chr21	21	q22.3	47830726	47856288	16	0	-2.13661	-2.13661	9.54E-13
252,152,934,023	10712	TT13	chr22	22	q11.21	18298515	18304789	4	0	-0.890752	-0.890752	2.433E-14
252,152,934,023	10713	TT13	chr22	22	q11.21	18321520	18328024	5	0	-0.649185	-0.649185	2.943E-10
252,152,934,023	10736	TT13	chr22	22	q11.21	20284563	20806765	44	0	-0.576299	-0.576299	7.965E-25
252,152,934,023	10739	TT13	chr22	22	q11.21	21269716	21273964	4	0	-1.618382	-1.618382	4.311E-28
252,152,934,023	10740	TT13	chr22	22	q11.21	21307890	21357982	26	0	-0.812453	-0.812453	3.266E-37
252,152,934,023	10745	TT13	chr22	22	q11.21	21984494	22014524	33	0	-0.888844	-0.888844	2.047E-57
252,152,934,023	10746	TT13	chr22	22	q11.21	22088145	22091451	3	0	-1.545951	-1.545951	9.173E-20
252,152,934,023	10747	TT13	chr22	22	q11.22	22200679	22236660	26	0	-0.748831	-0.748831	2.997E-35
252,152,934,023	10748	TT13	chr22	22	q11.22	22220751	22223363	3	0	-1.942869	-1.942869	2.502E-14
252,152,934,023	10751	TT13	chr22	22	q11.22	22862103	22866697	4	0	-1.524094	-1.524094	7.683E-33
252,152,934,023	10761	TT13	chr22	22	q11.23	24091038	24132473	24	0	-0.827208	-0.827208	1.866E-57
252,152,934,023	10769	TT13	chr22	22	q11.23	24711146	24715607	3	0	-1.902922	-1.902922	1.361E-34
252,152,934,023	10770	TT13	chr22	22	q11.23	24822769	24832438	8	0	-0.868656	-0.868656	8.672E-19
252,152,934,023	10771	TT13	chr22	22	q11.23	24885134	24893415	7	0	-0.887837	-0.887837	8.371E-24
252,152,934,023	10773	TT13	chr22	22	q11.23	24983109	25082694	9	0	-1.416586	-1.416586	1.577E-59
252,152,934,023	10774	TT13	chr22	22	q11.23	25344351	25352158	6	0	-1.09376	-1.09376	1.231E-27
252,152,934,023	10780	TT13	chr22	22	q12.1	25954957	25964979	4	0	-0.945694	-0.945694	9.823E-17
252,152,934,023	10781	TT13	chr22	22	q12.1	26146614	26150612	3	0	-1.409229	-1.409229	2.775E-22
252,152,934,023	10782	TT13	chr22	22	q12.1	26559760	26574014	9	0	-0.434582	-0.434582	1.812E-13
252,152,934,023	10783	TT13	chr22	22	q12.1	26820963	26830629	7	0	-0.824819	-0.824819	1.266E-18
252,152,934,023	10784	TT13	chr22	22	q12.1	26875592	26881519	4	0	-0.941405	-0.941405	2.893E-14
252,152,934,023	10785	TT13	chr22	22	q12.1	26934275	26940866	6	0	-1.008549	-1.008549	4.678E-25
252,152,934,023	10786	TT13	chr22	22	q12.1	26983604	26990902	7	0	-0.778515	-0.778515	3.089E-17
252,152,934,023	10787	TT13	chr22	22	q12.1	27038828	27055402	12	0	-0.845243	-0.845243	8.409E-32
252,152,934,023	10791	TT13	chr22	22	q12.1	28007396	28042272	24	0	-0.603879	-0.603879	1.269E-34
252,152,934,023	10792	TT13	chr22	22	q12.1	28313251	28316663	3	0	-1.864859	-1.864859	1.121E-30
252,152,934,023	10793	TT13	chr22	22	q12.1	28372264	28388689	14	0	-0.860009	-0.860009	9.001E-42
252,152,934,023	10794	TT13	chr22	22	q12.1	28837023	28841127	4	0	-1.796697	-1.796697	3.448E-36
252,152,934,023	10795	TT13	chr22	22	q12.1	28945743	28953972	3	0	-0.979333	-0.979333	3.817E-11
252,152,934,023	10798	TT13	chr22	22	q12.1	29278402	29283212	4	0	-1.374184	-1.374184	1.712E-21
252,152,934,023	10831	TT13	chr22	22	q12.2	32143727	32153697	5	0	-1.391625	-1.391625	2.157E-35
252,152,934,023	10832	TT13	chr22	22	q12.3	32336863	32345048	7	0	-1.01632	-1.01632	1.519E-25
252,152,934,023	10833	TT13	chr22	22	q12.3	32867583	32873786	5	0	-1.547861	-1.547861	3.561E-43
252,152,934,023	10835	TT13	chr22	22	q12.3	33194565	33201357	6	0	-1.232551	-1.232551	1.961E-41
252,152,934,023	10836	TT13	chr22	22	q12.3	33451774	33457137	5	0	-1.089101	-1.089101	6.436E-29
252,152,934,023	10837	TT13	chr22	22	q12.3	34042598	34049765	5	0	-0.932542	-0.932542	1.265E-23
252,152,934,023	10838	TT13	chr22	22	q12.3	34312764	34319568	5	0	-0.923379	-0.923379	1.157E-18
252,152,934,023	10839	TT13	chr22	22	q12.3	35653034	35656565	4	0	-1.543518	-1.543518	1.391E-32
252,152,934,023	10840	TT13	chr22	22	q12.3	35690935	35696208	4	0	-1.064893	-1.064893	1.684E-17
252,152,934,023	10841	TT13	chr22	22	q12.3	35767668	35781106	9	0	-1.004547	-1.004547	1.021E-36
252,152,934,023	10842	TT13	chr22	22	q12.3	36176497	36184030	6	0	-1.13846	-1.13846	3.687E-32
252,152,934,023	10843	TT13	chr22	22	q12.3	36421735	36426875	4	0	-1.552014	-1.552014	8.842E-32
252,152,934,023	10844	TT13	chr22	22	q12.3	36677709	36692011	9	0	-1.144044	-1.144044	5.885E-40
252,152,934,023	10845	TT13	chr22	22	q12.3	36722092	36773452	30	0.283316	0	0.283316	9.394E-12
252,152,934,023	10846	TT13	chr22	22	q12.3	36781085	36784842	3	0	-1.873117	-1.873117	2.308E-26
252,152,934,023	10847	TT13	chr22	22	q12.3	36895716	36906985	8	0	-0.75402	-0.75402	4.321E-19
252,152,934,023	10848	TT13	chr22	22	q12.3	37098840	37101511	3	0	-1.727682	-1.727682	1.031E-28
252,152,934,023	10850	TT13	chr22	22	q12.3	37413033	37421692	6	0	-1.595933	-1.595933	1.685E-37
252,152,934,023	10852	TT13	chr22	22	q12.3 - q13.1	37593735	37610129	10	0	-0.892612	-0.892612	6.435E-23
252,152,934,023	10853	TT13	chr22	22	q13.1	37717797	37733009	11	0	-0.999173	-0.999173	4.252E-30
252,152,934,023	10876	TT13	chr22	22	q13.1	39096121	39104279	6	0	-1.646003	-1.646003	3.802E-43
252,152,934,023	10881	TT13	chr22	22	q13.1	39528814	39544389	11	0	-1.156612	-1.156612	2.261E-34
252,152,934,023	10890	TT13	chr22	22	q13.1	40385682	40443984	34	0	-0.516417	-0.516417	2.026E-45
252,152,934,023	10891	TT13	chr22	22	q13.1	40388686	40392893	4	0	-1.422569	-1.422569	5.698E-13
252,152,934,023	10895	TT13	chr22	22	q13.2	41030874	41036350	6	0	-1.339187	-1.339187	2.695E-31
252,152,934,023	10912	TT13	chr22	22	q13.2	42349071	42398206	29	0	-0.512162	-0.512162	3.263E-18
252,152,934,023	10914	TT13	chr22	22	q13.2	42477780	42552427	17	0	-0.532148	-0.532148	4.06E-13
252,152,934,023	10922	TT13	chr22	22	q13.2	43364470	43381645	9	0	-1.32724	-1.32724	3.334E-48
252,152,934,023	10923	TT13	chr22	22	q13.2	43407475	43412309	4	0	-1.105147	-1.105147	1.558E-16
252,152,934,023	10927	TT13	chr22	22	q13.2	43793504	43833690	21	0	-0.895678	-0.895678	4.43E-66
252,152,934,023	10929	TT13	chr22	22	q13.2	43954156	43963329	7	0	-0.817309	-0.817309	3.465E-21
252,152,934,023	10931	TT13	chr22	22	q13.31	44348983	44355896	5	0	-1.402033	-1.402033	8.699E-39
252,152,934,023	10940	TT13	chr22	22	q13.31	45400411	45406464	6	0	-1.021759	-1.021759	1.299E-14
252,152,934,023	10942	TT13	chr22	22	q13.31	45588415	45607160	21	0	-1.035049	-1.035049	1.283E-54
252,152,934,023	10948	TT13	chr22	22	q13.31	46039104	46071070	13	0	-0.799072	-0.799072	1.727E-24
252,152,934,023	10949	TT13	chr22	22	q13.31	46257966	46370006	46	0	-0.483309	-0.483309	4.06E-20
252,152,934,023	10951	TT13	chr22	22	q13.31	46645150	46666414	11	0	-1.109054	-1.109054	4.331E-37
252,152,934,023	10952	TT13	chr22	22	q13.31	46682178	46706200	13	0	-0.726496	-0.726496	9.706E-20
252,152,934,023	10953	TT13	chr22	22	q13.31	46728659	46788035	33	0	-0.990568	-0.990568	3.136E-78
252,152,934,023	10954	TT13	chr22	22	q13.31	46783556	46788035	4	0	-2.642681	-2.642681	2.789E-19
252,152,934,023	10956	TT13	chr22	22	q13.31	46924234	46935002	7	0	-1.211586	-1.211586	5.948E-27
252,152,934,023	10961	TT13	chr22	22	q13.31	47187586	47192401	4	0	-1.42972	-1.42972	4.893E-25
252,152,934,023	10962	TT13	chr22	22	q13.31	47292485	47306019	10	0	-0.445962	-0.445962	3.129E-10
252,152,934,023	10963	TT13	chr22	22	q13.31	47360549	47369398	6	0	-0.991065	-0.991065	2.803E-23
252,152,934,023	10972	TT13	chr22	22	q13.32	49139607	49148253	8	0	-1.658017	-1.658017	9.341E-46
252,152,934,023	10978	TT13	chr22	22	q13.33	49991460	51224252	542	0	-0.536325	-0.536325	4.900e-324
252,152,934,023	10979	TT13	chr22	22	q13.33	50024946	50032089	6	0	-1.69879	-1.69879	6.422E-21
252,152,934,023	10980	TT13	chr22	22	q13.33	50055568	50062501	6	0	-1.976048	-1.976048	5.492E-26
252,152,934,023	10983	TT13	chr22	22	q13.33	50141999	50194079	32	0	-1.286079	-1.286079	2.829E-51
252,152,934,023	10989	TT13	chr22	22	q13.33	50622423	50634371	8	0	-1.42015	-1.42015	4.496E-17

Dataset S4. 3. List of common affected genes by CNAs in Human rh-PI reactive lymphocytes from newly diagnosed T1D patients and memory cells from PLNs of newly diabetic NOD mice (Chapter 3 of this thesis).

Common to Mouse and Human T1D	BioGPS Human T-cell or Hematopiotic expression	Immunebase Immun association	REF Pubmed PMID
ALKBH5	Yes		
ANKHD1-EIF4EBP3	Yes		
ANKRD13D	Yes		
ANKRD54	Yes		
ARIH2	Yes		
ARMC6	Yes		
ARRDC1	Yes		
ASF1B			
ATMIN	Yes		
ATN1			
ATP2A3	Yes		
BAHCC1			
BAHD1	Yes		
BOP1	Yes		
BRI3BP	Yes		
C11orf94			
C19orf38			
C19orf67			
C4orf48	Yes		
CARM1		**Psoriasis**	**23143594**
CASKIN1			
CASZ1	Yes		
CBX2			
CBX8	Yes		
CDC14B			
CGREF1	Yes		
CMPK1			
CNNM3	Yes		
CNNM4	Yes		
COPZ2			
CRY2	Yes		
CRYZL1	Yes		
CTXN1	Yes		
DENND4B	Yes		
DOCK5			
DTX1			
E2F1			
EHBP1L1			
ENO2	Yes		
ERF	Yes		
EVI5L	Yes		
EVX2			
FAM78A	Yes		
FIZ1	Yes		
FNDC4	Yes		
FOXI3			
FRMD8	Yes		
FURIN	Yes		
GAL3ST3	Yes		
GALNT7	Yes		
GATAD2A	Yes		
GATAD2B			
GCKR		**Crohn's disease**	**21102463**
GDF11	Yes		
GFER	Yes		
GJC2	Yes		
GMFG	Yes		
GNA12	Yes	**atory Bowel Disease, Crohn'**	**128233; 23128233, 21297633**
GSPT1	Yes		
GTPBP1	Yes		
HOXA10			
HOXA10-HOXA9			
HOXA11	Yes		
HOXA13			
HOXA2			
HOXA3	Yes		
HOXA4			
HOXA5	Yes		
HOXA6	Yes		
HOXA7	Yes		
HOXD10			
HOXD11	Yes		
HOXD12	Yes		
HOXD13			
HOXD3	Yes		

HOXD4	Yes		
HOXD8			
HOXD9			
HSF1	Yes		
HYOU1	Yes		
IQCE			
IVD			
JOSD1			
KCNH3	Yes		
KCNK7			
KDM2A	Yes		
KDM2B	Yes		
KDM3A			
KHSRP			
LLGL1	Yes		
LMNTD2	Yes		
LRFN1	Yes		
LRRC14	Yes		
LRRC24			
LRRC8E			
LTBP3	Yes		
MAP2K7	Yes		
MAP3K11			
MAPK8IP1	Yes		
MGAT4B	Yes		
MLST8			
NANOS3	Yes		
NAT8L			
NECAB3	Yes		
NKX2-3			
NPW			
P4HTM	Yes		
PCBP1			
PDE4A	Yes		
PEX14	Yes		
PGP	Yes		
PHRF1	**Yes**	**ystemic Lupus Erythematos**	**19838195**
PIK3R2	Yes		
PLEKHO1	Yes		
POGZ	Yes		
PRKACA			
PTCH1			
PURB			
PXMP4			
PXN			
RABEP1	Yes		
RAP2A			
RASIP1	**Yes**	**Crohn's Disease**	**21102463**
RASSF7			
REPIN1	Yes		
RNF103	Yes		
RNF157	Yes		
SAMD1	Yes		
SAMD4B			
SCYL1	Yes		
SF1	Yes		
SLC25A41	Yes		
SLC2A1	Yes		
SLC35E1			
SMARCD3	Yes		
SNAPC2	Yes		
SNW1	Yes		
SSSCA1	Yes		
SYNGR3			
TBKBP1	**Yes**	**sing Spondylitis, Multiple S**	**23749187, 22190364**
TEX22			
TIMM44	Yes		
TLE4	Yes		
TOB1	Yes		
TRAF7	Yes		
UBALD2	Yes		
UBE2F-SCLY			
UBTD2	Yes		
USP2	Yes		
WNT3A			
YPEL2			
ZBED4			
ZNF212	Yes		
ZNF282	Yes		
ZNF398	Yes		
ZNF524	Yes		
ZNF579			
ZNF598	Yes		
ZNF775	Yes		

Dataset S5. 1 List of CNAs in rh-PI- reactive lymphocytes of 10 tested CD patients (ADM-2 (LRRl0.25l, P- value ≤1x10-10) and CBS (LRRl0.25l, P-value ≤5 x 10-08)). Since we have no prior information in which to base power calculations the number of patients tested was determined by availability of funds.

ID	ID	NO.	chrom	chrom	chr region	loc.start	loc.end	num.mark	Amplification	Deletions	mean LRR	pval
252152940597	GP1	1	chr5	5	q34	168,193,912	168,207,095	15	0	0.345104	0	5.87E-10
252152940597	GP1	3	chr19	19	p13.12	14,195,682	14,208,674	8	0	0.598093	0	2.28E-12
252152940597	GP1	4	chr22	22	q13.31	47,770,715	47,777,489	4	0	0.771265	0	3.58E-11
252152940597	GP1	5	chr22	22	q13.33	51,116,107	51,146,462	16	0	0.406567	0	4.88E-11
252152942264	GP4	2	chr1	1	q31.3	198,601,789	198,668,629	35	0	0	-0.434116	2.53E-15
252152942264	GP4	3	chr2	2	p13.3	68,661,328	68,685,587	9	0	0	-0.572927	1.30E-14
252152942264	GP4	4	chr2	2	q31.1	169,816,992	169,839,906	12	0	0	-0.443942	5.56E-11
252152942264	GP4	5	chr2	2	q31.1	170,308,625	170,333,307	8	0	0	-0.553131	1.79E-11
252152942264	GP4	6	chr3	3	q11.2	98,252,951	98,281,633	13	0	0	-0.473663	1.11E-10
252152942264	GP4	8	chr5	5	p15.33	4,172,384	4,191,865	7	0	0	-0.599187	5.55E-10
252152942264	GP4	9	chr6	6	p12.1	55,925,943	55,968,474	23	0	0	-0.463639	4.78E-13
252152942264	GP4	10	chr6	6	q25.1	149,051,136	149,072,901	10	0	0	-0.534707	3.22E-12
252152942264	GP4	11	chr8	8	q21.3	87,157,803	87,193,605	17	0	0	-0.406836	2.16E-11
252152942264	GP4	12	chr11	11	q22.3	105,868,153	105,958,706	43	0	0	-0.266255	8.17E-10
252152942264	GP4	14	chr13	13	q14.2	50,605,714	50,667,472	56	0	0	-0.319792	1.23E-24
252152942264	GP4	16	chr14	14	q32.12	93,004,731	93,019,673	8	0	0	-0.517983	1.39E-12
252152942264	GP4	18	chr18	18	q12.2	34,019,085	34,056,714	21	0	0	-0.322554	7.99E-10
252152942264	GP4	20	chr22	22	q13.31	47,768,694	47,777,489	5	0	0	-0.710566	3.97E-11
252152942264	GP4	21	chrX	X	q12	65,252,087	65,261,948	12	0	0	-0.454295	4.48E-10
252152942264	GP4	22	chrX	X	q22.1	101,797,146	101,829,202	17	0	0	-0.372257	2.50E-10
252152942264	GP4	23	chrX	X	q25	123,458,618	123,520,850	34	0	0	-0.274604	6.55E-11
252152942272	GP6	1	chr7	7	p22.3	1,260,241	1,308,471	20	0	0	-0.379119	1.35E-10
252152942272	GP6	3	chr19	19	p12	21,055,920	21,098,244	14	0	0.589682	0	1.30E-20
252152942273	GP7	1	chr8	8	p23.3	1,706,041	1,719,102	7	0	0.787548	0	1.86E-16
252152942273	GP7	2	chr8	8	q12.1	61,586,383	61,596,459	6	0	0.682357	0	8.20E-11
252152942273	GP7	3	chr8	8	q24.3	146,271,091	146,294,098	8	0	0.592317	0	4.99E-12
252152942273	GP7	4	chr11	11	q25	134,934,137	134,945,165	3	0	1.036369	0	1.05E-11
252152942273	GP7	5	chr12	12	p13.31	7,778,761	7,783,075	3	0	1.107635	0	7.63E-14
252152942275	GP8	1	chr1	1	p36.33	1,707,749	1,711,288	3	0	0	-1.089197	7.62E-14
252152942275	GP8	2	chr1	1	p36.32	3,559,465	3,564,973	4	0	0	-1.077993	2.07E-18
252152942275	GP8	3	chr1	1	p36.31	6,843,990	6,853,409	5	0	0	-0.888753	2.14E-16
252152942275	GP8	4	chr1	1	p36.23	8,480,673	8,488,209	6	0	0	-0.999321	8.84E-21
252152942275	GP8	5	chr1	1	p36.22	9,963,375	9,973,761	6	0	0	-0.658164	7.92E-12
252152942275	GP8	6	chr1	1	p36.22	10,695,420	10,697,970	3	0	0	-1.619675	7.21E-22
252152942275	GP8	7	chr1	1	p36.22	10,751,866	10,758,535	4	0	0	-0.897584	4.68E-11
252152942275	GP8	8	chr1	1	p36.21	15,246,658	15,252,877	4	0	0	-0.848674	2.91E-12
252152942275	GP8	9	chr1	1	p36.13	17,758,118	17,769,964	7	0	0	-0.938476	1.34E-19
252152942275	GP8	10	chr1	1	p36.12	20,810,162	20,816,254	3	0	0	-0.940813	1.86E-13
252152942275	GP8	11	chr1	1	p36.12	21,107,922	21,117,873	6	0	0	-0.775144	7.62E-15
252152942275	GP8	12	chr1	1	p36.12	22,464,571	22,475,058	7	0	0	-0.735363	2.97E-15
252152942275	GP8	13	chr1	1	p36.12	23,031,836	23,042,142	6	0	0	-0.6606	1.83E-10
252152942275	GP8	14	chr1	1	p36.12	23,490,124	23,502,917	8	0	0	-0.590673	7.11E-13
252152942275	GP8	15	chr1	1	p36.11	25,935,729	25,951,052	8	0	0	-0.678587	1.04E-17
252152942275	GP8	16	chr1	1	p36.11	27,146,822	27,154,631	5	0	0	-0.75253	1.53E-12
252152942275	GP8	17	chr1	1	p35.3	29,562,293	29,565,728	3	0	0	-1.150238	1.42E-17
252152942275	GP8	22	chr1	1	p34.3	35,439,413	35,446,406	5	0	0	-0.848359	3.00E-14
252152942275	GP8	23	chr1	1	p34.3	36,035,259	36,041,478	4	0	0	-1.061806	1.67E-12
252152942275	GP8	24	chr1	1	p34.2	42,119,806	42,133,042	7	0	0	-0.811369	8.15E-18
252152942275	GP8	25	chr1	1	p34.2	43,143,795	43,151,801	5	0	0	-0.680255	1.28E-11
252152942275	GP8	26	chr1	1	p34.1	45,668,562	45,674,158	5	0	0	-0.916844	3.19E-17
252152942275	GP8	27	chr1	1	p32.3	51,419,525	51,452,142	18	0	0	-0.462833	5.99E-17
252152942275	GP8	28	chr1	1	p32.3	51,793,005	51,797,447	3	0	0	-0.861992	1.86E-10
252152942275	GP8	29	chr1	1	p32.3	53,921,950	53,928,221	4	0	0	-0.958544	8.64E-10
252152942275	GP8	30	chr1	1	p32.3	54,865,966	54,876,790	6	0	0	-0.622296	5.66E-12
252152942275	GP8	31	chr1	1	p31.3	61,542,403	61,556,385	8	0	0	-0.571183	9.02E-12
252152942275	GP8	32	chr1	1	p31.3	65,526,710	65,536,539	12	0	0	-0.76982	2.99E-28
252152942275	GP8	33	chr1	1	p13.3	109,100,537	109,105,616	4	0	0	-1.290291	2.82E-25
252152942275	GP8	34	chr1	1	p13.2	113,610,289	113,616,828	3	0	0	-1.025188	2.04E-13
252152942275	GP8	35	chr1	1	p12	120,162,251	120,169,523	5	0	0	-1.054384	9.60E-24
252152942275	GP8	36	chr1	1	q21.3	151,427,909	151,439,349	6	0	0	-0.645661	4.17E-11
252152942275	GP8	37	chr1	1	q21.3	154,526,394	154,534,270	5	0	0	-0.632671	9.50E-10
252152942275	GP8	38	chr1	1	q25.1	173,438,816	173,452,862	8	0	0	-0.692045	4.81E-18
252152942275	GP8	39	chr1	1	q25.2	178,990,493	179,002,099	7	0	0	-0.672225	8.67E-15
252152942275	GP8	40	chr1	1	q32.1	205,596,821	205,604,909	5	0	0	-0.887101	7.42E-19
252152942275	GP8	41	chr1	1	q32.2	207,986,475	207,998,531	12	0	0	-0.588226	3.67E-17
252152942275	GP8	42	chr1	1	q41	215,039,154	215,048,551	4	0	0	-0.733715	3.44E-10
252152942275	GP8	43	chr1	1	q41	215,252,377	215,260,866	6	0	0	-0.738057	3.18E-13
252152942275	GP8	44	chr1	1	q41	224,030,779	224,039,802	6	0	0	-0.595352	4.12E-11
252152942275	GP8	45	chr1	1	q42.12	224,617,495	224,625,108	5	0	0	-0.958329	1.96E-19
252152942275	GP8	46	chr1	1	q42.13	229,756,500	229,769,355	8	0	0	-0.893933	7.88E-28
252152942275	GP8	47	chr1	1	q42.13	230,557,140	230,564,552	5	0	0	-1.056257	1.59E-18
252152942275	GP8	48	chr1	1	q42.3	234,741,403	234,749,721	6	0	0	-0.842875	1.52E-18
252152942275	GP8	49	chr1	1	q44	244,209,483	244,216,663	5	0	0	-1.011626	2.30E-22
252152942275	GP8	50	chr1	1	q44	247,089,797	247,097,165	6	0	0	-0.812574	1.18E-17
252152942275	GP8	51	chr2	2	p25.3	421,180	428,543	3	0	0	-1.079416	1.02E-13

252152942275	GP8	52	chr2	2	p25.2	7,049,393	7,060,934	6	0	0	-0.582878	5.13E-10
252152942275	GP8	53	chr2	2	p25.1	9,341,867	9,349,480	4	0	0	-1.042722	3.43E-17
252152942275	GP8	54	chr2	2	p25.1	11,481,393	11,486,791	3	0	0	-1.220611	7.16E-19
252152942275	GP8	55	chr2	2	p24.2	16,842,198	16,850,569	6	0	0	-0.762947	6.32E-13
252152942275	GP8	56	chr2	2	p24.1	23,601,096	23,612,896	5	0	0	-0.813448	5.53E-13
252152942275	GP8	57	chr2	2	p23.3	24,708,885	24,715,739	4	0	0	-1.206744	2.66E-21
252152942275	GP8	58	chr2	2	p23.3	25,888,918	25,901,567	6	0	0	-0.921793	3.74E-20
252152942275	GP8	59	chr2	2	p23.3	26,393,711	26,408,832	8	0	0	-0.683161	7.89E-10
252152942275	GP8	60	chr2	2	p23.3	26,912,586	26,922,369	7	0	0	-0.534394	3.87E-10
252152942275	GP8	61	chr2	2	p22.3	32,230,743	32,237,389	4	0	0	-0.886755	7.70E-15
252152942275	GP8	62	chr2	2	p22.1	39,178,245	39,192,510	8	0	0	-0.522482	6.13E-12
252152942275	GP8	63	chr2	2	p22.1	40,672,359	40,685,964	9	0	0	-0.628336	9.55E-15
252152942275	GP8	64	chr2	2	p21	42,271,583	42,278,166	4	0	0	-0.914644	4.03E-11
252152942275	GP8	66	chr2	2	p21	47,397,620	47,408,107	6	0	0	-0.654382	1.74E-13
252152942275	GP8	67	chr2	2	p16.2	54,083,342	54,095,077	7	0	0	-0.586475	1.82E-12
252152942275	GP8	68	chr2	2	p16.1	59,289,705	59,296,510	3	0	0	-1.034569	1.09E-14
252152942275	GP8	69	chr2	2	p15	61,761,358	61,766,356	3	0	0	-1.205037	4.45E-13
252152942275	GP8	70	chr2	2	p14	64,878,424	64,882,195	3	0	0	-0.922947	2.27E-10
252152942275	GP8	71	chr2	2	p14	68,476,871	68,483,092	4	0	0	-0.894375	5.68E-11
252152942275	GP8	72	chr2	2	p13.2	72,370,041	72,389,755	13	0	0	-0.445229	4.12E-11
252152942275	GP8	73	chr2	2	p13.2	73,336,315	73,343,619	4	0	0	-0.727319	2.58E-11
252152942275	GP8	74	chr2	2	p13.1	74,208,046	74,218,368	5	0	0	-0.895415	1.31E-17
252152942275	GP8	75	chr2	2	p11.2	85,357,157	85,364,650	5	0	0	-0.689831	5.26E-10
252152942275	GP8	76	chr2	2	p11.2	88,748,583	88,755,682	4	0	0	-0.813981	9.22E-12
252152942275	GP8	77	chr2	2	q11.2	97,479,208	97,488,577	5	0	0	-0.766753	3.73E-13
252152942275	GP8	78	chr2	2	q11.2	99,342,816	99,349,698	5	0	0	-1.043309	6.47E-24
252152942275	GP8	79	chr2	2	q11.2	100,722,048	100,727,931	4	0	0	-1.44445	1.77E-22
252152942275	GP8	80	chr2	2	q11.2	100,935,735	100,939,766	3	0	0	-1.225577	9.43E-13
252152942275	GP8	81	chr2	2	q11.2	101,433,549	101,439,961	4	0	0	-0.753236	8.25E-10
252152942275	GP8	82	chr2	2	q11.2	102,311,073	102,320,605	6	0	0	-0.799597	1.47E-17
252152942275	GP8	83	chr2	2	q12.1	105,941,942	105,953,600	7	0	0	-0.740888	1.09E-17
252152942275	GP8	84	chr2	2	q14.2	121,736,879	121,757,158	9	0	0	-0.507564	4.24E-10
252152942275	GP8	85	chr2	2	q21.1	131,718,481	131,724,565	4	0	0	-1.127993	7.53E-10
252152942275	GP8	86	chr2	2	q21.1	132,172,024	132,217,492	15	0	0	-0.417397	1.46E-12
252152942275	GP8	87	chr2	2	q22.3	148,598,844	148,608,010	6	0	0	-0.653527	3.90E-12
252152942275	GP8	88	chr2	2	q24.1	158,726,275	158,735,778	5	0	0	-0.652615	4.09E-11
252152942275	GP8	89	chr2	2	q24.2	161,260,559	161,267,012	3	0	0	-1.122751	6.60E-17
252152942275	GP8	90	chr2	2	q24.3	169,099,929	169,108,741	6	0	0	-0.853061	2.71E-18
252152942275	GP8	91	chr2	2	q31.1	176,941,413	176,980,336	20	0	0	-0.456765	1.08E-17
252152942275	GP8	92	chr2	2	q31.3	181,842,356	181,850,949	5	0	0	-1.141445	1.08E-22
252152942275	GP8	93	chr2	2	q33.1	198,172,505	198,177,264	4	0	0	-1.098734	6.73E-13
252152942275	GP8	94	chr2	2	q33.2	203,496,151	203,501,123	3	0	0	-1.220585	2.74E-18
252152942275	GP8	95	chr2	2	q33.3	208,391,916	208,398,012	4	0	0	-0.975089	1.19E-16
252152942275	GP8	96	chr2	2	q34	214,013,299	214,025,522	6	0	0	-0.861208	1.95E-19
252152942275	GP8	97	chr2	2	q35	219,710,198	219,712,256	3	0	0	-0.940152	3.26E-11
252152942275	GP8	98	chr2	2	q36.1	223,179,732	223,187,382	3	0	0	-0.97613	3.45E-12
252152942275	GP8	100	chr2	2	q37.1	231,898,935	231,908,383	5	0	0	-0.956196	7.84E-16
252152942275	GP8	101	chr2	2	q37.1	233,789,612	233,794,044	3	0	0	-1.270706	1.70E-12
252152942275	GP8	102	chr2	2	q37.1	235,402,167	235,409,121	5	0	0	-0.827678	1.10E-15
252152942275	GP8	103	chr2	2	q37.2	235,854,426	235,865,195	5	0	0	-0.898782	4.54E-19
252152942275	GP8	104	chr2	2	q37.2	236,575,428	236,582,609	5	0	0	-1.02752	2.01E-16
252152942275	GP8	106	chr2	2	q37.3	240,317,128	240,324,140	5	0	0	-0.861852	1.61E-14
252152942275	GP8	107	chr2	2	q37.3	241,931,879	241,940,958	4	0	0	-0.892454	2.72E-10
252152942275	GP8	108	chr3	3	p25.2	12,043,740	12,050,170	5	0	0	-1.085132	2.95E-22
252152942275	GP8	109	chr3	3	p25.2	13,031,447	13,038,825	5	0	0	-0.672877	5.30E-11
252152942275	GP8	110	chr3	3	p24.3	23,243,526	23,248,243	3	0	0	-0.867347	3.91E-11
252152942275	GP8	111	chr3	3	p22.1	39,846,690	39,856,476	6	0	0	-0.613111	9.20E-12
252152942275	GP8	112	chr3	3	p22.1	43,325,893	43,331,904	5	0	0	-0.999623	3.64E-20
252152942275	GP8	113	chr3	3	p21.31	44,543,754	44,558,069	7	0	0	-0.579905	2.56E-11
252152942275	GP8	114	chr3	3	p21.31	45,266,031	45,268,609	3	0	0	-1.310582	3.34E-19
252152942275	GP8	115	chr3	3	p21.31	47,613,374	47,622,874	6	0	0	-0.79303	1.30E-13
252152942275	GP8	116	chr3	3	p21.1	53,077,137	53,081,754	3	0	0	-1.505965	6.88E-25
252152942275	GP8	117	chr3	3	p21.1	54,153,542	54,158,830	3	0	0	-1.149597	8.25E-15
252152942275	GP8	118	chr3	3	p14.3	56,492,419	56,509,727	8	0	0	-0.531897	1.97E-11
252152942275	GP8	119	chr3	3	p14.3	56,616,757	56,625,928	4	0	0	-0.887271	5.06E-13
252152942275	GP8	120	chr3	3	p14.3	58,475,161	58,484,245	5	0	0	-0.655202	4.98E-10
252152942275	GP8	121	chr3	3	p14.2	62,855,133	62,865,882	6	0	0	-0.77906	1.16E-17
252152942275	GP8	122	chr3	3	p14.1	63,846,162	63,852,530	4	0	0	-1.077338	1.88E-15
252152942275	GP8	123	chr3	3	p14.1	63,895,315	63,899,837	3	0	0	-1.1275	1.54E-16
252152942275	GP8	124	chr3	3	p13	71,105,087	71,118,524	7	0	0	-0.646218	9.11E-15
252152942275	GP8	125	chr3	3	p13	71,764,019	71,809,842	23	0	0	-0.52612	1.70E-25
252152942275	GP8	126	chr3	3	p13	72,491,502	72,499,565	5	0	0	-0.757543	2.44E-14
252152942275	GP8	127	chr3	3	p13	72,934,985	72,941,872	5	0	0	-0.921177	6.81E-17
252152942275	GP8	128	chr3	3	p13	73,668,625	73,677,105	6	0	0	-0.652562	4.43E-10
252152942275	GP8	129	chr3	3	q21.2	124,764,445	124,786,574	13	0	0	-0.473948	5.00E-14
252152942275	GP8	130	chr3	3	q21.3	126,258,119	126,266,266	5	0	0	-0.668339	3.68E-10
252152942275	GP8	131	chr3	3	q21.3	127,341,468	127,353,893	6	0	0	-0.841624	1.47E-18
252152942275	GP8	132	chr3	3	q22.1	129,606,445	129,614,295	4	0	0	-0.789361	3.55E-13
252152942275	GP8	133	chr3	3	q22.2	133,967,261	133,970,182	3	0	0	-1.614136	2.42E-24
252152942275	GP8	134	chr3	3	q23	141,198,445	141,210,822	7	0	0	-0.598553	2.53E-12
252152942275	GP8	135	chr3	3	q25.33	160,279,160	160,287,566	4	0	0	-0.829545	7.63E-14

252152942275	GP8	136	chr3	3	q26.32	176,912,261	176,917,249	3	0	0	-1.328245	2.65E-20
252152942275	GP8	137	chr3	3	q26.33	179,369,823	179,373,759	3	0	0	-0.925639	1.04E-12
252152942275	GP8	138	chr3	3	q27.1	183,866,855	183,875,594	5	0	0	-0.66294	2.91E-11
252152942275	GP8	139	chr3	3	q27.1	183,974,764	183,980,149	6	0	0	-0.917161	1.17E-16
252152942275	GP8	141	chr3	3	q29	194,202,266	194,210,302	5	0	0	-0.693931	2.10E-10
252152942275	GP8	142	chr3	3	q29	196,288,031	196,302,999	9	0	0	-0.521256	3.43E-13
252152942275	GP8	143	chr4	4	p16.2	5,893,148	5,899,333	4	0	0	-1.074163	2.14E-15
252152942275	GP8	144	chr4	4	p16.1	8,874,118	8,877,130	6	0	0	-0.626501	1.41E-10
252152942275	GP8	145	chr4	4	p15.33	13,627,412	13,629,980	3	0	0	-1.664108	2.00E-20
252152942275	GP8	146	chr4	4	p15.2	21,946,541	21,953,523	5	0	0	-1.02407	1.04E-22
252152942275	GP8	147	chr4	4	p15.2	22,513,948	22,523,985	4	0	0	-0.760734	4.80E-12
252152942275	GP8	148	chr4	4	p15.2	25,861,385	25,866,507	3	0	0	-0.882714	8.62E-11
252152942275	GP8	149	chr4	4	p15.2	26,318,560	26,326,546	5	0	0	-0.742269	3.24E-12
252152942275	GP8	150	chr4	4	p14	38,660,207	38,670,098	6	0	0	-0.634091	1.32E-10
252152942275	GP8	151	chr4	4	p13	41,743,665	41,753,541	6	0	0	-0.636045	1.88E-12
252152942275	GP8	152	chr4	4	q21.22	83,478,773	83,486,706	4	0	0	-0.941623	6.52E-13
252152942275	GP8	153	chr4	4	q22.3	95,676,916	95,683,995	5	0	0	-1.076655	1.11E-24
252152942275	GP8	154	chr4	4	q23	99,178,646	99,184,692	3	0	0	-1.01654	4.47E-14
252152942275	GP8	155	chr4	4	q24	103,419,353	103,425,936	5	0	0	-1.005029	7.46E-22
252152942275	GP8	156	chr4	4	q27	123,738,696	123,753,968	7	0	0	-0.541057	5.19E-10
252152942275	GP8	157	chr4	4	q28.2	129,726,223	129,740,953	10	0	0	-0.59971	1.57E-16
252152942275	GP8	158	chr4	4	q31.1	140,032,071	140,046,386	9	0	0	-0.512344	7.32E-11
252152942275	GP8	159	chr4	4	q32.1	157,990,308	158,000,885	7	0	0	-0.571969	5.54E-11
252152942275	GP8	160	chr4	4	q32.1	159,684,860	159,693,032	4	0	0	-0.991288	1.40E-15
252152942275	GP8	161	chr4	4	q34.3	177,710,134	177,719,273	4	0	0	-0.773187	6.98E-10
252152942275	GP8	162	chr4	4	q34.3	183,058,260	183,069,722	10	0	0	-0.534159	9.79E-12
252152942275	GP8	163	chr4	4	q35.1	183,715,829	183,724,473	5	0	0	-0.776565	7.29E-12
252152942275	GP8	164	chr4	4	q35.1	185,742,658	185,751,567	5	0	0	-0.881409	4.29E-14
252152942275	GP8	165	chr4	4	q35.1	187,058,627	187,068,952	5	0	0	-0.71904	2.70E-12
252152942275	GP8	166	chr5	5	p15.33	1,340,550	1,345,578	4	0	0	-0.985539	1.28E-11
252152942275	GP8	167	chr5	5	p15.33	2,745,603	2,754,445	5	0	0	-0.955905	1.25E-15
252152942275	GP8	168	chr5	5	p15.31	6,707,258	6,719,319	6	0	0	-0.648896	1.21E-10
252152942275	GP8	169	chr5	5	p15.31	7,392,725	7,403,130	6	0	0	-0.865122	2.09E-16
252152942275	GP8	170	chr5	5	p15.2	11,380,821	11,391,529	6	0	0	-0.81285	1.34E-15
252152942275	GP8	171	chr5	5	p15.2	11,902,118	11,910,391	6	0	0	-0.966029	1.57E-20
252152942275	GP8	172	chr5	5	p15.2	14,137,939	14,153,620	10	0	0	-0.666438	8.94E-18
252152942275	GP8	173	chr5	5	p15.2	14,484,401	14,491,038	4	0	0	-0.922371	5.44E-10
252152942275	GP8	174	chr5	5	p15.2	14,869,647	14,874,163	4	0	0	-1.124293	1.79E-15
252152942275	GP8	175	chr5	5	p15.1	17,271,126	17,282,524	8	0	0	-0.653777	6.25E-15
252152942275	GP8	176	chr5	5	p13.2	34,926,929	34,936,324	6	0	0	-0.877468	6.57E-18
252152942275	GP8	177	chr5	5	p13.1	38,554,012	38,562,339	5	0	0	-1.094581	9.49E-25
252152942275	GP8	178	chr5	5	q11.2	52,773,448	52,783,691	6	0	0	-0.625537	2.43E-10
252152942275	GP8	179	chr5	5	q11.2	56,246,302	56,251,031	3	0	0	-0.973805	3.79E-13
252152942275	GP8	180	chr5	5	q13.2	72,140,062	72,147,729	5	0	0	-1.011082	1.76E-16
252152942275	GP8	181	chr5	5	q13.2	72,736,905	72,750,671	7	0	0	-0.535837	2.37E-10
252152942275	GP8	182	chr5	5	q13.3	75,461,990	75,465,886	3	0	0	-0.892191	2.39E-11
252152942275	GP8	183	chr5	5	q13.3	76,332,185	76,344,673	7	0	0	-0.835347	1.46E-21
252152942275	GP8	184	chr5	5	q14.1	81,042,991	81,050,299	5	0	0	-0.665111	6.19E-11
252152942275	GP8	185	chr5	5	q15	92,905,359	92,931,987	16	0	0	-0.422675	3.27E-11
252152942275	GP8	186	chr5	5	q23.2	121,643,518	121,653,754	6	0	0	-0.714954	4.71E-15
252152942275	GP8	187	chr5	5	q31.3	141,378,541	141,381,856	3	0	0	-1.028731	8.64E-15
252152942275	GP8	188	chr5	5	q33.2	154,129,403	154,140,231	7	0	0	-0.580327	2.12E-10
252152942275	GP8	189	chr5	5	q34	167,281,175	167,290,959	5	0	0	-0.700475	1.31E-10
252152942275	GP8	190	chr5	5	q34	167,714,644	167,724,832	7	0	0	-0.820886	2.79E-19
252152942275	GP8	191	chr5	5	q34	167,950,549	167,962,156	8	0	0	-0.598885	5.04E-14
252152942275	GP8	192	chr5	5	q35.1	172,095,299	172,115,048	11	0	0	-0.811738	8.48E-25
252152942275	GP8	193	chr5	5	q35.2	176,555,344	176,569,797	8	0	0	-0.594386	4.15E-14
252152942275	GP8	197	chr6	6	p25.3	1,307,040	1,318,307	5	0	0	-0.715812	1.21E-12
252152942275	GP8	198	chr6	6	p25.2	4,074,026	4,085,375	6	0	0	-0.732728	3.09E-11
252152942275	GP8	199	chr6	6	p25.1	4,773,466	4,779,865	4	0	0	-1.204214	6.39E-22
252152942275	GP8	200	chr6	6	p24.3	7,907,323	7,912,516	3	0	0	-0.951124	8.22E-13
252152942275	GP8	201	chr6	6	p24.2	11,083,745	11,098,331	8	0	0	-0.553297	2.81E-11
252152942275	GP8	202	chr6	6	p24.1	12,008,097	12,013,632	4	0	0	-1.612083	4.74E-28
252152942275	GP8	203	chr6	6	p22.3	15,246,502	15,250,079	3	0	0	-1.397436	6.20E-23
252152942275	GP8	204	chr6	6	p22.3	17,979,612	17,993,673	8	0	0	-0.919567	4.13E-22
252152942275	GP8	205	chr6	6	p22.3	19,835,409	19,843,530	7	0	0	-0.561492	9.36E-11
252152942275	GP8	206	chr6	6	p21.2	38,922,027	38,938,015	5	0	0	-0.619409	5.84E-10
252152942275	GP8	207	chr6	6	p21.1	42,744,637	42,754,057	5	0	0	-0.835838	5.16E-12
252152942275	GP8	208	chr6	6	p21.1	43,540,869	43,554,917	7	0	0	-0.623529	3.21E-12
252152942275	GP8	209	chr6	6	q14.1	79,776,263	79,792,372	9	0	0	-0.529617	5.36E-13
252152942275	GP8	210	chr6	6	q21	105,581,288	105,588,496	5	0	0	-0.677932	1.00E-10
252152942275	GP8	211	chr6	6	q21	105,618,258	105,630,421	7	0	0	-0.791425	2.89E-18
252152942275	GP8	212	chr6	6	q21	107,432,843	107,438,412	3	0	0	-1.034097	2.41E-13
252152942275	GP8	213	chr6	6	q21	108,878,143	108,886,264	5	0	0	-0.593513	9.35E-10
252152942275	GP8	214	chr6	6	q21	110,678,406	110,681,221	3	0	0	-1.430314	1.37E-23
252152942275	GP8	215	chr6	6	q21	114,177,937	114,183,824	4	0	0	-0.909094	5.57E-14
252152942275	GP8	216	chr6	6	q22.31	124,121,057	124,131,078	6	0	0	-0.966134	2.80E-21
252152942275	GP8	217	chr6	6	q23.1	130,337,779	130,343,379	3	0	0	-1.083438	1.21E-13
252152942275	GP8	218	chr6	6	q23.2	132,127,910	132,132,234	3	0	0	-0.992113	6.55E-13
252152942275	GP8	219	chr6	6	q24.1	139,455,284	139,461,526	3	0	0	-0.852798	3.93E-11
252152942275	GP8	220	chr6	6	q24.2	143,378,370	143,384,299	4	0	0	-1.174223	5.70E-22

252152942275	GP8	221	chr6	6	q25.2	153,445,515	153,458,190	8	0	0	-0.729425	1.12E-17
252152942275	GP8	223	chr6	6	q25.3	157,095,149	157,102,992	4	0	0	-1.097061	5.17E-18
252152942275	GP8	224	chr6	6	q25.3	158,650,888	158,655,597	3	0	0	-1.202387	2.91E-14
252152942275	GP8	225	chr6	6	q25.3	160,384,952	160,394,627	6	0	0	-0.543243	7.25E-10
252152942275	GP8	226	chr6	6	q27	168,433,568	168,449,845	11	0	0	-0.501388	7.28E-11
252152942275	GP8	227	chr6	6	q27	170,121,435	170,127,040	4	0	0	-1.131081	2.12E-20
252152942275	GP8	229	chr7	7	p22.3	2,613,788	2,623,881	6	0	0	-1.19899	6.41E-29
252152942275	GP8	230	chr7	7	p22.2	3,333,654	3,345,281	6	0	0	-0.69867	8.94E-12
252152942275	GP8	232	chr7	7	p22.1	6,654,359	6,663,938	5	0	0	-1.290406	8.21E-19
252152942275	GP8	233	chr7	7	p21.3	9,759,552	9,769,966	6	0	0	-0.635851	1.18E-10
252152942275	GP8	234	chr7	7	p21.3	12,592,758	12,599,309	4	0	0	-0.850353	1.88E-11
252152942275	GP8	235	chr7	7	p21.2	15,433,336	15,440,570	6	0	0	-0.736909	5.10E-15
252152942275	GP8	236	chr7	7	p21.1	19,150,921	19,159,147	6	0	0	-0.912391	1.40E-18
252152942275	GP8	237	chr7	7	p15.3	24,609,515	24,616,405	4	0	0	-0.987756	4.15E-16
252152942275	GP8	238	chr7	7	p15.2	26,327,209	26,334,736	6	0	0	-0.692637	1.47E-14
252152942275	GP8	239	chr7	7	p15.2	27,165,814	27,176,949	8	0	0	-0.623797	6.95E-16
252152942275	GP8	240	chr7	7	p15.2	27,234,943	27,242,413	6	0	0	-1.043221	7.87E-27
252152942275	GP8	241	chr7	7	p15.1	28,214,941	28,224,936	6	0	0	-0.906798	9.70E-21
252152942275	GP8	242	chr7	7	p14.3	30,170,881	30,177,387	4	0	0	-0.973082	3.28E-17
252152942275	GP8	243	chr7	7	p14.3	30,321,278	30,323,722	3	0	0	-0.917612	1.71E-12
252152942275	GP8	244	chr7	7	p14.3	32,930,034	32,934,261	3	0	0	-1.386842	2.02E-16
252152942275	GP8	245	chr7	7	p14.2	35,075,152	35,080,318	3	0	0	-1.158356	3.42E-16
252152942275	GP8	246	chr7	7	p14.1	39,869,979	39,876,354	4	0	0	-0.884547	2.74E-15
252152942275	GP8	247	chr7	7	p14.1	42,270,288	42,284,209	8	0	0	-0.69041	2.58E-17
252152942275	GP8	248	chr7	7	p13	44,922,602	44,927,821	4	0	0	-1.109555	2.54E-20
252152942275	GP8	249	chr7	7	p13	45,025,335	45,045,206	10	0	0	-0.52653	1.82E-12
252152942275	GP8	250	chr7	7	p12.1	50,846,702	50,862,024	7	0	0	-0.774391	5.20E-18
252152942275	GP8	251	chr7	7	p11.2	55,635,209	55,641,423	4	0	0	-0.861822	2.37E-13
252152942275	GP8	253	chr7	7	q21.11	77,644,551	77,652,021	5	0	0	-1.075255	8.61E-22
252152942275	GP8	254	chr7	7	q21.3	94,532,156	94,542,174	8	0	0	-0.583914	1.08E-12
252152942275	GP8	255	chr7	7	q22.1	98,742,296	98,745,745	3	0	0	-1.202657	6.10E-19
252152942275	GP8	256	chr7	7	q22.1	100,290,206	100,295,137	3	0	0	-0.913553	2.43E-10
252152942275	GP8	257	chr7	7	q22.1	101,455,968	101,462,497	4	0	0	-1.21739	6.75E-21
252152942275	GP8	258	chr7	7	q22.1	101,888,196	101,895,138	7	0	0	-0.845394	1.64E-15
252152942275	GP8	259	chr7	7	q22.3	106,671,221	106,695,005	12	0	0	-0.497658	4.94E-15
252152942275	GP8	260	chr7	7	q31.1	113,717,797	113,734,372	9	0	0	-0.535174	1.21E-11
252152942275	GP8	261	chr7	7	q31.2	116,591,420	116,597,335	4	0	0	-1.067903	9.98E-16
252152942275	GP8	262	chr7	7	q31.31	119,911,666	119,916,550	4	0	0	-0.878113	1.82E-15
252152942275	GP8	263	chr7	7	q32.1	128,762,715	128,787,460	14	0	0	-0.411122	6.52E-11
252152942275	GP8	264	chr7	7	q32.2	130,130,099	130,134,916	7	0	0	-0.616801	1.85E-11
252152942275	GP8	265	chr7	7	q33	137,524,453	137,535,075	5	0	0	-0.683564	1.58E-11
252152942275	GP8	266	chr7	7	q34	139,206,623	139,212,526	3	0	0	-0.949425	4.77E-13
252152942275	GP8	267	chr7	7	q34	139,473,298	139,484,440	5	0	0	-0.921402	2.18E-19
252152942275	GP8	268	chr7	7	q34	139,873,465	139,877,877	3	0	0	-1.307944	3.18E-20
252152942275	GP8	269	chr7	7	q34	141,397,369	141,408,076	6	0	0	-0.82555	9.05E-17
252152942275	GP8	270	chr7	7	q35	145,383,862	145,397,672	6	0	0	-0.733986	8.10E-14
252152942275	GP8	271	chr7	7	q36.1	149,121,022	149,130,294	5	0	0	-0.862141	1.03E-12
252152942275	GP8	272	chr7	7	q36.1	149,152,121	149,173,798	12	0	0	-0.832848	2.24E-32
252152942275	GP8	273	chr7	7	q36.1	150,091,096	150,104,056	8	0	0	-0.866146	5.33E-23
252152942275	GP8	274	chr7	7	q36.1	150,947,708	150,957,515	7	0	0	-0.555069	9.67E-10
252152942275	GP8	275	chr7	7	q36.2	154,791,894	154,801,863	5	0	0	-0.81726	3.38E-15
252152942275	GP8	276	chr7	7	q36.3	156,792,950	156,809,249	9	0	0	-0.632672	9.81E-13
252152942275	GP8	277	chr7	7	q36.3	158,179,318	158,203,133	14	0	0	-0.485109	3.40E-14
252152942275	GP8	278	chr8	8	p23.3	609,939	659,569	21	0	0	-0.467391	1.49E-19
252152942275	GP8	280	chr8	8	p23.3	1,943,388	1,953,478	6	0	0	-0.814081	2.66E-18
252152942275	GP8	281	chr8	8	p23.1	12,610,902	12,614,610	3	0	0	-1.355623	1.34E-20
252152942275	GP8	282	chr8	8	p21.2	25,038,131	25,045,706	5	0	0	-0.90685	1.87E-19
252152942275	GP8	283	chr8	8	p21.1	28,239,796	28,246,703	5	0	0	-0.760001	5.82E-14
252152942275	GP8	284	chr8	8	p12	28,924,978	28,935,048	6	0	0	-0.615694	7.53E-10
252152942275	GP8	285	chr8	8	p12	30,886,622	30,892,125	4	0	0	-1.105448	1.37E-18
252152942275	GP8	286	chr8	8	p11.21	41,905,520	41,908,043	3	0	0	-1.110626	2.50E-15
252152942275	GP8	287	chr8	8	p11.21	42,392,855	42,398,201	4	0	0	-0.763683	4.19E-11
252152942275	GP8	288	chr8	8	p11.21	42,745,197	42,757,937	8	0	0	-0.596331	1.46E-12
252152942275	GP8	289	chr8	8	q11.23	54,623,338	54,632,965	6	0	0	-0.726343	2.83E-14
252152942275	GP8	290	chr8	8	q12.1	56,012,260	56,020,371	7	0	0	-0.763792	5.42E-12
252152942275	GP8	291	chr8	8	q12.1	61,586,383	61,596,459	6	0	0	-1.115903	1.01E-25
252152942275	GP8	292	chr8	8	q13.1	67,870,216	67,879,176	5	0	0	-1.149613	1.27E-13
252152942275	GP8	293	chr8	8	q13.3	71,309,017	71,320,250	7	0	0	-0.638412	2.28E-12
252152942275	GP8	294	chr8	8	q21.13	80,678,241	80,683,749	4	0	0	-0.994484	5.99E-14
252152942275	GP8	295	chr8	8	q21.13	81,784,315	81,792,623	5	0	0	-0.85328	2.69E-11
252152942275	GP8	296	chr8	8	q21.2	86,083,804	86,091,715	5	0	0	-1.082182	2.92E-21
252152942275	GP8	297	chr8	8	q21.3	87,353,171	87,360,952	6	0	0	-0.564742	1.23E-10
252152942275	GP8	298	chr8	8	q21.3	91,656,006	91,662,776	4	0	0	-0.853332	1.53E-14
252152942275	GP8	299	chr8	8	q22.2	99,834,020	99,843,368	5	0	0	-0.793066	4.26E-14
252152942275	GP8	300	chr8	8	q22.3	103,660,801	103,669,471	5	0	0	-0.719565	6.30E-11
252152942275	GP8	301	chr8	8	q23.1	106,328,850	106,335,008	5	0	0	-0.694019	9.86E-11
252152942275	GP8	302	chr8	8	q23.3	116,676,719	116,686,400	5	0	0	-0.927506	2.38E-18
252152942275	GP8	303	chr8	8	q24.11	117,957,571	117,965,855	5	0	0	-0.87213	1.93E-16
252152942275	GP8	304	chr8	8	q24.11	119,120,552	119,129,732	5	0	0	-0.749662	2.39E-12
252152942275	GP8	305	chr8	8	q24.13	125,379,343	125,383,397	3	0	0	-0.804514	2.36E-10
252152942275	GP8	306	chr8	8	q24.23	136,452,927	136,485,030	15	0	0	-0.419701	8.99E-14

252152942275	GP8	307	chr8	8	q24.3	141,637,442	141,647,348	5	0	0	-0.699998	1.36E-10
252152942275	GP8	308	chr8	8	q24.3	144,440,732	144,446,966	3	0	0	-0.920321	1.54E-12
252152942275	GP8	309	chr8	8	q24.3	144,938,537	144,941,946	4	0	0	-1.074366	8.36E-20
2.52153E+11	GP8	310	chr8	8	q24.3	146274776	146280020	4	0	0	-1.145917	1.178E-19
252152942275	GP8	311	chr9	9	p24.3	2,040,909	2,053,837	8	0	0	-0.823666	4.24E-20
252152942275	GP8	312	chr9	9	p24.1	5,084,349	5,089,199	3	0	0	-1.004358	2.39E-12
252152942275	GP8	313	chr9	9	p13.3	34,954,671	34,961,045	5	0	0	-1.017135	2.51E-21
252152942275	GP8	314	chr9	9	p13.3	35,787,162	35,798,193	7	0	0	-0.564374	2.33E-11
252152942275	GP8	315	chr9	9	q21.11	71,623,658	71,645,898	13	0	0	-0.401668	3.54E-11
252152942275	GP8	316	chr9	9	q21.11	71,937,907	71,944,494	5	0	0	-1.019743	1.71E-22
252152942275	GP8	317	chr9	9	q21.11	72,128,514	72,133,993	4	0	0	-1.239518	3.78E-22
252152942275	GP8	318	chr9	9	q21.33	88,709,484	88,718,692	5	0	0	-0.759513	4.07E-14
252152942275	GP8	319	chr9	9	q22.1	91,790,359	91,796,056	4	0	0	-0.797892	1.90E-12
252152942275	GP8	320	chr9	9	q22.2	92,109,062	92,116,097	3	0	0	-0.826478	1.61E-10
252152942275	GP8	321	chr9	9	q22.31	94,182,549	94,190,452	5	0	0	-0.994931	2.07E-17
252152942275	GP8	322	chr9	9	q22.31	96,208,809	96,218,449	5	0	0	-0.864473	3.19E-13
252152942275	GP8	324	chr9	9	q22.32	97,752,769	97,774,216	13	0	0	-0.516037	3.91E-16
252152942275	GP8	325	chr9	9	q22.32	98,052,971	98,058,562	3	0	0	-0.821603	6.98E-11
252152942275	GP8	326	chr9	9	q22.32	98,274,246	98,282,413	6	0	0	-0.95177	3.35E-18
252152942275	GP8	327	chr9	9	q22.33	100,258,515	100,269,783	8	0	0	-0.542375	3.69E-12
252152942275	GP8	328	chr9	9	q22.33	101,467,897	101,475,417	4	0	0	-0.815158	1.04E-10
252152942275	GP8	329	chr9	9	q22.33	101,554,879	101,573,553	10	0	0	-0.773611	4.38E-23
252152942275	GP8	330	chr9	9	q22.33	101,863,999	101,873,345	6	0	0	-0.818833	6.51E-17
252152942275	GP8	331	chr9	9	q22.33	102,585,646	102,593,896	5	0	0	-0.791441	7.28E-15
252152942275	GP8	332	chr9	9	q31.1	103,185,084	103,192,529	5	0	0	-0.894311	8.43E-14
252152942275	GP8	333	chr9	9	q31.3	112,079,831	112,086,535	4	0	0	-1.036144	5.98E-17
252152942275	GP8	334	chr9	9	q31.3	112,254,319	112,263,808	5	0	0	-0.845425	1.07E-14
252152942275	GP8	335	chr9	9	q31.3	114,240,106	114,246,914	5	0	0	-0.804196	2.13E-13
252152942275	GP8	336	chr9	9	q32	115,246,657	115,254,208	6	0	0	-1.016804	3.99E-23
252152942275	GP8	337	chr9	9	q32	115,509,310	115,518,534	7	0	0	-0.748791	1.23E-15
252152942275	GP8	338	chr9	9	q32	116,632,755	116,642,488	6	0	0	-0.651516	3.34E-12
252152942275	GP8	339	chr9	9	q32	117,369,058	117,375,910	5	0	0	-0.774777	3.63E-13
252152942275	GP8	340	chr9	9	q33.1	118,912,806	118,918,857	4	0	0	-1.037455	4.42E-17
252152942275	GP8	341	chr9	9	q33.3	126,011,315	126,080,889	24	0	0	-0.281989	2.66E-10
252152942275	GP8	342	chr9	9	q33.3	128,650,152	128,654,591	4	0	0	-1.459257	2.15E-29
252152942275	GP8	343	chr9	9	q33.3	129,086,622	129,090,455	3	0	0	-1.577254	3.67E-24
252152942275	GP8	344	chr9	9	q34.11	131,449,302	131,453,220	3	0	0	-1.244352	1.26E-18
252152942275	GP8	345	chr9	9	q34.12	133,705,609	133,720,711	9	0	0	-0.814099	2.36E-25
252152942275	GP8	347	chr9	9	q34.13	134,267,935	134,271,587	3	0	0	-1.277255	2.37E-18
252152942275	GP8	348	chr10	10	p15.3	728,425	740,247	6	0	0	-0.615558	2.16E-10
252152942275	GP8	349	chr10	10	p14	8,042,937	8,060,912	10	0	0	-0.512423	9.12E-13
252152942275	GP8	350	chr10	10	p14	11,054,073	11,068,538	7	0	0	-0.655282	1.86E-14
252152942275	GP8	351	chr10	10	p14	11,780,466	11,791,384	6	0	0	-0.716139	1.35E-10
252152942275	GP8	352	chr10	10	p14	11,905,729	11,916,733	6	0	0	-0.587436	9.85E-10
252152942275	GP8	353	chr10	10	p13	13,690,710	13,706,280	8	0	0	-0.564628	2.45E-10
252152942275	GP8	354	chr10	10	p13	13,930,667	13,935,510	3	0	0	-0.948678	2.25E-10
252152942275	GP8	355	chr10	10	p13	14,642,514	14,650,987	4	0	0	-0.90399	2.35E-12
252152942275	GP8	356	chr10	10	p13	15,403,945	15,418,293	9	0	0	-0.664442	1.19E-17
252152942275	GP8	357	chr10	10	p12.31	21,801,632	21,811,066	10	0	0	-0.724982	2.41E-24
252152942275	GP8	359	chr10	10	p12.2	22,998,933	23,008,720	6	0	0	-0.813385	6.48E-18
252152942275	GP8	360	chr10	10	p12.1	26,851,965	26,858,737	5	0	0	-0.90227	9.42E-16
252152942275	GP8	361	chr10	10	p11.21	35,100,625	35,107,608	4	0	0	-1.022581	1.97E-15
252152942275	GP8	362	chr10	10	p11.21	35,617,339	35,641,021	12	0	0	-0.440434	1.17E-12
252152942275	GP8	363	chr10	10	p11.21	35,924,660	35,934,470	5	0	0	-0.828035	1.93E-13
252152942275	GP8	364	chr10	10	q11.23	50,317,458	50,327,075	5	0	0	-0.890661	1.59E-15
252152942275	GP8	365	chr10	10	q21.1	60,267,554	60,275,899	4	0	0	-0.836451	3.90E-12
252152942275	GP8	366	chr10	10	q21.3	65,276,892	65,285,540	5	0	0	-0.89723	4.43E-18
252152942275	GP8	367	chr10	10	q22.3	79,390,905	79,405,358	9	0	0	-0.574867	1.55E-10
252152942275	GP8	368	chr10	10	q23.1	83,631,734	83,641,436	6	0	0	-0.921455	7.54E-21
252152942275	GP8	369	chr10	10	q23.2	88,852,158	88,857,016	4	0	0	-1.10516	1.48E-15
252152942275	GP8	370	chr10	10	q23.31	92,614,476	92,623,734	6	0	0	-0.78857	1.15E-17
252152942275	GP8	371	chr10	10	q23.32	92,917,816	92,927,117	5	0	0	-0.847573	1.37E-14
252152942275	GP8	372	chr10	10	q23.32	93,165,067	93,172,879	5	0	0	-0.705055	1.08E-12
252152942275	GP8	373	chr10	10	q24.1	98,588,727	98,596,596	11	0	0	-0.811334	1.12E-24
252152942275	GP8	374	chr10	10	q24.1	99,092,039	99,096,440	3	0	0	-0.801947	2.06E-10
252152942275	GP8	375	chr10	10	q24.2	101,596,627	101,603,171	4	0	0	-0.95658	1.11E-14
252152942275	GP8	376	chr10	10	q25.1	108,922,569	108,927,235	3	0	0	-1.147789	7.94E-17
252152942275	GP8	377	chr10	10	q25.3	115,800,455	115,809,422	4	0	0	-0.861377	1.47E-12
252152942275	GP8	378	chr10	10	q26.11	120,783,526	120,805,881	10	0	0	-0.529052	8.05E-13
252152942275	GP8	379	chr10	10	q26.13	123,350,591	123,364,732	7	0	0	-0.56753	3.42E-10
252152942275	GP8	380	chr10	10	q26.13	126,427,698	126,439,690	7	0	0	-0.693386	5.98E-14
252152942275	GP8	382	chr10	10	q26.2	130,084,164	130,090,772	3	0	0	-0.889057	7.09E-11
252152942275	GP8	383	chr10	10	q26.3	133,102,865	133,115,664	8	0	0	-0.723722	1.05E-16
252152942275	GP8	384	chr11	11	p15.4	2,903,609	2,908,625	3	0	0	-1.153553	4.43E-11
252152942275	GP8	385	chr11	11	p15.4	6,674,905	6,683,662	5	0	0	-0.702616	6.81E-12
252152942275	GP8	386	chr11	11	p15.4	9,282,219	9,289,996	5	0	0	-0.726925	1.37E-12
252152942275	GP8	387	chr11	11	p15.3 - p15.2	12,693,768	12,700,048	5	0	0	-0.798003	3.02E-11
252152942275	GP8	388	chr11	11	p11.2	46,138,777	46,148,703	7	0	0	-0.774504	1.31E-16
252152942275	GP8	389	chr11	11	q13.1	63,528,548	63,538,252	4	0	0	-1.283761	2.03E-15
252152942275	GP8	390	chr11	11	q13.1	64,542,025	64,546,879	4	0	0	-1.239055	1.32E-21
252152942275	GP8	391	chr11	11	q13.1	65,807,239	65,845,801	21	0	0	-0.437173	8.30E-19

252152942275	GP8	392	chr11	11	q13.2	66,494,511	66,498,204	3	0	0	-1.466315	6.69E-21
252152942275	GP8	393	chr11	11	q13.4	74,436,544	74,465,067	14	0	0	-0.64812	7.53E-28
252152942275	GP8	394	chr11	11	q14.1	77,905,483	77,910,028	3	0	0	-1.035509	4.41E-13
252152942275	GP8	395	chr11	11	q14.1	78,125,466	78,132,165	5	0	0	-0.822876	3.48E-12
252152942275	GP8	396	chr11	11	q21	93,270,505	93,285,125	8	0	0	-0.831651	2.22E-24
252152942275	GP8	397	chr11	11	q22.3	106,880,356	106,894,972	8	0	0	-0.770088	5.80E-20
252152942275	GP8	399	chr11	11	q24.3	129,861,936	129,966,838	44	0	0	-0.257118	1.53E-13
252152942275	GP8	404	chr12	12	p13.33	2,155,792	2,170,018	9	0	0	-0.554015	3.49E-10
252152942275	GP8	405	chr12	12	p13.33	3,065,223	3,072,388	5	0	0	-0.760447	1.43E-12
252152942275	GP8	406	chr12	12	p13.31	7,034,415	7,040,293	4	0	0	-0.850692	1.73E-13
252152942275	GP8	407	chr12	12	p13.31	8,845,605	8,855,207	6	0	0	-0.648777	9.42E-12
252152942275	GP8	408	chr12	12	p12.3	19,282,053	19,285,386	3	0	0	-1.072535	4.84E-15
252152942275	GP8	409	chr12	12	p12.1	26,110,307	26,116,097	4	0	0	-1.361856	4.29E-26
252152942275	GP8	410	chr12	12	p12.1	26,272,787	26,278,447	4	0	0	-1.087642	4.50E-16
252152942275	GP8	411	chr12	12	q12	42,614,238	42,631,224	8	0	0	-0.744569	7.33E-20
252152942275	GP8	412	chr12	12	q12	42,982,644	42,987,900	4	0	0	-1.025834	4.93E-18
252152942275	GP8	413	chr12	12	q12	46,120,090	46,127,415	4	0	0	-1.046511	2.10E-18
252152942275	GP8	414	chr12	12	q13.13	52,206,600	52,220,537	8	0	0	-0.572892	2.08E-13
252152942275	GP8	415	chr12	12	q13.13	52,344,104	52,348,294	3	0	0	-1.03879	2.52E-15
252152942275	GP8	416	chr12	12	q13.13	54,769,385	54,777,950	5	0	0	-0.637543	4.87E-11
252152942275	GP8	417	chr12	12	q13.2	56,572,877	56,588,347	10	0	0	-0.466151	3.88E-11
252152942275	GP8	418	chr12	12	q13.3	57,397,465	57,405,881	6	0	0	-0.737472	6.94E-15
252152942275	GP8	419	chr12	12	q23.1	96,584,136	96,593,111	6	0	0	-0.55436	9.67E-10
252152942275	GP8	420	chr12	12	q23.1	99,283,634	99,292,190	5	0	0	-1.048357	5.60E-22
252152942275	GP8	421	chr12	12	q23.1	100,375,167	100,384,831	6	0	0	-0.969169	2.07E-23
252152942275	GP8	422	chr12	12	q23.2	102,219,910	102,229,260	6	0	0	-0.660999	5.21E-12
252152942275	GP8	423	chr12	12	q23.3	104,524,154	104,537,481	9	0	0	-0.605344	1.59E-15
252152942275	GP8	424	chr12	12	q24.11	109,246,968	109,256,006	8	0	0	-0.822479	1.41E-19
252152942275	GP8	425	chr12	12	q24.11	109,744,643	109,749,290	4	0	0	-0.901661	3.72E-15
252152942275	GP8	426	chr12	12	q24.21	116,709,610	116,717,834	5	0	0	-0.997835	1.43E-20
252152942275	GP8	427	chr12	12	q24.23	118,495,892	118,503,589	4	0	0	-0.876795	9.06E-13
252152942275	GP8	428	chr12	12	q24.23	120,421,625	120,436,087	7	0	0	-0.681703	7.78E-15
252152942275	GP8	430	chr12	12	q24.31	122,902,888	122,909,814	5	0	0	-0.958196	1.06E-16
252152942275	GP8	431	chr12	12	q24.31	123,632,154	123,639,185	5	0	0	-1.024326	2.50E-18
252152942275	GP8	432	chr12	12	q24.31	125,470,644	125,481,289	7	0	0	-0.62927	2.22E-11
252152942275	GP8	433	chr12	12	q24.33	130,384,657	130,390,490	4	0	0	-0.95868	8.49E-15
252152942275	GP8	434	chr12	12	q24.33	131,353,633	131,361,379	6	0	0	-0.690005	1.16E-14
252152942275	GP8	435	chr12	12	q24.33	132,377,111	132,381,896	4	0	0	-1.047685	2.73E-11
252152942275	GP8	436	chr13	13	q12.11	21,275,506	21,280,504	4	0	0	-1.04807	7.77E-13
252152942275	GP8	437	chr13	13	q12.13	27,329,861	27,343,744	9	0	0	-0.543892	2.38E-10
252152942275	GP8	438	chr13	13	q12.13	27,738,859	27,752,573	9	0	0	-0.982571	1.34E-34
252152942275	GP8	439	chr13	13	q12.3	29,393,179	29,401,441	3	0	0	-0.820401	4.12E-10
252152942275	GP8	440	chr13	13	q12.3	31,035,934	31,042,977	4	0	0	-0.948524	3.95E-17
252152942275	GP8	441	chr13	13	q13.1	33,159,254	33,163,859	3	0	0	-1.36804	2.19E-21
252152942275	GP8	442	chr13	13	q13.1	33,587,382	33,592,252	3	0	0	-1.27217	3.68E-18
252152942275	GP8	443	chr13	13	q13.3	37,490,354	37,500,436	6	0	0	-0.587126	9.44E-10
252152942275	GP8	444	chr13	13	q14.11	42,611,231	42,620,793	5	0	0	-0.854518	2.45E-17
252152942275	GP8	445	chr13	13	q14.3	51,793,637	51,798,133	3	0	0	-1.301309	1.73E-18
252152942275	GP8	446	chr13	13	q14.3	53,767,631	53,782,875	7	0	0	-0.565521	5.41E-12
252152942275	GP8	447	chr13	13	q21.33	72,434,812	72,446,162	7	0	0	-0.563662	3.54E-11
252152942275	GP8	448	chr13	13	q31.3	91,993,757	92,005,613	15	0	0	-0.712362	1.57E-32
252152942275	GP8	449	chr13	13	q32.1	96,738,891	96,746,735	6	0	0	-0.862854	1.08E-14
252152942275	GP8	450	chr13	13	q32.1	98,083,941	98,088,971	3	0	0	-1.249814	6.39E-18
252152942275	GP8	451	chr13	13	q32.2	99,215,658	99,235,678	12	0	0	-0.580296	1.17E-18
252152942275	GP8	452	chr13	13	q32.3	100,615,203	100,640,555	13	0	0	-0.753752	7.01E-26
252152942275	GP8	453	chr13	13	q32.3	101,317,446	101,335,405	10	0	0	-0.498634	3.13E-12
252152942275	GP8	454	chr13	13	q33.3	107,186,045	107,194,652	6	0	0	-0.839465	7.49E-12
252152942275	GP8	455	chr13	13	q34	110,430,371	110,442,785	7	0	0	-0.696851	1.73E-14
252152942275	GP8	456	chr13	13	q34	113,857,818	113,868,734	6	0	0	-0.819465	7.55E-16
252152942275	GP8	457	chr13	13	q34	114,229,628	114,250,467	16	0	0	-0.408763	8.83E-11
252152942275	GP8	458	chr14	14	q11.2	21,559,808	21,568,120	5	0	0	-1.010764	5.15E-21
252152942275	GP8	459	chr14	14	q11.2	23,514,833	23,522,469	6	0	0	-0.832548	2.60E-16
252152942275	GP8	460	chr14	14	q13.1	33,399,986	33,413,544	8	0	0	-0.709458	8.01E-18
252152942275	GP8	461	chr14	14	q21.3	48,092,745	48,100,867	5	0	0	-0.668243	6.11E-11
252152942275	GP8	462	chr14	14	q22.3	56,044,103	56,049,680	3	0	0	-1.020666	4.65E-12
252152942275	GP8	463	chr14	14	q23.2	62,274,705	62,281,091	4	0	0	-0.840584	2.26E-12
252152942275	GP8	464	chr14	14	q23.3	65,435,275	65,445,017	6	0	0	-0.586257	6.32E-10
252152942275	GP8	465	chr14	14	q24.2	70,719,730	70,724,229	4	0	0	-1.349759	1.20E-20
252152942275	GP8	466	chr14	14	q24.3	74,888,741	74,896,530	5	0	0	-0.683597	4.97E-11
252152942275	GP8	467	chr14	14	q31.1	81,679,352	81,694,062	8	0	0	-0.502594	2.58E-10
252152942275	GP8	468	chr14	14	q32.11	89,879,335	89,887,444	6	0	0	-0.880603	2.24E-17
252152942275	GP8	469	chr14	14	q32.11	91,280,043	91,286,449	4	0	0	-0.774978	1.37E-10
252152942275	GP8	470	chr14	14	q32.11	91,522,555	91,531,647	7	0	0	-0.604444	2.24E-13
252152942275	GP8	471	chr14	14	q32.13	95,784,221	95,788,362	3	0	0	-1.12645	4.55E-14
252152942275	GP8	472	chr14	14	q32.2	100,254,687	100,264,021	6	0	0	-0.910139	2.93E-18
252152942275	GP8	474	chr14	14	q32.32	103,240,021	103,253,658	10	0	0	-0.735132	2.00E-17
252152942275	GP8	475	chr14	14	q32.32	103,518,590	103,522,534	3	0	0	-1.012111	2.83E-11
252152942275	GP8	476	chr14	14	q32.32	103,801,861	103,804,489	3	0	0	-0.968351	3.07E-13
252152942275	GP8	477	chr14	14	q32.33	104,391,294	104,400,363	6	0	0	-0.590402	7.88E-10
252152942275	GP8	478	chr14	14	q32.33	105,709,978	105,713,174	3	0	0	-0.789987	3.19E-10
252152942275	GP8	479	chr15	15	q12	27,213,885	27,221,993	6	0	0	-0.882296	5.69E-19

252152942275	GP8	480	chr15	15	q13.1	29,859,183	29,870,718	6	0	0	-0.994139	6.60E-23
252152942275	GP8	481	chr15	15	q13.1	30,110,497	30,118,025	5	0	0	-0.943139	2.07E-17
252152942275	GP8	482	chr15	15	q13.1	30,259,899	30,263,524	3	0	0	-1.313704	3.03E-18
252152942275	GP8	483	chr15	15	q15.1	40,614,168	40,621,719	4	0	0	-0.683536	6.89E-10
252152942275	GP8	484	chr15	15	q21.2	51,382,032	51,394,633	8	0	0	-0.586217	2.83E-13
252152942275	GP8	485	chr15	15	q21.3	55,875,068	55,886,364	7	0	0	-0.736171	4.89E-15
252152942275	GP8	486	chr15	15	q21.3	56,529,713	56,539,897	8	0	0	-0.7187	8.56E-19
252152942275	GP8	487	chr15	15	q22.2	59,726,607	59,733,211	5	0	0	-1.022159	8.91E-19
252152942275	GP8	488	chr15	15	q22.2	62,355,836	62,368,774	9	0	0	-0.497144	1.44E-10
252152942275	GP8	489	chr15	15	q22.31	65,063,279	65,070,621	10	0	0	-0.649127	4.32E-16
252152942275	GP8	491	chr15	15	q22.31	65,711,824	65,718,974	4	0	0	-0.879138	3.92E-12
252152942275	GP8	492	chr15	15	q23	71,403,932	71,410,596	5	0	0	-0.922134	2.24E-18
252152942275	GP8	493	chr15	15	q24.1	73,342,280	73,347,803	3	0	0	-0.866581	1.95E-11
252152942275	GP8	495	chr15	15	q24.3	77,359,805	77,366,720	6	0	0	-0.846347	2.44E-18
252152942275	GP8	496	chr15	15	q24.3	77,707,943	77,714,605	5	0	0	-0.721893	1.00E-12
252152942275	GP8	497	chr15	15	q25.1	78,365,306	78,374,037	4	0	0	-0.757694	1.59E-11
252152942275	GP8	498	chr15	15	q25.1	80,982,431	80,993,442	6	0	0	-0.930807	4.69E-23
252152942275	GP8	499	chr15	15	q25.2	83,614,855	83,631,616	10	0	0	-0.579408	3.95E-14
252152942275	GP8	500	chr15	15	q25.2	83,948,050	83,960,718	9	0	0	-0.551808	3.42E-11
252152942275	GP8	501	chr15	15	q26.1	90,166,827	90,211,786	33	0	0	-0.253694	9.72E-10
252152942275	GP8	502	chr15	15	q26.1	90,534,644	90,549,541	9	0	0	-0.552915	1.79E-11
252152942275	GP8	503	chr15	15	q26.1	93,629,482	93,636,735	5	0	0	-0.77664	8.04E-13
252152942275	GP8	504	chr15	15	q26.2	96,867,525	96,878,995	14	0	0	-0.776588	1.08E-28
252152942275	GP8	505	chr15	15	q26.3	99,183,604	99,205,894	13	0	0	-0.402435	2.17E-10
252152942275	GP8	506	chr15	15	q26.3	100,874,206	100,889,231	9	0	0	-0.649291	4.52E-14
252152942275	GP8	507	chr15	15	q26.3	101,452,803	101,465,055	8	0	0	-0.788453	1.03E-19
252152942275	GP8	508	chr15	15	q26.3	101,787,757	101,795,263	5	0	0	-0.923809	2.74E-18
252152942275	GP8	509	chr15	15	q26.3	102,026,679	102,034,423	5	0	0	-0.830893	6.07E-14
252152942275	GP8	511	chr16	16	p13.3	474,598	479,473	3	0	0	-1.153256	7.34E-14
252152942275	GP8	512	chr16	16	p13.3	1,647,705	1,667,960	11	0	0	-0.650432	3.19E-14
252152942275	GP8	515	chr16	16	p13.2	9,054,847	9,060,119	4	0	0	-1.324332	1.24E-25
252152942275	GP8	516	chr16	16	p13.11	16,041,539	16,045,173	3	0	0	-1.176593	4.16E-14
252152942275	GP8	517	chr16	16	p12.3	17,558,648	17,572,276	7	0	0	-0.606849	2.33E-11
252152942275	GP8	518	chr16	16	p12.2	22,016,268	22,028,461	9	0	0	-0.460434	2.83E-10
252152942275	GP8	519	chr16	16	p12.1	24,738,205	24,743,696	4	0	0	-0.841371	1.28E-13
252152942275	GP8	520	chr16	16	p12.1	25,699,068	25,707,443	5	0	0	-0.886899	1.41E-17
252152942275	GP8	521	chr16	16	q12.1	47,171,585	47,180,965	5	0	0	-0.828288	1.52E-15
252152942275	GP8	522	chr16	16	q12.1	48,413,813	48,426,836	6	0	0	-0.720379	4.58E-14
252152942275	GP8	523	chr16	16	q12.1	49,312,440	49,319,655	4	0	0	-0.90972	1.85E-10
252152942275	GP8	524	chr16	16	q12.1	50,185,053	50,196,775	7	0	0	-0.573119	1.04E-11
252152942275	GP8	525	chr16	16	q12.1	50,400,863	50,404,671	3	0	0	-1.165362	6.62E-15
252152942275	GP8	526	chr16	16	q12.1	52,575,553	52,587,753	6	0	0	-0.81344	2.25E-17
252152942275	GP8	527	chr16	16	q12.2	56,220,623	56,229,842	4	0	0	-0.834875	3.95E-12
252152942275	GP8	528	chr16	16	q12.2	56,455,764	56,467,976	7	0	0	-0.648219	2.18E-13
252152942275	GP8	529	chr16	16	q21	58,227,960	58,233,859	3	0	0	-1.122485	1.50E-16
252152942275	GP8	530	chr16	16	q21	66,457,969	66,464,528	3	0	0	-0.821862	1.36E-10
252152942275	GP8	531	chr16	16	q23.1	75,030,799	75,035,555	3	0	0	-1.215294	3.76E-15
252152942275	GP8	532	chr16	16	q23.2	79,610,991	79,642,281	18	0	0	-0.379887	6.42E-13
252152942275	GP8	533	chr16	16	q23.2	80,831,794	80,843,034	6	0	0	-0.832271	6.59E-18
252152942275	GP8	534	chr16	16	q23.2	81,068,752	81,073,644	4	0	0	-0.832331	9.30E-13
252152942275	GP8	536	chr16	16	q24.3	89,552,470	89,559,189	5	0	0	-1.107251	5.89E-24
252152942275	GP8	537	chr16	16	q24.3	89,894,035	89,898,890	4	0	0	-0.828552	7.91E-13
252152942275	GP8	538	chr17	17	p13.2	5,182,104	5,186,897	3	0	0	-1.096952	1.06E-15
252152942275	GP8	539	chr17	17	p12	11,140,998	11,153,351	7	0	0	-0.794271	2.06E-18
252152942275	GP8	540	chr17	17	p11.2	16,253,216	16,261,839	5	0	0	-0.760973	4.50E-12
252152942275	GP8	541	chr17	17	p11.2	16,941,187	16,951,761	5	0	0	-0.758213	1.19E-11
252152942275	GP8	542	chr17	17	q11.2	29,879,264	29,892,456	14	0	0	-0.417064	3.27E-11
252152942275	GP8	543	chr17	17	q12	35,763,772	35,771,339	5	0	0	-0.62753	1.64E-10
252152942275	GP8	544	chr17	17	q12	35,848,572	35,852,908	3	0	0	-0.938086	3.09E-12
252152942275	GP8	545	chr17	17	q21.2	40,425,013	40,432,141	4	0	0	-0.792477	1.73E-12
252152942275	GP8	546	chr17	17	q21.31	42,904,317	42,909,288	3	0	0	-1.147099	6.90E-17
252152942275	GP8	547	chr17	17	q21.31	44,265,697	44,275,777	6	0	0	-0.789809	9.69E-19
252152942275	GP8	548	chr17	17	q21.32	46,624,272	46,639,989	13	0	0	-0.51879	2.75E-15
252152942275	GP8	549	chr17	17	q21.33	49,196,414	49,200,031	3	0	0	-0.89209	1.09E-11
252152942275	GP8	550	chr17	17	q23.2	60,139,533	60,148,466	5	0	0	-1.063932	1.15E-16
252152942275	GP8	551	chr17	17	q23.2	61,040,408	61,048,521	5	0	0	-0.929822	2.23E-18
252152942275	GP8	552	chr17	17	q23.3	61,697,921	61,704,790	3	0	0	-0.828664	7.17E-10
252152942275	GP8	553	chr17	17	q24.2	64,295,954	64,300,380	3	0	0	-1.280486	1.34E-18
252152942275	GP8	554	chr17	17	q24.2	65,987,167	65,996,608	5	0	0	-0.765374	3.34E-11
252152942275	GP8	555	chr17	17	q25.1	74,232,394	74,240,537	5	0	0	-0.954262	6.14E-19
252152942275	GP8	556	chr17	17	q25.1	74,701,184	74,711,353	9	0	0	-0.679745	1.23E-17
252152942275	GP8	557	chr17	17	q25.3	76,770,956	76,780,311	7	0	0	-0.690386	5.87E-13
252152942275	GP8	558	chr17	17	q25.3	78,006,260	78,011,214	3	0	0	-1.126631	7.52E-13
252152942275	GP8	560	chr17	17	q25.3	80,476,337	80,481,025	3	0	0	-1.107148	6.13E-13
252152942275	GP8	561	chr18	18	p11.32	495,257	513,267	8	0	0	-0.574937	1.66E-11
252152942275	GP8	562	chr18	18	p11.31	5,290,748	5,298,074	4	0	0	-1.017872	8.06E-18
252152942275	GP8	563	chr18	18	p11.31	5,539,898	5,546,661	4	0	0	-0.896078	6.43E-15
252152942275	GP8	564	chr18	18	p11.22	8,607,655	8,614,347	4	0	0	-0.983181	1.77E-15
252152942275	GP8	566	chr18	18	p11.22	9,610,119	9,619,910	7	0	0	-0.810918	9.50E-17
252152942275	GP8	567	chr18	18	p11.22	10,450,513	10,457,834	4	0	0	-0.940827	8.67E-17
252152942275	GP8	568	chr18	18	q11.2	20,711,787	20,719,488	4	0	0	-0.855984	2.88E-11

252152942275	GP8	569	chr18	18	q11.2	22,928,725	22,936,070	4	0	0	-1.130925	4.65E-19
252152942275	GP8	570	chr18	18	q12.1	25,751,556	25,760,426	5	0	0	-1.084238	3.53E-23
252152942275	GP8	571	chr18	18	q12.1	29,261,192	29,269,937	5	0	0	-0.898635	5.47E-15
252152942275	GP8	572	chr18	18	q12.1	30,047,907	30,053,695	4	0	0	-1.116893	5.78E-17
252152942275	GP8	573	chr18	18	q12.1	31,157,460	31,162,296	3	0	0	-1.056287	6.49E-13
252152942275	GP8	574	chr18	18	q12.2	33,156,966	33,164,337	5	0	0	-0.981767	2.57E-18
252152942275	GP8	575	chr18	18	q12.2	33,874,101	33,885,038	6	0	0	-0.621857	4.43E-10
252152942275	GP8	576	chr18	18	q12.3	42,254,966	42,269,449	9	0	0	-0.558322	6.30E-13
252152942275	GP8	577	chr18	18	q21.1	43,912,416	43,916,566	3	0	0	-1.345732	5.97E-22
252152942275	GP8	578	chr18	18	q21.1	48,085,147	48,089,559	3	0	0	-1.172602	1.77E-17
252152942275	GP8	579	chr18	18	q21.2	48,718,408	48,728,192	6	0	0	-0.702138	5.91E-12
252152942275	GP8	580	chr18	18	q21.2	51,733,798	51,759,561	14	0	0	-0.51279	1.90E-16
252152942275	GP8	581	chr18	18	q21.2	53,249,313	53,257,825	5	0	0	-0.798901	1.02E-12
252152942275	GP8	582	chr18	18	q21.31	54,811,205	54,819,823	4	0	0	-1.120448	4.19E-21
252152942275	GP8	583	chr18	18	q21.32	56,529,328	56,534,019	3	0	0	-1.315437	2.00E-20
252152942275	GP8	585	chr18	18	q21.33	60,187,607	60,192,468	3	0	0	-1.279753	7.94E-19
252152942275	GP8	586	chr18	18	q21.33	60,376,316	60,393,327	9	0	0	-0.485753	6.18E-11
252152942275	GP8	587	chr18	18	q22.2	67,952,819	67,959,972	4	0	0	-1.017928	6.21E-17
252152942275	GP8	588	chr18	18	q22.3	72,117,411	72,127,847	7	0	0	-0.652515	4.54E-13
252152942275	GP8	589	chr18	18	q22.3	72,922,090	72,928,199	3	0	0	-1.187258	1.64E-14
252152942275	GP8	590	chr18	18	q23	74,201,322	74,211,566	6	0	0	-0.801722	5.49E-15
252152942275	GP8	591	chr18	18	q23	76,734,862	76,756,679	11	0	0	-0.73603	5.45E-21
252152942275	GP8	592	chr18	18	q23	77,161,323	77,176,231	8	0	0	-0.629411	6.18E-13
252152942275	GP8	595	chr19	19	p13.12	15,435,498	15,446,236	7	0	0	-0.872471	7.57E-20
252152942275	GP8	596	chr19	19	p13.12	15,527,652	15,573,466	39	0	0	-0.264078	6.92E-12
252152942275	GP8	597	chr19	19	p13.11	19,492,309	19,519,948	18	0	0	-0.605817	1.78E-27
252152942275	GP8	598	chr19	19	q12	30,301,243	30,305,837	3	0	0	-0.889527	4.44E-11
252152942275	GP8	599	chr19	19	q12	30,430,964	30,443,474	6	0	0	-1.259674	8.86E-36
252152942275	GP8	600	chr19	19	q13.11	34,744,862	34,751,825	6	0	0	-0.651328	4.01E-12
252152942275	GP8	601	chr19	19	q13.2	39,808,628	39,836,057	13	0	0	-0.538029	5.50E-18
252152942275	GP8	603	chr19	19	q13.32	47,248,031	47,264,283	8	0	0	-0.729183	1.60E-16
252152942275	GP8	604	chr19	19	q13.33	48,941,148	48,948,460	5	0	0	-0.837211	1.18E-15
252152942275	GP8	605	chr19	19	q13.33	49,228,471	49,235,045	4	0	0	-1.029092	3.47E-16
252152942275	GP8	606	chr19	19	q13.41	51,602,857	51,608,914	4	0	0	-1.826176	1.51E-31
252152942275	GP8	607	chr19	19	q13.42	54,971,115	54,979,536	6	0	0	-0.683937	3.28E-10
252152942275	GP8	608	chr19	19	q13.42	56,083,629	56,131,788	29	0	0	-0.352025	9.79E-17
252152942275	GP8	609	chr19	19	q13.43	56,596,052	56,637,533	19	0	0	-0.411511	5.48E-12
252152942275	GP8	610	chr19	19	q13.43	57,678,918	57,686,917	5	0	0	-1.062696	5.76E-24
252152942275	GP8	611	chr20	20	p13	642,377	649,337	5	0	0	-0.730765	2.00E-10
252152942275	GP8	612	chr20	20	p13	2,668,677	2,680,081	6	0	0	-0.851841	3.31E-13
252152942275	GP8	613	chr20	20	p13	4,976,620	4,986,113	6	0	0	-0.673344	1.73E-12
252152942275	GP8	614	chr20	20	p12.3	6,743,214	6,755,817	7	0	0	-0.596158	1.90E-12
252152942275	GP8	615	chr20	20	p12.1	17,199,016	17,213,707	9	0	0	-0.553735	5.49E-14
252152942275	GP8	616	chr20	20	p12.1	17,651,140	17,671,774	10	0	0	-0.479827	8.45E-12
252152942275	GP8	617	chr20	20	p11.23	19,190,772	19,196,437	3	0	0	-1.15332	1.87E-16
252152942275	GP8	618	chr20	20	p11.23	20,346,283	20,355,980	6	0	0	-0.703877	2.39E-14
252152942275	GP8	619	chr20	20	q11.21	30,943,377	30,950,795	4	0	0	-1.201329	2.18E-19
252152942275	GP8	620	chr20	20	q11.21	32,069,617	32,081,667	7	0	0	-0.793738	2.54E-15
252152942275	GP8	621	chr20	20	q11.22	33,811,525	33,818,916	4	0	0	-0.756642	1.47E-10
252152942275	GP8	622	chr20	20	q12	40,237,934	40,251,584	8	0	0	-0.548667	9.92E-12
252152942275	GP8	623	chr20	20	q13.13	47,437,036	47,453,650	9	0	0	-0.603352	3.32E-15
252152942275	GP8	624	chr20	20	q13.13	48,325,865	48,334,030	4	0	0	-0.908407	9.52E-13
252152942275	GP8	625	chr20	20	q13.13	49,539,776	49,552,600	8	0	0	-0.697468	1.65E-16
252152942275	GP8	626	chr20	20	q13.2	50,382,615	50,389,993	5	0	0	-0.998163	2.83E-17
252152942275	GP8	627	chr20	20	q13.31	56,282,373	56,289,544	4	0	0	-0.760039	9.80E-11
252152942275	GP8	628	chr20	20	q13.33	59,824,185	59,831,399	4	0	0	-1.088121	3.07E-19
252152942275	GP8	629	chr20	20	q13.33	60,634,471	60,644,631	6	0	0	-0.869972	3.37E-20
252152942275	GP8	630	chr20	20	q13.33	60,707,909	60,720,138	8	0	0	-0.625502	3.41E-15
252152942275	GP8	631	chr20	20	q13.33	61,487,662	61,494,313	4	0	0	-1.042206	1.41E-18
252152942275	GP8	632	chr20	20	q13.33	61,842,410	61,846,469	4	0	0	-0.814475	4.50E-13
252152942275	GP8	633	chr20	20	q13.33	62,459,161	62,465,177	3	0	0	-1.085001	1.60E-13
252152942275	GP8	634	chr20	20	q13.33	62,525,378	62,529,749	5	0	0	-1.336388	1.29E-26
252152942275	GP8	635	chr20	20	q13.33	62,597,892	62,625,032	15	0	0	-0.393228	8.07E-11
252152942275	GP8	636	chr21	21	q21.1	17,099,436	17,108,071	7	0	0	-0.790033	4.41E-20
252152942275	GP8	637	chr21	21	q22.11	35,442,302	35,451,261	7	0	0	-0.843455	6.24E-18
252152942275	GP8	638	chr21	21	q22.12	35,978,782	35,990,686	15	0	0	-0.369467	9.50E-10
252152942275	GP8	639	chr21	21	q22.13	38,118,759	38,125,435	5	0	0	-1.012095	5.37E-19
252152942275	GP8	640	chr21	21	q22.13	38,734,125	38,742,471	6	0	0	-0.855581	6.63E-17
252152942275	GP8	641	chr21	21	q22.2	40,980,317	40,987,317	5	0	0	-0.888795	1.55E-14
252152942275	GP8	642	chr21	21	q22.2	42,214,433	42,219,559	5	0	0	-1.285789	2.10E-26
252152942275	GP8	643	chr21	21	q22.3	43,294,540	43,306,511	7	0	0	-0.817601	1.06E-17
252152942275	GP8	644	chr21	21	q22.3	44,841,883	44,849,541	5	0	0	-1.135762	7.11E-24
252152942275	GP8	645	chr21	21	q22.3	45,283,580	45,289,242	4	0	0	-1.049104	4.41E-15
252152942275	GP8	646	chr21	21	q22.3	46,490,681	46,496,996	5	0	0	-1.027366	4.98E-19
252152942275	GP8	648	chr22	22	q11.1	17,843,829	17,857,097	8	0	0	-0.720469	1.45E-18
252152942275	GP8	649	chr22	22	q11.21	19,413,126	19,423,081	7	0	0	-0.688456	3.42E-14
252152942275	GP8	651	chr22	22	q11.22	23,352,999	23,360,910	6	0	0	-0.579662	5.07E-11
252152942275	GP8	652	chr22	22	q12.1	29,280,366	29,286,716	6	0	0	-0.798363	7.51E-13
252152942275	GP8	653	chr22	22	q12.1	29,465,342	29,475,204	6	0	0	-0.609971	1.61E-10
252152942275	GP8	654	chr22	22	q12.2	31,669,588	31,675,187	4	0	0	-1.32522	5.47E-21
252152942275	GP8	655	chr22	22	q12.3	34,307,761	34,321,417	10	0	0	-0.548355	2.37E-13

252152942275	GP8	656	chr22	22	q12.3	36,417,486	36,434,084	11	0	0	-0.4271	1.00E-09
252152942275	GP8	657	chr22	22	q13.1	38,709,494	38,714,333	3	0	0	-0.909659	5.70E-11
252152942275	GP8	658	chr22	22	q13.1	40,387,103	40,392,893	5	0	0	-0.82491	2.60E-15
252152942275	GP8	659	chr22	22	q13.1	40,435,785	40,445,472	6	0	0	-0.693022	2.01E-13
252152942275	GP8	660	chr22	22	q13.1	40,885,148	40,941,249	33	0	0	-0.285771	2.21E-13
252152942275	GP8	661	chr22	22	q13.2	43,804,711	43,812,404	6	0	0	-0.687969	1.58E-13
252152942275	GP8	662	chr22	22	q13.31	45,401,274	45,409,120	7	0	0	-0.570995	8.91E-10
252152942275	GP8	663	chr22	22	q13.31	46,453,356	46,473,812	13	0	0	-0.680609	6.55E-20
252152942275	GP8	665	chr22	22	q13.31	47,772,729	47,777,489	3	0	0	-1.287124	6.21E-17
252152942275	GP8	666	chr22	22	q13.32	48,878,859	48,889,348	6	0	0	-0.984236	1.86E-20
252152942275	GP8	667	chr22	22	q13.33	50,213,887	50,252,911	18	0	0	-0.416658	2.09E-13
252152942275	GP8	668	chr22	22	q13.33	50,493,660	50,533,779	24	0	0	-0.367128	1.54E-12
252152942275	GP8	669	chrX	X	p22.2	9,978,638	9,985,907	5	0	0	-1.036052	1.08E-18
252152942275	GP8	670	chrX	X	p22.2	11,770,867	11,780,145	5	0	0	-0.832353	2.35E-17
252152942275	GP8	671	chrX	X	p22.2	16,881,021	16,897,305	9	0	0	-0.558621	5.86E-14
252152942275	GP8	672	chrX	X	p22.13	17,874,877	17,883,783	4	0	0	-0.894572	5.79E-15
252152942275	GP8	673	chrX	X	p22.13	19,134,822	19,147,556	8	0	0	-0.535106	9.85E-11
252152942275	GP8	674	chrX	X	p22.12	19,903,357	19,910,305	5	0	0	-0.660897	6.79E-11
252152942275	GP8	675	chrX	X	p22.12	20,005,288	20,011,347	4	0	0	-0.720213	2.48E-11
252152942275	GP8	676	chrX	X	p22.12	20,281,024	20,285,815	3	0	0	-0.941699	1.12E-12
252152942275	GP8	677	chrX	X	p22.12	21,389,597	21,394,845	3	0	0	-0.843783	1.06E-10
252152942275	GP8	678	chrX	X	p22.11	21,956,832	21,963,378	5	0	0	-0.778363	3.54E-13
252152942275	GP8	679	chrX	X	p21.3	25,018,306	25,032,502	9	0	0	-0.71032	2.19E-16
252152942275	GP8	680	chrX	X	p21.3	27,822,886	27,835,542	7	0	0	-0.745535	1.98E-17
252152942275	GP8	681	chrX	X	p21.1	34,668,860	34,686,322	10	0	0	-0.435525	1.44E-10
252152942275	GP8	682	chrX	X	p11.4	38,415,657	38,425,540	5	0	0	-0.765402	1.97E-12
252152942275	GP8	683	chrX	X	p11.4	41,776,335	41,785,104	7	0	0	-0.868479	2.37E-21
252152942275	GP8	684	chrX	X	p11.23	48,811,040	48,818,299	6	0	0	-0.666281	1.50E-11
252152942275	GP8	685	chrX	X	p11.22	50,548,484	50,566,468	10	0	0	-0.386797	5.91E-10
252152942275	GP8	686	chrX	X	p11.22	53,347,498	53,354,425	5	0	0	-0.627693	1.30E-10
252152942275	GP8	687	chrX	X	p11.22	53,648,607	53,658,099	7	0	0	-0.754492	1.96E-19
252152942275	GP8	688	chrX	X	q13.2	71,896,246	71,909,052	8	0	0	-0.446506	2.86E-10
252152942275	GP8	689	chrX	X	q13.3	74,959,895	74,972,331	7	0	0	-0.765534	9.63E-19
252152942275	GP8	690	chrX	X	q22.2	103,489,499	103,497,336	5	0	0	-0.854518	3.27E-14
252152942275	GP8	691	chrX	X	q23	109,553,974	109,563,687	7	0	0	-0.666924	7.30E-16
252152942275	GP8	692	chrX	X	q25	125,295,264	125,307,834	8	0	0	-0.591925	1.79E-13
252152942275	GP8	693	chrX	X	q26.1	129,119,047	129,122,322	3	0	0	-1.152318	2.33E-16
252152942275	GP8	694	chrX	X	q26.2	131,622,296	131,627,188	4	0	0	-0.756909	8.53E-11
252152942275	GP8	695	chrX	X	q26.3	135,573,438	135,582,572	5	0	0	-0.621384	5.79E-10
252152942275	GP8	696	chrX	X	q27.1	139,011,211	139,016,429	8	0	0	-0.702017	6.07E-15
252152942275	GP8	697	chrX	X	q27.1	139,167,128	139,178,596	7	0	0	-0.788719	3.17E-18
252152942275	GP8	698	chrX	X	q27.3	146,989,770	146,999,058	7	0	0	-0.845372	4.79E-23
252152942275	GP8	699	chrX	X	q28	147,577,601	147,590,160	9	0	0	-0.581298	1.77E-14
252152942275	GP8	700	chrX	X	q28	149,857,696	149,867,677	6	0	0	-0.735428	2.44E-12
252152942275	GP8	701	chrX	X	q28	150,153,607	150,156,062	3	0	0	-1.296539	1.61E-19
252152942275	GP8	702	chrX	X	q28	153,359,641	153,365,973	4	0	0	-1.190789	1.21E-22
252152942275	GP8	703	chrX	X	q28	153,659,667	153,687,751	14	0	0	-0.476668	2.47E-12
252152942275	GP8	704	chrX	X	q28	154,297,080	154,303,774	5	0	0	-0.684273	1.21E-10
252152942267	GP9	1	chr3	3	p25.1	15,804,666	15,852,708	23	0	0	-0.262131	2.36E-10
252152942267	GP9	2	chr3	3	q25.33	160,124,003	160,139,096	18	0	0	-0.340667	2.57E-11
252152942267	GP9	3	chr6	6	q25.3	158,243,414	158,320,443	38	0	0	-0.262004	4.63E-15
252152942267	GP9	5	chr20	20	q11.21	31,724,750	31,733,371	5	0	0.717848	0	1.22E-10
252152942267	GP9	6	chr20	20	q11.22	34,292,715	34,326,672	19	0	0	-0.284399	2.16E-10
252152942267	GP9	7	chr21	21	q11.2	15,890,020	15,941,127	31	0	0	-0.255091	5.33E-11
252152942269	GP10	2	chr19	19	p13.2	8,979,402	9,018,643	22	0	0	-0.310169	2.64E-11

Dataset S5. 2 List of CNAs in TT- reactive lymphocytes of seven tested CD patients (ADM-2 (LRRl0.25l, P- value ≤1x10-10) and CBS (LRRl0.25l, P-value ≤5 x 10-08)).

ID	ID	NO.	chrom	chrom	chr region	loc.start	loc.end	num.mark	Amplification	Deletions	mean LRR	pval
252152942263	1	TT 1	chr12	12	p13.31	7,778,761	7,783,075	3	0	0	-1.439242	3.02E-21
252152942268	1	TT 6	chr1	1	p22.2	89,686,311	89,744,074	18	0	0.39112	0	2.41E-12
252152942270	2	TT 7	chr19	19	p13.2	8,994,725	9,021,017	16	0	0.485592	0	1.65E-14
252152941975	1	TT3	chr1	1	p36.23	9,173,343	9,186,672	8	0	0	-0.672097	4.84E-19
252152941975	2	TT3	chr1	1	p36.11	27,810,977	27,817,017	4	0	0	-0.726433	2.78E-12
252152941975	3	TT3	chr1	1	p32.3	53,255,095	53,271,751	9	0	0	-0.45696	1.62E-10
252152941975	4	TT3	chr1	1	p31.1	70,378,450	70,386,514	5	0	0	-0.763881	5.85E-15
252152941975	5	TT3	chr1	1	p31.1	76,344,741	76,378,859	17	0	0	-0.358943	1.76E-12
252152941975	6	TT3	chr1	1	p22.3	87,258,359	87,266,450	5	0	0	-0.681496	1.47E-11
252152941975	7	TT3	chr1	1	q23.3	162,693,747	162,710,832	9	0	0	-0.431191	5.99E-10
252152941975	8	TT3	chr1	1	q24.2	169,046,869	169,063,999	8	0	0	-0.518578	3.13E-12
252152941975	9	TT3	chr1	1	q25.1	174,994,448	174,998,424	3	0	0	-0.92076	2.01E-12
252152941975	10	TT3	chr1	1	q32.1	198,806,652	198,816,318	8	0	0	-0.515523	1.19E-11
252152941975	11	TT3	chr1	1	q32.1	206,694,361	206,699,924	4	0	0	-0.672834	4.80E-11
252152941975	12	TT3	chr1	1	q41	215,373,446	215,387,375	9	0	0	-0.462009	7.41E-10
252152941975	13	TT3	chr1	1	q42.2	231,254,738	231,261,830	4	0	0	-0.695793	4.56E-11
252152941975	14	TT3	chr1	1	q43	238,649,511	238,667,665	10	0	0	-0.448092	3.97E-11
252152941975	15	TT3	chr2	2	p25.1	11,224,926	11,238,255	6	0	0	-0.565265	1.05E-10
252152941975	16	TT3	chr2	2	p22.3	36,172,867	36,190,268	9	0	0	-0.438641	2.22E-10
252152941975	17	TT3	chr2	2	q11.2	100,649,876	100,659,077	7	0	0	-0.502543	2.57E-10
252152941975	18	TT3	chr2	2	q12.1	102,963,487	102,975,880	7	0	0	-0.559594	1.92E-11
252152941975	19	TT3	chr2	2	q14.1	115,916,975	115,942,052	13	0	0	-0.392875	7.19E-12
252152941975	20	TT3	chr2	2	q24.1	155,151,737	155,158,867	5	0	0	-0.622515	3.89E-10
252152941975	21	TT3	chr2	2	q24.2	160,728,916	160,735,871	4	0	0	-0.77643	3.51E-12
252152941975	22	TT3	chr2	2	q31.1	175,112,470	175,120,682	5	0	0	-0.745162	4.45E-14
252152941975	23	TT3	chr2	2	q31.1	175,196,741	175,222,415	13	0	0	-0.41008	7.02E-11
252152941975	24	TT3	chr2	2	q33.3	208,977,828	208,993,534	9	0	0	-0.507688	3.26E-12
252152941975	25	TT3	chr2	2	q37.2	237,260,219	237,269,534	6	0	0	-0.615543	1.04E-10
252152941975	26	TT3	chr3	3	p26.3	2,744,616	2,753,481	6	0	0	-0.607161	2.74E-12
252152941975	27	TT3	chr3	3	p24.3	16,440,646	16,450,472	7	0	0	-0.665099	9.96E-16
252152941975	28	TT3	chr3	3	p24.3	21,181,429	21,190,317	4	0	0	-0.678035	2.96E-10
252152941975	29	TT3	chr3	3	p22.1	40,242,089	40,251,165	6	0	0	-0.647395	6.55E-13
252152941975	30	TT3	chr3	3	p14.3	56,995,001	57,008,878	7	0	0	-0.50384	3.94E-10
252152941975	31	TT3	chr3	3	p12.3	77,368,097	77,373,385	3	0	0	-0.845912	5.35E-10
252152941975	32	TT3	chr3	3	p12.3	79,601,949	79,632,258	16	0	0	-0.384483	6.59E-10
252152941975	33	TT3	chr3	3	p11.2	87,308,969	87,321,023	8	0	0	-0.545301	1.35E-10
252152941975	34	TT3	chr3	3	q12.3	102,089,582	102,096,757	5	0	0	-0.728544	2.71E-13
252152941975	35	TT3	chr3	3	q13.13	107,920,307	107,941,739	12	0	0	-0.417417	5.22E-12
252152941975	36	TT3	chr3	3	q13.2	111,545,423	111,554,970	6	0	0	-0.612827	2.84E-12
252152941975	37	TT3	chr3	3	q23	142,143,733	142,155,974	8	0	0	-0.545056	3.39E-13
252152941975	38	TT3	chr3	3	q25.1	151,999,373	152,007,767	5	0	0	-0.677629	1.54E-12
252152941975	39	TT3	chr3	3	q25.2	154,777,828	154,783,820	4	0	0	-0.956682	1.37E-17
252152941975	40	TT3	chr3	3	q25.33	160,027,758	160,033,647	4	0	0	-0.925429	1.70E-16
252152941975	41	TT3	chr3	3	q26.2	169,483,860	169,491,968	5	0	0	-0.863286	3.98E-17
252152941975	42	TT3	chr3	3	q26.31	175,385,457	175,395,905	6	0	0	-0.58605	1.37E-11
252152941975	43	TT3	chr3	3	q28	190,564,452	190,581,538	9	0	0	-0.423816	9.27E-10
252152941975	44	TT3	chr4	4	q12	56,263,540	56,273,975	7	0	0	-0.582316	8.51E-12
252152941975	45	TT3	chr4	4	q13.3	73,390,941	73,400,529	5	0	0	-0.737517	1.23E-13
252152941975	46	TT3	chr4	4	q21.23	86,405,224	86,411,961	4	0	0	-0.983606	1.44E-17
252152941975	47	TT3	chr4	4	q21.23	86,788,469	86,800,363	6	0	0	-0.699999	2.28E-14
252152941975	48	TT3	chr4	4	q22.1	88,144,971	88,153,165	5	0	0	-0.710982	1.20E-12
252152941975	49	TT3	chr4	4	q22.1	89,297,672	89,305,070	4	0	0	-0.749029	7.28E-10
252152941975	50	TT3	chr4	4	q22.3	96,116,103	96,120,705	4	0	0	-0.884434	3.63E-15
252152941975	51	TT3	chr4	4	q24	104,569,195	104,581,216	7	0	0	-0.487577	6.88E-10
252152941975	52	TT3	chr4	4	q26	119,216,681	119,225,896	6	0	0	-0.654546	3.54E-13
252152941975	53	TT3	chr4	4	q31.23	148,701,026	148,709,872	6	0	0	-0.633597	6.14E-12
252152941975	54	TT3	chr4	4	q32.3	168,117,144	168,156,940	21	0	0	-0.429387	9.62E-19
252152941975	55	TT3	chr4	4	q32.3	169,070,647	169,083,480	7	0	0	-0.541708	6.83E-11
252152941975	56	TT3	chr5	5	p15.2	10,344,519	10,357,011	6	0	0	-0.692337	6.02E-15
252152941975	57	TT3	chr5	5	p14.1	28,614,217	28,629,694	7	0	0	-0.650593	1.33E-12
252152941975	58	TT3	chr5	5	p12	43,030,838	43,046,183	7	0	0	-0.800913	7.19E-20
252152941975	59	TT3	chr5	5	q11.2	53,805,675	53,812,412	4	0	0	-0.687661	8.48E-11
252152941975	60	TT3	chr5	5	q11.2	58,463,152	58,475,906	8	0	0	-0.490228	3.33E-11
252152941975	61	TT3	chr5	5	q12.1	60,331,496	60,352,430	11	0	0	-0.452603	6.27E-13
252152941975	62	TT3	chr5	5	q12.3	66,371,564	66,379,986	4	0	0	-0.753412	2.87E-12
252152941975	63	TT3	chr5	5	q14.1	79,887,953	79,905,362	7	0	0	-0.546073	5.11E-11
252152941975	64	TT3	chr5	5	q14.3	83,423,661	83,430,430	5	0	0	-0.741705	1.55E-13
252152941975	65	TT3	chr5	5	q14.3	86,549,591	86,557,064	6	0	0	-0.765273	7.73E-17
252152941975	67	TT3	chr5	5	q21.1	100,055,779	100,070,662	6	0	0	-0.59394	3.64E-11
252152941975	68	TT3	chr5	5	q23.1	118,391,248	118,407,721	8	0	0	-0.476631	1.97E-10
252152941975	69	TT3	chr5	5	q31.1	131,508,676	131,516,574	6	0	0	-0.629428	4.25E-13
252152941975	70	TT3	chr5	5	q35.3	180,639,923	180,656,093	9	0	0	-0.54006	2.53E-13
252152941975	71	TT3	chr6	6	p22.3	24,353,789	24,366,951	9	0	0	-0.577407	5.49E-16
252152941975	72	TT3	chr6	6	p22.1	28,677,922	28,685,737	5	0	0	-0.679241	3.38E-10
252152941975	73	TT3	chr6	6	p12.1	55,950,998	55,968,474	10	0	0	-0.447551	2.00E-11
252152941975	74	TT3	chr6	6	p12.1	56,187,439	56,194,649	5	0	0	-0.777953	1.04E-15

252152941975	75	TT3	chr6	6	q13	72,077,120	72,095,274	18	0	0	-0.376039	6.79E-13
252152941975	76	TT3	chr6	6	q14.2	83,947,409	83,956,924	6	0	0	-0.587182	9.28E-11
252152941975	77	TT3	chr6	6	q16.3	101,052,687	101,064,590	7	0	0	-0.69943	6.54E-17
252152941975	78	TT3	chr6	6	q16.3	105,463,844	105,475,574	8	0	0	-0.514955	3.71E-10
252152941975	79	TT3	chr6	6	q22.33	130,035,786	130,042,427	4	0	0	-0.751623	2.10E-11
252152941975	80	TT3	chr6	6	q23.3	135,227,793	135,232,002	3	0	0	-0.864053	2.52E-11
252152941975	81	TT3	chr6	6	q23.3	136,250,460	136,263,036	8	0	0	-0.569657	7.04E-13
252152941975	82	TT3	chr6	6	q23.3	137,517,986	137,523,180	4	0	0	-0.757679	1.24E-11
252152941975	83	TT3	chr6	6	q25.3	158,243,414	158,250,063	5	0	0	-0.788712	9.59E-14
252152941975	84	TT3	chr6	6	q25.3	158,571,462	158,593,726	11	0	0	-0.52708	1.27E-15
252152941975	85	TT3	chr6	6	q26	162,290,562	162,302,746	7	0	0	-0.505369	6.35E-10
252152941975	86	TT3	chr6	6	q27	166,439,027	166,449,564	4	0	0	-0.722723	5.53E-11
252152941975	87	TT3	chr7	7	p21.3	11,194,274	11,224,316	14	0	0	-0.445489	7.66E-13
252152941975	88	TT3	chr7	7	p21.2	14,598,897	14,619,688	11	0	0	-0.53345	2.23E-14
252152941975	89	TT3	chr7	7	q21.11	82,719,740	82,731,074	6	0	0	-0.699451	9.08E-13
252152941975	90	TT3	chr7	7	q21.12	87,338,966	87,352,705	5	0	0	-0.724762	2.96E-13
252152941975	91	TT3	chr7	7	q22.3	107,232,160	107,245,981	8	0	0	-0.488906	5.26E-11
252152941975	92	TT3	chr7	7	q31.31	120,435,301	120,444,533	6	0	0	-0.649479	9.78E-13
252152941975	93	TT3	chr7	7	q32.2	129,689,287	129,713,502	12	0	0	-0.383267	2.83E-10
252152941975	94	TT3	chr7	7	q33	133,785,725	133,788,973	3	0	0	-0.801558	1.56E-10
252152941975	95	TT3	chr7	7	q33	135,252,476	135,258,974	5	0	0	-0.603069	2.01E-10
252152941975	96	TT3	chr7	7	q34	141,830,701	141,838,515	5	0	0	-0.671135	1.60E-10
252152941975	97	TT3	chr7	7	q35	147,463,626	147,476,400	9	0	0	-0.463572	6.07E-10
252152941975	98	TT3	chr7	7	q36.1	152,365,525	152,375,249	8	0	0	-0.541795	2.36E-12
252152941975	99	TT3	chr8	8	p23.3	1,914,827	1,923,434	5	0	0	-0.928539	4.83E-17
252152941975	100	TT3	chr8	8	p23.2	3,240,825	3,243,327	3	0	0	-1.13465	4.97E-12
252152941975	101	TT3	chr8	8	p23.2	3,694,676	3,708,992	7	0	0	-0.577986	1.41E-11
252152941975	102	TT3	chr8	8	p22	16,040,684	16,051,417	7	0	0	-0.640359	4.17E-14
252152941975	103	TT3	chr8	8	p22	17,731,832	17,749,229	11	0	0	-0.503731	8.57E-14
252152941975	104	TT3	chr8	8	p21.2	25,856,558	25,866,340	7	0	0	-0.544002	1.14E-11
252152941975	105	TT3	chr8	8	p12	35,092,371	35,110,711	11	0	0	-0.477151	5.04E-14
252152941975	106	TT3	chr8	8	q12.1	59,464,990	59,470,565	4	0	0	-0.703971	1.58E-10
252152941975	107	TT3	chr8	8	q12.3	64,032,144	64,038,200	3	0	0	-0.809074	2.42E-10
252152941975	108	TT3	chr8	8	q21.3	87,170,764	87,178,252	4	0	0	-0.69883	2.82E-10
252152941975	109	TT3	chr8	8	q21.3	88,143,898	88,156,210	7	0	0	-0.538613	1.27E-10
252152941975	110	TT3	chr8	8	q21.3	91,003,829	91,013,136	5	0	0	-0.670874	3.45E-11
252152941975	111	TT3	chr8	8	q22.2	101,055,626	101,067,039	9	0	0	-0.530018	3.94E-13
252152941975	113	TT3	chr8	8	q24.11	118,105,309	118,111,999	5	0	0	-0.770153	3.78E-13
252152941975	114	TT3	chr8	8	q24.13	125,486,684	125,502,398	11	0	0	-0.452657	9.35E-13
252152941975	115	TT3	chr9	9	p24.2	3,497,920	3,508,312	5	0	0	-0.723658	6.67E-14
252152941975	116	TT3	chr9	9	p21.1	28,852,844	28,869,102	18	0	0	-0.529589	2.97E-25
252152941975	117	TT3	chr9	9	p13.2	37,802,509	37,811,474	4	0	0	-0.765455	6.79E-12
252152941975	118	TT3	chr9	9	q22.32	99,175,933	99,196,933	10	0	0	-0.423876	2.40E-10
252152941975	119	TT3	chr9	9	q31.1	105,770,114	105,785,144	8	0	0	-0.598321	2.62E-15
252152941975	120	TT3	chr9	9	q31.3	113,440,083	113,453,846	6	0	0	-0.727446	2.01E-16
252152941975	121	TT3	chr10	10	p13	12,727,344	12,749,426	10	0	0	-0.429132	7.91E-11
252152941975	122	TT3	chr10	10	p13	13,906,412	13,913,578	5	0	0	-0.668419	1.32E-12
252152941975	123	TT3	chr10	10	p12.31	22,191,023	22,205,707	9	0	0	-0.502068	7.54E-13
252152941975	124	TT3	chr10	10	p11.21	35,468,477	35,485,762	11	0	0	-0.493295	1.94E-14
252152941975	125	TT3	chr10	10	q11.23	52,731,345	52,741,805	7	0	0	-0.492035	7.54E-10
252152941975	126	TT3	chr10	10	q21.1	53,999,354	54,008,603	7	0	0	-0.566371	1.25E-10
252152941975	127	TT3	chr10	10	q21.2	63,417,882	63,438,894	11	0	0	-0.436637	5.45E-12
252152941975	129	TT3	chr10	10	q23.33	94,277,064	94,291,895	9	0	0	-0.456525	3.98E-11
252152941975	130	TT3	chr10	10	q26.13	126,159,561	126,163,142	3	0	0	-0.899838	7.87E-12
252152941975	131	TT3	chr11	11	p15.1	18,068,371	18,085,548	8	0	0	-0.461044	5.73E-11
252152941975	132	TT3	chr11	11	p13	32,852,043	32,868,239	10	0	0	-0.42835	1.25E-10
252152941975	133	TT3	chr11	11	p12	43,331,871	43,339,039	5	0	0	-0.6659	6.07E-12
252152941975	134	TT3	chr11	11	q13.4	72,957,267	72,963,660	3	0	0	-0.820191	1.62E-11
252152941975	135	TT3	chr11	11	q14.3	89,168,896	89,175,805	5	0	0	-0.608325	5.46E-10
252152941975	136	TT3	chr11	11	q22.3	106,570,259	106,581,519	7	0	0	-0.526839	3.99E-11
252152941975	137	TT3	chr12	12	p13.31	9,344,825	9,358,371	8	0	0	-0.476642	1.79E-10
252152941975	138	TT3	chr12	12	p12.2	20,534,533	20,543,713	6	0	0	-0.526221	6.00E-10
252152941975	139	TT3	chr12	12	p11.22	29,857,357	29,865,337	5	0	0	-0.684708	9.31E-13
252152941975	140	TT3	chr12	12	q12	44,537,314	44,550,816	8	0	0	-0.533381	8.37E-13
252152941975	141	TT3	chr12	12	q15	69,225,927	69,233,396	6	0	0	-0.635032	2.59E-13
252152941975	142	TT3	chr12	12	q21.31	81,971,139	81,984,207	9	0	0	-0.521076	2.04E-11
252152941975	143	TT3	chr12	12	q21.31	85,577,483	85,685,565	44	0	0	-0.284404	1.18E-13
252152941975	144	TT3	chr12	12	q21.31	86,271,609	86,276,158	3	0	0	-0.840916	4.16E-10
252152941975	145	TT3	chr12	12	q23.1	97,869,836	97,881,493	12	0	0	-0.372026	8.01E-10
252152941975	146	TT3	chr12	12	q24.31	124,337,534	124,342,821	4	0	0	-0.715324	7.52E-12
252152941975	147	TT3	chr12	12	q24.32	128,546,018	128,593,838	9	0	0	-0.482357	7.36E-12
252152941975	148	TT3	chr13	13	q13.3	39,557,929	39,564,841	4	0	0	-0.673577	3.25E-10
252152941975	149	TT3	chr13	13	q14.13	45,991,680	46,002,307	10	0	0	-0.421692	2.80E-10
252152941975	150	TT3	chr13	13	q14.2	50,630,606	50,645,155	15	0	0	-0.453095	1.28E-16
252152941975	151	TT3	chr13	13	q31.1	79,942,581	79,953,261	7	0	0	-0.643188	7.36E-13
252152941975	152	TT3	chr13	13	q31.3	93,252,593	93,273,148	12	0	0	-0.3754	7.08E-10
252152941975	153	TT3	chr13	13	q33.2	106,162,566	106,176,474	6	0	0	-0.572464	3.51E-10
252152941975	154	TT3	chr13	13	q33.3	109,671,677	109,685,434	9	0	0	-0.538295	2.98E-12
252152941975	155	TT3	chr14	14	q11.2	20,706,801	20,709,630	4	0	0	-0.777427	2.02E-12
252152941975	159	TT3	chr14	14	q13.3	37,253,149	37,261,568	6	0	0	-0.664896	2.76E-14
252152941975	160	TT3	chr14	14	q22.1	52,988,345	53,008,114	14	0	0	-0.404036	6.10E-13
252152941975	161	TT3	chr14	14	q23.1	60,212,731	60,221,973	5	0	0	-0.651343	6.34E-12

252152941975	162	TT3	chr14	14	q31.3	89,257,590	89,264,915	4	0	0	-0.763385	6.51E-10
252152941975	163	TT3	chr14	14	q32.12	93,004,731	93,019,673	8	0	0	-0.574302	1.13E-14
252152941975	164	TT3	chr15	15	q21.2	49,659,331	49,672,752	8	0	0	-0.740237	5.64E-21
252152941975	165	TT3	chr15	15	q21.3	55,722,135	55,727,209	3	0	0	-0.780282	6.57E-10
252152941975	166	TT3	chr15	15	q22.31	66,083,524	66,098,730	9	0	0	-0.557119	2.16E-15
252152941975	167	TT3	chr15	15	q24.1	75,001,741	75,007,318	4	0	0	-0.652925	2.96E-10
252152941975	168	TT3	chr15	15	q25.3	87,514,635	87,524,971	9	0	0	-0.470759	3.53E-11
252152941975	170	TT3	chr16	16	p13.3	6,684,146	6,687,776	3	0	0	-0.895325	1.42E-12
252152941975	171	TT3	chr16	16	p11.1	34,777,185	34,784,380	4	0	0	-0.727853	9.56E-10
252152941975	172	TT3	chr16	16	q12.1	48,504,256	48,520,527	6	0	0	-0.534035	4.20E-10
252152941975	173	TT3	chr17	17	p13.1	6,905,390	6,908,787	5	0	0	-0.80536	2.74E-15
252152941975	174	TT3	chr17	17	q12	37,096,222	37,101,642	5	0	0	-0.716733	9.62E-14
252152941975	175	TT3	chr17	17	q21.31	43,976,988	43,984,385	4	0	0	-0.691339	1.00E-09
252152941975	177	TT3	chr18	18	q21.2	50,948,903	50,958,958	6	0	0	-0.82914	1.62E-19
252152941975	178	TT3	chr18	18	q22.1	66,512,703	66,535,954	10	0	0	-0.460384	7.50E-10
252152941975	179	TT3	chr18	18	q22.3	72,027,746	72,034,954	4	0	0	-0.769556	1.64E-10
252152941975	180	TT3	chr18	18	q23	74,216,306	74,222,479	5	0	0	-0.653173	4.18E-10
252152941975	181	TT3	chr19	19	q13.11	33,601,497	33,616,017	10	0	0	-0.447535	1.52E-11
252152941975	183	TT3	chr19	19	q13.43	57,619,113	57,625,986	5	0	0	-0.698941	4.90E-14
252152941975	185	TT3	chr20	20	p12.1	14,928,568	14,940,824	8	0	0	-0.617762	2.30E-16
252152941975	186	TT3	chr20	20	q13.12	42,759,326	42,765,572	4	0	0	-0.757137	7.85E-12
252152941975	187	TT3	chr21	21	q21.1	17,729,053	17,735,860	4	0	0	-0.870123	8.39E-15
252152941975	188	TT3	chr21	21	q21.1	19,614,098	19,630,490	14	0	0	-0.5101	2.74E-13
252152941975	189	TT3	chr21	21	q21.1	22,900,882	22,911,661	8	0	0	-0.63234	6.69E-12
252152941975	192	TT3	chr21	21	q22.3	44,305,291	44,317,227	9	0	0	-0.471042	8.99E-11
252152941975	193	TT3	chrX	X	p22.33	437,220	447,397	9	0	0	-0.47595	2.84E-10
252152941975	194	TT3	chrX	X	p22.33	776,045	812,564	26	0	0	-0.317973	7.04E-15
252152941975	195	TT3	chrX	X	p22.33	2,027,029	2,032,353	5	0	0	-0.558675	9.00E-11
252152941975	196	TT3	chrX	X	p22.33	2,939,649	2,955,730	11	0	0	-0.435771	4.24E-12
252152941975	197	TT3	chrX	X	p22.33	3,258,345	3,262,390	4	0	0	-0.862574	9.18E-15
252152941975	198	TT3	chrX	X	p22.31	8,448,259	8,457,876	5	0	0	-0.658583	5.67E-11
252152941975	199	TT3	chrX	X	p22.12	19,566,859	19,607,037	25	0	0	-0.255318	8.60E-10
252152941975	200	TT3	chrX	X	p21.3	27,411,769	27,431,671	10	0	0	-0.543265	2.42E-15
252152941975	201	TT3	chrX	X	q12	65,253,243	65,261,948	11	0	0	-0.388771	1.45E-10
252152941975	202	TT3	chrX	X	q13.1	70,282,010	70,296,278	9	0	0	-0.485718	7.89E-12
252152941975	203	TT3	chrX	X	q21.1	77,522,287	77,529,070	5	0	0	-0.631545	1.07E-10
252152941975	204	TT3	chrX	X	q21.1	83,125,105	83,137,716	9	0	0	-0.463637	9.44E-12
252152941975	205	TT3	chrX	X	q22.1	101,804,551	101,816,888	9	0	0	-0.517441	3.71E-14
252152941975	206	TT3	chrX	X	q22.3	106,440,967	106,454,146	9	0	0	-0.579134	7.00E-17
252152941975	207	TT3	chrX	X	q24	117,772,075	117,790,576	12	0	0	-0.413241	2.62E-12
252152941975	208	TT3	chrX	X	q26.2	131,519,987	131,543,128	14	0	0	-0.325082	7.32E-10
252152941975	209	TT3	chrX	X	q26.2	133,289,175	133,293,166	5	0	0	-0.685824	2.69E-12
252152941975	210	TT3	chrX	X	q28	149,749,342	149,754,238	5	0	0	-0.60648	3.69E-10
252152941975	211	TT3	chrY	Y	p11.32	387,220	397,397	9	0	0	-0.47595	2.84E-10
252152941975	212	TT3	chrY	Y	p11.32	726,045	762,564	26	0	0	-0.317973	7.04E-15
252152941975	213	TT3	chrY	Y	p11.32	1,978,785	1,982,353	4	0	0	-0.626792	1.94E-10

Dataset S5. 3 List of common affected genes by CNAs in Human CD patients and memory cells from PLNs of newly diabetic NOD mice (Chapter 3) and rh-PI reactive lymphocytes from newly diagnosed T1D patients (Chapter 4).

Common to Celiac and T1D NOD	Common to Human T1D and CD	Common to Human T1D and CD	Common to Human T1D and CD	Common to Human T1D and CD	Common to Human T1D and CD	Common to Human T1D and CD	Common to Human T1D and CD	Common to Human T1D and CD	Common to All
ANKRD11	ABHD17C	CECR2	FOXD1	JARID2-AS1	MIR17HG	POLH	SLC30A8	USP25	ATMIN
APLP2	ABL1	CHD7	FOXI3	JAZF1	MIR18A	POPDC3	SLC5A3	USP7	ATN1
ATMIN	ACSL1	CHRDL2	FOXK2	JAZF1-AS1	MIR193A	PPP1R9A	SLIT3	VEGFC	BRI3BP
ATN1	ACVR1	CHSY1	FOXN3	JMJD6	MIR19A	PPP4R1	SMAD9	VSTM4	C19orf67
BRF1	ACVR1B	CLIP1	FOXN3-AS1	KAT6A	MIR19B1	PPP4R1-AS1	SMARCA2	WDR26	CASZ1
BRI3BP	ACVR2A	CLMN	FOXQ1	KBTBD2	MIR20A	PRDM15	SMARCD3	WIZ	CNNM3
C19orf67	ADARB1	CNIH3	FRMD4A	KCND2	MIR29B2CHG	PRDX6	SMCO4	WNT4	DOCK5
CAMTA1	ADGRA3	CNNM3	FZD8	KCNIP4	MIR3195	PREX1	SMIM13	WRAP73	EVX2
CASZ1	ADNP	CNNM3-DT	GAB2	KCNK2	MIR3650	PRICKLE1	SNORA37	WRN	FIZ1
CBFA2T2	ADNP-AS1	COL21A1	GAL3ST3	KCNK3	MIR4466	PRKACA	SNRK	WWC1	FOXI3
CDKN1C	AFF3	CREB1	GALNT12	KCNMA1	MIR4469	PRKACG	SNX10	XKR4	GAL3ST3
CNNM3	AGGF1	CRMP1	GAREM2	KCTD6	MIR4683	PROSER2	SNX30	XYLT1	GATAD2A
DHX37	AGO2	CSNK2A2	GATAD2A	KHDRBS3	MIR4713HG	PROSER2-AS1	SNX9	YAF2	GMFG
DOCK5	AHCTF1	CSPG5	GLI2	KIAA1958	MIR5091	PRR34-AS1	SOCS6	ZBED4	HOXA13
EIF5	AIG1	CT62	GLI3	KIF13A	MIR5095	PTCH1	SPAG9	ZBTB14	HOXA3
EVX2	ALDH1A3	CTNND2	GLRB	KIF7	MIR92A1	PTPN3	SPIRE2	ZBTB18	HOXA4
FIZ1	ANKH	CTU1	GLUD1	KL	MMP24	PTPRN2	SSBP2	ZBTB39	HOXD11
FOXI3	ANKRD28	CUX1	GMFG	KPNA4	MMP24-AS1-EDEM2	PTPRU	SSBP3	ZCCHC2	HOXD12
FOXN4	ANKRD44	CYP26B1	GNAO1	L3MBTL3	MNX1	PURB	SSH1	ZDHHC18	HOXD13
FRAT2	ANKS1B	CYTH1	GPR12	LCOR	MNX1-AS1	PURG	ST7	ZFPM2	IQCE
GAL3ST3	ANKS6	DCHS1	GPR27	LIFR	MNX1-AS2	RAB12	ST7-AS1	ZIC2	POGZ
GATAD2A	APBA1	DGKH	GRB10	LIFR-AS1	MOV10L1	RABEP1	ST7-OT4	ZIC5	PRKACA
GMFG	APBB1IP	DGLUCY	GUCY1A2	LINC00938	MPP6	RAN	STK24	ZNF219	PTCH1
GRIN2D	ARID1B	DGUOK-AS1	GXYLT2	LINC01607	MPPED1	RAP1GDS1	STK24-AS1	ZNF385A	PURB
HOXA13	ARID2	DKFZP434H168	Gene Names	LINC01639	MRPS6	RAP2A	STK3	ZNF516	RABEP1
HOXA3	ASAP2	DLEU2	HDAC4	LINC02102	MSANTD3	RASAL3	STK39	ZNF524	RAP2A
HOXA4	ATMIN	DNAJC21	HECA	LOC100506023	MUC16	RASIP1	SYN2	ZNF532	RASIP1
HOXD11	ATN1	DOCK5	HECTD2	LOC101927040	MVB12B	RBFOX2	TAC3	ZNF579	RNF157
HOXD12	ATP9A	DPM1	HECTD2-AS1	LOC101927751	MXRA7	RBPJ	TAF3	ZNF618	SAMD1
HOXD13	ATXN7	DPY19L1	HEG1	LOC101928111	NADK	RBPMS2	TAF4	ZNF697	SAMD4B
HP1BP3	B3GALT5	DSCAM	HEY1	LOC102723322	NCOA2	RCAN1	TAF5L	ZNF704	SF1
IFT140	B3GALT5-AS1	DTNB	HIVEP1	LOC102723665	NEURL1B	RCC2	TALAM1	ZNF710	SMARCD3
IQCE	B4GALT5	DUSP14	HIVEP3	LOC102724050	NFIA	REEP3	TBL1XR1	ZNF746	ZBED4
JAK2	BASP1	DVL3	HLCS	LOC105375218	NFKB1	RFX7	TCERG1L	ZNF775	ZNF524
LSM14B	BEND3	DYRK1A	HMG20A	LOC105377621	NKAIN2	RGS17	TCF24	ZNF777	ZNF579
MAP3K3	BHLHE41	E2F5	HMGB1	LOC148696	NPAS3	RIMKLB	TCF4	ZNF787	ZNF775
MKL1	BLOC1S5-TXNDC5	EFNB2	HOOK3	LOC283856	NPR2	RNF144A	TENM2	ZNF853	
MPRIP	BOD1L1	EIF4E3	HOTTIP	LOC339529	NR2F1	RNF144A-AS1	TENM3	ZNF865	
MRPL40	BOD1L2	ELF2	HOXA-AS2	LOC407835	NR2F1-AS1	RNF157	TET3	ZNRF3	
OTUD5	BRD1	ELK3	HOXA13	LOC642648	NR2F2	RNF165	TFDP1	ZSWIM5	
PACS1	BRD4	EPB41L4B	HOXA3	LOC653160	NR2F2-AS1	RNF169	TGFBR1		
POGZ	BRI3BP	ERICH1	HOXA4	LOC728743	NR4A3	RNF170	TGFBRAP1		
PRKACA	BVES	EVX2	HOXB-AS1	LOC90768	NRG3	ROCK2	THOC7		
PSMA7	BVES-AS1	EXT1	HOXB3	LONRF1	PAPD5	RPS6KA5	THOC7-AS1		
PTCH1	C11orf95	FAF1	HOXD11	LONRF2	PAPD7	RYBP	TJP1		
PURB	C17orf58	FAM102B	HOXD12	LRRK1	PAPPA	RYK	TMEM158		
RAB11FIP5	C18orf65	FAM107B	HOXD13	LUZP1	PAXIP1	SALL3	TMEM253		
RABEP1	C19orf67	FAM120A	HS3ST4	MAF	PAXIP1-AS1	SAMD1	TMOD1		
RAP2A	C2CD4A	FAM120AOS	HS6ST3	MAGI2	PBX3	SAMD4B	TNFAIP8L3		
RASIP1	C2orf72	FAM124A	HTR7	MALAT1	PCGF5	SCN8A	TNRC6B		
RNF157	C5orf38	FAM149A	ID4	MAN1C1	PCSK6	SCRT2	TOP1MT		
SAMD1	C9orf147	FAM171A1	IGDCC4	MAP4K4	PEAK1	SDK1	TRAF3		
SAMD4B	C9orf3	FAM189A1	IGF1R	MAPK4	PGBD5	SERTAD2	TRIO		
SF1	CACNA1C	FAM189A2	IGF2R	MARCKS	PHF10	SET	TSHZ1		
SF3B2	CACNA1C-IT2	FAM19A5	IKZF2	MASCRNA	PHF21B	SF1	TTC7B		
SMARCC2	CADPS	FAM35A	IL17D	MBD2	PHF24	SFMBT1	TWIST1		
SMARCD3	CASZ1	FAM69C	INAFM2	MED13	PHIP	SHANK3	TXNDC5		
SS18L1	CCM2	FAM81A	INSM1	MED13L	PHOX2B	SHC3	UBE2E3		
ULK1	CCNE1	FAM83F	IQCE	MEST	PIP4K2A	SHISA6	UBE2Q1		
XPO1	CCNY	FANCC	IRAIN	MESTIT1	PIP5K1B	SIAH1	UNCX		
YBX1	CDH24	FBLL1	IRF2BP2	MEX3C	PKDCC	SIK1	URB2		
ZBED4	CDH4	FGF2	IRX2	MGAT4A	PLEKHA5	SIK1B	URI1		
ZNF524	CDKN2C	FGFR2	JADE1	MIR1469	PLIN1	SIM2	USP12		
ZNF579	CDYL	FIGNL2	JAK1	MIR1470	PODXL2	SKIDA1	USP12-AS2		
ZNF775	CDYL2	FIZ1	JARID2	MIR17	POGZ	SLC24A3	USP13		

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