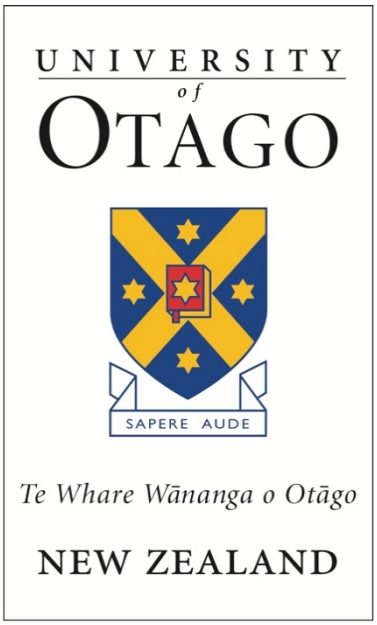
SLC2A9 and Hyperuricemia

A Locus-Wide Association Study To Identify Population-Specific Genetic Variants In New Zealand Māori and Pacific People

Padmini Parthasarathy
Supervisor: Professor Tony R. Merriman



A thesis submitted for the degree of
Master of Science (MSc) in Biochemistry

University of Otago, Dunedin, New Zealand

July 2018

BLANK

ACKNOWLEDGEMENTS

"Matha Pitha Guru Deivam"

Translation: "Mother Father Teacher God"

My profound gratitude and reverence to my Parents, my Supervisor and The Supreme Almighty.

To my Supervisor Professor Tony R Merriman- Thank you for inspiring and guiding me throughout this journey and comforting me at times of adversity. Without your valuable inputs, your unfailing support and encouragement, this would not have been possible. Your belief in me is a very big reason why I have been able to complete this task against all odds.

To my lab members- Marilyn Merriman, Mandy Phipps-Green, Ruth Topless, Tanya Major, Murray Cadzow and Matt Bixley- it was wonderful sharing the lab with all of you. Special thanks to Marilyn and Mandy for all the help and guidance.

To my friends: Karan Bali, Tahzeeb Fatima, Renu, Jiffin, Amara, Umair, Sepideh, Jaye, Karesoma and Denise, for the wonderful times and the laughter sessions we have had and the timely help that you have all generously offered. These memories will never fade away. Special thanks to Hakimeh for all the lovely times. Special thanks to my bestie, Tahzeeb, for being an incredible labmate, guide and an amazing friend for a lifetime. Special thanks to Karan for all the care and affection, thank you is the least I could say.

My family is my pillar of strength. To my family: My grandparents- late Padma Rajagopalan and Thirumaal Azhagi, my parents- Parimala Devi and Parthasarathy, my parents-in-law- Emerencial and Charles, my sister and brother-in-law- Sripriya and Rahul Singh, my adorable nieces- Sathakshi and Druti, my husband- Colin Antony and my daughter- Saanvi - For the unconditional love and support that you give me, for all the sacrifices you have made and for believing in me at all times, 'thank you' is too small to say. Whatever I am today, I owe it to you. Special thanks to my beloved husband- if not for you, I would not have been here today.

I dedicate this thesis to my beloved daughter, my little princess, Saanvi.

BLANK

ABSTRACT

Hyperuricemia, pathologically defined as the presence of an elevated level of serum urate, is a prerequisite for gouty arthritis. The solute carrier family 2 member 9 (*SLC2A9)* gene that encodes a urate transporter tops the list of hyperuricemic genes. It is a key genetic determinant of serum urate levels and explains about 3% of urate variance. Gout is highly prevalent in the New Zealand Māori and other Polynesian populations. As an attempt to understand the reason for this increased prevalence, this study focused on the identification and characterisation of Polynesian-specific genetic variants within the *SLC2A9* locus conferring susceptibility to hyperuricemia.

The *SLC2A9* locus was resequenced in 809 individuals (Polynesian, n = 440 and European, n = 369) comprising hyperuricemic cases and normouricemic controls**.** All Polynesians were from New Zealand while Europeans were from New Zealand and the United States. Association analysis was carried out to identify variants within the *SLC2A9* locus that confer risk for hyperuricemia. Multiple adjusted logistic regression analysis was carried out using R version 3.4.1. A number of data visualization techniques and variant annotation tools were used to interpret and represent data and variant annotations.

A total of 3963 variants was identified within the locus, of which 25 and 53 variants displayed nominal significance (p-value ≤ 0.05) with hyperuricemia in the East and West Polynesians, respectively. These significant signals were further analysed. Five variants were chosen for replication via genotyping (VAR_CHR4_9914056, rs373311989, VAR_CHR4_9452283, VAR_CHR4_10160679 and VAR_CHR4_10457448). The A allele of VAR_CHR4_9914056, located in intron 7 of the *SLC2A9* gene, was found to be associated with hyperuricemia in the East Polynesians in the Discovery Cohort (adjusted OR = 28.30, $P_{OR} = 0.003$) and the association was successfully replicated in the larger independent Replication Cohort, although with a relatively smaller effect size (adjusted OR = 2.93, $P_{OR} = 0.004$).

BLANK

The variants prioritized for replication were also tested for the association with gout in Polynesians. The A allele of the intergenic variant, VAR_CHR4_10160679, showed a significant protective association with gout both during discovery (adjusted OR = 0.04, P_{OR} = 0.03) and replication (adjusted OR = 0.32, P_{OR} = 0.01) in West Polynesians. The region containing this variant (4:10120364 – 4:10494666) displayed variation in the haplotype structure in Polynesians compared to Europeans, as revealed by haplotype analysis and visualization.

This research was conducted to provide a greater insight into the genetic causes of gout and understand the reason for the higher prevalence of hyperuricemia in Polynesians. The work signifies the usefulness of targeted resequencing, especially in a bespoke fashion, in studying the genetic basis of a trait/disease that is highly prevalent in a particular population and further evinces the association of non-coding variants in the *SLC2A9* locus, mapping to the human 4p16.1 chromosomal region, with hyperuricemia and gout in Polynesians. The study also demonstrates the utility of data visualization tools and techniques in exploratory big data analysis. The identification of the Polynesian-specific hyperuricemia-associated variant can be applied in precision medicine and public health genomics to improve health outcomes for the target population.

BLANK

NOTE

This research was presented at the Otago Medical School Research Society Scientific Meeting on 1st Nov 2017, following which the research abstract was published in the 'New Zealand Medical Journal'.

An art model illustrating this research was in display at the Art and Genetics Exhibition 2017, in collaboration with Josephine Waring, a ceramic diploma student at the Dunedin School of Art, Otago Polytechnic. An article about this was published in the journal 'Junctures'.

This thesis won the 'Best 3-minute Oral Presentation' at the Biochemistry and Microbiology and Immunology Research Celebration held on 1st Dec 2017 at the University of Otago.

BLANK

TABLE OF CONTENTS

LIST OF FIGURES

LIST OF TABLES

LIST OF ABBREVIATIONS

Gene Names	
SLC2A9	Solute Carrier Family 2 Member 9
SLC22A12	Solute Carrier Family 22 Member 12
SLC16A9	Solute Carrier Family 16 Member 9
SLC5A8	Solute Carrier Family 5 Member 8
SLC5A12	Solute Carrier Family 5 Member 12
SLC22A11	Solute Carrier Family 22 Member 11
SLC22A13	Solute Carrier Family 22 Member 13
ABCG2	ATP Binding Cassette Subfamily G Member 2
ABCC4	ATP Binding Cassette Subfamily C Member 4
SLC17A1	Solute Carrier Family 17 Member 1
SLC17A3	Solute Carrier Family 17 Member 3
SLC22A6	Solute Carrier Family 22 Member 6
SLC22A7	Solute Carrier Family 22 Member 7
SLC22A8	Solute Carrier Family 22 Member 8
PDZK1	PDZ Domain Containing 1
DEFB131A	Defensin Beta 131A
DRD5	Dopamine Receptor D5
WDR1	WD Repeat Domain 1
ZNF518B	Zinc Finger Protein 518B
CLNK	Cytokine Dependent Hematopoietic Cell Linker
Others	
DNA	Deoxyribonucleic Acid
RNA	Ribonucleic Acid
MR	Mendelian Randomization
BMD	Bone Mineral Density
RCT	Randomized Control Trial
CKD	Chronic Kidney Disease
FEUA	Fractional Excretion Of Urate
GWAS	Genome-Wide Association Study
URAT1	Urate Transporter 1

GLUT9	Glucose Transporter 9
MSU	Monosodium Urate
MRI	Magnetic Resonance Imaging
BMI	Body Mass Index
ATP	Adenosine Triphosphate
AMP	Adenosine Monophosphate
PRPP	Phosphoribosyl Pyrophosphate
HGPRT	Hypoxanthine-Guanine Phosphoribosyl Transferase
FJHN	Familial Juvenile Hyperuricemic Nephropathy
MCKD	Medullary Cystic Kidney Disease
PESPR	Proline-Glutamate-Serine-Proline-Arginine Motif
PETK	Proline-Glutamate-Threonine-Lysine Motif
GPK	Glycine-Proline-Lysine Motif
GRR	Glycine-Arginine-Arginine
NZ	New Zealand
EP	East Polynesian
WP	West Polynesian
ACR	American College Of Rheumatology
HPFS	The Health Professionals Follow-Up Study
NHS	The Nurses' Health Study
NGS	Next Generation Sequencing
UTR	Untranslated Region
GATK	Genome Analysis Tool Kit
SAM	Sequence Alignment/Map
BAM	Binary Alignment/Map
VCF	Variant Call Format
SNP	Single Nucleotide Polymorphism
HMM	Hidden Markov Model
PCA	Principal Component Analysis
OR	Odds Ratio
CI	Confidence Interval
TE	Natural Log of OR

seTE	Standard Error
P	P-value
LD	Linkage Disequilibrium
HWE	Hardy-Weinberg equilibrium
LWAS	Locus-Wide Association Study
Ve!P	Variant Effect Predictor
SnpEff	Snp Effect
CADD	Combined Annotation Dependent Depletion
GWAVA	Genome Wide Annotation of Variants
inPHAP	Interactive Visualization of Genotype And Phased Haplotype Data

Chapter 1

Introduction

CHAPTER 1

INTRODUCTION

1.1 BACKGROUND

1.1.1 URATE

FIRST PRINCIPLES

It is hard to overemphasize the universal importance of purines (adenine and guanine) in the body. Besides their obvious roles as monomeric precursors of deoxyribonucleic acid (DNA) and ribonucleic acid (RNA), they also participate in signal transduction, neurotransmission and various enzymatic processes. They are indispensable for the survival of cells. Purines in the body are derived exogenously via the consumption of purine-containing foods and endogenously via the degradation of nucleic acids. Exogenous and endogenous purines are further broken down during metabolism.

Uric acid (called 'urate' in its anionic form) has the chemical formula 2,6,8-trihydroxypurine ($C_5H_4N_4O_3$) and a molecular mass of 168 Da. It is the end product of purine degradation in humans. Karl Wilhelm Scheele isolated this acidic substance from a bladder stone and named it lithic acid (lithos in Greek means stone). George Pearson and Antoine Fourcroy later changed the name from lithic acid to uric acid to indicate its presence in normal urine (Richet, 1995).

This weak diprotic acid has two dissociable protons with pKa_1~5.4 and pKa_2~10.3. At physiological pH (pH=7.4), uric acid is present mostly as monovalent urate anion (figure 1.1). The presence of divalent urate anion in the extracellular fluid is negligible (~1%) owing to the very high value of pKa_2. For this reason, the term urate is used, in biomedical literature, to describe monovalent urate anion in circulation (Bobulescu et al.,

2012). The lower pH of urine allows urate to be contained in the form of unprotonated uric acid while excreted (Hyndman et al., 2016).

NOTE: In order to maintain consistency, the term 'urate' is used, throughout this thesis, to refer to uric acid in its protonated or deprotonated form.

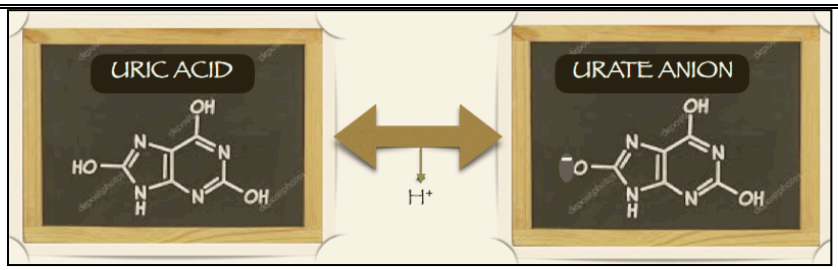


FIGURE 1.1 STRUCTURE OF URATE ($C_5H_3N_4O_3$).

1.1.2 PHYLOGENY OF THE URICASE GENE

EVOLUTIONARY CUES

As shown in figure 1.2, purine catabolism yields urate, but whether urate is itself the terminal metabolite or is it subject to further degradation is species-dependent. In most mammals, weakly soluble urate undergoes oxidative degradation to yield allantoin. Allantoin, being a more soluble metabolite, is easily excreted by the kidney. In most non-mammals, allantoin is further degraded to urea or ammonia. The copper-binding enzyme called urate oxidase, also called uricase, oxidizes urate to allantoin (Oda et al., 2002; Lee et al., 2013).

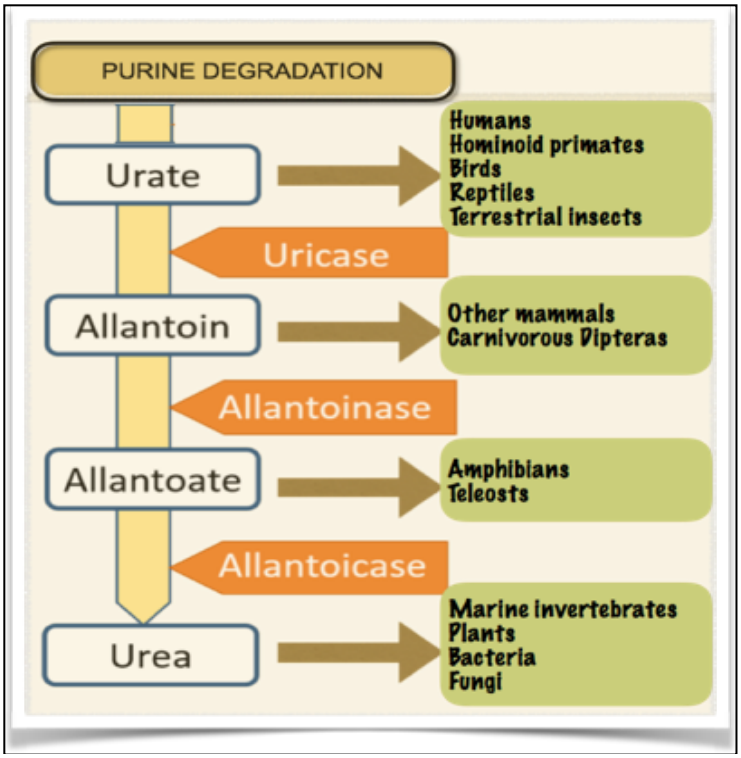


FIGURE 1.2 TERMINAL METABOLITE IN THE PURINE DEGRADATION PATHWAY IS SPECIES-DEPENDENT. *Marine invertebrates, plants, bacteria and fungi excrete nitrogenous wastes in the form of urea. Amphibians and teleosts excrete allantoate. Other mammals and carnivorous dipteras excrete allantoin while humans, other primates, birds, reptiles and terrestrial insects excrete urate as such without further degrading it.*
(Own illustration)

Differential conservation of the uricase gene is observed in various species. While an active form of this gene is carried by most non-mammalian and mammalian species, humans and other great apes have been evolutionarily constrained to completely lack any uricase activity (Oda et al., 2002).

During hominoid evolution, the uricase gene was subjected to negative pressure. Several parallel mutations were incurred in the promoter and coding regions of the gene, resulting in a gradual loss of enzyme activity along the primate lineage. In *Hylobates* (gibbon), either a 13-base pair deletion in exon 2 (Wu et al., 1992), a nonsense mutation in exon 2, a 1-base pair deletion in exon 3 or a 1-base pair deletion in exon 5 disrupted the uricase reading frame, rendering the gene inactive (Oda et al., 2002). According to Oda et al., the most likely inactivating mutation in gibbons was an independent nonsense mutation in

exon 2. In *Pan troglodytes* (chimpanzee), *Pongo pygmaeus* (orangutan) and *Homo sapiens* (human), the occurrence of two nonsense mutations at codons 33 and 187 subsequently resulted in the pseudogenisation of the uricase gene and a complete loss of enzyme activity in these species, compelling urate to be excreted as such by the kidneys (Wu et al., 1992). Owing to this, the serum urate level in humans is ~10 times higher than most other mammals (Bobulescu et al., 2012). The figure 1.3 (own illustration) depicts the phylogeny of the uricase gene.

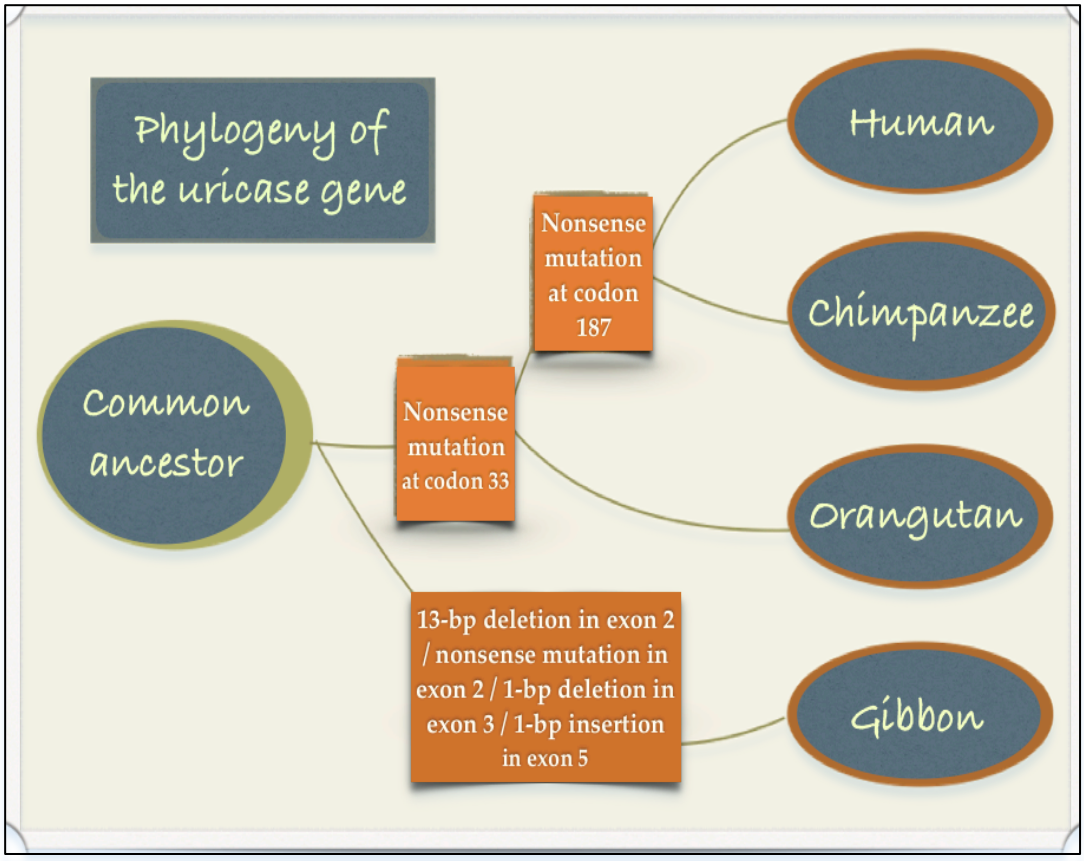


FIGURE 1.3 PHYLOGENY OF THE URICASE GENE. *Parallel mutations in the uricase gene resulted in the pseudogenisation of the gene and the loss of uricase activity along the primate lineage. (Own illustration)*

The fact that evolutionary pressures have worked in concert to completely pseudogenise the uricase gene in humans and great apes invokes a thought that there must be some sort of selective advantage that higher serum urate levels had to offer in these species. This thought is further supported by the remarkable ability of the kidney to reabsorb ~90% of

the filtered urate back into the blood stream (discussed later). Intuitively, why would the kidney invest resources to reclaim urate, if the sole mission of urate was merely to excrete nitrogen from the body?

1.1.3 THE JEKYLL AND HYDE TENDENCIES OF URATE

FRIEND OR FOE?

Compared to most other species, human beings possess a propensity for higher urate levels (~240-360μM) in the blood stream. With the available evolutionary and physiological clues, it would be unwise to regard urate as an inert metabolic waste that simply serves as a means of excreting nitrogenous wastes.

Varying degrees of evidence suggest a spectrum of roles for urate in human physiology and health. While numerous reports illustrate protective roles of serum urate, some recent reports suggest a causal role of elevated serum urate in disease pathogenicity.

1.1.3.1 PROTECTIVE ROLES OF URATE IN HUMAN HEALTH

- ANTIOXIDANT Urate has been considered an important antioxidant that protects the body from oxidative stress. In fact, circulating urate contributes to at least 50% of the total antioxidant capacity of the blood plasma. A theory put forth by Ames et al. in 1981 states that the relative intrinsic hyperuricemia (elevated serum urate level) observed in humans following the loss of uricase activity evolved as a strategy to cope with the loss of the vitamin-C synthesizing enzyme, L-gulonolactone oxidase, during the hominoid evolution. Although, urate is not as efficient an antioxidant as vitamin-C, a larger concentration is likely to compensate for its relatively lower antioxidant capacity (Ames et al., 1981). The intrinsic antioxidant capacity of urate makes it an effective scavenger of free radicals and a chelator of metal ions. It has also been postulated to be a powerful peroxynitrite neutralizer (Kuzkaya et al., 2005). It prevents the peroxidation and nitrosylation of proteins and lipids and reduces the production of reactive oxygen species (Ames et al., 1981). It has been postulated to serve as an antioxidant in the

liver, vascular endothelial cells and the nasal airways (Shi et al., 2003; Peden et al., 1990; Peden et al., 1993).

- ANTI-NATRIURETIC EFFECT One of the significant evolutionary benefits that higher serum urate has been postulated to offer in humans is the survival under low-salt dietary conditions that prevailed during the Miocene era. During this time, elevated urate was likely advantageous to better conserve sodium and maintain blood pressure (Watanabe et al., 2002).

- TISSUE HEALING AND REPAIR Urate is an important danger signal that alerts the innate immune system during cell injury by stimulating the maturation of dendritic cells and thereby initiating an innate immune response (Shi et al., 2003). It is a major alarmin secreted by dying cells in order to initiate the inflammatory cascade that enables tissue reconstruction (Bianchi et al., 2007). Further, it has been shown, using an animal model, to mediate the mobilization and recruitment of endothelial progenitor cells during ischemic tissue injury (Patschan et al., 2007)

- RESISTANCE TO PARASITES Urate has been shown to be protective against schistosomiasis, a tropical parasitic infection (Amaral et al., 2016).

- PROTECTION AGAINST NEURODEGENERATIVE DISEASES Urate has been postulated to play a protective role in several neurodegenerative diseases including multiple sclerosis, Parkinson's disease, dementia and Alzheimer's disease. High serum urate levels have been shown to block myelin degradation by scavenging peroxynitrites and reactive oxygen species. There is documented evidence linking low serum urate levels to multiple sclerosis (Hooper et al., 1998; Zoccolella et al., 2012). Interestingly, gout patients are naturally protected from multiple sclerosis and the two diseases are almost mutually exclusive (Hooper et al., 1998). Serum urate levels have been shown to be low in patients with myasthenia gravis, an autoimmune neuromuscular disease (Yang et al., 2016). Further, there is compelling evidence for urate being protective in Parkinson's

disease (Weisskopf et al., 2007; Schwarzschild et al., 2008) and Alzheimer's disease (Bowman et al., 2010). Oxidative damage is a known cause of these central nervous system disorders. With its well-known antioxidant potential, it is not surprising that urate protects against the progression of these disorders.

- BONE METABOLISM DISORDERS Observational studies have reported a positive correlation between elevated serum urate and high bone mineral density (BMD) (Ishii et al., 2014, Veronese et al., 2016). However, Mendelian randomization (MR) studies provide no evidence of a causal association between elevated urate and high bone mineral density (Dalbeth et al., 2015) or other bone-related outcomes (Xiong et al., 2016).

1.1.3.2 ROLES OF URATE IN DISEASE PATHOGENICITY

Urate has some emerging and some proven roles in disease pathogenicity. Hyperuricemia has been postulated, on the basis of observational studies, to be a risk factor for conditions such as cardio-renal disorders (Hsu et al., 2009, Weiner et al., 2008, Hare et al., 2003, Bos et al., 2006) and metabolic syndrome (encompassing conditions such as hypertension, visceral obesity, dyslipidaemia and insulin resistance) (Yoo et al., 2005; Chen et al., 2007; Lin et al., 2007; Conen et al., 2004; Klein et al., 2002; Facchini et al., 1991).

However, the inferences from observational studies alone (based on the co-occurrence of two conditions) cannot be used to ascribe a causal relationship between a risk factor (cause) and disease (effect), especially for complex traits wherein, observational studies tend to be prone to biases due to the presence of unaccounted confounders and reverse causation. In such scenarios, MR studies, analogous to randomized control trials (RCT), can be useful in drawing inferences regarding a possible causal relationship between the risk factor and the disease (Robinson et al., 2016; Bowden et al., 2017, Smith and Hemani, 2014).

- OXIDATIVE STRESS Contrary to the antioxidant roles stated in section 1.1.3.1, elevated plasma urate has been linked to cardio-renal disorders that are well known to be influenced by an increase in oxidative stress (Gagliardi et al., 2009). One plausible explanation for these paradoxical findings could be that urate, like any other redox agent, is capable of behaving both as an antioxidant and a prooxidant. Based on the microenvironmental milieu and the concentrations of free radicals and other antioxidant molecules, urate may take up either role (Hayden et al., 2004).

- HYPERTENSION Observational studies suggest a possible role of chronic hyperuricemia in the development of hypertension. Considering its earlier anti-natriuretic effect, the link between hyperuricemia and hypertension has been attributed to the shift from a low-salt to a high-salt diet during the post-industrialization era (Feig et al., 2008). The dramatic increase in sodium intake has been postulated to have transmuted the trait that once provided a survival benefit to early hominoids into a possible risk factor for hypertension in today's world. Probable mechanisms by which elevated serum urate may elevate blood pressure have been hypothesized. These include the stimulation of oxidative stress (Sánchez-Lozada et al., 2008), the proliferation of vascular smooth muscle cells (Sánchez-Lozada et al., 2007), the reduction of endothelial nitric oxide levels (Khosla et al., 2005) and the activation of the renin-angiotensin system (Mazzali et al., 2002). Contradicting these observations, Palmer et al. (2013) reported no evidence for a causal association of hyperuricemia and increased risk of hypertension, using the MR approach in two large cohorts, comprising 10602 participants from the Copenhagen City Heart Study and 58072 participants from the Copenhagen General Population Study (Palmer et al., 2013).

- KIDNEY DISEASES Elevated serum urate has been postulated to be an independent risk factor for end-stage renal disease (Hsu et al., 2009), incident kidney disease (Weiner et al., 2008) as well as prevalent chronic kidney disease (CKD) (Chonchol et al., 2007), based on observational studies. A 7-year follow-up study of 21475 individuals reported a significant increase in the risk of CKD with higher blood urate levels (Obermayr et al., 2008). High blood urate level has

been reported to correlate with urate nephrolithiasis in an appreciable number of patients (Gutman et al., 1968). However, an MR study in the Finnish Caucasian population suggests no causal association of elevated urate and diabetic nephropathy and suggests urate to be a probable downstream marker, rather than a cause, of kidney damage (Ahola et al., 2017). More MR studies to replicate these results in other populations are therefore necessary to understand and assess the role for hyperuricemia in kidney disease (Gul et al., 2017)

- OBESITY Various reports suggest a positive association of hyperuricemia and obesity, central (visceral) body fat distribution (Matsuura et al., 1998; Bonora et al., 1996) and waist circumference in men (Chen et al., 2007). However, MR studies describe elevated urate as a consequence rather than a cause of an increased adiposity (Lyngdoh et al., 2012; Rasheed et al., 2014).

- CARDIOVASCULAR DISEASES Serum urate has been postulated, on the basis of observational studies, to be associated with cardiovascular diseases such as stroke, myocardial infarction (Bos et al., 2006), heart failure (Hare et al., 2003), atherosclerosis (Neogi et al., 2009), peripheral arterial disease (Shankar et al., 2008), incident heart failure (Ekundayo et al., 2010) and death from all major forms of cardiovascular disease (Strasak et al., 2008). On the contrary, MR studies have established no such causal role of elevated urate in increasing the triglyceride levels (Rashhed et al., 2014) or ischemic heart disease (Palmer et al., 2013; White et al., 2016; Keenan et al., 2016).

- DIABETES Observational studies suggest elevated urate to be associated with type 2 diabetes mellitus (Dehghan et al., 2008), impaired renal function (Rosolowsky et al., 2008) and albuminuria (Jalal et al., 2010) in type 1 diabetic patients. However, findings from MR studies report no causal association between serum urate and risk of Type 2 diabetes mellitus and suggest that urate lowering therapy may not be beneficial in preventing/reducing the risk of diabetes (Pfister et al., 2011; Keenan et al., 2016; Sluijs et al., 2015).

- GOUT Convincing sets of data linking hyperuricemia and disease causation are available for gout, an excruciatingly painful type of inflammatory arthritis. Gout is by far the most common clinical manifestation of hyperuricemia, with mounting evidence suggesting a significant association between these two traits in various populations. Hyperuricemia in the context of gout is described in detail in section 1.2 of this chapter.

A summary of the various postulated roles of serum urate in health and disease, reported in literature to date, is depicted as a plot in figure 1.4. Whether urate is beneficial or pathogenic, helpful or harmful, is an on-going age-old debate that defies explanation. However, the unifying theme that emerges is that urate is not merely an inert waste product of purine metabolism but has many more roles to play in human physiology.

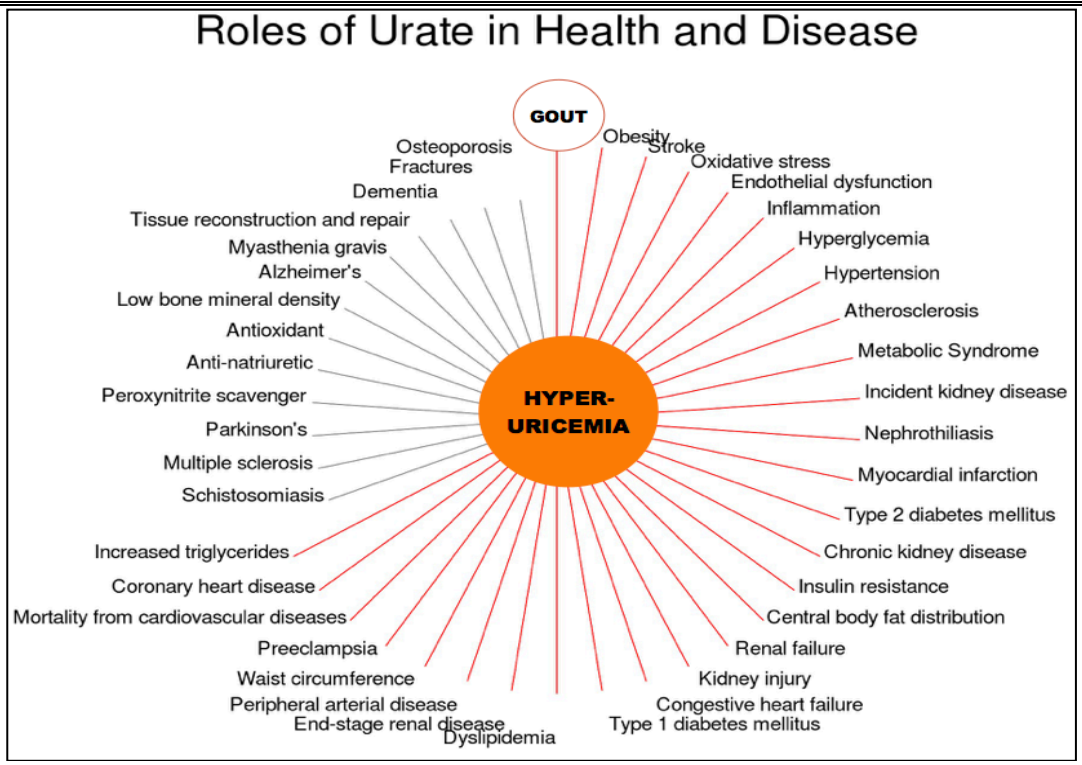


FIGURE 1.4: PLOT ILLUSTRATING THE POSTULATED PATHOGENIC AND PROTECTIVE ROLES OF SERUM URATE IN HUMANS. *Hyperuricemia has been postulated to be protective against neurodegenerative diseases and have antioxidant roles but has also been postulated to be a risk factor for cardio-renal disorders and components of the metabolic syndrome. Convincing evidence linking hyperuricemia and disease causation are available for gout. Red strokes indicate the postulated pathogenic roles and grey strokes indicate the postulated protective roles.*
(Own illustration)

1.1.4 URATE HOMEOSTASIS

STRIKING THE RIGHT BALANCE

Urate is produced in the liver and excreted primarily by the kidneys. Specifically, about two-thirds of the total excretion occurs via the kidneys (renal excretion), while the rest of the urate reaches the intestine where it undergoes uricolysis by the colonic bacteria and is then eliminated (extra-renal elimination) (Sorensen et al., 1975). In order to maintain a constant level of urate in the blood stream, the body's homeostatic mechanisms serve to strike an overall balance between its net production and excretion (Lipkowitz et al., 2001). Urate handling is therefore a balancing act involving the tight regulation between three processes namely, hepatic production, renal excretion and intestinal elimination. An alteration in any one of these processes disrupts the steady-state urate concentration and

may result in an abnormally higher or lower level of urate in the blood stream. The overproduction or the under-excretion of urate may result in an elevated level of serum urate, a condition termed hyperuricemia. Similarly, the excessive excretion of the substance may end up in serum urate level being lower than normal, a condition termed hypouricemia. These concepts are depicted in figure 1.5.

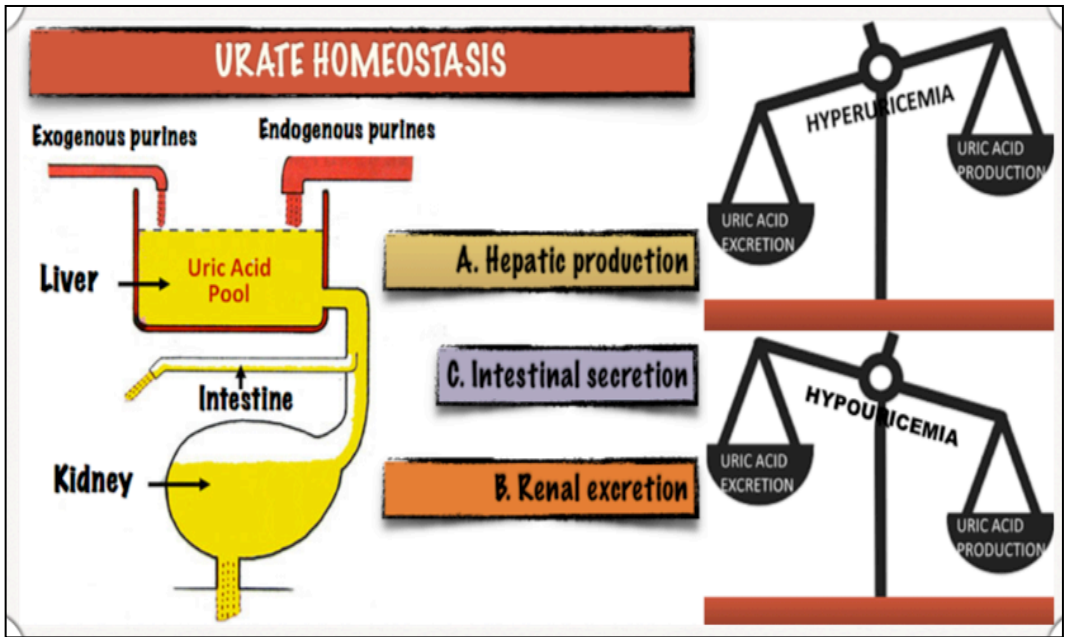


FIGURE 1.5: URATE HOMEOSTASIS. *Urate is produced in the liver and excreted by the kidneys (two-third) and the intestine (one-third). Homeostatic mechanisms maintain a tight balance between hepatic production, renal excretion and intestinal elimination. An overproduction and/or the under-excretion of urate result in hyperuricemia while excessive excretion of urate results in hypouricemia. (Own illustration)*

1.1.4.1 HEPATIC PRODUCTION OF URATE

As mentioned earlier, urate, in humans, is the final degradation product of metabolism of purines that are derived exogenously through the diet and endogenously from normal cellular breakdown of nucleic acids. The purine degradation pathway is illustrated in figure 1.6.

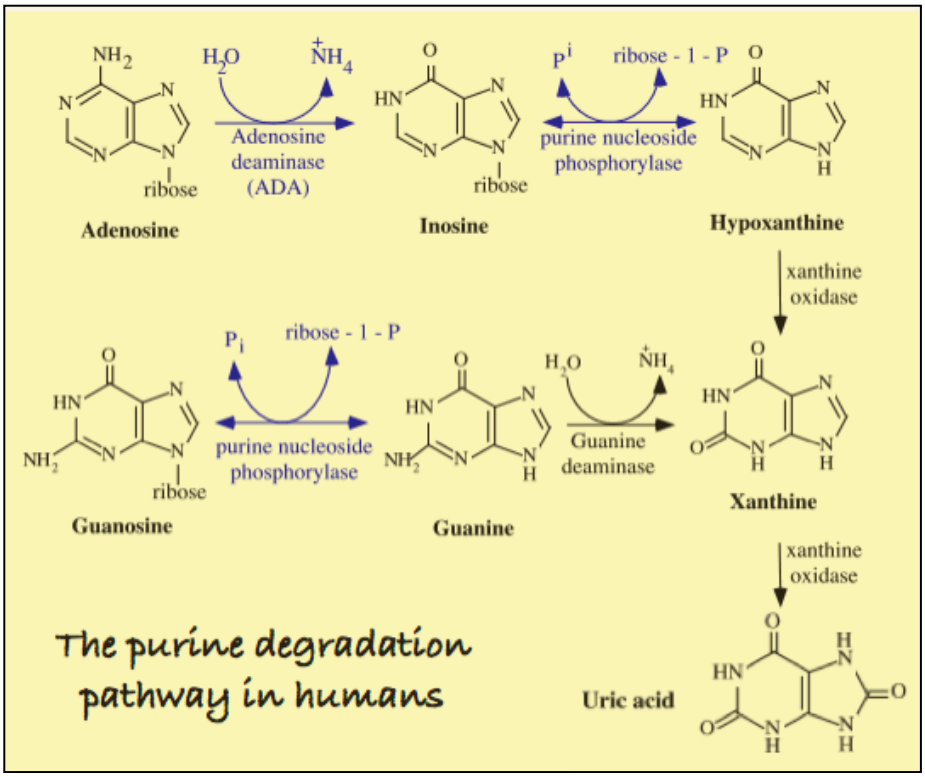


FIGURE 1.6: THE PURINE DEGRADATION PATHWAY. *Adenosine and guanosine are both converted to xanthine, which is converted to uric acid by xanthine oxidase (Adapted from: Robert Lyons, 2008)*

1.1.4.2 RENAL HANDLING OF URATE

Renal urate handling is a dynamic process involving a number of transporters for the import/export of urate along the epithelium of the proximal convoluted tubules of the kidney. The majority of urate in the blood stream is freely circulating and a very small percentage (< 5%) is bound to plasma proteins. It is therefore freely filtered at the kidney glomeruli. Although freely filterable, most of the filtered urate (> 90%) is reabsorbed back into the blood stream with very little of it (< 10%) being excreted in the urine, under normal conditions.

The percentage of urate that, after glomerular filtration, is eventually excreted in the final urine is described as the fractional excretion of urate (FEUA). FEUA is indicative of the renal urate reabsorption efficiency (Hyndman et al., 2016). Unlike the uricotelic species that display an FEUA > 100%, its value in humans, under normal conditions, is approximately 10% or less. The lower the FEUA, the higher the serum urate

concentration. Normally, FEUA is around 6-8%, as against 3-5% in gout patients (Levinson et al., 1980). The FEUA values are higher in women than in men, consistent with the fact that the serum urate levels are generally higher in men than women (Bobulescu et al., 2012). Also, FEUA is higher in newborns (< 3 weeks old) when compared to children less than 12 months of age. It further decreases progressively in adults (Passwell et al., 1974), owing to the maturational changes in the kidney urate transport system (Baum et al., 2003).

The renal urate transport occurs bidirectionally wherein the reabsorptive and the secretory mechanisms act in concert along the apical and basolateral surfaces of the renal proximal tubules in order to establish the necessary transepithelial urate flux. The classical physiological model describing this process comprises four stages namely- glomerular ultrafiltration, tubular reabsorption, secretion and post secretory resorption (Levinson et al., 1980). However, recent advances in the field have deepened our understanding of the molecular physiology of urate transport and question some assumptions that formed the basis of the four-component model, warranting further speculation and revision.

As per the current understanding, glomerular filtration definitely occurs, followed by tubular reabsorption. Whether secretion is concomitant with reabsorption remains unclear. However, there is emerging evidence indicating the occurrence of concomitant tubular secretion and post-reabsorptive secretion (Dinour et al., 2010; Puig et al., 2012; Perez-Ruiz et al., 2002).

1.1.4.2.1 THE URATE TRANSPORTOSOME

Brief notes on the important reabsorptive and secretory urate transporters are added below followed by a quadrant diagram illustrating the current understanding of the urate transportosome, drawn based on published literature (figure 1.7).

TRANSPORTERS FOR URATE REABSORPTION

The transporters involved in the reabsorption pathway include three proteins that function at the apical surface- URAT1, OAT4 and OAT10, and the GLUT9 protein that functions at the basolateral surface (discussed below). The uptake of urate by the apical membrane transporters is promoted by intracellular mono- and di-carboxylates. The apical monocarboxylate transporters, MCT9 (encoded by *SLC16A9*, solute carrier family 16 member 9), SMCT1 (encoded by *SLC5A8*, solute carrier family 5 member 8) and SMCT2 (encoded by *SLC5A12*, solute carrier family 5 member 12), participate in this process (Halestrap et al., 1999; Thangaraju., 2006).

- URAT1 The URAT1 (urate transporter 1) protein is encoded by the *SLC22A12* (solute carrier family 22 member 12) gene. It is expressed on the apical membrane of the proximal tubule. This urate/anion exchanger is one of the two most important reabsorptive urate transporters and plays a key role in urate handling by the kidneys. It functions in the uptake of urate by the tubular epithelial cells from the glomerular filtrate. Loss of function variations in the *SLC22A12* gene are a known cause of renal hypouricemia. Such patients exhibit FEUA of 40-100% and therefore very low serum urate levels (Enomoto et al., 2002; Ichida et al., 2004). This gene has been identified as an important signal in hyperuricemia and gout genome-wide association study (GWAS) (Kottgen et al., 2013). Most urate-lowering therapies for hyperuricemia and gout work by inhibiting URAT1 ((Enomoto et al., 2002).

- GLUT9 The GLUT9 (glucose transporter 9) protein is encoded by the *SLC2A9* (solute carrier family 2 member 9) gene. This protein is present in two isoforms, long and short. The long isoform is best characterized and localizes to the basolateral side of the proximal tubule. GLUT9 is a voltage-dependent high-capacity facilitative urate transporter and is the other important reabsorptive transporter playing a fundamental role in renal urate handling and regulating serum urate levels, as identified by a large number of studies including GWA studies (table 1.1). This is the key protein that functions to transport urate from the

proximal tubular cells back into the blood stream. Loss of function variations in the *SLC2A9* gene have been linked to renal hypouricemia (Dinour et al., 2010; Matsuo et al., 2008).

- OAT4 AND OAT10 The OAT4 and the OAT10 proteins are encoded by the *SLC22A11* (solute carrier family 22 member 11) and the *SLC22A13* (solute carrier family 22 member 13) genes, respectively. These organic anion transporters, expressed on the apical surface of the membrane, have a relatively low affinity for urate. Like URAT1, these proteins transport urate from the glomerulus into the cytosol of the proximal tubular epithelium (Hagos et al., 2007; Zhou et al., 2010). Studies suggest an association between OAT4 and diuretic-induced hyperuricemia (McAdams-DeMarco et al., 2013) and the risk of gout (Flynn et al., 2013; Sakiyama et al., 2014). However, evidence suggesting the role of OAT10 in urate handling is sparing.

TRANSPORTERS FOR URATE SECRETION

The transporters involved in the urate secretion pathway include four proteins at the apical surface- two ATP-binding cassette proteins, MRP4 and ABCG2, and two sodium/phosphate cotransporters, NPT1 and NPT4; and the OAT proteins (OAT1, OAT2 and OAT3) at the basolateral surface (discussed below). The sodium/dicarboxylate cotransporters, NaDC1 and NaDC3, play roles similar to those of the SMCT proteins (apical membrane transporters) and contribute to urate secretion (Ho et al., 2007). The hUAT/galectin 9 protein, encoded by the *LGALS9* gene, localizes at both the luminal and the basolateral surfaces of the proximal tubules and is proposed to function as a urate uniporter, but whether its role is reabsorptive or secretory remains unclear (Hyink et al., 2001; Lipkowitz et al., 2006).

- ABCG2 The ABCG2 protein is encoded by the *ABCG2* (ATP binding cassette subfamily G member 2) gene. This urate efflux transporter localizes to the luminal membrane of the proximal tubule and is also called BRCP (breast cancer resistance protein). GWASs have revealed an association of this gene with

hyperuricemia and gout (Woodward et al., 2009; Jiri et al., 2016). An *ABCG2* variant, rs2231142 (Q141K), has been reported to be associated with gout risk in the Western Polynesian sub-population (Phipps-Green et al., 2010).

- **MRP4** The MRP4 protein is encoded by the *ABCC4* (ATP binding cassette subfamily C member 4) gene. Like ABCG2, this protein is also an ATP-binding cassette protein that is expressed on the apical side of the membrane (Lee et al., 1998; van Aubel et al., 2002). An *ABCC4* variant, rs4148500, has been reported to be significantly associated with FEUA, hyperuricemia and gout in the Polynesian population (Tanner et al., 2017).

- **NPT1 and NPT4** The NPT1 and the NPT4 proteins are encoded by the *SLC17A1* (solute carrier family 17 member 1) and the *SLC17A3* (solute carrier family 17 member 3) genes, respectively. These sodium-dependent phosphate cotransporters are expressed on the luminal side of the proximal tubule. Hollis-Moffatt et al. (2012) provide evidence for the association of the *SLC17A1* locus with gout, attaining a genome-wide level of significance (Hollis-Moffatt et al., 2012). Gain of function variations in the *SLC17A1* and *SLC17A3* genes have been reported to be protective against gout (Chiba et al., 2015; Jutabha et al., 2011).

- **OAT1, OAT2 and OAT3** The OAT1, OAT2 and OAT3 proteins are encoded by the SLC22A6 (solute carrier family 22 member 6), SLC22A7 (solute carrier family 22 member 7) and SLC22A8 (solute carrier family 22 member 8) genes, respectively, located on the human chromosome 11, in tandem. These dicarboxylate/urate exchangers localize to the basolateral surface of the proximal tubule. *In vitro* and animal model studies have confirmed their expression and indicate a probable role of these transporters in renal urate secretion (Bakhiya et al., 2003; Eraly et al., 2008; Sato et al., 2010; Ichida et al., 2003).

PDZK1- A FACILITATOR OF URATE TRANSPORT

The PDZ domain-containing protein, encoded by the *PDZK1* gene, is expressed on the luminal side of the renal proximal tubule. Through the PDZ interaction domain, this protein has been shown to interact with several apical membrane proteins including URAT1, OAT4, NPT1, SMCT1 and SMCT2 (Anzai et al., 2004; Miyazaki et al., 2005). It functions as a scaffold, holding these proteins in close proximity in order to facilitate urate transport across the tubular membrane. This gene has been identified in GWAS as a modulator of urate levels (Yang et al., 2010), while Phipps-Green et al. (2016) have provided the first evidence for the association of *PDZK1* with gout (Phipps-Green et al., 2016).

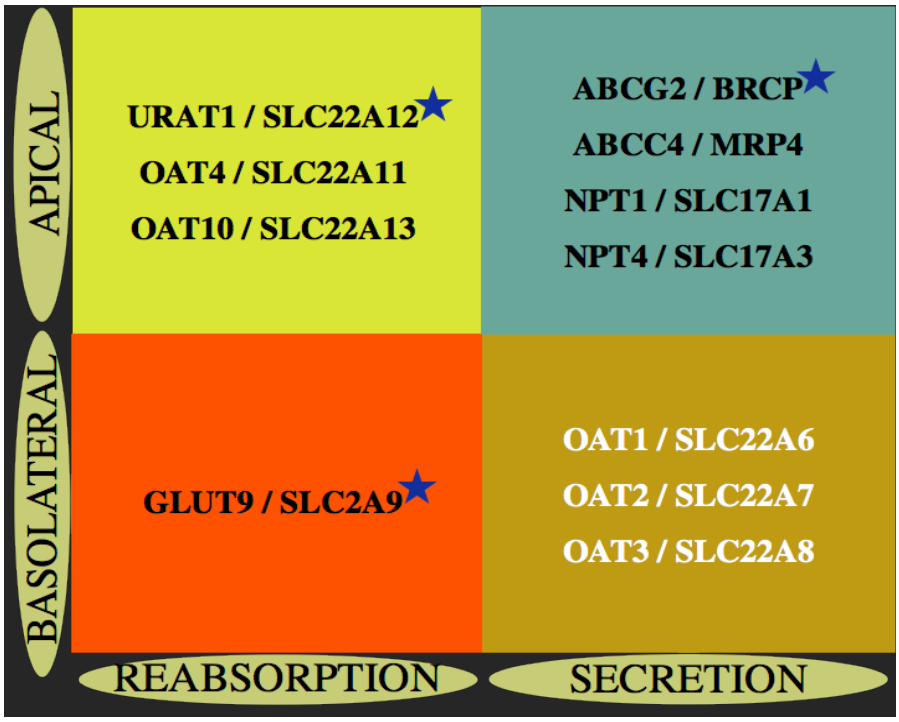


FIGURE 1.7: QUADRANT DIAGRAM ILLUSTRATING THE CURRENT UNDERSTANDING OF THE URATE TRANSPORTOSOME. *URAT1, OAT4 and OAT10 play a role in urate reabsorption at the apical surface while SLC2A9 plays a role in urate reabsorption at the basolateral surface. ABCG2, ABCC4, NPT1 and NPT4 play a role in urate secretion at the apical surface while OAT1, OAT2 and OAT3 play a role in urate secretion at the basolateral surface. The most important transporters are starred. transporters whose roles in disease are yet to be well-established are indicated in white.*
(Own illustration)

1.1.4.3 INTESTINAL URICOLYSIS

Uricolysis as a process to eliminate urate from the body was described several decades ago. It was conceived that a reduced rate of uricolysis in gout patients was responsible for the hyperuricemic status observed in these individuals (Bien et al., 1955). Urate that enters the intestine from the blood or as a component of the peptic juices, saliva or the bile is either reabsorbed or degraded by the colonic bacteria that are able to utilize urate as a metabolic substrate. Owing to this, no urate is normally detected in the faeces (Sorenson., 1959, Braun et al., 1989). Intestinal uricolysis is especially crucial in individuals with suboptimal renal excretion, as is seen in most subjects with gout or renal failure.

Most urate transporters that function in the kidney have also been identified in the intestine including ABCG2 (Dehghan et al., 2008), MRP2 and MRP4 (Grandvuinet et al., 2012), GLUT9 (Phay et al., 2000), MCT9 (Nakayama et al., 2013), NPT4 (Reimer et al., 2004) and OAT10 (Bahn et al., 2008).

1.2 ELEMENTS OF THIS STUDY

"***SLC2A9*** and **Hyperuricemia**: A Locus-Wide Association Study To Identify Population-Specific Genetic Variants In **New Zealand Māori and Pacific People**"

The key elements of this study (highlighted in the title above) are discussed in detail in this section.

1.2.1 HYPERURICEMIA– A CLINICAL PERSPECTIVE

TOO MUCH OF A GOOD THING

The presence of increased concentration of urate in the blood stream is termed hyperuricemia. At physiological pH, the solubility threshold of urate in the extracellular fluid is approximately 6.8 mg/dL (408 μmol/L). This threshold is also the commonly accepted cut-off value to clinically define hyperuricemia, so that individuals with a serum urate concentration greater than 6.8 mg/dL are generally considered hyperuricemic. An upper threshold value of 6.0 mg/dL (360 μmol/L) has been identified as optimal to define normouricemia (normal serum urate level) and prevent the occurrence of gout (Desideri et al., 2014).

Concentrations of urate beyond the solubility threshold induce crystallization of urate in the form of monosodium urate (MSU) crystals in the synovial fluid of the joints, soft tissues and/or in the kidneys (Martillo et al., 2014). These MSU crystals mediate the detrimental effects of hyperuricemia. However, some hyperuricemic individuals display no clinical manifestations of gouty arthritis and may remain asymptomatic throughout life. Such individuals are said to have asymptomatic hyperuricemia.

The current international recommendations and treatment guidelines suggest therapies to curtail blood urate concentrations to levels < 6.0 mg/dL in all cases of symptomatic hyperuricemia or gouty arthritis, and to levels < 5.0 mg/dL in all cases of severe (tophaceous) gout (Khanna et al., 2012a; Khanna et al., 2012b). In any case, it must be noted that while these threshold values are more convenient for clinical purposes, treating

urate as a continuous rather than a dichotomous variable has a better biological rationale. Figure 1.8 illustrates the current clinical classification of hyperuricemia.

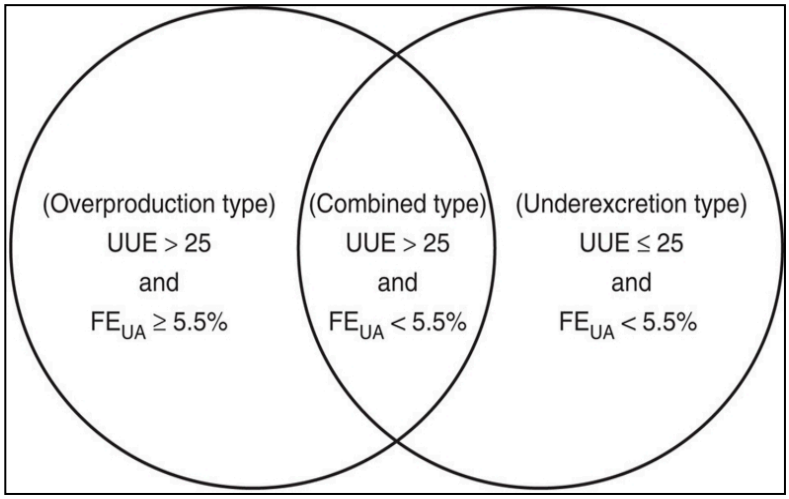


FIGURE I.8: CURRENT CLINICAL CLASSIFICATION OF HYPERURICEMIA. *UUE- Urinary Urate Excretion, FE$_{UA}$- Fractional Excretion Of Urate Clearance (Source: Ichida et al., 2012).*

Hyperuricemia is influenced by multiple genetic and environmental (dietary) factors. In a broader sense, hyperuricemia may result from either the overproduction and/or the under-excretion of urate in the body. Overproduction of urate can in turn be the consequence of endogenous metabolic defect(s) in the purine degradation pathway or an excessive intake of purine-rich diet (Bobulescu et al., 2012). Regulatory impairments in purine metabolism can result in the expansion of the blood urate pool. On the other hand, under-excretion of urate may result from endogenous defects in renal/gut urate handling. Since 70% of urate excretion occurs via the kidneys, defective renal urate excretion is the main cause of hyperuricemia. Gain of function variants in the urate reabsorptive genes and/or loss of function variants in the urate secretory genes may lead to suboptimal FEUA and hyperuricemia (Terkeltaub et al., 2003; Gutman, 1965; Pascual et al., 2006).

1.2.2 Gout
More Than Meets the Eye

1.2.2.1 History

Gout, an excruciatingly painful form of inflammatory arthritis, is the most common manifestation of symptomatic hyperuricemia (VanItallie et al., 2010). The first reference to gout symptoms, as swollen and painful toes (described by the Egyptians as podagra), traces back to 2640BC. Hippocrates described gout as "the unwalkable disease" way back in the fifth century BC (Nuki et al., 2006). The earliest documented description of a gout attack was given by an English physician, Thomas Sydenham, who himself had gout (Dorwart et al., 2004).

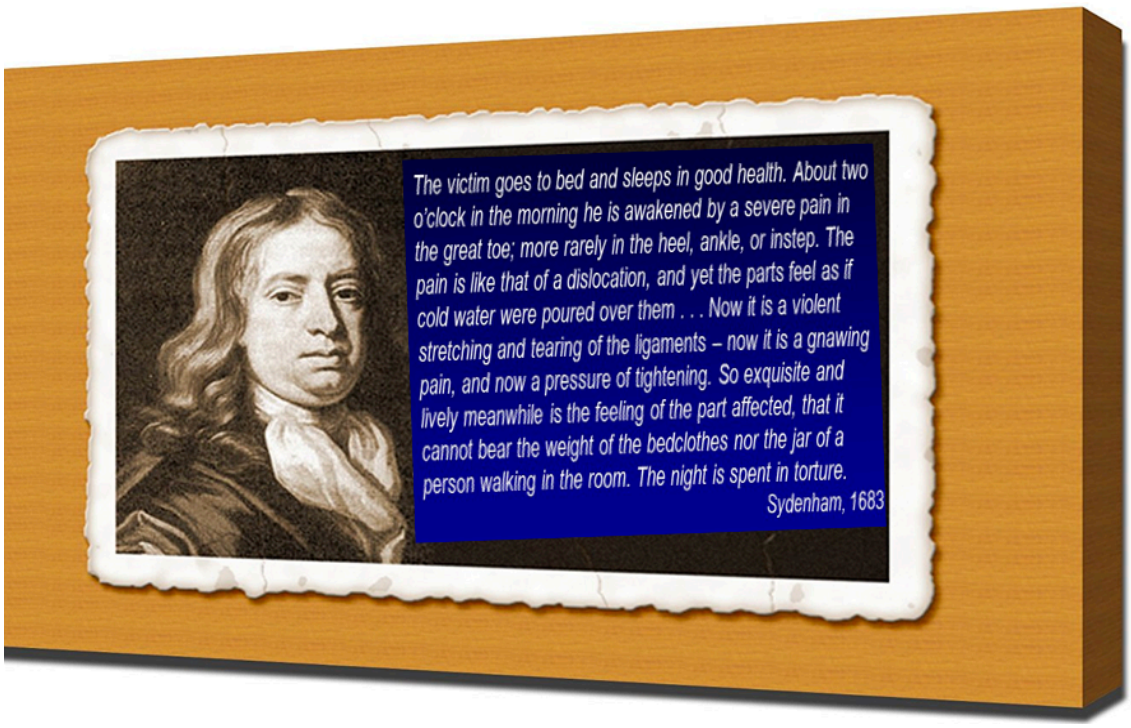


Figure 1.9: Narration, By The English Physician, Thomas Sydenham, Of His Own Experience, Is Still Considered One Of The Most Accurate Descriptions Of A Gout Flare.
(Quote sourced from: Sydenham,T: The works of Thomas Sydenham, London, New Sydenham Soc.1850.)

1.2.2.2 Pathophysiology

Long-standing hyperuricemia predisposes individuals to gout. This being said, not all hyperuricemic individuals develop gout. This shows that hyperuricemia is not sufficiently causative of gout. In the presence of long-standing hyperuricemia, MSU may form in the joints and the periarticular tissues (Martillo et al., 2014). These MSU crystals are implicated in the aetiology of gout. Being pro-inflammatory, they mediate inflammasome-mediated inflammation (tender, warm and swollen joints). This is the fundamental pathophysiological feature of a gout flare. The activation of the NALP3 inflammasome complex followed by the production of interleukin-1beta are crucial events in establishing the inflammatory response during acute gout flares (Martinon et al., 2006).

In the pathophysiological context, four stages of the disease progression can be described (Dalbeth et al., 2014), as follows:

- Stage 1 Asymptomatic hyperuricemia (hyperuricemia with no traces of MSU crystal deposits).
- Stage 2 Appearance of MSU crystals but without symptoms of gout.
- Stage 3 Acute gout attacks (intermittent self-limiting gout flares).
- Stage 4 Advanced/chronic tophaceous gout.

It is not obligatory for the disease to progress from stage 1 through to stage 4 in any individual. A number of checkpoints operate during the development and progression of the disease. For example, the solubility of MSU crystals is lower at relatively lower physiological temperature and pH conditions that prevail in the peripheral joints of the body (Loeb et al., 1972). Other factors such as intraarticular hydration and reduction in extracellular matrix components (proteoglycans, chondroitin sulphate and collagen) also influence the solubility of urate in the synovial fluid (Roddy et al., 2007).

Initial gout flares usually affect a single joint, most often the first metatarsophalangeal joint (big toe). It may then affect more joints such as the arms, knees, ankles and the

midtarsi. Advanced gout is the consequence of neglected hyperuricemia over many years and is characterized by the presence of polyarticular inflammation and tophi. A tophus is an aggregation of large MSU crystal and infiltrated immune cells, representing the cumulative (innate and adaptive) immune response to chronic MSU crystal deposits. Formation of tophi can cause irreparable damage to the joints, leading to joint disability (Dalbeth et al., 2010). About 30% of untreated acute gout patients, in about 5-10 years, develop tophaceous gout (Schumacher et al., 2005). Such patients lead a poor quality of life (Alvarez-Hernández et al., 2008).

1.2.2.3 DIAGNOSIS

Diagnosis of gout is supported by elevated blood urate concentration and characteristic changes in radiographs. The presence of needle-shaped MSU crystals along with immune cells in the synovial fluid aspirated from the joint spaces establishes gout diagnosis (Perez-Ruiz et al., 2007). Ultrasonography and magnetic resonance imaging (MRI) scan can also be used in the diagnosis and assessment of gout. Differential diagnosis of gout includes conditions like psoriatic arthritis, reactive arthritis, rheumatoid arthritis and pseudo-gout (calcium pyrophosphate crystal arthropathy) (Pascal et al., 2015; Popovich et al., 2015).

Allopurinol is the most frequently prescribed drug to lower serum urate levels. It is a xanthine oxidase inhibitor that prevents the production of urate in the body. Other urate-lowering drugs used to treat gout include febuxostat, probenecid and benzbromarone. Combination therapy has also proven to be very effective in treating gout patients (Maekawa 2014 et al., 2014). Patient education around daily administration of allopurinol, lifestyle modifications and regular comorbidity screening are strongly recommended for the effective management of gout.

1.2.2.4 EPIDEMIOLOGY

Gout is the most prevalent inflammatory crystal arthritis in the world today and is more common in the developed nations. The worldwide prevalence of hyperuricemia and gout is on a constant rise, attributable to the lifestyle and dietary changes embraced and

adopted by the modern man. Given that the risk of gout increases with age, extended longevity also has a role to play in this regard (Smith et al., 2014). The prevalence of hyperuricemia and gout is higher in males, especially older males. In women, it is generally lower, but dramatically increases after menopause (Conen et al., 2004; Kuo et al., 2016; (Hak et al., 2008).

The prevalence of gout varies amongst the different populations of the world. Most world populations have urate levels in the normouricemic range (< 6.0 mg/dL). However, some populations are inherently hyperuricemic and therefore display a higher predisposition to gout. Populations such as the Taiwanese aboriginals and the Polynesians generally have higher average blood urate levels, as is evident from figure 1.10. Such populations are therefore more prone to gout (Gosling et al., 2014). However, it must be noted that a higher rate of hyperuricemia does not necessarily mean a higher risk for gout, since development of gout in hyperuricemic individuals is not mandatory, as discussed before.

Skeletal remains from ancient Polynesians show presence of gouty lesions (Buckley et al., 2007). Furthermore, numerous studies report the mean serum urate levels to be higher in the various Polynesians subgroups such as the Māoris (~7.1 mg/dL) (Brauer et al., 1978), Cook Islanders (~7.0 mg/dL) (Prior et al., 1966), Tongans urban (urban ~6.5 mg/dL) (Finau et al., 1983), Samoans (urban- ~6.7 mg/dL, rural- ~6.9 mg/dL) (Jackson et al., 1981), Tokelauans (~6.6 mg/dL) (Østbye et al., 1989) and Tuvaluans (~6.6 mg/dL) (Jackson et al., 1980). Study of blood urate concentrations in 342 Māoris and 315 Europeans in New Zealand, belonging to different age groups, revealed that the mean serum urate concentration is higher in Māoris compared to Europeans of all age groups (Klemp et al., 1997).

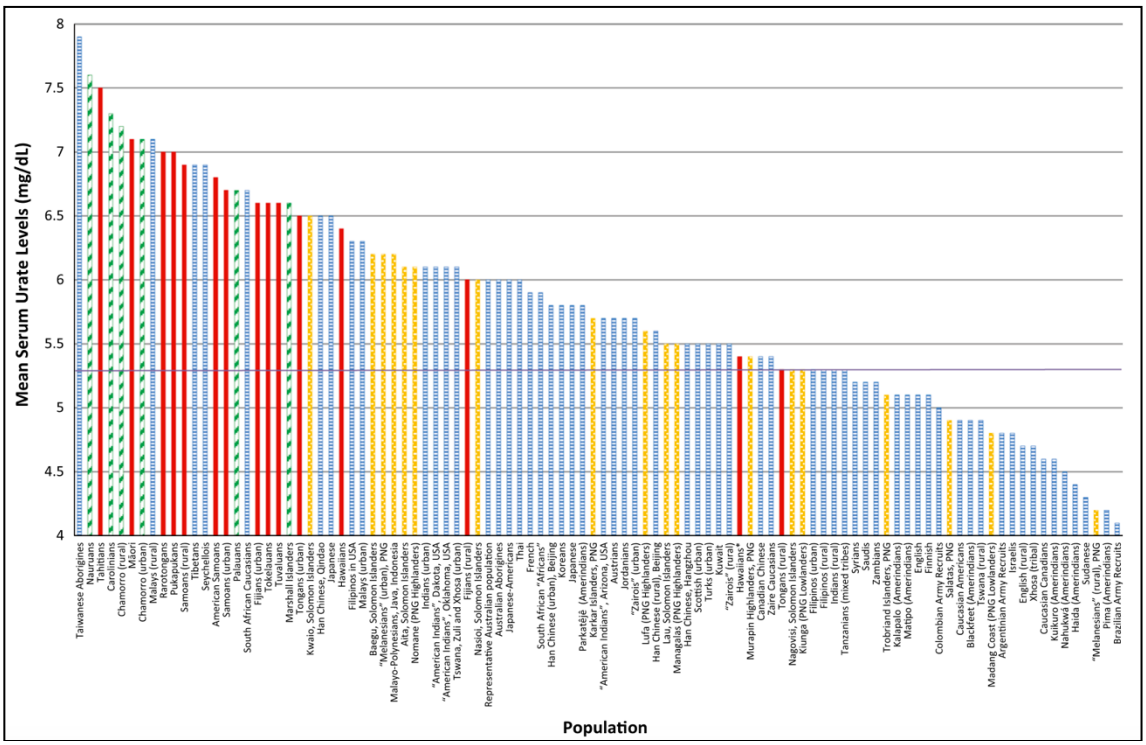


Figure 1.10 Mean Serum Urate Levels (Measured In mg/dL) In Various Populations. *The red bars indicate Polynesian subpopulations. Source: Gosling et al., 2014. License # 4377481174318. Publication: Rheumatology International. Title: Hyperuricaemia in the Pacific: why the elevated serum urate levels?*

1.2.3 Hyperuricemia & Gout are Complex Traits

Wheels within Wheels

Over the past decade, scientists across the globe have worked towards understanding the genetic architecture of gout. Studying hyperuricemia and gout has been challenging for several reasons. These disease phenotypes are complex genetic traits with many genomic loci contributing to disease susceptibility. Moreover, a number of environmental factors also play a substantial role in disease development, given an individual is genetically predisposed. As if that were not enough, these traits are plagued with an exceptional number of comorbidities and confounding factors that add more layers of complexity to the problem. Multiple bidirectional associations exist between hyperuricemia and gout and a spectrum of cardio-renal diseases, as discussed in section 1.1.3.2. Confounders such

as age, sex, BMI and ancestry greatly influence the development of hyperuricemia and gout, necessitating adjustment to these covariates during genetic studies.

1.2.3.1 GENETICS

Serum urate and gout are heritable traits. Although dietary factors do influence blood urate levels, the development of hyperuricemia is mainly attributable to genetic factors. The heritability (amount of phenotypic variability ascribable to genetic variability) of urate is considered to be about 60% (Krishnan et al., 2012).

Genetic studies using animal models are more often than not inadequate models for urate studies. The rodent kidney is ill-equipped to handle hyperuricemia/high filtered load. This is evident from studies that have shown that uricase knockout mice face death by renal failure, being unable to tolerate urate levels typically found in normouricemic humans (Wu et al., 1994). Moreover, the mechanisms of urate reabsorption/secretion as well as the distribution of these transporters differ in humans compared to other mammals (So et al., 2010).

The real breakthrough in understanding the genetic components of hyperuricemia and gout came from GWASs that scan the genome to identify SNPs and loci associated with the trait under study. The largest urate GWAS to date is the study carried out by Kottgen and colleagues on a large European sample set (>140,000 individuals). They reported a total of 28 genomic loci that potentially contain variants collectively affecting serum urate concentrations. This included 18 loci newly identified and replicated in this study (*TRIM46, SFMBT1, HLF, TMEM171, INHBB, VEGFA, BAZ1B, UBE2Q2, PRKAG2, STC1, HNF4G, A1CF, ATXN2, B3GNT4, IGF1R, NFAT5, MAF and ACVR1B-ACVRL1*) plus 10 previously known loci, the associations of which were confirmed in this study (*SLC2A9, ABCG2, RREB1, PDZK1, GCKR, SLC17A1, SLC16A9, SLC22A11, INHBC and NRXN2*) (Kottgen et al., 2013).

Although as many as 28 urate-associated loci have been identified thus far, they are cumulatively able to explain only 7% of variance in serum urate levels, of which 3.4% variance can be attributed to genetic variants in the *SLC2A9* and *ABCG2* genes alone

(Kottgen et al., 2013). Taking into account the fact that the heritability of urate is about 60% (Krishnan et al., 2012), there must be some key genetic players hidden and yet to be identified, playing a significant role in urate genetics. Unleashing the 'missing heritability' (Manolio et al., 2009) will undoubtedly better our understanding on the genetic architecture of these common yet complex disease traits.

1.2.3.2 Environmental Triggers

- **Red Meat and Seafood** Studies reveal sea food and red meat to be important triggers for gout attacks. In a study documenting self-reported food triggers for gout in NZ Polynesian and European individuals, 62.54% participants reported either seafood/fish, while 35.18% reported red meat as a trigger for gout flares (figure 1.11) (Flynn et al., 2015). Multiple other reports also suggest a positive correlation between red meat consumption and hyperuricemia (Choi et al., 2004) and the risk of incident gout (Williams et al., 2008; Choi et al., 2004). Osturk et al. (2013) suggested meat consumption to be a precipitating factor for gout (Ozturk et al., 2013).

- **Alcohol Intake** Alcohol consumption (most notably beer) has been shown to strongly associate with an increased risk of hyperuricemia and gout (Choi et al., 2004).

- **Ketoacidosis** Starvation and consumption of extremely low-carbohydrate diet have both been reported to cause hyperuricemia (Drenick et al., 1965; Shah et al., 2006).

- **Dairy Intake (Protective)** The consumption of dairy has been shown, in a randomized controlled study, to be protective against elevated urate and gout, attributable to the urate-lowering capacity of milk (Dalbeth et al., 2010).

- **Tomato Consumption** A positive correlation between tomato consumption and blood urate levels has been reported (Flynn et al., 2015).

- **Diuretic Use** In a nested case-control study, it was shown that the use of diuretics elevates blood urate levels and thereby imposes an adverse effect on the development of incident gout (Choi et al., 2012).

- **Drugs/Medications** The uricosuric drugs such as probenecid and lesinurad, and the antihypertensive drug, losartan, lower serum urate levels. On the other hand, drugs such as pyrazinamide and low-dose aspirin increase serum urate levels (Enomoto et al., 2002; Shin et al., 2011). Administration of niacin for hypercholesterolemia has also been reported to increase blood urate levels (Gershon et al., 1974).

- **Fructose** Fructose, the fruit sugar, is capable of causing intracellular ATP depletion by conversion to AMP, increased turnover of adenine and increased serum urate levels. Consumption of sugar-sweetened beverages has been shown to increase urate levels in the blood and increase the risk of gout (Le et al., 2008; Batt et al., 2014).

- **Defects In Purine Metabolism** Increased activity of phosphoribosyl pyrophosphate (PRPP) or reduced activity of hypoxanthine-guanine phosphoribosyl transferase (HGPRT) can cause hyperuricemia. Hyperuricemia resulting from partial and complete deficiencies of HGPRT are termed Kelley-Seegmiller syndrome and Lesch-Nyhan syndrome, respectively (Fathallah-Shaykh et al., 2014).

- **Uromodulin-Associated Defects** Familial juvenile hyperuricemic nephropathy (FJHN) and medullary cystic kidney disease (MCKD) are autosomal dominant disorders caused by variations in the *UMOD* gene characterised by

normal urate production but reduced FEUA, causing hyperuricemia (Vylet'al et al., 2006).

- **Age, Sex, Body mass index (BMI) and Ancestral Origin** Hyperuricemia is common in older men. Male sex and increasing age are by themselves risk factors for hyperuricemia (Conen et al., 2004; Kuo et al., 2016). Hyperuricemia, in women, mostly develop after menopause (Hak et al., 2008). Moreover, ancestral origin of the individual also influences the chance of developing the trait, as does BMI. The risk of gout increases with higher BMI and body weight (Choi et al., 2005).

- **Other Rare Conditions** Other conditions that can result in the overproduction of urate as a result of excess purine degradation include glycogenosis, Lymphoma and leukaemia (Fathallah-Shaykh et al., 2014).

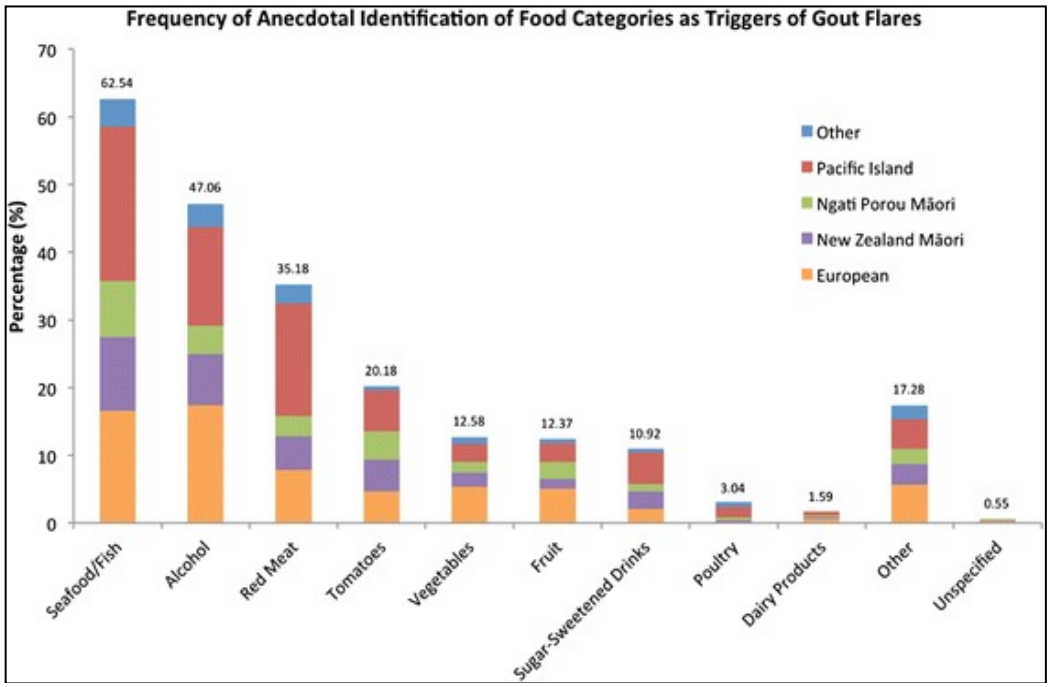


Figure 1.11 Food Triggers For Gout Flares As Reported In The Study By Flynn et al. (2015). *Seafood, alcohol and red meat were reported as the most important triggers of gout flares. (Source: Flynn et al., 2015.)*

1.2.4 SLC2A9

A Key Player in Urate and Gout Genetics

Initial observations on urate levels in gout patients vs. normal individuals unearthed the fact that in humans, the majority of urate is drawn back into the bloodstream via largely uncharacterised mechanisms. The discovery of URAT1 provided some clarity on how urate from the kidney lumen is reabsorbed into the tubular epithelial cells. But how does this intracellular urate make its way back into the interstitium? This was the next obvious question, answered by the discovery of the urate efflux transporter, SLC2A9, that works in tandem with URAT1.

The *SLC2A9* (solute carrier family 2 member 9) gene, mapping to the 4p16.1 region on chromosome 4 in humans (genomic coordinates 4:9446200 - 4: 10686500), is one of the most influential genes in the context of urate genetics. It encodes the SLC2A9 protein, a voltage-driven high-capacity urate transporter (Anzai et al., 2008), which was originally identified, on the basis of predicted topology, as a member of the facilitative glucose transporter (GLUT) family and therefore named as GLUT9 (Phay et al., 2000). The protein is, in fact, a high affinity-low capacity glucose/fructose transporter that shares sequence/structural homology with the other members of the GLUT (SLC2A) family. For example, it contains 12 transmembrane helical domains like all other members of the GLUT family, as well as the motifs- PESPR (Proline-Glutamate-Serine-Proline-Arginine) in helix 2, PETK (Proline-Glutamate-Threonine-Lysine) in helix 12, GPK (Glycine-Proline-Lysine) in loop 2 and GRR (Glycine-Arginine-Arginine) in loop 8 (Augustin et al., 2004). The obvious structural difference between SLC2A9 and the other members of the SLC2A family is the presence of a relatively longer cytoplasmic N-terminus (Phay et al., 2000).

Although the protein does have a high affinity for hexoses, there is sufficient evidence illustrating that it predominantly transports urate in a voltage-dependent manner. Comprehensive analyses indicate that the SLC2A9 protein is capable of hexose/hexose trans-acceleration as well as urate/hexose exchange across membranes (Caulfield et al., 2008; Witkowska et al., 2012).

1.2.4.1 SLC2A9- SPLICING AND EXPRESSION

Transcriptional regulation of two different upstream promoters enables alternative splicing of the gene that results in the production of two splice variants, the long and the short isoforms, described as SLC2A9-L (GLUT9-L; accession number- NM_020041) and SLC2A9-S (GLUT9-S; accession number- NM_001001290), respectively. The RNA of the longer splice variant spans 195kb, consists of 12 exons and codes for a 540-amino acid residue protein. The RNA of the shorter splice variant is 215kb long, comprises 13 exons and encodes a shorter putative protein of length 512 amino acid residues (Anzai et al., 2008). The C-terminal 490 residues in both of these isoforms are identical so that they differ only in their N-terminal amino acid composition (Kimura et al., 2014), as shown in figure 1.12.

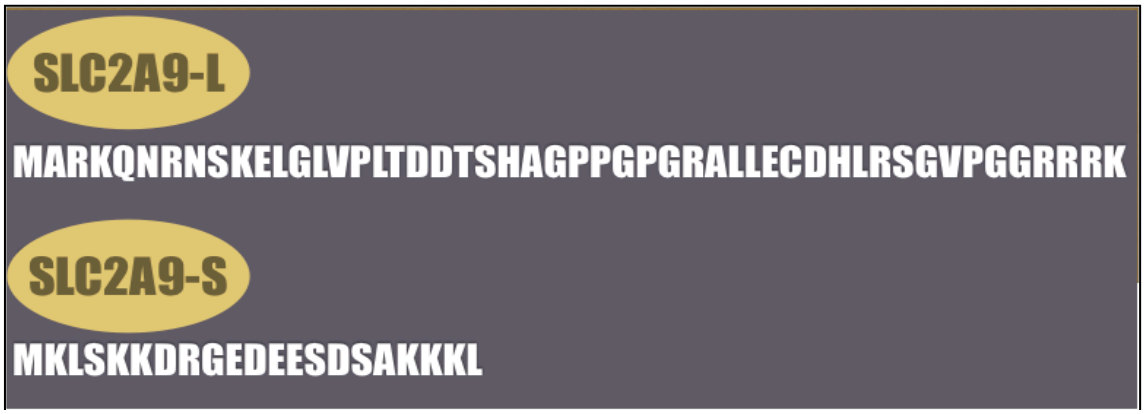


FIGURE 1.12: THE N-TERMINI OF THE TWO SPLICE VARIANTS OF THE SLC2A9 GENE THAT ARE RESPONSIBLE FOR THE DIFFERENTIAL SORTING OF THESE ISOFORMS IN THE HUMAN KIDNEY. *The N-terminal amino acid sequence of SLC2A9-S is shorter (21 residues) than that of SLC2A9-L by 50 residues. (Own illustration)*

The difference in the N-termini of the two isoforms plausibly affects their tissue-specific expression patterns. SLC2A9-L is predominantly expressed in the kidney followed by the liver and placenta, and to a lesser extent in the lung, brain and leukocytes. SLC2A9-S, on the other hand, is expressed only in the kidney and placenta, as revealed by reverse-transcription Polymerase Chain Reaction (RT-PCR) studies (Augustin et al., 2004).

Although both isoforms are expressed in the kidney, their intracellular distributions within the kidney vary, the differential sorting being attributable to the differences in their N-termini. Immunohistochemistry reveals that the SLC2A9-L protein localizes to the

basolateral membrane of the epithelial cells of the renal proximal tubules in humans. This is the isoform responsible for the renal tubular reabsorption of urate (Augustin et al., 2004). The N-terminal amino acid stretch unique to this isoform plays a role in the basolateral sorting of the protein. However, the critical residues specifically responsible for the intracellular trafficking are yet to be identified (Kimura et al., 2014).

The shorter isoform has been shown to localize to the apical membrane of the collecting tubule (Kimura et al., 2014). Evidence illustrating the roles of this isoform is scanty. Therefore, unless otherwise mentioned, 'SLC2A9' refers to the well-characterized SLC2A9-L throughout this report.

1.2.4.2 SLC2A9 IN THE CONTEXT OF HYPERURICEMIA AND GOUT

As mentioned before, the SLC2A9 protein is an important modulator of serum urate. The crucial significance of SLC2A9 in urate homeostasis is evident from both GWASs and functional studies. Single nucleotide polymorphisms in the gene have been shown to be very strongly associated with hyperuricemia. A number of variants, including those in the noncoding regions, have been shown to be associated with reduced FEUA and increased serum urate (Vitart et al., 2008; Doring et al., 2008). Moreover, loss of function variations in the gene have been shown to be causative of hypouricemia (Dinour et al., 2010; Dinour et al., 2012; Matsuo et al., 2008). The gene has showed up as a peak signal in a vast number of urate GWASs and meta-analysis studies in various populations (Urate: European: Kolz et al. (2009), Kottgen et al. (2013), Scharpf et al. (2014), Wallace et al. (2008); Hispanic: Voruganti et al. (2015); American Indian: Voruganti. (2014); African American: Tin et al. (2011), Charles et al. (2011); Mexican American: Voruganti et al. (2013); Mauritius: Cummings et al. (2010), Germany: Stark et al. (2009), Doring et al. (2008), American: Dehghan et al. (2008), Yang et al. (2010); Sadinia: Li et al. (2007); Gout: Chinese: Li et al. (2012), Li et al. (2017); Japanese: Mat suo et al. (2016); African American: Tin et al. (2011))

Variations in *SLC2A9*, together with *ABCG2*, explain up to 3.4% variance in serum urate levels, as discussed previously in section 1.2.3.1. Variants in *SLC2A9* have been reported to have population-specific effects. For instance, the variant rs11942223 has been

reported to play a role in conferring susceptibility to gout in both Caucasians (odds ratio (OR=2) and NZ Polynesians (OR=5) but with different effect sizes (Hollis-Moffatt et al., 2009). *SLC2A9* variants have also been reported to have sex-specific effects on risk of hyperuricemia (Brandstatter et al., 2008). Doring et al. (2008) showed that the variants in *SLC2A9* modulate urate concentrations and are significantly associated with self-reported gout. They also reported the presence of the majority of significantly associated variants to be located within intronic regions of the gene. These variants were also found to have sex-specific effects, so that the serum urate variance explained by *SLC2A9* genotypes was 1.2% and 6% in men and women, respectively in this study (Doring et al., 2008).

Apart from the evidence for urate-associated variants located within the introns of *SLC2A9*, there is evidence for the presence of intergenic variants and epistatic interactions in the *SLC2A9* locus (Wei et al., 2014). Based on this rationale, I have analysed the entire *SLC2A9* locus, rather than focusing only on the exons. My study is therefore a 'locus-wide association study' (LWAS).

1.3 Specific Aims Of This Study

This research is based on the hypothesis that the Polynesian genome likely contains population-specific variants in the *SLC2A9* locus, which has been implicated in the control of serum urate at a genome-wide significance level (Kottgen et al., 2013). The main focus of the study is to identify Polynesian-specific hyperuricemia-associated genetic variants, if any, in the *SLC2A9* locus. The specific aims of the study include:

- To identify and visualize variants in the *SLC2A9* locus.
- To phase and visualize haplotypes for the *SLC2A9* locus and then compare the Polynesian and European haplotypes.
- To conduct single variant association analysis using logistic regression to test for the association of identified genetic variants with hyperuricemia in the East and West Polynesians.
- To prioritize variants and replicate their association with hyperuricemia in a larger independent Polynesian cohort.
- To test the prioritized variants for their association with gout in Polynesians.

Chapter 2

Methods

CHAPTER 2
METHODS

2.1 PARTICIPANTS IN THE STUDY

All Polynesian samples in this study were drawn from the New Zealand (NZ) gout case-control cohort, which consists of Polynesian and European participants recruited from all over NZ during the period 2006-2013. Sample recruitment was carried out under the overall supervision of Professor Tony Merriman, University of Otago, Dunedin, New Zealand. This dataset was developed with the aim of evaluating the genetic and environmental risk factors for hyperuricaemia and gout in the Polynesian and European people residing in NZ. All gout cases were recruited from the Waikato, Canterbury and Auckland regions and fulfilled the American College of Rheumatology (ACR) criteria for gout classification. All healthy controls were recruited from Otago and Auckland regions and self-reported no diagnosis of gout. All Polynesian controls also satisfied the ACR criteria for not having gout. All Polynesians self-reported Polynesian grandparental ancestry for at least three grandparents.

Written informed consent was given by all individuals who participated in the study. Ethical approval was granted by the Lower South Ethics Committee (OTA/99/11/098) and the New Zealand Multi-Region Ethics Committee (MEC/05/10/130).

Apart from the NZ gout case-control cohort, European cases and controls were obtained from two more cohorts including (a) The Health Professionals Follow-up Study (HPFS)- an all-male health based longitudinal study that began in 1986, with the aim of evaluating the potential relationship between nutritional factors and men's health (www.hsph.harvard.edu.hpfs) and (b) The Nurses' Health Study (NHS)- a female-based longitudinal study, established in 1976, with the initial aim of investigating the long-term health effects of oral contraceptives in the US female population (www.channing.harvard.edu/nhs).[1]

[1] Samples from the HPFS and NHS were kindly provided by Professor Hyon K Choi (Gout and Crystal Arthropathy Center, Massachusetts General Hospital, Boston).

2.2 RESEQUENCING

Targeted resequencing, an important application of next generation sequencing (NGS) technology, is a method that can be employed to capture all variants within a target region of interest by scanning the genomes of a given sample set, rather than detecting a limited number of predetermined genotypes. An important application of the resequencing technology is the identification of population-specific genetic variants (Keller et al., 2011).

In 2014, Professor Tony R Merriman at the Department of Biochemistry, University of Otago, undertook a resequencing project with the aim of specifically identifying Polynesian-specific genetic variants within genes and regulatory regions previously known to be associated with serum urate levels and/or gout.

2.2.1 THE RESEQUENCE COHORT

A subset of the NZ gout case-control cohort, comprising 440 Polynesian samples (East Polynesians (EP): n = 223, West Polynesians (WP): n = 186 and Mixed East/West Polynesian: n = 31) with either very high serum urate levels ($\geq$ 0.41 mmol/L) or very low serum urate levels ($\leq$ 0.37 mmol/L), were selected for resequencing (table 2.1). Similarly, three hundred and sixty nine European samples were also resequenced. These samples were obtained from three different cohorts- (a) 82 samples from the NZ gout case-control cohort (b) 169 samples from the HPFS and (c) 125 samples from the NHS cohorts. The Cohort comprised hyperuricemic cases (average serum urate level = 0.53 mmol/L) and normouricemic controls (average serum urate level = 0.27 mmol/L).

In this thesis, the Resequence Cohort is referred to as the 'Discovery Cohort', as it was used to discover the potential association of genetic variants with hyperuricemia (and gout) in the Polynesian population.

2.2.1.1 SUB-SETTING THE DISCOVERY COHORT

"Allele frequency differences between cases and controls due to systematic ancestry differences- can cause spurious associations in disease studies" (Price et al., 2006). The

differences in allele frequencies across different populations can impact genotype-phenotype association studies (Pritchard et al., 1999). Heterogeneity may be introduced in a population via genetic drift (changes in allele frequencies in a population over time by chance) and/or genetic admixture (introduction of new genetic lineages as a result of interbreeding events between previously isolated populations) (Long J., 1991). One method to deal with stratification is to assign samples to discrete sub-populations before analysing associations (Price et al., 2006).

Since the main focus of this project was to identify population-specific genetic variants associated with hyperuricemia (and gout), population stratification was a key component of the study design. Individuals belonging to the European ancestry were not greatly influenced by population admixture. This European cohort was, therefore, not further subdivided (n = 369). Unlike the European cohort, the Polynesian cohort represented an European-admixed population displaying significant genetic heterogeneity. Therefore, the NZ Polynesian cohort (n = 440) was further classified as EP (primarily including Cook Island and NZ Māori; n = 223), WP (primarily including Samoa, Tuvalu, Tonga, Niue and Tokelau; n = 186) and Mixed East/West Polynesian (n = 31) subgroups. The Mixed East/West Polynesian subgroup (not represented in table 2.1) was excluded from most analyses, in order to be able to identify EP-specific and WP-specific hyperuricemia/gout-associated genetic variants.

2.2.1.2 THE DEMOGRAPHIC AND CLINICAL INFORMATION FOR THE DISCOVERY COHORT

The demographic and clinical details for the Discovery Cohort are presented in table 2.1. Data was exported from BC|SNPmax, an efficient repository for data storage and management, provided by the Biocomputing (BC) Platforms (http://www.bcplatforms.com/).

TABLE 2.1 THE DEMOGRAPHIC AND CLINICAL INFORMATION FOR THE DISCOVERY COHORT

	NZ Polynesian		European
	EP	WP	
N	223	186	369
Hyperuricemic Cases (n, %)	106, 47.5	108, 58	196, 53.1
Normouricemic Controls (n, %)	117, 52.5	78, 42	173, 47.8
Sex (male n, %)	134, 60.1	128, 68.8	236, 64
Average age (years)	47.5	47.5	48.4*
Gout cases (n, %)	71, 31.8	90, 48.4	74*
Non-gout controls (n, %)	152, 68.2	96, 51.6	8*

** Data based on NZ samples only (n = 82). EP: East Polynesian, WP: West Polynesian*

2.2.2 RESEQUENCING PROCEDURE

2.2.2.1 REGION SELECTION

An approximately 2.5Mb region across the human genome was selected for resequencing, including both genic and regulatory regions. A total of 790 genes were selected including 182 genes reported in the largest urate GWAS conducted by Kottgen et al. (2013), 14 BMI and renal function genes, 45 genes involved in allopurinol metabolism and 12 candidate genes associated with the risk of gout development and 6 urate transporter genes not previously known to be associated with gout. All exons along with 10bp flanking regions plus the 3'- and 5'- UTRs for all transcripts were extracted using Ensembl version v74. Regulatory regions including the *SLC22A7*/*ABCC10* region, thirty association regions (P < 1e-8) identified in the Kottgen et al. GWA study and 14 DNase hypersensitivity regions identified from 19 renal cell samples available on the Gene Expression Omnibus database were also included in the project.[2]

The *SLC2A9* gene, mapping to the 4p16.1 region on chromosome 4 in humans (genomic coordinates 4:9446200 - 4: 10686500), has been reported to be significantly associated with serum urate and gout (discussed in Chapter 1, section 1.2.4). There is evidence for the presence of intergenic variants and epistatic interactions within the *SLC2A9* locus (Wei et al., 2014). Therefore, rather than selecting only the exons of the gene, the resequencing project covered the entire *SLC2A9* locus, including the complete gene (all exons, all introns and the 5'- and 3'- UTR regions), the neighbouring genes as well as the inter-genic regions (table 2.2).

2.2.2.2 SEQUENCING PROTOCOL

All DNA samples (250ng of DNA/sample) were sent to McDonnell Genome Institute, Washington University for sequencing and library preparation. The Illumina indexed libraries were constructed as per the manufacturer's protocol and Nextera DNA Sample Prep kit (Illumina Inc., San Diego).[3]

The protocol comprised the following steps:

- DNA fragmentation using Covaris E220 DNA Sonicator (Covaris Inc., Woburn)
- Ligation of sequence adapters on to the DNA fragments
- Eight cycles of DNA amplification using primers and indices to adapter ligated DNA fragments
- Library purification and size selection using Solid Phase Reversible Immobilization (SPRI) technique
- Hybridization and amplification of fragments using custom Roche NimbleGen SeqCap kit (Roche NimbleGen Inc., Madison)
- Sequencing on Illumina HiSeq 2500 (Illumina, San Diego) with an average of 51.2X coverage across the complete target sequence

[2] The specific regions for targeted resequencing were selected by Professor Tony R Merriman (Project Supervisor; Department of Biochemistry, University of Otago), Professor Hyon K Choi (Gout and Crystal Arthropathy Center, Massachusetts General Hospital, Boston, MA), Assistant Professor Eli Stahl (Icahn School of Medicine, Mount Sinai, New York) and Assistant Professor David B Mount (Brigham and Women's Hospital, Boston). The exact genome positions to be sequenced were identified by Ruth Topless (Assistant Research Fellow, Merriman Laboratory) and Murray Cadzow (Assistant Research Fellow, Merriman Laboratory).

2.2.2.3 SEQUENCE ALIGNMENT AND VARIANT CALLING

The entire sequence alignment and variant calling procedure was carried out in the Merriman Laboratory, following the Genome Analysis Tool Kit (GATK) Best Practices guidelines (Auwera et al., 2013).[3]

The variant calling protocol comprised the following steps:

- Extraction of FASTQ files from raw sequence files using Sequence alignment/map (SAM) tools software package version 1.1.2
- Alignment of FASTQ files to human reference genome (build GRCh37) using the Burrows-Wheeler Aligner (BWA 0.7.12) (Li et al., 2009) to create binary alignment/map (BAM) files
- Processing of the BAM files using Picard 1.114 from the github repository (www.github.com/broadinstitute/picard)
- Base recalibration and alignment of insertion/deletions (indels) using the GATK 3.3.0 framework (McKenna et al., 2010)
- The creation of Variant call format (VCF) files using the GNU Parallel command-line (Tange, 2011) and the GATK HaplotypeCaller (DePristo et al., 2011)

The variants in the resulting variant call format (VCF) file were recalibrated using the GATK variant quality score recalibration utility. Variants with a truth sensitivity of less than 99.00 were removed during recalibration of the VCF file.

[3] Sample shipping was carried out by Amanda Phipps-Green (Assistant Research Fellow, Merriman Laboratory). Library preparation, sequence alignment and variant calling steps were carried out by James Boocock (ex-Research Assistant, Merriman Laboratory).

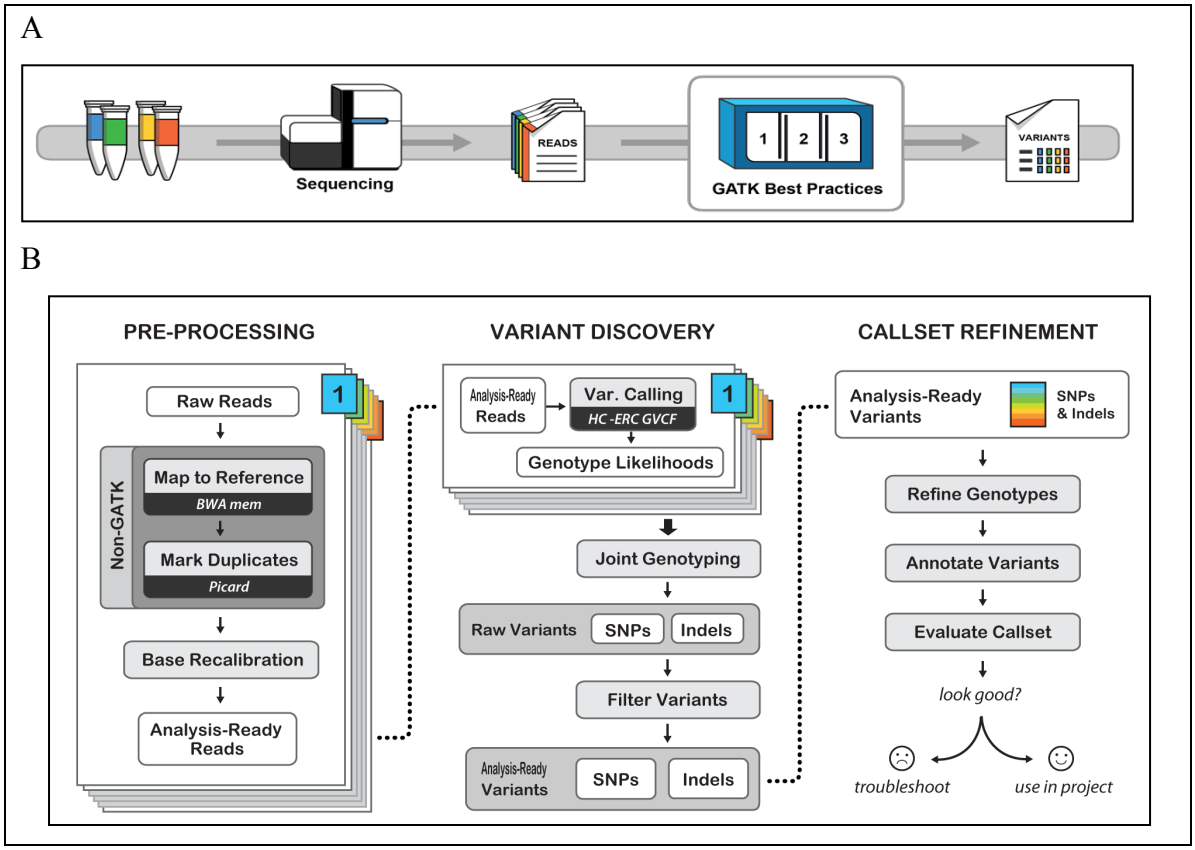


FIGURE 2.1: SCHEMATIC REPRESENTATION OF GATK BEST PRACTICES: *(A) GATK Best Practices workflow and (B) GATK Best Practices pipeline. Source: https://software.broadinstitute.org/gatk/documentation/presentations.php*

2.3 GENOMIC REGION ANALYSED AND VARIANTS IDENTIFIED

The complete *SLC2A9* locus was analysed in this study. All introns, exons and untranslated regions (5'- and 3'- UTRs) of each of the following genes were analysed. The intergenic regions, pseudogenes (RNA5SP154 (RNA, 5S ribosomal pseudogene 154) and RNA5SP155 (RNA, 5S ribosomal pseudogene 155)) and other annotated sequences (RP11-448G15.3, RP11-480G3.1, AC006499.7, AC006499.9, AC006499.2, RP11-136113.1) in the locus were also included in the analysis. Annotations were extracted using Ensembl Variant Effect Predictor.

- *DEFB131A (*defensin beta 131A*)*
- *SLC2A9* (solute carrier family 2 member 9)
- *DRD5* (dopamine receptor D5)
- *WDR1* (WD repeat domain 1)

- *ZNF518B* (zinc finger protein 518B)
- *CLNK (*cytokine dependent hematopoietic cell linker)

The genomic coordinates for all genes in the *SLC2A9* locus were noted from the Ensembl human reference genome (build GRCh37). The genes were arranged in order of their chromosomal position in order to mark the complete region of interest, as shown in table 2.2.

TABLE 2.2 THE GENOMIC REGION ANALYSED IN THIS STUDY

GENE/REGION	CHROMOSOME	START POSITION	END POSITION
DEFB131A	4	9446260	9452240
SLC2A9	4	9772777	10056560
DRD5	4	9783258	9785632
RNA5SP154	4	9794375	9794485
RP11-448G15.3	4	10069713	10074643
WDR1	4	10075963	10118573
RNA5SP155	4	10117380	10117508
RP11-480G3.1	4	10144991	10145279
AC006499.7	4	10168783	10169389
AC006499.9	4	10239837	10239859
AC006499.2	4	10293819	10294332
RP11-136113.1	4	10412620	10413268
ZNF518B	4	10441498	10459034
CLNK	4	10488019	10686489
OVERALL REGION	**4**	**9446200**	**10686500**

The number of variants within the *SLC2A9* locus identified using the resequencing procedure was 3963. A complete list of all variants is provided in appendix 1. Variants that were previously reported/deposited in the dbSNP database were identified by their unique identifiers (rsid #), while variants that did not have an rsid number (novel variants) were annotated based on their location on the chromosome. For example, a variant at the genomic location 4:9914056 was annotated as VAR_CHR4_9914056.

2.4 PRELIMINARY EXPLORATORY DATA VISUALIZATION

A series of data visualization tools and techniques were used in this project aimed towards addressing the following goals:

- Visualize where the variants are located
- Identify the different types/categories of variants
- Identify polymorphic sub-regions within the locus
- Understand the functional relevance of variants based on their location
- Identify missing data patterns, if any
- Visualize haplotypes in the region
- Identify unique haplotypes in the Polynesian population

2.4.1 VISUALIZING MISSING GENOTYPES

Visdat (Visualisation of Data) is a tool in R version 3.4.1 that can be used to visualize dataframes (RStudio Team, 2015). Variables in a dataframe can be plotted to check for missing data. The visdat tool was used in this study to check for the percentage of missing genotypes prior to genotypic analyses.

2.4.2 ANNOTATING VARIANTS

In order to predict the deleteriousness of the discovered variants, tools that are able to annotate and/or predict the functional relevance of both coding and noncoding variants, were employed. These include:

2.4.2.1 ENSEMBL VARIANT EFFECT PREDICTOR (VE!P)

AVAILABLE AT HTTPS://WWW.ENSEMBL.ORG/VEP

VE!P is a widely used tool to predict the effect of genomic variants of all types including single base substitutions, insertion and deletions (indels), copy number variations and structural variations. The two widely used algorithms to predict the deleteriousness of nonsynonymous variants within coding regions of human genes, Sorting Intolerant from Tolerant (SIFT, http://sift.jcvi.org, Sim et al., 2012) and Polymorphism Phenotyping v2

(PolyPhen-2, http://genetics.bwh.harvard.edu/pph2, Adzhubei et al., 2010), are now incorporated within Ve!P (McLaren et al., 2016).

2.4.2.2 SNP EFFECT (SNPEFF)

AVAIABLE FOR DOWNLOAD AT HTTP://SNPEFF.SOURCEFORGE.NET

SnpEff is a java-based program that can be used to functionally annotate and classify variants based on the variant type (SNPs, indels etc), location (upstream, intergenic, splice site etc) and effect (synonymous, nonsynonymous, stop lost, frameshift etc) (Cingolani et al., 2012).

2.4.2.3 COMBINED ANNOTATION DEPENDENT DEPLETION (CADD)

AVAILABLE AT HTTP://CADD.GS.WASHINGTON.EDU

The CADD framework scores the deleteriousness of variants, both coding and non-coding, based on diverse variant information such as conservation, regulatory effects, allelic diversity etc. It works on the principle of comparing and contrasting simulated variants with those that have survived natural selection (Kircher et al., 2014).

2.4.2.4 GENOCANYON

AVAILABLE AT HTTP://GENOCANYON.MED.YALE.EDU

GenoCanyon is an unsupervised statistical learning-based approach to functionally annotate whole genomes, based on biochemical signals and conservation scores (Lu et al., 2015).

2.4.2.5 GENOME WIDE ANNOTATION OF VARIANTS (GWAVA)

AVAILABLE AT HTTPS://WWW.SANGER.AC.UK/SANGER/STATGEN_GWAVA

GWAVA is a tool for the prioritisation of non-coding variants based on various parameters such as the GC content, evolutionary conservation and the ENCODE/GENCODE annotations (Ritchie et al., 2014).

2.4.3 VISUALIZING VARIANT ANNOTATIONS WITH CIRCOS

AVAILABLE FOR DOWNLOAD AT HTTP://CIRCOS.CA

Circos plots were used to visualize where variants are located, mark regions of high variant density and, more importantly, to display variant annotations.

The circos package, written in Perl, can be deployed on any operating system where Perl is available. This command-line tool is a useful software to visualize data in a circular layout. Circos has emerged to be one of the standard tools used to visualize genomic data. Configuration files, input files and command-line flags can be used to input data and specify parameters to generate image files as output. The biggest advantage of circos is the ability to plot multiple layers of information in a single plot to explore and understand the relationship between different objects (Krzywinski et al., 2009).

2.4.4 VISUALIZING HAPLOTYPES

"Combinations of genetic variants occurring on the same DNA molecule are known as haplotypes" (Jager et al., 2014). In order to better understand genetic information in the context of phenotypes/diseases, haplotype visualization is a valuable approach. Visualization of haplotypes and their comparisons across different populations can provide valuable insights into the patterns of variations associated with a phenotype/disease.

2.4.4.1 PHASING HAPLOTYPES WITH SHAPEIT

AVAILABLE FOR DOWNLOAD AT
HTTP://MATHGEN.STATS.OX.AC.UK/GENETICS_SOFTWARE/SHAPEIT/SHAPEIT.HTML

Haplotype phasing is the estimation of haplotypes from SNP genotypes (Delaneau et al., 2014). Individuals sequenced/genotyped for any particular study may exhibit some degree of relatedness by chance or by design. In such sample sets, estimation of haplotypes is a key task before proceeding further with genotypic/association analyses.

SHAPEIT v2.r790, a Hidden Markov Model (HMM)-based approach to infer haplotypes from genotype data (Delaneau et al., 2014; O'Connell et al., 2014), was used in this study for haplotype estimation/phasing.

SHAPEIT v2.r790 is a command-line tool that takes a set of genotypes (in the .ped/.map format) and a genetic map (in the .txt format) as input and gives the estimated haplotypes (in the .haps format) as output. SHAPEIT offers several advantages to the user. For example, it can be used to phase low-coverage sequence data, allows multithreading to reduce computational times and can be used to phase individuals with any level of relatedness.

2.4 4.2 VISUALIZING HAPLOTYPES WITH INPHAP

AVAILABLE FOR DOWNLOAD AT HTTP://IT.INF.UNI-TUEBINGEN.DE/?PAGE_ID=193

The inPHAP (Interactive visualization of genotype and phased haplotype data) software package was used for the interactive visualization of genotypes and phased haplotypes.

The inPHAP software is a java-based application and can run on Java 7 Runtime Environment. The tool provides a graphical user interface and supports a wide range of interactions with the data. It allows for filtering and/or aggregation of large data based on meta-information to reduce the amount of time spent in data investigation and reduce data complexity while enabling the assessment of hidden/underlying patterns (Jager et al., 2014).

2.5 LWAS

The *SLC2A9* LWAS was designed to address the following goals:

- Test the association of the identified variants with hyperuricemia
- Identify association signals specific to the EP and WP populations
- Identify significant associations, characterize them and analyse linkage disequilibrium patterns in the EP and WP groups
- Replicate significant associations in a larger independent Polynesian cohort

2.5.1 ASSOCIATION ANALYSIS – DISCOVERY PHASE

2.5.1.1 LOGISTIC REGRESSION

Logistic regression is a statistical method used to describe the relationship between a dichotomous dependent (response/outcome) variable and a set of independent

(predictor/explanatory) variables (Sperandei et al., 2014). Multivariate logistic regression analysis (model with multiple explanatory variables) generates the p-value, the beta estimate and the standard error for each variable.

In this study, the association of alleles with hyperuricemia was analysed. Logistic regression, treating the dependent variable as dichotomous (hyperuricemic versus normouricemic) was the statistical approach employed to identify discovery-phase associations. Multiple-adjusted logistic regression was carried out using R version 3.4.1 (RStudio Team, 2015). All 3963 variants were individually tested for association with hyperuricemia in each of the three population cohorts (West Polynesian, East Polynesian and European).

NOTE: The R programming language was extensively used in this project. Data extraction for various analyses, file management and processing, all calculations, statistical analyses and plotting were carried out using R version 3.4.1 (RStudio Team, 2015).

2.5.1.1.1 ADJUSTING FOR CONFOUNDERS

A confounder is any factor/variable that influences the dependent (response/outcome) or the independent (predictor/explanatory) variable under study (Skelly et al., 2012). Since confounders can mask real associations (false negative results) or reveal spurious associations (false positive results), it is important to adjust for potential confounders while studying associations between explanatory and response variables. Logistic regression allows for confounder-adjustment. Both unadjusted and confounder-adjusted analyses were performed to test for the association of each variant with hyperuricemia in all three population cohorts. The regression model was adjusted for age, sex (well-known confounding factors for hyperuricemia) and principal components (discussed below).

Principal component analysis (PCA) is a dimension reduction statistical technique for modelling genotypic data (ancestral differences between cases and controls) along continuous axes of genetic variation (Price et al., 2006). The first principal component (PCA1) accounts for maximum variance in the data and identifies large ancestral clusters.

The second principal component (PCA2) accounts for as much of the remaining variance in the data as possible while the third component accounts for much of the remainder of the variance and so on, so that the last principal component accounts for the least amount of variance in the data.

Ancestry adjustment is crucial prior to computation of association statistics. Although the Polynesian sample set was already sub-divided into East Polynesian and West Polynesian subgroups on the basis of self-reported ethnicity, the model was further adjusted for principal components. This was done to account for population admixture, since the principal components calculations were based on genetic ancestries of participants rather than their self-reported (grand-parental) ethnicities. Principal components 1 through 10 (PCA1-10) were used for confounder adjustment.[4]

2.5.1.1.2 COMPUTING STATISTICAL SIGNIFICANCE

Statistical significance (p-value) is the likelihood that an observation is owing to chance. A p-value higher than the alpha significance level (a pre-chosen threshold usually set at 5%, equivalent to 95% confidence interval i.e., a 5% risk of a false positive result), indicates that the observation can probably be explained by sampling variability. On the other hand, a p-value lower than the alpha threshold means that the observed result has nominal statistical significance (Sullivan et al., 2012). In this study, the significance level was set at 5%, so that any variant with a p-value ≤ 0.05 was considered as displaying a nominally significant association with hyperuricemia.

All significant variants (variants displaying a statistically significant association between its minor/altered allele and hyperuricemia) in the EP, WP and European cohorts were further analysed.

NOTE: Since replication via genotyping was incorporated in the study design to validate discovery-phase associations, Bonferroni correction (that accounts for multiple testing) was not applied in this study.

[4] PCA was carried out by Ruth Topless (Assistant Research Fellow, Merriman Laboratory). The data for PCA was obtained by genotyping on the CoreExome bead chip platform, which was carried out by Amanda Phipps-Green (Assistant Research Fellow, Merriman Laboratory), Tanya Flynn (Assistant Research Fellow, Merriman Laboratory) and Murray Cadzow (Assistant Research Fellow, Merriman Laboratory).

2.5.1.1.3 COMPUTING THE EFFECT SIZE

A common effect size index used in epidemiological studies is the odds ratio (OR). The odds ratios and confidence intervals for all variants displaying statistically significant association in each population group were computed from the beta estimate and standard error values generated through logistic regression analysis. The allelic odds ratios were calculated with respect to the minor allele.

2.5.1.2 PLOTTING WITH LOCUSZOOM

AVAILABLE AT LOCUSZOOM.ORG

The LocusZoom plotting tool visually displays results of association analysis for a specified genomic region. Both web-based and standalone versions are available. The software utilizes publicly available genetic data (gene annotations from the UCSC browser, variant information from the 1000 Genomes/dbSNP databases and Linkage disequilibrium (LD) data provided by the HapMap Phase II project) to generate plots displaying the strength of association signals (Pruim et al., 2010).

2.5.1.3 IDENTIFYING SIGNIFICANT SIGNALS UNIQUE TO OR COMMON ACROSS POPULATIONS

The main aim of this study was the identification of significant associations unique to the Polynesian population. Significant signals overlapping across populations and those specific to the EP and WP subgroups were therefore identified and represented using a Venn diagram.

2.5.1.4 ANALYSING LINKAGE DISEQUILIBRIUM WITH HAPLOVIEW

AVAILABLE AT HTTP://WWW.BROAD.MIT.EDU/MPG/HAPLOVIEW/

LD is the non-random association of alleles. Alleles in strong/complete LD are inherited together (Slatkin et al., 2008). The pairwise LD between all significant signals in East and West Polynesian subsets was calculated using the Haploview software package. Haploview, written in Java, can be deployed on any operating system where Java 1.3 or

later is installed. The command-line interface was used to generate LD plots from genotype data. An $r^2 \geq 60$ indicates LD between the variants, the threshold LD for strong LD was set at $r^2 \geq 80$ while an $r^2 = 100$ indicates complete LD. Using Haploview has the advantage of visually appealing graphical representation of results (Barrett et al., 2005).

2.5.1.5 META-ANALYSIS WITH 'META'

Meta-analysis is a statistical technique employed to increase the overall power of a study. Two possible statistical models can be used for meta-analysis depending on the population heterogeneity - the fixed effect model (for more homogenous datasets) and the random effect model (for more heterogenous datasets) (Haidich et al., 2010).

Meta-analysis was performed using the statistical package 'meta' in R version 3.4.1 (RStudio Team, 2015). The heterogeneity between the sample sets was calculated (Q-statistic) and an overall p-value, the heterogeneity p-value and the OR for combined analysis were generated. The fixed-effect model was used wherever the population heterogeneity was greater than 0.05 ($P_{het}>0.05$) and the random effect model was chosen when the population heterogeneity was less than 0.05 ($P_{het}<0.05$). The significance threshold for meta-analysis was set at 0.05 (p-value ≤ 0.05), similar to that of the logistic regression model.

2.5.1.6 CALCULATING THE POWER OF STUDY

The power of a study indicates whether the sample size used is large enough to detect statistically significant associations between alleles and the phenotype. The power to detect P_{OR} (p-value for odds ratio) < 0.05 was calculated for the East Polynesian, West Polynesian and the combined dataset used for meta-analysis, using the methodology outlined by Johnson and colleagues (Johnson et al., 2001). Power $\geq 80\%$ was considered adequate. All power calculations were done in R version 3.4.1 (RStudio Team, 2015).

2.5.2 REPLICATING ASSOCIATIONS

Replication is the technique of reproducing associations to validate the findings made initially. Replication is important to ensure that the discovery-phase associations were not a result of chance or uncontrolled biases (Kraft et al., 2009). The discovery-phase associations were replicated by genotyping in a larger, independent sample set.

2.5.2.1 STUDY PARTICIPANTS

Subsets of individuals were drawn from the NZ gout case-control cohort (section 2.1) to create two Replication Cohorts- Replication Cohort A and Replication Cohort B. The demographic and clinical details for the Replication Cohorts A and B are provided in table 2.3.

The Replication Cohort A consisted of 1221 Polynesians (EP: n = 707, WP: n = 514) who were genotyped on the Sequenom MassARRAY platform and the Replication Cohort B consisted of 1577 Polynesians (EP: n = 932, WP: n = 645) who were genotyped on the TaqMan® SNP Genotyping platform. All individuals who were a part of the Discovery Cohort were excluded from the Replication Cohorts, so that replication could be carried out in completely independent sample sets. All Mixed East/West Polynesians were excluded from analysis. The Replication Cohorts comprised hyperuricemic cases (serum urate levels $\geq$ 0.41 mmol/L) and normouricemic controls (serum urate levels $\leq$ 0.37 mmol/L). Individuals with serum urate levels > 0.37 mmol/L and < 0.41 mmol/L were excluded from analysis. Individuals whose serum urate levels were unknown were excluded from analysis, except for gout cases who were considered to be hyperuricemic. Similarly, normouricemic individuals, whose gout status was unknown, were considered to be non-gout controls.

TABLE 2.3 THE DEMOGRAPHIC AND CLINICAL INFORMATION FOR THE REPLICATION COHORTS A AND B

	Replication Cohort A		Replication Cohort B	
	EP	**WP**	**EP**	**WP**
N	707	514	932	645
Hyperuricemic Cases (n, %)	318, 45	305, 59.3	367, 39.4	345, 53.5
Normouricemic Controls (n, %)	389, 55	209, 40.7	565, 60.6	300, 46.5
Sex (male n, %)	393, 55.6	390, 76	536, 57.5	472, 73.2
Average Age (years)	50.6	50.6	47.4	47.4
Average BMI	32.4	32.45	34.1	34.1
Gout Cases (n, %)^	312, 44.1	291, 56.6	400, 42.9	334, 51.8
Non-gout Controls (n, %)^	395, 55.9	223, 43.4	515, 55.3	300, 46.5

^Number based on individuals whose gout status (case or control) could be clearly ascertained. EP: East Polynesian, WP: West Polynesian.

2.5.2.2 PRIORITISING VARIANTS FOR REPLICATION

For replication, some of the nominally significant signals obtained from the initial (discovery-phase) association analysis were prioritised based on several criteria outlined below. Only those variants that satisfied all of the following criteria were chosen for replication.

- **STATISTICAL SIGNIFICANCE** The variant has a p-value ≤ 0.05 as computed during the initial association analysis
- **EFFECT SIZE** The variant (minor allele) has an OR (95% CI) ≤ 0.5 (direction of association- protective) or OR (95% CI) ≥ 2 (direction of association- risk)
- **POPULATION-SPECIFIC SIGNAL** The variant was found to be specific to the Polynesian population (present in either the East and/or West Polynesian cohort but absent in the European cohort)

- **LINKAGE DISEQUILIBRIUM** Where multiple significant signals were found to be in strong LD with each other, only one of those variants were chosen for replication based on the above mentioned criteria

2.5.2.3 GENOTYPING

A common and reliable technique for replicating single variant-signals is genotyping the prioritised variants in a new, larger and completely independent (nonoverlapping) cohort (Kraft et al., 2009).

Five variants (VAR_CHR4_9914056, rs373311989, VAR_CHR4_9452283, VAR_CHR4_10160679 and VAR_CHR4_10457448) were shortlisted for replication based on the criteria outlined in section 2.5.2.2.

Before directly genotyping on the Taqman® Genotyping platform, it was checked if any of the variants prioritised for replication in this study, were previously genotyped on either the Infinium® CoreExome-24 v1.2 bead chip platform or the Sequenom MassARRAY platform, as part of the genotyping projects undertaken by the Merriman Laboratory aimed at studying the association of important urate-associated loci, reported in literature, with gout, using subsets of the NZ gout case-control cohort (section 2.1).[5] A flowchart depicting how the genotype data for the replication-phase was sourced is provided in figure 2.2.

None of the prioritized variants were genotyped on the Infinium® CoreExome-24 v1.2 bead chip platform. Two of the prioritized variants (VAR_CHR4_10160679 and VAR_CHR4_10457448) were previously genotyped on the Sequenom MassARRAY platform. Therefore, the genotype data for the variants, VAR_CHR4_10160679 and VAR_CHR4_10457448, were sourced from the Sequenom genotype dataset. The remaining three variants (VAR_CHR4_9914056, rs373311989 and VAR_CHR4_9452283) were genotyped using Taqman® methodology.

[5] The prep work for the Sequenom genotyping project was done by Amanda Phipps-Green (Assistant Research Fellow, Merriman Laboratory). Genotyping on the CoreExome bead chip platform was carried out by Amanda Phipps-Green (Assistant Research Fellow, Merriman Laboratory), Tanya Flynn (Assistant Research Fellow, Merriman Laboratory) and Murray Cadzow (Assistant Research Fellow, Merriman Laboratory).

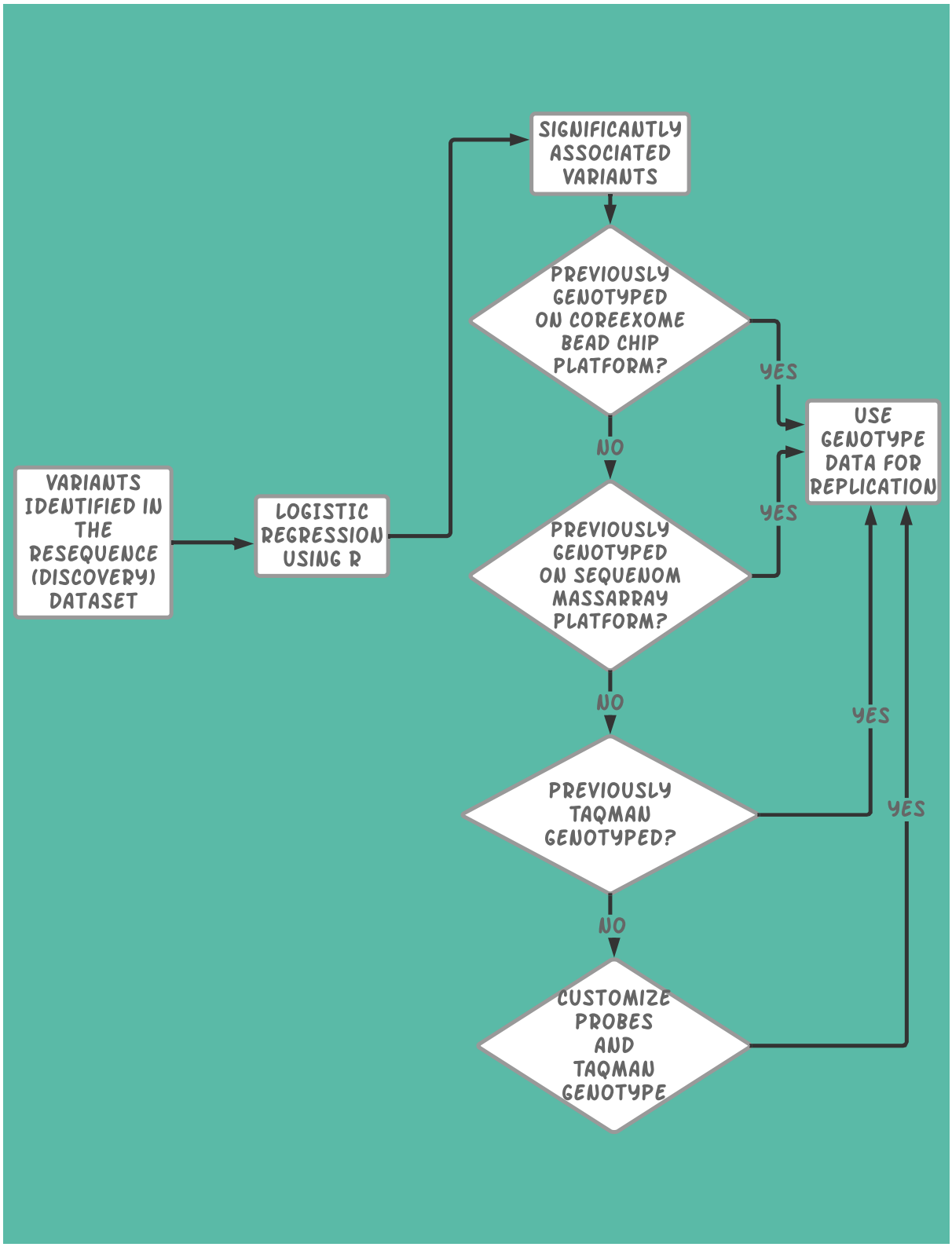


FIGURE 2.2 APPROACH USED FOR SOURCING GENOTYPE DATA FOR REPLICATION. *Variants prioritised for replication were genotyped using Taqman® methodology, if they were not previously genotyped either on the CoreExome-24 v1.2 bead chip platform or the Sequenom MassARRAY platform.*

2.5.2.3.1 TAQMAN® GENOTYPING

The TaqMan® SNP Genotyping platform (Applied Biosystems, Foster City, USA) is used to carry out allele discrimination assays using the Lightcycler® 480 version 15 Real-Time Polymerase Chain Reaction (RT-PCR) System (Roche Applied Science, Indianapolis, IN, USA).

2.5.2.3.1.1 CUSTOMIZING PROBES WITH ANNOTATE_SEQUENCE-V2.0

AVAILABLE AT HTTPS://ZENODO.ORG/RECORD/56250

For common variants, commercial probes are usually readily available for use in assays. However, for novel or uncommon variants, custom probes are usually required to be designed. While designing custom probes, it is crucial to ensure that the probe is able to uniquely identify and bind to the sequence of interest carrying the variant. The first step in designing a custom probe is therefore sequence annotation. The snp_design: annotate_sequence-v2.0 is a program that can be used for this purpose (Flynn and Boocock, 2016).

Since all the three variants to be genotyped using Taqman® methodology in this study were novel and/or uncommon, commercial probes for these variants were not already available. Therefore, custom probes had to be designed for each of the variants to carry out the PCR assays. The following steps were carried out for each variant using the annotate_sequence program.

- The Polynesian-specific consensus sequence around the variant of interest (~200 bases on either side) was identified.
- Any other common/uncommon SNPs in the selected sequence were masked so that the Taqman probes/primers are not designed over these variants but are rather unique to detect the SNP of interest.
- Any indels in the selected sequence were masked so that the Taqman probes/primers are not designed over indels in the region, if any.

Probes were then designed and ordered based on the annotated sequence using Life Technologies custom design tool (https://www.thermofisher.com).[6]

2.5.2.3.1.2 RUNNING THE ASSAYS

The Taqman assays were run using 384-well plates. Each well contained 2 µL (6-10 ng/µL) DNA plus 5 µL of the kapa master mix (2.5 µL kapa mix + 2.43 µL water + 0.07 µL probe). Each assay also included quality controls (QC) to confirm accurate genotyping. The assays were autocalled by the Light Cycler 480 machine. Each run took approximately 45 minutes. The signal plots obtained were manually inspected to verify the genotype clusters. The results were recorded in the form of haploped files. The genotypes recorded were uploaded onto BC|SNPmax and the biochemical/phenotypic characteristics for the corresponding individuals were retrieved.[7]

[6] Custom probes were designed under the guidance of Amanda Phipps-Green (Assistant Research Fellow, Merriman Laboratory).

[7] The Taqman PCR assays were run by Tahzeeb Fatima (Assistant Research Fellow, Merriman Laboratory).

2.5.2.4 STATISTICAL ANALYSES

2.5.2.4.1 TESTING FOR ASSOCIATION WITH HYPERURICEMIA

The genotype data were analysed for deviation from Hardy-Weinberg equilibrium (HWE). HWE was calculated individually for each sample subset. Multiple-adjusted logistic regression, treating the dependent variable as dichotomous (hyperuricemic versus normouricemic) was carried out using R version 3.4.1 (RStudio Team, 2015). All five variants were tested for association with hyperuricemia in the EP and WP sample sets. Both unadjusted and confounder-adjusted analyses were performed. The logistic regression model was adjusted for age, sex and grandparental ancestry (since PCA data was not available for the replication cohorts). The statistical significance and the effect size of variants were calculated for all associations. The significance threshold was set at alpha = 0.05 (equivalent to 95 % confidence interval). The allelic odds ratios were calculated with respect to the minor allele. Meta-analysis was performed using the statistical package 'meta' in R version 3.4.1 (RStudio Team, 2015), as in the discovery-phase. Power ≥ 80% was considered adequate. All power calculations were done in R version 3.4.1 (RStudio Team, 2015).

2.5.2.4.2 TESTING FOR ASSOCIATION WITH GOUT

The five variants chosen for replicating association with hyperuricemia (VAR_CHR4_9914056, rs373311989, VAR_CHR4_9452283, VAR_CHR4_10160679 and VAR_CHR4_10457448) were also tested for their association with gout, both in the Discovery and the Replication Cohorts. The cohorts comprised gout cases and controls. The Discovery Cohort consisted of 161 cases (EP: n = 71, WP: n = 90) and 248 controls (EP: n = 152, WP: n = 96), the Replication Cohort A consisted of 603 cases (EP: n = 312, WP: n = 291) and 618 controls (EP: n = 395, WP: n = 223) and the Replication Cohort B consisted of 734 cases (EP: n = 400, WP: n = 334) and 815 controls (EP: n = 515, WP: n = 300) (table 2.1 and table 2.3). Individuals whose gout affection status was unknown were considered as non-gout controls, if they were normouricemic. Testing for association of variants with gout was done using the same approach as for hyperuricemia (outlined in section 2.5.2.4.1), treating the dependent variable as dichotomous (gout cases versus controls).

[8]VAR_CHR4_9914056 has recently been assigned an rsid number: rs931756502 (Date: 30 Oct 2018)

Chapter 3

Results

Chapter 3

Results

3.1 Data Visualization

3.1.1 Variants Identified

A total of 3963 variants spread over the entire *SLC2A9* locus were identified by targeted sequencing. Of these, 2430 (61%) variants had dbSNP identifiers (allocated rsid numbers) and 1533 (39%) variants were novel. About 97% of the variants were found to be located within noncoding regions of the locus, including introns, untranslated, regulatory and intergenic regions. 70% of the variants were intronic. The coding region variants accounted to < 3% of the total number. Amongst the coding variants, a majority of them were either missense or synonymous. Figure 3.1 summarizes the type of variants identified. The summary data was obtained used the Ensembl Variant Effect Predictor tool. The complete list of the variants identified is provided in the Appendix section (appendix 1).

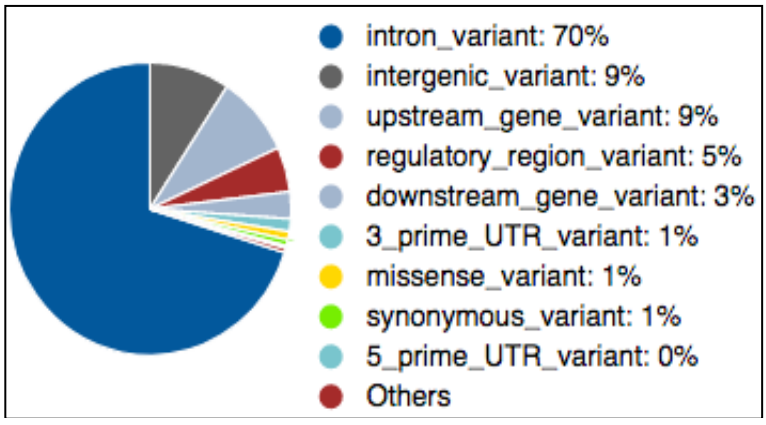


Figure 3.1 Summary Of The Types Of Variants Identified. *About 97% of the variants were located in the noncoding regions of the locus, of which 70% were intronic. Less than 3% of the variants were located in the coding regions of the locus.*

3.1.2 VARIANT ANNOTATION AND FUNCTION PREDICTION

All variants have been elaborately annotated using the tools described in section 2.4.2. The following annotations are provided in the Appendix section (appendix 2).

- Variant id
- Genomic notation
- Gene name
- Variant location (intronic / exonic / regulatory / 3'UTR / 5"UTR / intergenic)
- Variant type (missense / synonymous / nonsynonymous / stop lost / stop gained / frameshift / splice site)
- CADD score (for both known and novel variants)
- GWAVA score (for novel variants only)

3.1.2.1 CIRCOS PLOT

The circos plot below (figure 3.2) summarizes the annotations for each variant, including the genomic location, the gene within which each variant resides, and the CADD and GWAVA scores (prediction values) that predict deleteriousness and functional potential of the variant.

INTERPRETATION OF THE CADD AND GWAVA SCORES CADD assigns a score for each variant, called a 'C-score' (a measure that correlates with the functionality and pathogenicity of the variant. For example, known pathogenic variants are ranked high, i.e., given a higher C-score) and a phred-score (scaled C-scores for easier interpretation). Phred-score values range from 1 – 99. The higher the phred-score, the higher the predicted deleteriousness of the variant (Kircher et al., 2014). The highest CADD phred-score for any variant in this set was 39, which was assigned for the variant VAR_CHR4_10089949 (genomic location: 10089949) located within the *WDR1* gene (4:10075963 – 4:10118573).

Unlike CADD that predicts the deleteriousness of both known and novel variants, GWAVA predicts the deleteriousness of only the known variants (with rsid numbers assigned). The GWAVA scores range from 0 to 1. The higher the score, the higher the predicted deleteriousness/functional relevance of the variant. The highest GWAVA score in this set of

variants (a value of 0.7) was assigned for the variant rs883041 (genomic location 4:9868346) located within the *SLC2A9* gene (4:9772777 – 4:10056560).

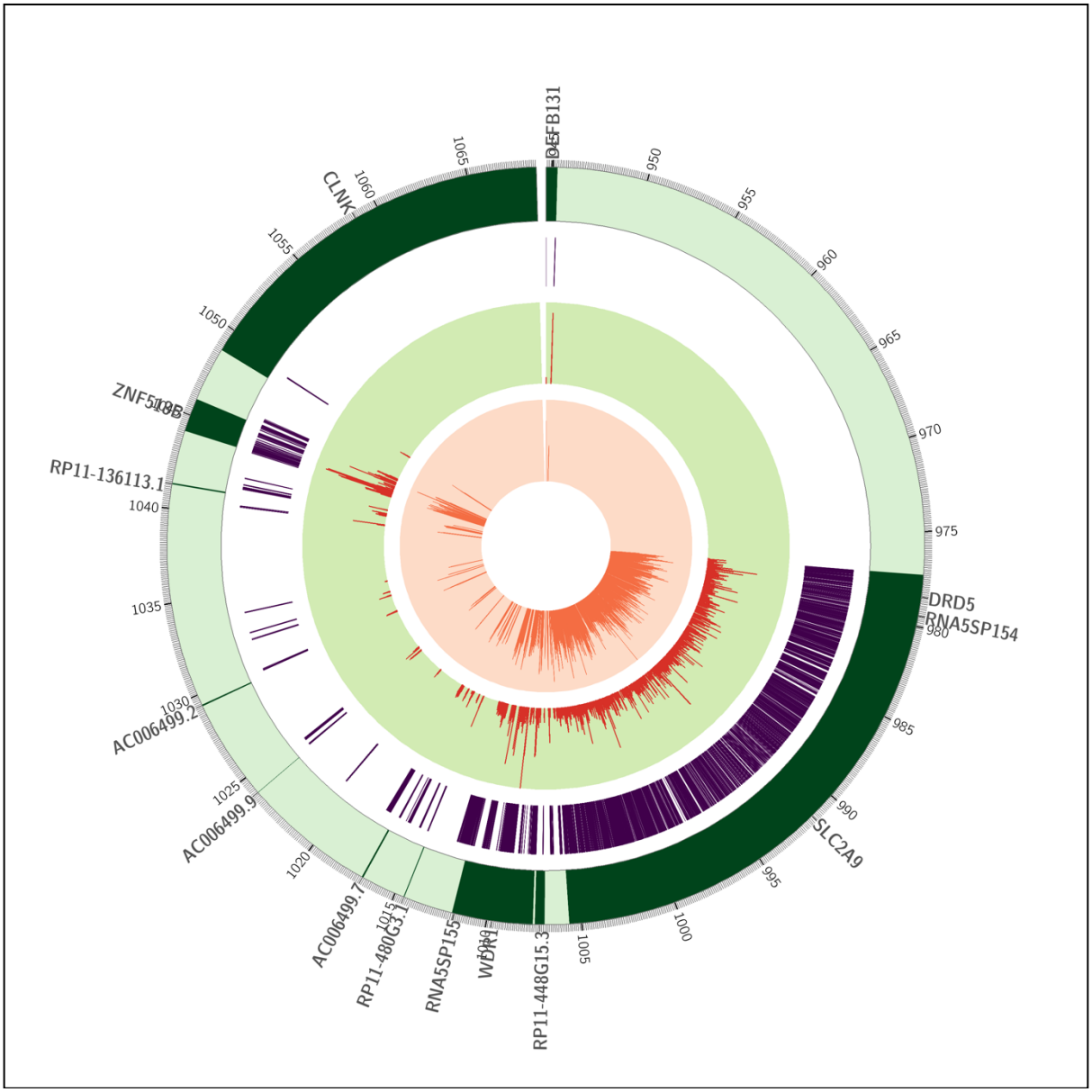


Figure 3.2 Circos Plot Displaying A Summary Of The Variant Annotations. *Track 1 (the outermost track) displays the location of each gene (the regions painted in green). Track 2 (inner to the outermost track) displays the genomic location of the variants (the purple strokes). Track 3 displays the CADD scores for the variants. The height of each peak (red strokes) represents the value. The greater the height of the peak, the greater the predicted deleteriousness of the variant. Track 4 (the innermost track) displays the GWAVA scores for the variants. The height of each peak (orange strokes) represents the value. The greater the height of the peak, the greater the predicted deleteriousness of the variant. Plot was generated using the circos software package.*

3.1.2.2 FUNCTION PREDICTION REGIONAL PLOTS

The functional potential of the *SLC2A9* locus (chromosomal coordinates 4:9446200 - 4:10686500) was investigated using the GenoCanyon functional prediction tool (figure 3.3A). The tool assigns a prediction score for every genomic position in the region analysed, based on the biochemical signals and the genomic conservation scores obtained from the ENCyclopedia Of DNA Elements (ENCODE) project (ENCODE Project Consortium, 2004). The prediction scores represent the functional relevance of the location/region and ranges from 0.0 – 1.0 (Lu et al., 2015). Similar to CADD and GWAVA scores, the higher the prediction score, the higher the conservation and functional potential at the genomic location. The genomic region from 4:9855000 to 4:10686500 was predicted to be conserved and functionally relevant (mean prediction score for the region = 0.744) (figure 3.3B). On the other hand, a sub-region within the locus (chromosomal coordinates 4:9446200 - 4:9750000) encompassing the *DEFB131A* gene through the intergenic region and into the beginning of the *SLC2A9* gene, was predicted to have a low functional potential (mean prediction score for the region = 0.011) (figure 3.3C).

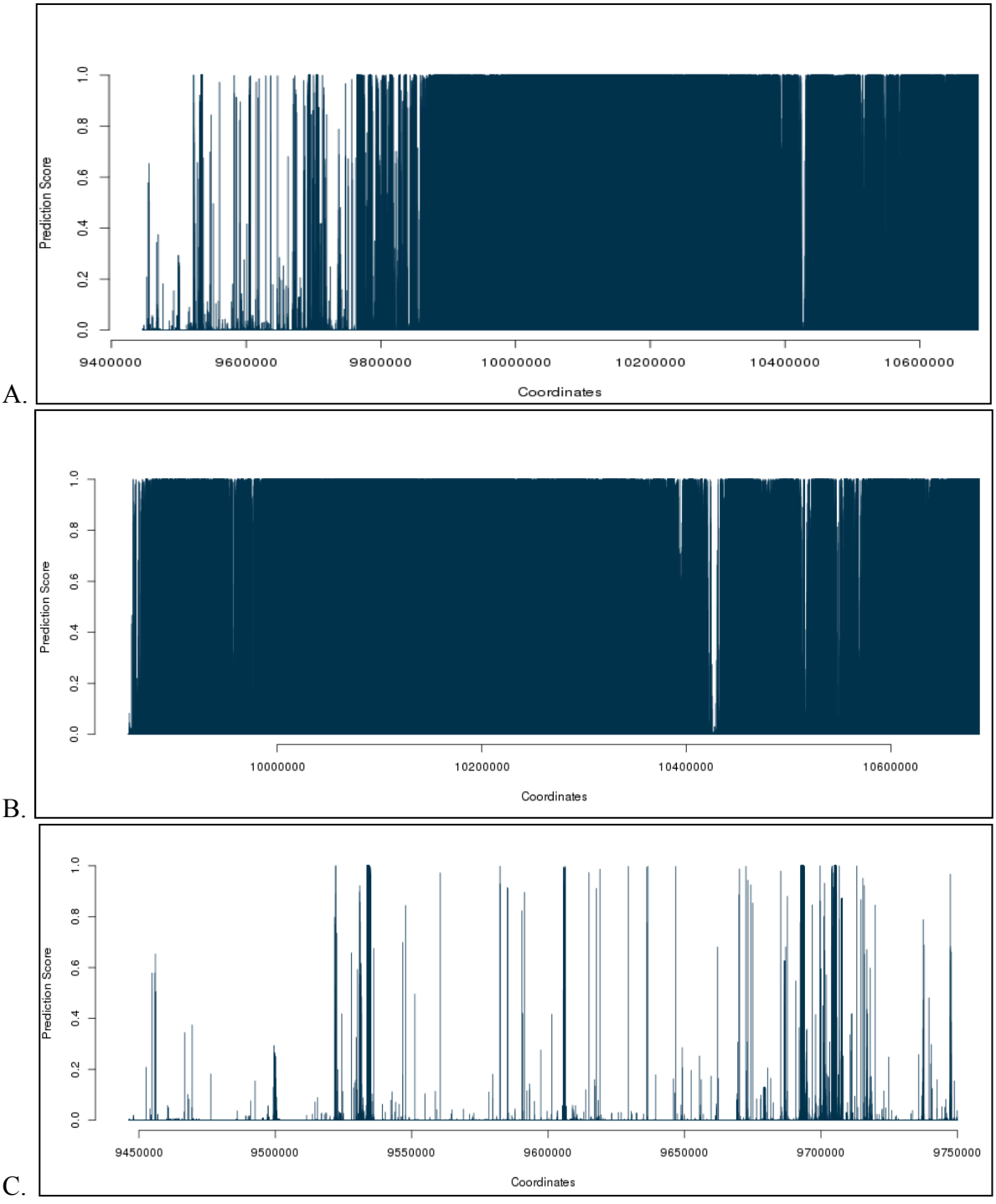


Figure 3.3 Plots Representing the Functional Potential of the SLC2A9 Locus (4:9446200 – 4: 10686500) *The plots represent the functional potential of A. the entire locus (genomic coordinates- 4:9446200 – 4: 10686500). B: a sub-region predicted to have high functional potential (genomic coordinates- 4:9855000 to 4:10686500) and C: a sub-region predicted to have low functional potential (genomic coordinates- 4:9446200 - 4:9750000). The blue peaks represent the prediction values for each genomic location. The height of the peak is proportional to the functional potential at that genomic location. Tall peaks represent conserved locations with higher predicted functional potential. Plots were generated using the GenoCanyon function prediction software.*

3.1.3 PERCENTAGE OF MISSING GENOTYPES

Using the visdat tool in R, the percentage of missing genotypes for the Discovery Cohort was calculated. Genotype data were available for 99.9% of the study participants (figure 3.4). Therefore, imputation of genotype data prior to various analyses was not necessary.

FIGURE 3.4 PLOT DISPLAYING THE PERCENTAGE OF MISSING GENOTYPES FOR THE DISCOVERY COHORT.
Variants are plotted along the x-axis and subjects (denoted as observations) are plotted along the y-axis. Every point in the plot represents the genotype data for a subject at a particular variant location and coded as zero (if the genotype data is available; represented in grey) or one (if the genotype data is missing; represented in black). Genotype data were available for 99.9% of the study participants. The percentage of missing genotypes was calculated using the visdat tool in R version 3.4.1.

3.1.4 HAPLOTYPES FROM PHASED DATA

The SHAPEIT v2.r790 software was used to infer/phase haplotypes. The inPHAP software package was used for the visualization of genotypes and phased haplotypes. The haplotypes inferred from phased genotypes data for all subjects in the Discovery Cohort (n = 809) and all variants identified in the study (n = 809) revealed that the genomic structures for the East and West Polynesians are similar. Therefore, they were subsequently combined to represent the overall 'Polynesian' population. Comparing the Polynesian haplotypes with the European haplotypes exposed two genomic segments where the Polynesians showed a relatively higher variability compared to the Europeans (figures 3.5 and 3.6).

The two variable regions include:

- Variable region1: 4:9446207 - 4:9823478
- Variable region 2: 4:10120364 - 4:10494666

The first variable region was located at the very beginning of the locus covering the entire *DEFB131A* gene, the intergenic region and a portion of the *SLC2A9* gene that includes the *DRD5* gene. The second variable region was located towards the end of the locus starting with the intergenic region outside of the *WDR1* gene through the *ZNF518B* and *CLNK* genes.

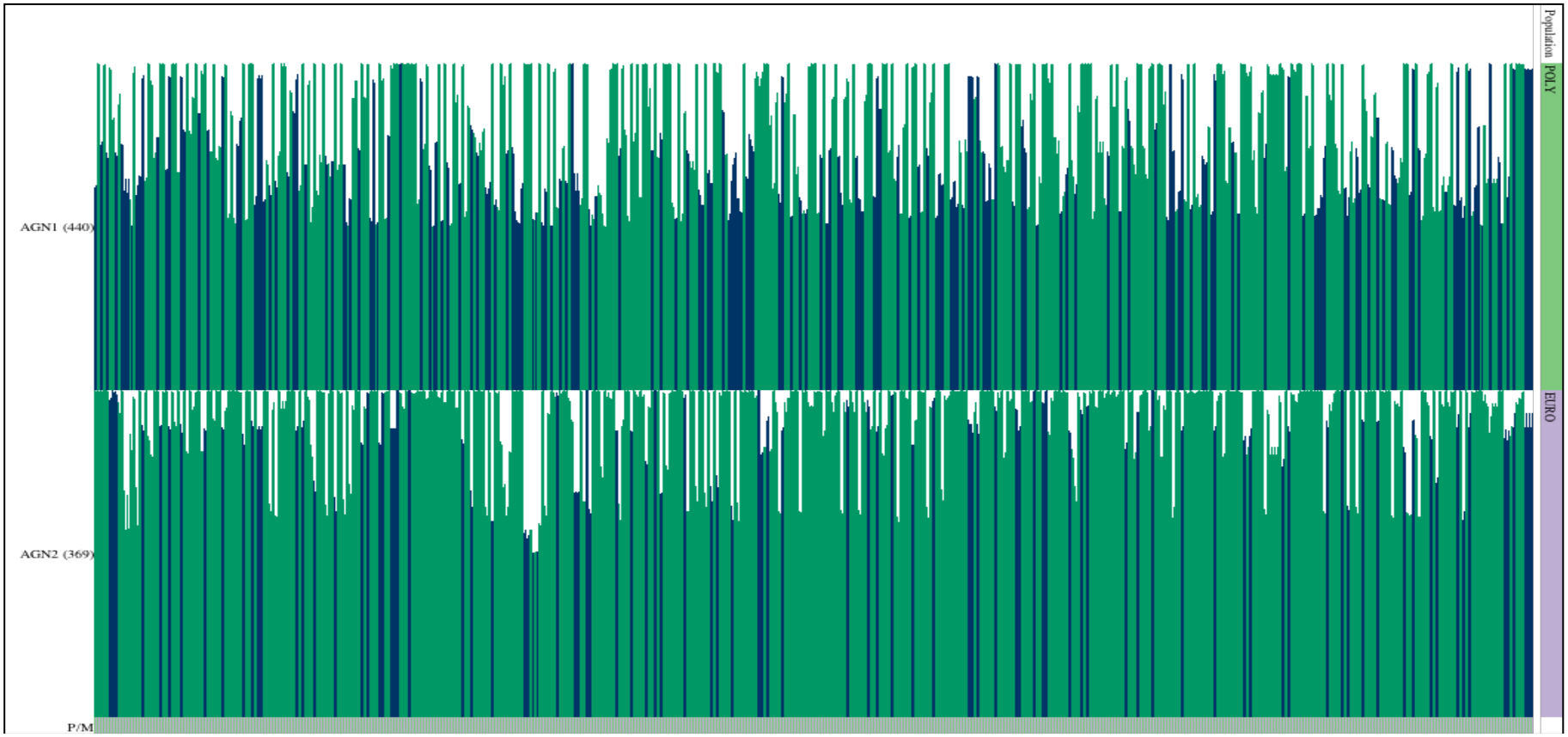


Figure 3.5The Polynesian and European haplotypes inferred from phased data for all 809 subjects (Discovery Cohort) and 3963 variants in the SLC2A9 locus for the variable region 1 (4:94462O7 - 4:9823478). *AGN1: Polynesians (n = 440). AGN2: Europeans (n = 369). The green peaks represent reference alleles, blue peaks represent alternate alleles. The panel at the bottom (P/M) refers to the paternal/ maternal chromosome. The plot shows greater number of carriers for the alternate alleles of variants in Polynesians. Haplotype phasing was carried out using the SHAPEIT v2.r790 software. Haplotype visualization was carried out using the inPHAP software package.*

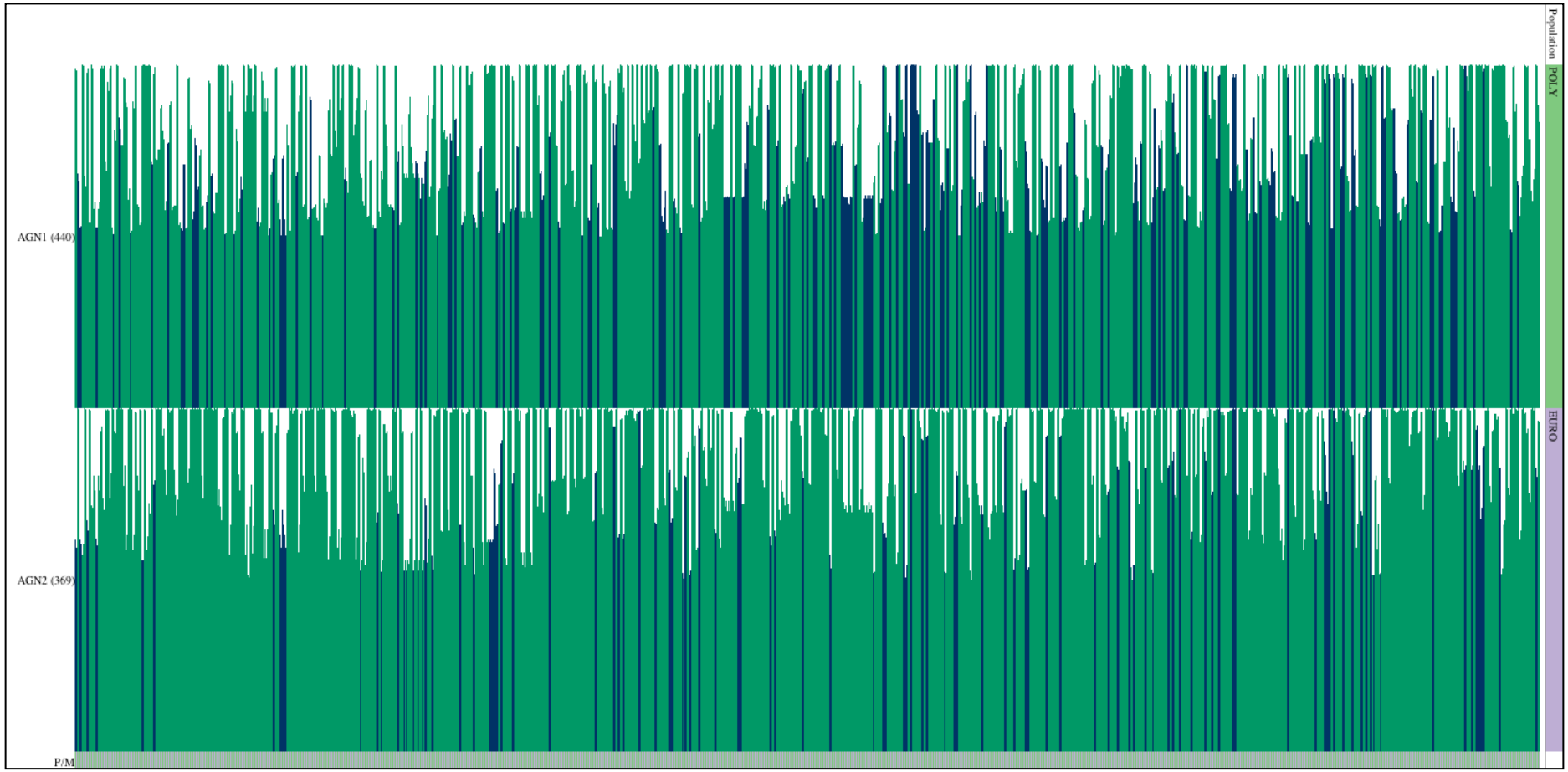


Figure 3.6 The Polynesian and European haplotypes inferred from phased data for all 809 subjects and 3963 variants in the SLC2A9 locus for the variable region 2 (4:101203̲64 - 4:10494666). *AGN1: Polynesians (n = 440). AGN2: Europeans (n = 369). The green peaks represent reference alleles, blue peaks represent alternate alleles. The panel at the bottom (P/M) refers to the paternal/ maternal chromosome. The plot shows greater number of carriers for the alternate alleles of variants in Polynesians. Haplotype phasing was carried out using the SHAPEIT v2.r790 software. Haplotype visualization was carried out using the inPHAP software package.*

3.2 LWAS- DISCOVERY PHASE

3.2.1 POWER OF STUDY

The Power of a study indicates whether the size of the dataset is large enough to detect statistically significant associations between alleles and the phenotype. Detection power ≥ 80% was considered adequate. The power calculated for the Discovery Cohort, consisting of 410 cases (106 East Polynesians, 108 West Polynesians and 196 Europeans) and 368 controls (117 East Polynesians, 78 West Polynesians and 173 Europeans), indicated that the study was 100% powered to detect effect sizes of variants with OR ≥ 2.0 having a minor allele frequency (MAF) ≥ 0.1 and adequately powered (≥ 80%) to detect significant associations for variants with OR ≥ 1.5 and MAF ≥ 0.15 (figure 3.7).

NOTE: Since replication (visa genotyping) was incorporated in the study design to validate discovery-phase associations, Bonferroni correction was not applied in this study.

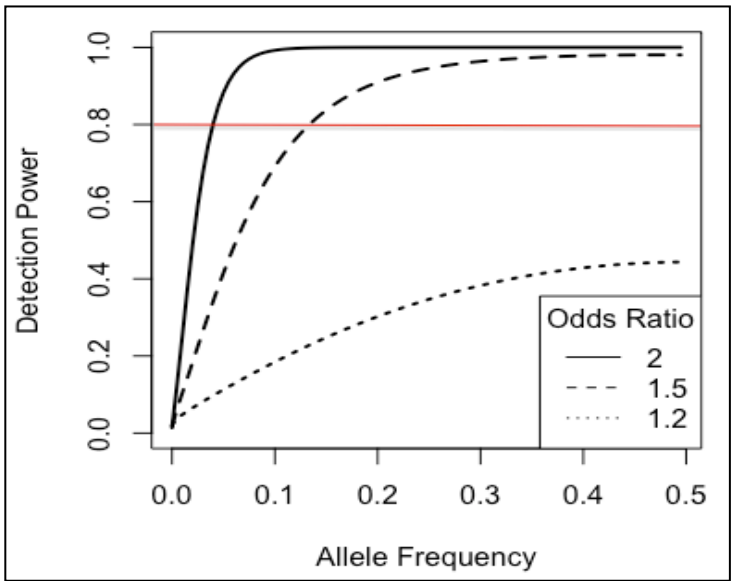


FIGURE 3.7 THE POWER OF STUDY FOR THE DISCOVERY COHORT, CALCULATED OVER A RANGE OF EFFECT SIZES (LOW EFFECT SIZE- OR = 1.2, MODERATE EFFECT SIZE- OR = 1.5, HIGH EFFECT SIZE- OR = 2) AND MINOR ALLELE FREQUENCIES. *The red line indicates detection power that was considered adequate for this study. Power calculation was carried out using R version 3.4.1.*

3.2.2 LOGISTIC REGRESSION

In this study, the association of genetic variants with hyperuricemia was analysed. Logistic regression, treating the dependent variable as dichotomous (hyperuricemic versus normouricemic) was the statistical approach employed to identify discovery-phase associations. Multiple-adjusted logistic regression was carried out using R version 3.4.1 (RStudio Team, 2015).

3.2.2.1 OVERVIEW OF DISCOVERY-PHASE RESULTS

Testing of all 3963 variants for association with hyperuricemia in each of the three population datasets (West Polynesian, East Polynesian and European) using multiple-adjusted logistic regression yielded the following results. Figure 3.8 and figure 3.9 summarize the results.

3.2.2.1.1 SIGNIFICANT SIGNALS IN EAST POLYNESIANS

Analyses using three models- unadjusted, age/sex-adjusted and age/sex/PCA-adjusted- were performed. Association analysis without confounder-adjustment returned 38 variants showing nominally significant association with hyperuricemia (p-value ≤ 0.05). Thirteen of these and three other variants were found to be significant after adjusting for age and sex. Adjusting for age, sex and PCA 1 through 10 yielded 25 nominally significant signals; 10 of these were returned as significant in the analysis without confounder adjustment and 8 of them were significant after adjusting for age and sex. Only six variants were found to be significant in all three instances. These are listed in table 3.1.

NOTE: Wherever a variant is said to be significant, it refers to the altered allele of the variant showing a nominally significant association (p-value ≤ 0.05) with hyperuricaemia.

TABLE 3.1 VARIANTS FOUND TO BE SIGNIFICANTLY ASSOCIATED WITH HYPERURICEMIA IN THE EAST POLYNESIANS BOTH BEFORE AND AFTER CONFOUNDER-ADJUSTMENT

Variant	Ref allele	Alt allele	Unadjusted		Age,Sex-Adjusted		Age,Sex,PCA-Adjusted	
			OR (95%CI)	P_{OR}	OR (95%CI)	P_{OR}	OR (95%CI)	P_{OR}
rs139180190	C	T	7.26[2.06;25.54]	0.002	10.65[2.74;41.32]	0.0006	10.69[2.49;45.88]	0.001
rs149628125	T	G	7.26[2.06;25.54]	0.002	10.65[2.74;41.32]	0.0006	10.69[2.49;45.88]	0.001
rs7659924	G	C	0.57[0.36;0.89]	0.013	0.58[0.36;0.93]	0.024	0.55[0.33;0.94]	0.028
VAR_CHR4_10122489	G	A	16.22[2.08;126.23]	0.007	22.63[2.70;189.87]	0.004	23.96[2.64;217.53]	0.004
VAR_CHR4_9820317	G	C	13.43[1.70;105.83]	0.013	21.18[2.47;181.49]	0.005	17.04[1.85;156.78]	0.012
VAR_CHR4_9914056	G	A	17.65[2.28;136.73]	0.005	27.86[3.34;232.69]	0.002	28.30[3.17;252.31]	0.002

The significance threshold was set at 0.05. Ref: reference. Alt: alternate. OR: odds ratio for the alternate (minor) allele. 95% CI: 95% confidence interval. P_{OR}: p-value for odds ratio.

3.2.2.1.2 SIGNIFICANT SIGNALS IN WEST POLYNESIANS

Analyses using three models- unadjusted, age/sex-adjusted and age/sex/PCA-adjusted- were performed. Association analysis without confounder-adjustment returned 181 variants showing nominally significant association with hyperuricemia (p-value $\leq$ 0.05). After adjusting for age and sex, 73 variants were found to be significant. Adjusting for age, sex and PCA 1 through 10 yielded 53 nominally significant variants; 27 of these were returned as significant in the analysis without confounder adjustment and 45 of them were significant after adjusting for age and sex. Twenty seven variants were found to be significant in all three instances. These are listed in table 3.2.

Table 3.2 Variants found to be significantly associated with hyperuricemia in the West Polynesians both before and after confounder-adjustment

Variant	Ref allele	Alt allele	Unadjusted		Age,Sex-Adjusted		Age,Sex,PCA-Adjusted	
			OR (95%CI)	P_{OR}	OR (95%CI)	P_{OR}	OR (95%CI)	P_{OR}
rs117443909	**C**	**T**	0.19[0.04;0.95]	0.043	0.13[0.02;0.67]	0.015	0.11[0.02;0.65]	0.015
rs13126279	**T**	**C**	0.54[0.34;0.87]	0.011	0.50[0.29;0.88]	0.015	0.48[0.26;0.87]	0.016
rs141354936	**T**	**G**	0.19[0.04;0.95]	0.043	0.13[0.02;0.67]	0.015	0.11[0.02;0.65]	0.015
rs145058214	**G**	**T**	0.19[0.04;0.95]	0.043	0.13[0.02;0.67]	0.015	0.11[0.02;0.65]	0.015
rs16889260	**C**	**T**	0.35[0.15;0.82]	0.016	0.36[0.14;0.94]	0.037	0.34[0.12;0.96]	0.040
rs182701836	**C**	**T**	0.11[0.01;0.95]	0.045	0.06[0.01;0.53]	0.012	0.05[0.01;0.50]	0.010
rs183640684	**C**	**T**	0.09[0.01;0.79]	0.029	0.06[0.01;0.53]	0.011	0.05[0.01;0.46]	0.008
rs184866950	**T**	**C**	0.11[0.01;0.95]	0.044	0.06[0.01;0.53]	0.011	0.05[0.01;0.50]	0.010
rs188311840	**G**	**A**	0.11[0.01;0.95]	0.044	0.06[0.01;0.53]	0.011	0.05[0.01;0.50]	0.010
rs1980220	**G**	**A**	0.37[0.16;0.83]	0.016	0.35[0.14;0.88]	0.026	0.35[0.13;0.95]	0.039
rs28643326	**T**	**C**	1.65[1.07;2.55]	0.023	1.72[1.04;2.83]	0.033	1.80[1.05;3.08]	0.033
rs28798076	**C**	**A**	1.54[1.00;2.37]	0.049	1.83[1.11;3.03]	0.017	2.06[1.19;3.56]	0.009
rs373311989	**A**	**G**	0.09[0.01;0.79]	0.029	0.05[0.01;0.44]	0.006	0.04[0.00;0.40]	0.0056
rs4621429	**A**	**G**	0.37[0.16;0.83]	0.016	0.35[0.14;0.88]	0.026	0.35[0.13;0.95]	0.039
rs4697704	**T**	**G**	1.65[1.05;2.61]	0.029	2.00[1.18;3.40]	0.010	2.10[1.17;3.75]	0.012
rs4697705	**G**	**A**	0.54[0.35;0.85]	0.007	0.57[0.35;0.95]	0.031	0.57[0.33;0.98]	0.042
rs4697892	**C**	**A**	0.37[0.16;0.83]	0.016	0.35[0.14;0.88]	0.026	0.35[0.13;0.95]	0.039
rs4697895	**T**	**C**	0.37[0.16;0.83]	0.016	0.35[0.14;0.88]	0.026	0.35[0.13;0.95]	0.039
VAR_CHR4_10008732	**T**	**C**	0.09[0.01;0.73]	0.024	0.08[0.01;0.70]	0.022	0.05[0.00;0.66]	0.023
VAR_CHR4_10108441	**G**	**C**	0.09[0.01;0.73]	0.024	0.08[0.01;0.70]	0.022	0.05[0.00;0.66]	0.023

Variant	Ref allele	Alt allele	Unadjusted		Age,Sex-Adjusted		Age,Sex,PCA-Adjusted	
			OR (95%CI)	P_{OR}	OR (95%CI)	P_{OR}	OR (95%CI)	P_{OR}
VAR_CHR4_10120485	**C**	**T**	0.09[0.01;0.73]	0.024	0.08[0.01;0.70]	0.022	0.05[0.00;0.66]	0.023
VAR_CHR4_10160679	**A**	**G**	0.09[0.01;0.73]	0.024	0.08[0.01;0.70]	0.022	0.05[0.00;0.66]	0.023
VAR_CHR4_10298641	**G**	**A**	0.09[0.01;0.73]	0.024	0.08[0.01;0.70]	0.022	0.05[0.00;0.66]	0.023
VAR_CHR4_9452283	**T**	**A**	0.11[0.01;0.95]	0.045	0.06[0.01;0.53]	0.011	0.05[0.01;0.50]	0.010
VAR_CHR4_9946797	**T**	**C**	0.09[0.01;0.73]	0.024	0.08[0.01;0.70]	0.022	0.05[0.00;0.66]	0.023
VAR_CHR4_9950432	**C**	**T**	0.09[0.01;0.73]	0.024	0.08[0.01;0.70]	0.022	0.05[0.00;0.66]	0.023
VAR_CHR4_9981322	**C**	**G**	0.09[0.01;0.73]	0.024	0.08[0.01;0.70]	0.022	0.05[0.00;0.66]	0.023

The significance threshold was set at 0.05. Ref: reference. Alt: alternate. OR: odds ratio for the alternate (minor) allele. 95% CI: 95% confidence interval. P_{OR}: p-value for odds ratio.

3.2.2.1.3 Significant Signals in Europeans

Analyses using two models- unadjusted and sex-adjusted- were performed. Since age and PCA data were available only for European samples recruited from New Zealand, the model could not be adjusted for these confounders. This was not a major concern as the main focus of the study was to identify Polynesian-specific variants and European samples were used for comparison purposes only. Association analysis without confounder-adjustment returned 596 variants displaying nominally significant association with hyperuricemia (p-value $\leq$ 0.05). Five hundred and thirty six of these and 23 other variants were found to be significant after adjusting for sex.

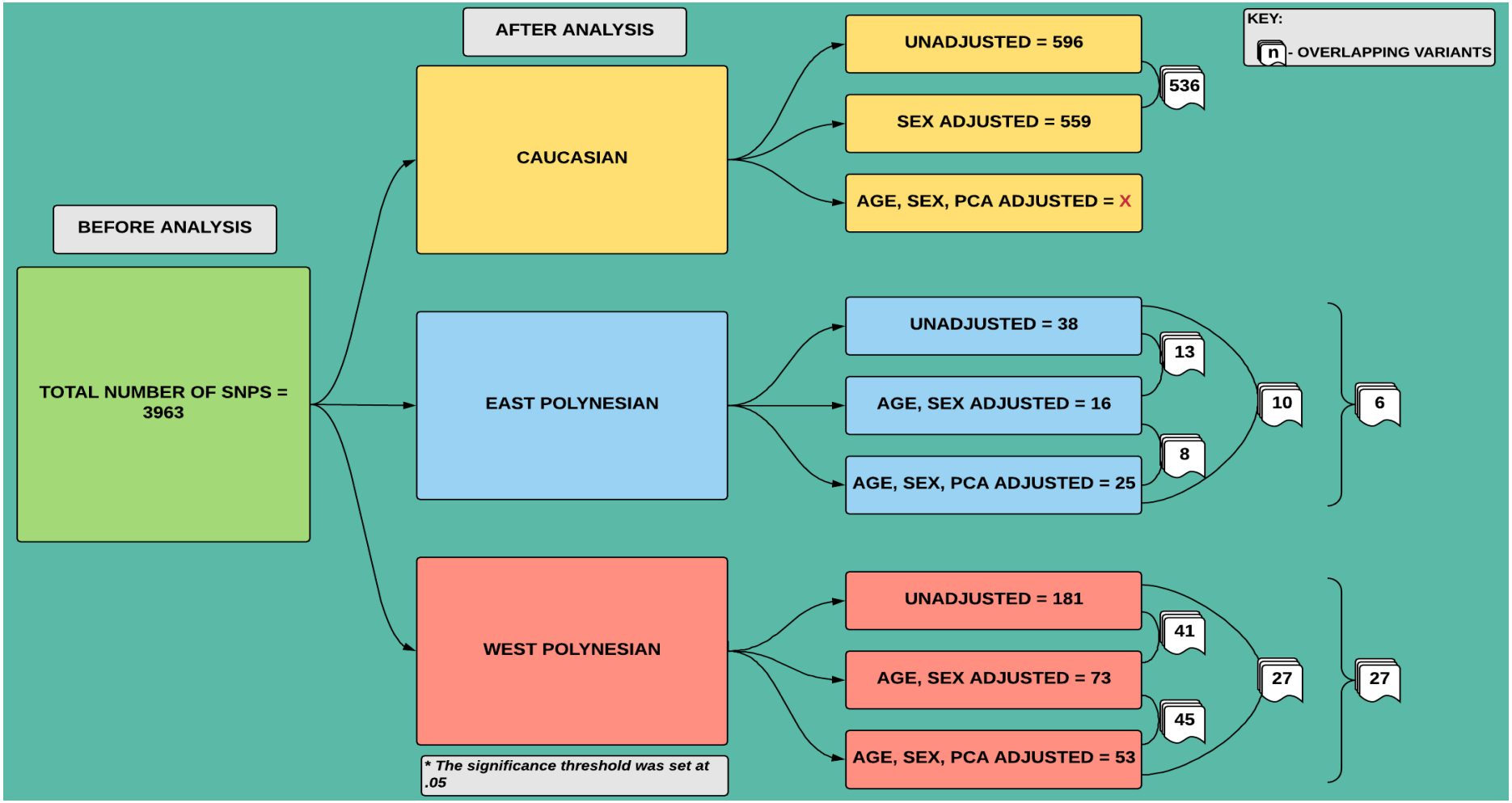


Figure 3.8 Summary of unadjusted and confounder-adjusted logistic regression analyses performed in a population-stratified manner. *The significance threshold was set at 0.05. Logistic regression was carried out using R version 3.4.1.*

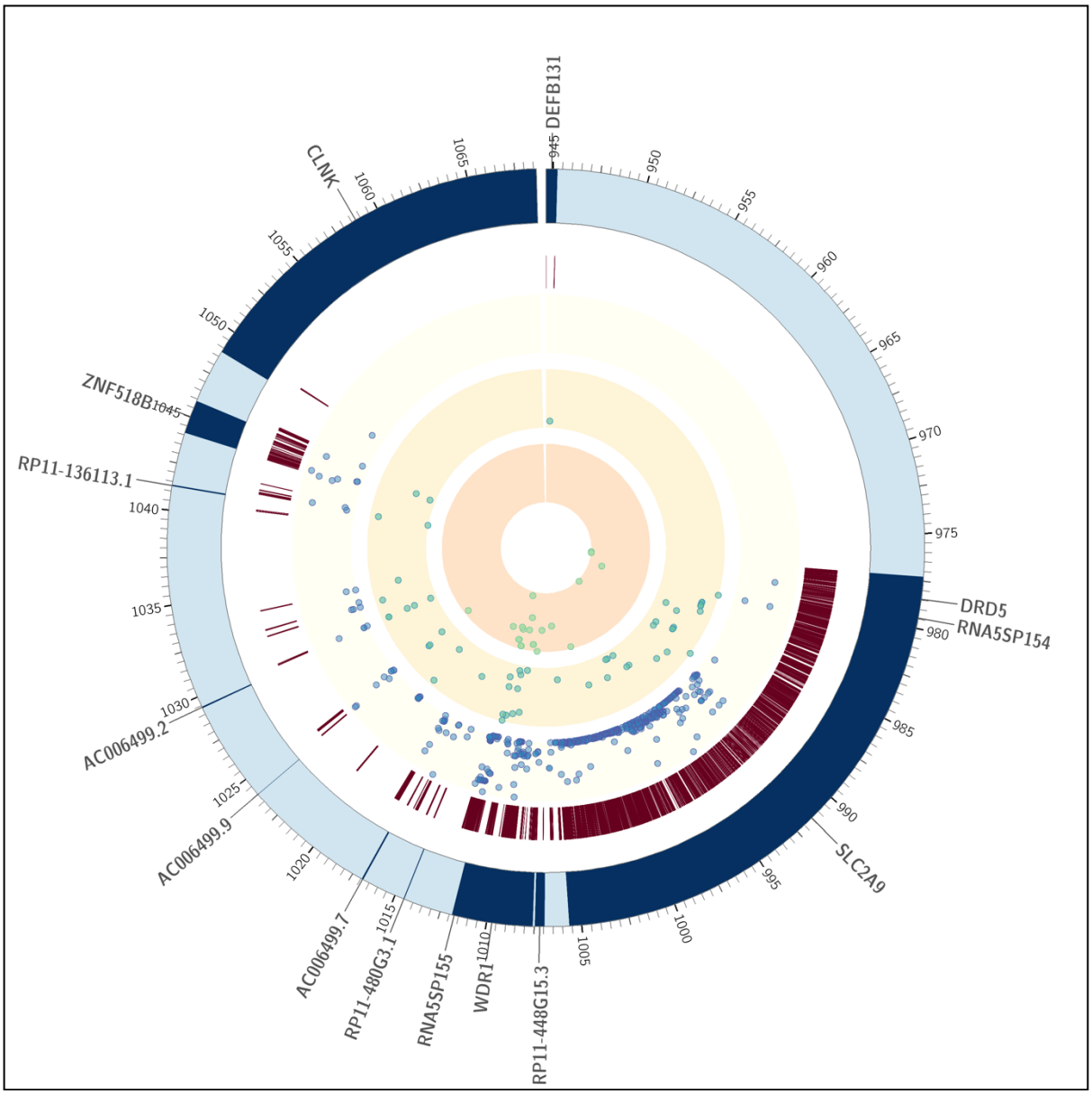


Figure 3.9 Circos Plot Displaying A Summary Of The Significant Signals. *Track 1 (the outermost track) displays the location of each gene (the regions painted in dark blue). Track 2 (inner to the outermost track) displays the genomic location of the variants (the marron strokes). Track 3 is a scatterplot of the significant signals in the European population. Track 4 is a scatterplot of the significant signals in the West Polynesian population. Track 5 (the innermost track) is a scatterplot of the significant signals in the East Polynesian population. Plot was generated using the circos software package.*

3.2.2.1.4 SIGNIFICANT SIGNALS OVERLAPPING / NONOVERLAPPING ACROSS POPULATIONS

A large number of variants were uniquely significant in specific populations. This does not necessarily mean that such variants were absent in the other populations but rather that they were not found to have significant signals in the other populations. Forty one of the 53 variants significant in the West Polynesians were specific to this population. Similarly, 11 variants were specifically significant in the East Polynesians. Of the significant signals in Europeans, 529 variants were uniquely significant in this population, eight of them overlapped with the West Polynesians and 13 of them overlapped with the East Polynesians. Two Polynesian-specific variants (VAR_CHR4_9452283 and VAR_CHR4_10122489) were significant in both East and West Polynesian groups. Two other variants (rs13126279 and rs4697705) were significant across all three populations. These results are represented in the Venn diagram below (figure 3.10).

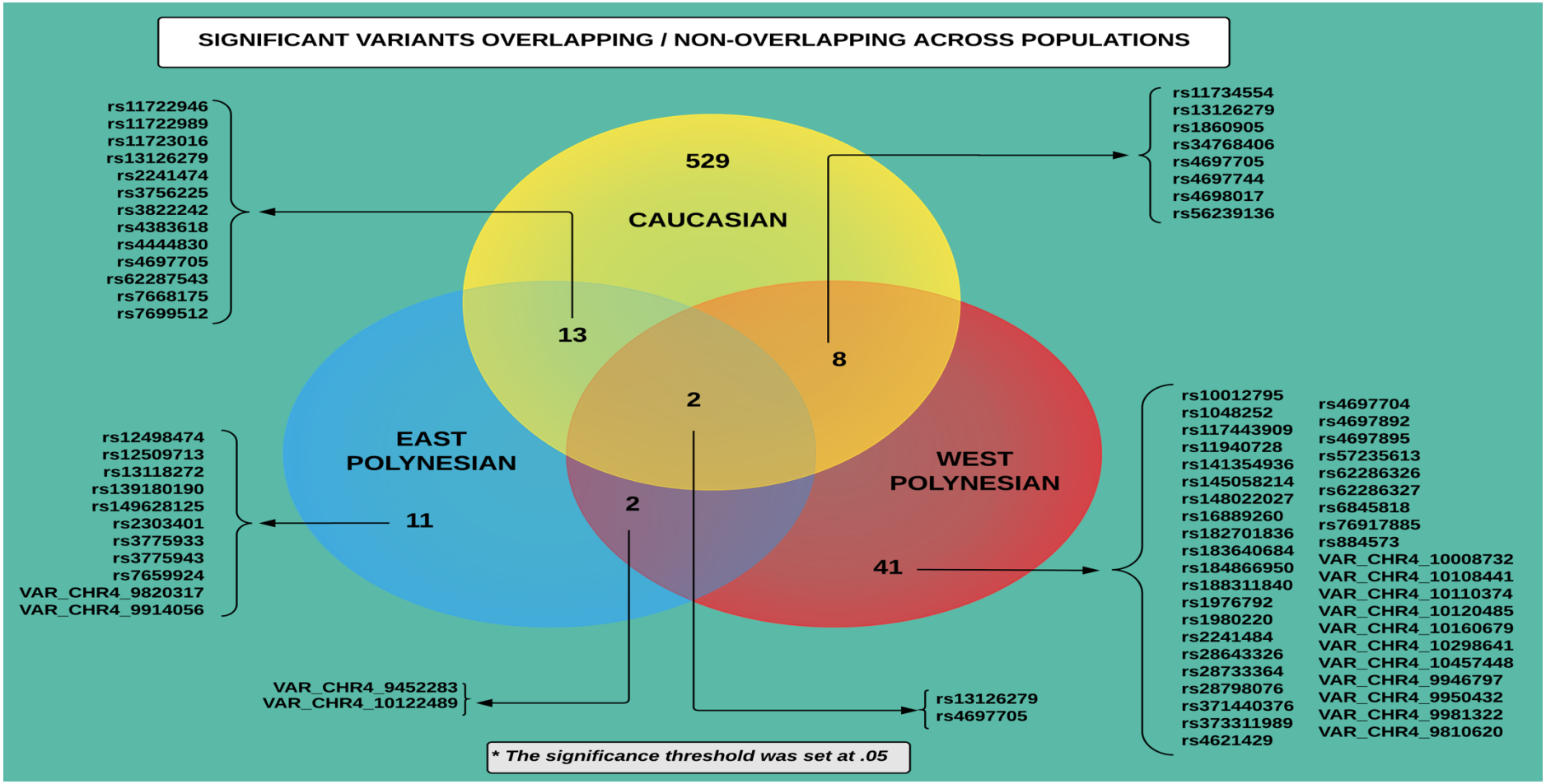


FIGURE 3.10 VENN DIAGRAM ILLUSTRATING SIGNIFICANT VARIANTS THAT ARE OVERLAPPING / NONOVERLAPPING ACROSS THE THREE POPULATIONS. *The significance threshold was set at 0.05.Eight significant signals overlapped between the Europeans and West Polynesians, 13 overlapped between the Europeans and East Polynesians and 2 were common to the East and West Polynesians. Only 2 variants displayed nominal significance across all three populations.*

3.2.2.2 FURTHER ANALYSIS OF SIGNIFICANT SIGNALS IN POLYNESIANS

3.2.2.2.1 EAST POLYNESIANS

The regional LocusZoom plot depicting the association of *SLC2A9* locus variants with hyperuricemia in East Polynesians is provided in figure 3.11. The 25 variants significantly associated with hyperuricemia after confounder-adjustment (age, sex and PCA 1 through 10) were further analysed. The complete results are tabulated in table 3.3 and the LD plot is shown in figure 3.12.

Five of the variants mapped to the introns of *SLC2A9* (rs149628125, VAR_CHR4_9820317, VAR_CHR4_9914056, rs3775943, rs7659924), one variant was present upstream of *DRD5* (rs139180190), nine in the intronic/upstream regions of *WDR1* (rs12498474, rs3756225, rs3822242, rs12509713, rs4697705, rs2303401, rs2241474, VAR_CHR4_10122489 and rs13118272) while the others were mostly intergenic.

Of the 25 variants, five were Polynesian-specific (rs149628125, rs139180190, VAR_CHR4_9820317, VAR_CHR4_9914056 and VAR_CHR4_10122489), amongst which three were novel (VAR_CHR4_9820317, VAR_CHR4_9914056 and VAR_CHR4_10122489). All these three Polynesian-specific novel variants were found to have very large effect sizes with the alternate/minor allele conferring risk for hyperuricemia (VAR_CHR4_9820317: OR = 17.04, P_{OR} = 0.01, VAR_CHR4_9914056: OR = 28.30, P_{OR} = 0.003 and VAR_CHR4_10122489: OR = 23.96, P_{OR} = 0.004) (table 3.3).

Linkage disequilibrium (LD) is the non-random association of alleles. Alleles in strong/complete LD inherit together (Slatkin et al., 2008). The pairwise LD between all significant signals in the East Polynesian population revealed 17 of the 25 variants to belong to a single large haplotype block. Six of these variants (rs4444830, rs4383618, rs7668175, rs7699512, rs11722946 and rs11722989) were in complete LD with each other (r^2 = 100) and in strong LD ($r^2 \geq 80$) with rs12498474, rs3756225, rs3822242 and rs11723016. These variants could therefore be regarded as a single signal. The three Polynesian-specific novel variants were also linked, VAR_CHR4_9914056 being in 93% LD with VAR_CHR4_10122489 and 79 % LD with VAR_CHR4_9820317 (figure 3.12).

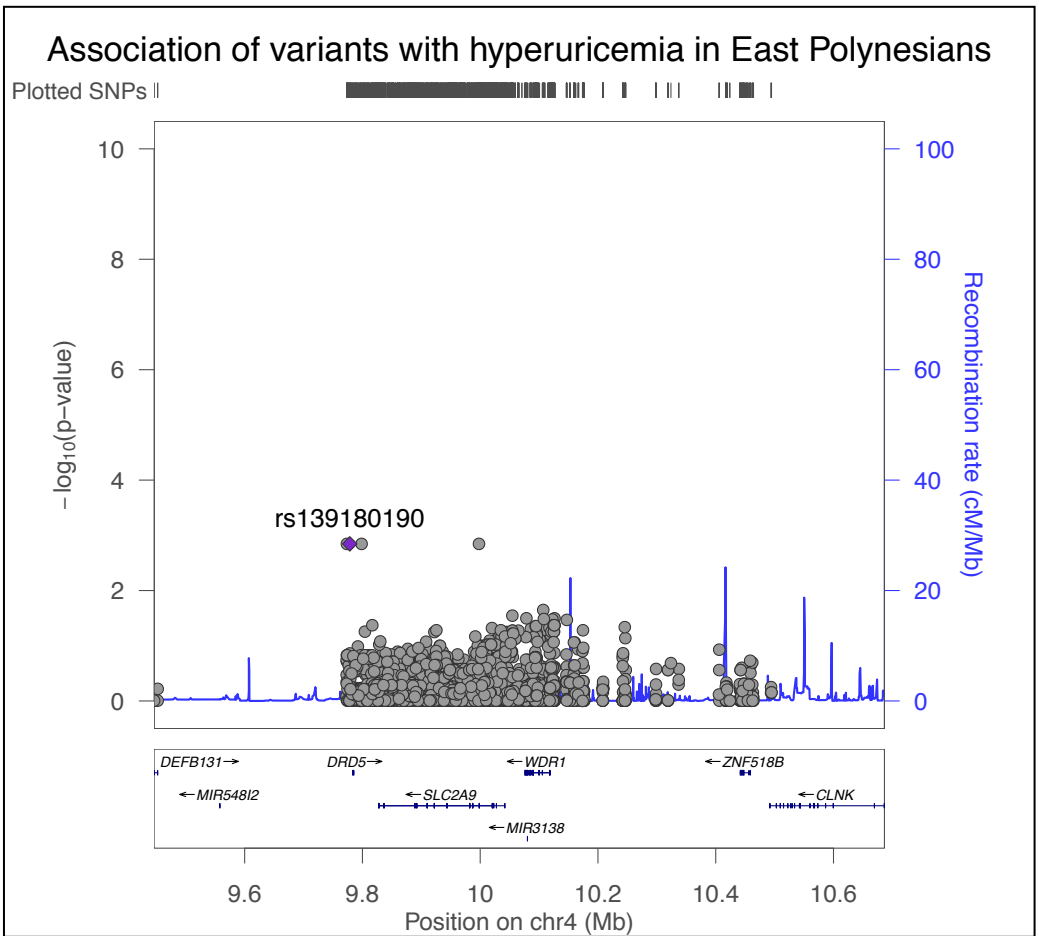


Figure 3.11 Regional LocusZoom plot depicting the association of SLC2A9 locus (genomic region: 4:9446200-4:10686500) variants with hyperuricemia in East Polynesians. *P-values were calculated after adjusting the model for sex, age and PCA1-10. P-value calculations were done using R version 3.4.1. Plot was generated using the LocusZoom software.*

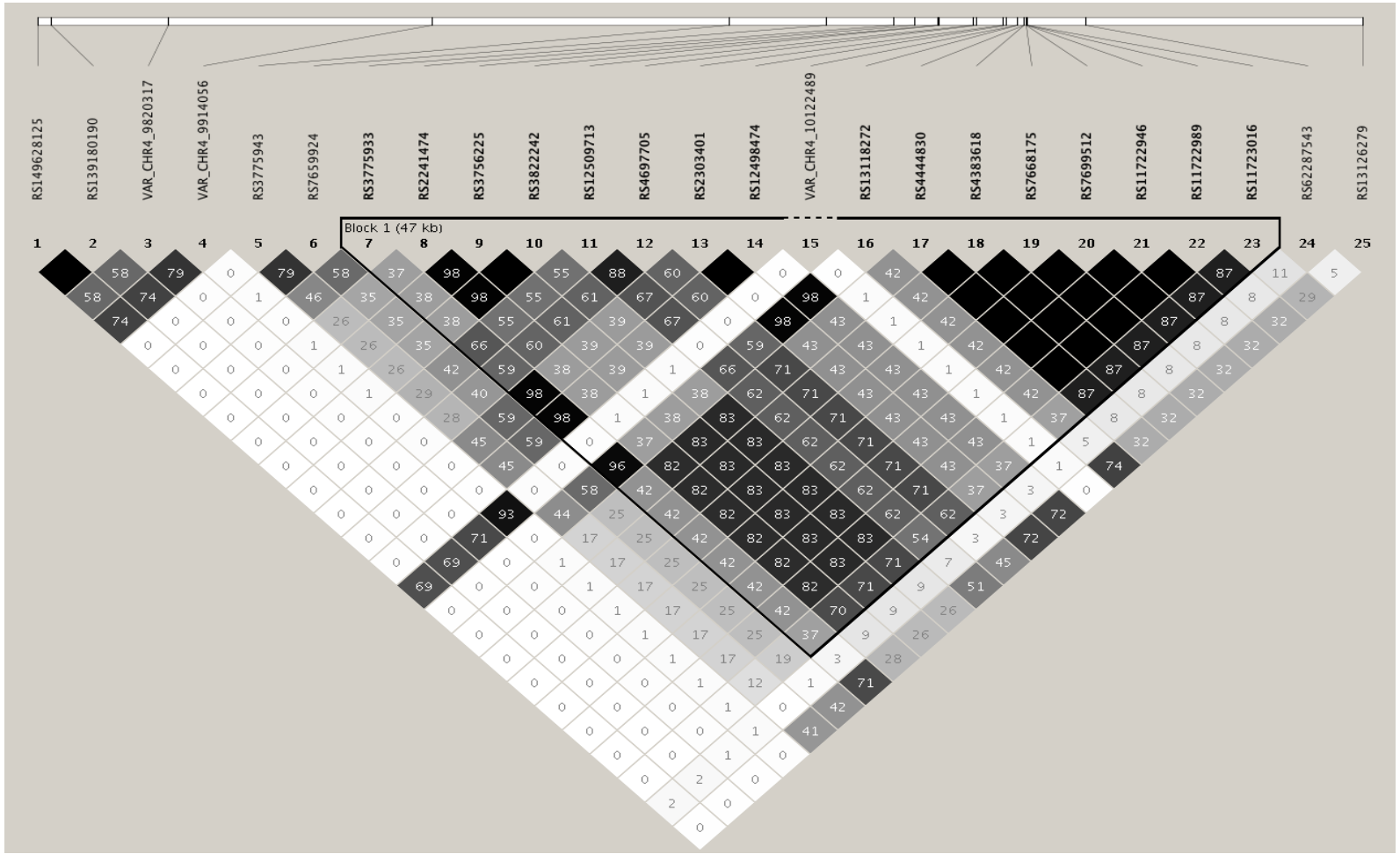


Figure 3.12 The pairwise linkage disequilibrium (LD) plot indicating the 'R-squared (r^2)' values between the 25 significant signals in East Polynesians. *An $r^2 \geq 60$ in the above plot indicates an LD between the particular variants. The number inside each square indicates the r^2 value between the two variants. Pairwise LD calculations were done using the Haploview software package.*

Table 3.3 Variants significantly associated with hyperuricemia in East Polynesians after confounder-adjustment

VARIANT	GENE	TYPE	Ref allele	Alt allele	EAST POLYNESIAN				WEST POLYNESIAN				EUROPEAN			
					HU-freq	NU-freq	OR(95%CI)*	P_{OR}*	HU-freq	NU-freq	OR(95%CI)*	P_{OR}*	HU-freq	NU-freq	OR(95%CI)#	P_{OR}#
rs149628125	*SLC2A9*	intronic	T	G	0.08	0.01	10.69[2.49;45.88]	0.0014	0.07	0.09	0.74[0.29;1.89]	0.5276	0.00	0.00	NA	NA
rs139180190	*DRD5*	upstream	C	T	0.08	0.01	10.69[2.49;45.88]	0.0014	0.07	0.09	0.74[0.29;1.89]	0.5276	0.00	0.00	NA	NA
VAR_CHR4_9820317	*SLC2A9*	intronic	G	C	0.05	0.00	17.04[1.85;156.78]	0.0123	0.04	0.03	4.32[0.96;19.44]	0.0566	0.00	0.00	NA	NA
VAR_CHR4_9914056	*SLC2A9*	intronic	G	A	0.07	0.00	28.30[3.17;252.31]	0.0027	0.07	0.04	2.86[0.82;9.92]	0.0982	0.00	0.00	NA	NA
rs3775943	*SLC2A9*	intronic	T	C	0.14	0.23	0.55[0.31;0.99]	0.0478	0.44	0.42	1.11[0.68;1.81]	0.6756	0.05	0.03	1.71[0.72;4.06]	0.227
rs7659924	*SLC2A9*	intronic	G	C	0.17	0.27	0.55[0.33;0.94]	0.0285	0.44	0.44	1.01[0.62;1.64]	0.9764	0.10	0.11	0.90[0.53;1.54]	0.7001
rs3775933	*MIR3138*	downstream	G	T	0.10	0.18	0.50[0.26;0.94]	0.0318	0.22	0.31	0.70[0.39;1.26]	0.2326	0.06	0.05	0.86[0.43;1.73]	0.6728
rs12498474	*WDR1*	upstream	C	T	0.11	0.18	0.53[0.28;0.99]	0.0471	0.22	0.31	0.70[0.39;1.24]	0.2217	0.07	0.06	0.99[0.52;1.89]	0.9790
rs3756225	*WDR1*	intronic	G	C	0.25	0.34	0.61[0.37;0.99]	0.0442	0.40	0.49	0.86[0.52;1.43]	0.5686	0.56	0.41	1.79[1.29;2.49]	0.0005
RS3822242	*WDR1*	intronic	T	C	0.25	0.34	0.61[0.37;0.99]	0.0442	0.40	0.49	0.86[0.52;1.43]	0.5686	0.44	0.59	0.56[0.40;0.78]	0.0005
rs12509713	*WDR1*	intronic	C	T	0.16	0.22	0.50[0.28;0.91]	0.0225	0.25	0.35	0.67[0.39;1.16]	0.1541	0.29	0.31	0.95[0.67;1.35]	0.7780
rs4697705	*WDR1*	intronic	G	A	0.17	0.24	0.53[0.30;0.95]	0.0328	0.25	0.39	0.57[0.33;0.98]	0.0426	0.43	0.57	0.60[0.43;0.83]	0.0023
rs2303401	*WDR1*	intronic	G	C	0.11	0.18	0.53[0.28;0.99]	0.0471	0.22	0.31	0.67[0.38;1.20]	0.1787	0.07	0.06	0.99[0.52;1.89]	0.9790
rs2241474	*WDR1*	intronic	C	T	0.26	0.34	0.61[0.37;1.00]	0.0495	0.40	0.49	0.86[0.52;1.43]	0.5686	0.44	0.59	0.58[0.42;0.80]	0.0011
VAR_CHR4_10122489	*WDR1*	upstream	G	A	0.06	0.00	23.96[2.64;217.53]	0.0048	0.09	0.05	4.20[1.31;13.50]	0.0159	0.00	0.00	NA	NA
rs13118272	*WDR1*	upstream	T	C	0.10	0.18	0.50[0.26;0.95]	0.0335	0.22	0.32	0.64[0.36;1.14]	0.1315	0.07	0.06	0.99[0.52;1.89]	0.9790
rs4444830	-	intergenic	T	C	0.23	0.30	0.59[0.35;0.98]	0.0425	0.33	0.44	0.67[0.40;1.13]	0.1327	0.42	0.56	0.60[0.43;0.83]	0.0024
rs4383618	-	intergenic	T	C	0.23	0.30	0.59[0.35;0.98]	0.0425	0.33	0.44	0.67[0.40;1.13]	0.1327	0.42	0.55	0.61[0.44;0.85]	0.0033
rs7668175	-	intergenic	T	C	0.23	0.30	0.59[0.35;0.98]	0.0425	0.33	0.44	0.67[0.40;1.13]	0.1327	0.42	0.56	0.60[0.43;0.83]	0.0024
rs7699512	-	intergenic	C	T	0.23	0.30	0.59[0.35;0.98]	0.0425	0.33	0.44	0.67[0.40;1.13]	0.1327	0.42	0.56	0.60[0.43;0.83]	0.0024

VARIANT	GENE	TYPE	Ref allele	Alt allele	EAST POLYNESIAN				WEST POLYNESIAN				EUROPEAN			
					HU-freq	NU-freq	OR(95%CI)*	P_{OR}*	HU-freq	NU-freq	OR(95%CI)*	P_{OR}*	HU-freq	NU-freq	OR(95%CI)#	P_{OR}#
rs11722946	-	intergenic	A	G	0.23	0.30	0.59[0.35;0.98]	0.0425	0.33	0.44	0.67[0.40;1.13]	0.1327	0.42	0.56	0.60[0.43;0.83]	0.0024
rs11722989	-	intergenic	A	G	0.23	0.30	0.59[0.35;0.98]	0.0425	0.33	0.44	0.67[0.40;1.13]	0.1327	0.42	0.56	0.60[0.43;0.83]	0.0024
rs11723016	-	intergenic	A	G	0.26	0.33	0.57[0.34;0.95]	0.0318	0.35	0.46	0.65[0.39;1.08]	0.0991	0.42	0.56	0.60[0.43;0.83]	0.0024
rs62287543	*RP11-480G3.1*	upstream	G	A	0.25	0.16	2.22[1.06;4.65]	0.0340	0.23	0.22	1.43[0.62;3.32]	0.4017	0.20	0.34	0.56[0.37;0.86]	0.0086
rs13126279	-	intergenic	T	C	0.11	0.18	0.51[0.26;0.99]	0.0461	0.18	0.31	0.48[0.26;0.87]	0.0158	0.11	0.04	2.18[1.13;4.21]	0.0202

*The significance threshold was set at 0.05. Variants in LD with each other are highlighted with the same color. Ref: reference. Alt: alternate. HU-freq: minor allele frequency (MAF) in hyperuricemic cases. NU-freq: MAF in normouricemic controls. OR: odds ratio for the alternate (minor) allele. 95% CI: 95% confidence interval. P_{OR}: p-value for odds ratio. *: Odds ratio adjusted for age, sex and PCA1-10, #: Odds ratio adjusted for sex.*

3.2.2.2.2 WEST POLYNESIANS

The regional LocusZoom plot depicting the association of *SLC2A9* locus variants with hyperuricemia in West Polynesians is provided in figure 3.13. The 53 variants significantly associated with hyperuricemia after confounder-adjustment (age, sex and PCA 1 through 10) were further analysed. The complete results are tabulated in table 3.4 and the LD plot is shown in figure 3.14.

Twenty four of the 53 variants were within the noncoding regions (21 intronic, 3 downstream) of *SLC2A9* (VAR_CHR4_9810620, rs4697892, rs1980220, rs4621429, rs4697895, rs16889260, VAR_CHR4_9842261, rs1976792, rs57235613, rs884573, rs1048252, rs141354936, rs145058214, VAR_CHR4_9882651, rs56239136, rs28643326, VAR_CHR4_9946797, VAR_CHR4_9950432, rs182701836, rs184866950, rs188311840, VAR_CHR4_9981322, VAR_CHR4_10008732, rs117443909), one variant was downstream of *DEFB131A* (VAR_CHR4_9452283), eleven of them were in the noncoding regions (intronic/5'UTR/downstream/upstream) of *WDR1* (rs183640684, rs2241484, rs4697704, rs4697705, VAR_CHR4_10108441, VAR_CHR4_10110374, rs148022027, rs34768406, rs371440376, VAR_CHR4_10120485, VAR_CHR4_10122489) and two variants mapped to the introns of *ZNF518B* (VAR_CHR4_10457448, rs76917885) (table 3.4).

A large number of Polynesian-specific and novel variants were identified. Of the 53 variants, twenty five were Polynesian-specific (VAR_CHR4_9452283, VAR_CHR4_9810620, VAR_CHR4_9842261, rs141354936, rs145058214, VAR_CHR4_9882651, VAR_CHR4_9946797, VAR_CHR4_9950432, rs182701836, rs184866950, rs188311840, VAR_CHR4_9981322, VAR_CHR4_10008732, rs117443909, rs183640684, VAR_CHR4_10108441, VAR_CHR4_10110374, rs148022027, rs34768406, rs371440376, VAR_CHR4_10120485, VAR_CHR4_10122489, VAR_CHR4_10160679, rs373311989, VAR_CHR4_10457448) and amongst these, fourteen were novel (VAR_CHR4_9452283, VAR_CHR4_9810620, VAR_CHR4_9842261, VAR_CHR4_9882651, VAR_CHR4_9946797, VAR_CHR4_9950432, VAR_CHR4_9981322, VAR_CHR4_10008732, VAR_CHR4_10108441, VAR_CHR4_10110374, VAR_CHR4_10120485, VAR_CHR4_10122489, VAR_CHR4_10160679, VAR_CHR4_10457448) (table 3.4).

For most Polynesian-specific variants, the direction of association with hyperuricemia was protective for the variants' alternate alleles, the only exceptions being variants rs148022027, rs371440376 and VAR_CHR4_10122489. For both rs148022027 and rs371440376, the OR = 2.3 and the P_{OR} = 0.05. Given that the p-value was in the borderline of the significance threshold, there is a probability that these were false-positive signals. However, VAR_CHR4_10122489, located upstream of *WDR1*, appeared to be an important signal with its A allele (alternate allele) conferring risk for hyperuricemia (OR = 4.2, P_{OR} = 0.016). Of note, this variant was found to be associated with hyperuricemia in the East Polynesians with a larger effect size (OR = 23.96, P_{OR} = 0.005) (table 3.4).

The pairwise LD between all significant signals in the West Polynesian population revealed three haplotype blocks. Haplotype block 1 contained five variants (rs4697892, rs1980220, rs4621429, rs4697895 and rs16889260), all in strong or complete LD with each other. Seven variants (rs4697704, rs4697705, VAR_CHR4_10108441, VAR_CHR4_10110374, rs148022027, rs34768406 and rs371440376) belonged to the second haplotype block and eighteen variants (VAR_CHR4_10122489, VAR_CHR4_10160679, rs11734554, rs6845818, rs62286326, rs62286327, rs13126279, rs4698017, rs4697744, VAR_CHR4_10298641, rs11940728, rs28798076, rs1860905, rs10012795, rs28733364, rs373311989, VAR_CHR4_10457448, rs76917885) to the third and larger haplotype block (figure 3.14).

The figure 3.15 illustrates the variants significant in the East and West Polynesian sub-populations, variants prioritised for replication and their gene annotations.

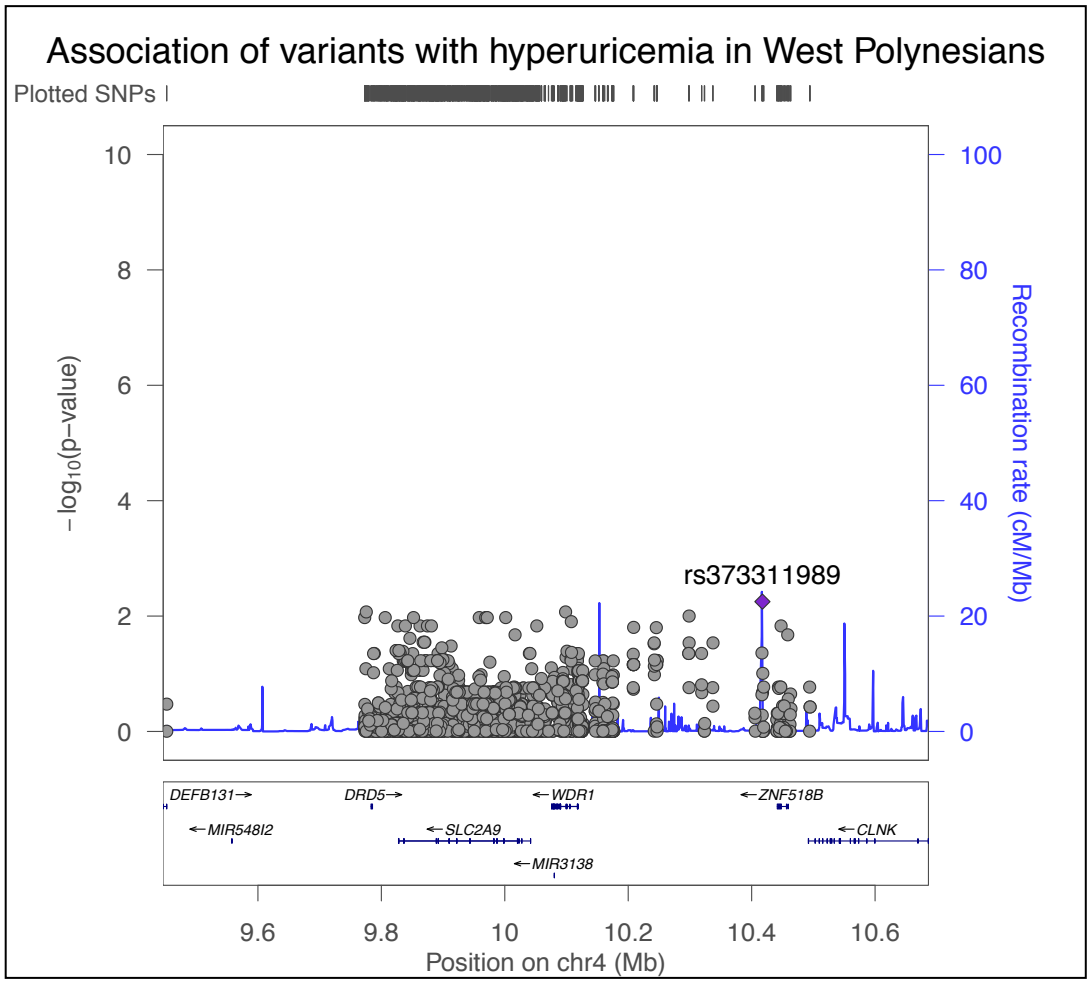


Figure 3.13 Regional LocusZoom plot depicting the association of SLC2A9 locus (genomic region: 4:94462200-4:10686500) variants with hyperuricemia in West Polynesians. *P-values were calculated after adjusting the model for sex, age and PCA1-10. P-value calculations were done using R version 3.4.1. Plot was generated using the LocusZoom software.*

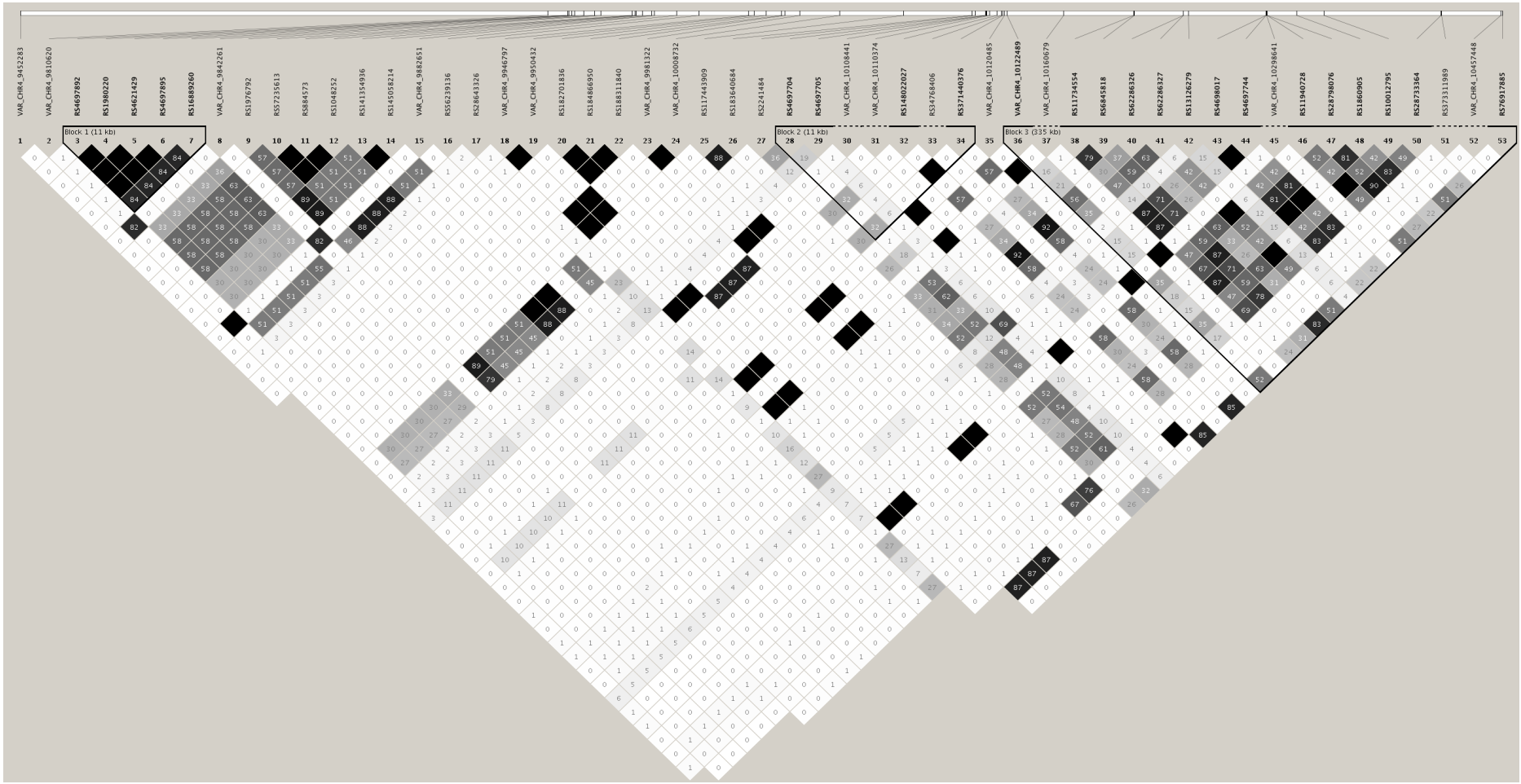


FIGURE 3.14 THE PAIRWISE LINKAGE DISEQUILIBRIUM (LD) PLOT INDICATING THE 'R-SQUARED (r^2)' VALUES BETWEEN THE 53 SIGNIFICANT SIGNALS IN WEST POLYNESIANS. *An $r^2 \geq 60$ in the above plot indicates an LD between the particular variants. The number inside each square indicates the r^2 value between the two variants. Pairwise LD calculations were done using the Haploview software package.*

Table 3.4 Variants significantly associated with hyperuricemia in the West Polynesians after confounder-adjustment

VARIANT	GENE	TYPE	Ref allele	Alt allele	WEST POLYNESIAN				EAST POLYNESIAN				EUROPEAN			
					HU-freq	NU-freq	OR(95%CI)*	P_{OR}*	HU-freq	NU-freq	OR(95%CI)*	P_{OR}*	HU-freq	NU-freq	OR(95%CI)#	P_{OR}#
VAR_CHR4_9452283	*DEFB131A*	downstream	T	A	0.01	0.04	0.05[0.01;0.50]	0.011	0.01	0.02	0.72[0.16;3.22]	0.669	0.00	0.00	-	-
VAR_CHR4_9810620	*SLC2A9*	intronic	T	C	0.02	0.04	0.06[0.00;1.00]	0.050	0.00	0.00	-	-	0.00	0.00	-	-
rs4697892	*SLC2A9*	downstream	C	A	0.05	0.12	0.35[0.13;0.95]	0.040	0.07	0.09	0.59[0.26;1.31]	0.196	0.23	0.26	0.77[0.54;1.11]	0.161
rs1980220	*SLC2A9*	downstream	G	A	0.05	0.12	0.35[0.13;0.95]	0.040	0.07	0.09	0.59[0.26;1.31]	0.196	0.23	0.26	0.77[0.54;1.11]	0.161
rs4621429	*SLC2A9*	downstream	A	G	0.05	0.12	0.35[0.13;0.95]	0.040	0.07	0.09	0.59[0.26;1.31]	0.196	0.23	0.26	0.77[0.54;1.11]	0.161
rs4697895	*SLC2A9*	intronic	T	C	0.05	0.12	0.35[0.13;0.95]	0.040	0.07	0.09	0.59[0.26;1.31]	0.196	0.23	0.26	0.77[0.54;1.11]	0.161
rs16889260	*SLC2A9*	intronic	C	T	0.04	0.11	0.34[0.12;0.96]	0.041	0.07	0.07	0.71[0.31;1.60]	0.405	0.20	0.22	0.73[0.49;1.08]	0.112
VAR_CHR4_9842261	*SLC2A9*	intronic	T	C	0.03	0.04	0.03[0.00;0.50]	0.014	0.00	0.00	-	-	0.00	0.00	-	-
rs1976792	*SLC2A9*	intronic	G	A	0.01	0.05	0.17[0.04;0.79]	0.024	0.04	0.06	0.64[0.24;1.69]	0.369	0.18	0.20	0.73[0.48;1.11]	0.141
rs57235613	*SLC2A9*	intronic	C	T	0.03	0.07	0.26[0.08;0.87]	0.028	0.05	0.06	0.76[0.31;1.91]	0.564	0.18	0.20	0.72[0.48;1.09]	0.125
rs884573	*SLC2A9*	intronic	G	C	0.03	0.07	0.26[0.08;0.87]	0.028	0.05	0.06	0.66[0.27;1.61]	0.361	0.18	0.20	0.72[0.47;1.08]	0.113
rs1048252	*SLC2A9*	intronic	C	T	0.03	0.07	0.26[0.08;0.87]	0.028	0.05	0.06	0.66[0.27;1.61]	0.361	0.18	0.20	0.72[0.47;1.08]	0.113
rs141354936	*SLC2A9*	intronic	T	G	0.01	0.05	0.11[0.02;0.65]	0.015	0.02	0.01	1.81[0.35;9.44]	0.484	0.00	0.00	-	-
rs145058214	*SLC2A9*	intronic	G	T	0.01	0.05	0.11[0.02;0.65]	0.015	0.02	0.01	1.81[0.35;9.44]	0.484	0.00	0.00	-	-
VAR_CHR4_9882651	*SLC2A9*	intronic	T	C	0.02	0.04	0.06[0.00;1.00]	0.050	0.00	0.00	-	-	0.00	0.00	-	-
rs56239136	*SLC2A9*	intronic	T	C	0.03	0.07	0.28[0.08;0.92]	0.035	0.06	0.08	0.59[0.23;1.47]	0.256	0.21	0.33	0.52[0.36;0.76]	0.001
rs28643326	*SLC2A9*	intronic	T	C	0.37	0.25	1.80[1.05;3.08]	0.033	0.61	0.51	1.27[0.84;1.93]	0.257	0.27	0.23	1.39[0.94;2.05]	0.097
VAR_CHR4_9946797	*SLC2A9*	intronic	T	C	0.01	0.06	0.05[0.00;0.66]	0.023	0.01	0.00	-	-	0.00	0.00	-	-
VAR_CHR4_9950432	*SLC2A9*	intronic	C	T	0.01	0.06	0.05[0.00;0.66]	0.023	0.01	0.00	-	-	0.00	0.00	-	-
rs182701836	*SLC2A9*	intronic	C	T	0.01	0.04	0.05[0.01;0.50]	0.011	0.01	0.01	0.70[0.03;15.49]	0.820	0.00	0.00	-	-
rs184866950	*SLC2A9*	intronic	T	C	0.01	0.04	0.05[0.01;0.50]	0.011	0.01	0.01	0.70[0.03;15.49]	0.820	0.00	0.00	-	-
rs188311840	*SLC2A9*	intronic	G	A	0.01	0.04	0.05[0.01;0.50]	0.011	0.01	0.01	0.70[0.03;15.49]	0.820	0.00	0.00	-	-

VARIANT	GENE	TYPE	Ref allele	Alt allele	WEST POLYNESIAN				EAST POLYNESIAN				EUROPEAN			
					HU-freq	NU-freq	OR(95%CI)*	P_{OR}*	HU-freq	NU-freq	OR(95%CI)*	P_{OR}*	HU-freq	NU-freq	OR(95%CI)#	P_{OR}#
VAR_CHR4_9981322	*SLC2A9*	intronic	C	G	0.01	0.06	0.05[0.00;0.66]	0.023	0.01	0.00	-	-	0.00	0.00	-	-
VAR_CHR4_10008732	*SLC2A9*	intronic	T	C	0.01	0.06	0.05[0.00;0.66]	0.023	0.01	0.00	-	-	0.00	0.00	-	-
rs117443909	*SLC2A9*	intronic	C	T	0.01	0.05	0.11[0.02;0.65]	0.015	0.02	0.03	1.03[0.25;4.27]	0.966	0.00	0.00	-	-
rs183640684	*WDR1*	intronic	C	T	0.01	0.05	0.05[0.01;0.46]	0.008	0.02	0.03	1.03[0.25;4.27]	0.966	0.00	0.00	-	-
rs2241484	*WDR1*	intronic	C	T	0.26	0.17	1.85[1.03;3.33]	0.041	0.42	0.32	1.44[0.96;2.16]	0.077	0.38	0.33	1.15[0.84;1.57]	0.371
rs4697704	*WDR1*	intronic	T	G	0.35	0.24	2.10[1.17;3.75]	0.012	0.42	0.36	1.28[0.83;1.97]	0.268	0.32	0.27	1.21[0.84;1.73]	0.301
rs4697705	*WDR1*	intronic	G	A	0.26	0.39	0.57[0.33;0.98]	0.043	0.18	0.24	0.53[0.30;0.95]	0.033	0.43	0.57	0.60[0.43;0.83]	0.002
VAR_CHR4_10108441	*WDR1*	intronic	G	C	0.01	0.06	0.05[0.00;0.66]	0.023	0.01	0.00	-	-	0.00	0.00	-	-
VAR_CHR4_10110374	*WDR1*	intronic	C	T	0.01	0.04	0.10[0.02;0.57]	0.010	0.01	0.01	0.27[0.02;3.98]	0.343	0.00	0.00	-	-
rs148022027	*WDR1*	downstream	T	A	0.14	0.10	2.30[1.02;5.20]	0.045	0.22	0.17	1.34[0.78;2.31]	0.290	0.00	0.00	-	-
rs34768406	*WDR1*	5'UTR	C	A	0.01	0.03	0.08[0.01;0.99]	0.049	0.01	0.02	2.12[0.35;12.64]	0.410	0.10	0.24	0.39[0.25;0.62]	0.000 05
rs371440376	*WDR1*	upstream	C	T	0.14	0.10	2.30[1.02;5.20]	0.045	0.22	0.17	1.34[0.78;2.31]	0.290	0.00	0.00	-	-
VAR_CHR4_10120485	*WDR1*	upstream	C	T	0.01	0.06	0.05[0.00;0.66]	0.023	0.01	0.00	-	-	0.00	0.00	-	-
VAR_CHR4_10122489	*WDR1*	upstream	G	A	0.09	0.05	4.20[1.31;13.50]	0.016	0.06	0.00	23.96[2.64;217.53]	0.005	0.00	0.00	-	-
VAR_CHR4_10160679	-	intergenic	A	G	0.01	0.06	0.05[0.00;0.66]	0.023	0.01	0.00	-	-	0.00	0.00	-	-
rs11734554	-	intergenic	T	C	0.65	0.71	0.58[0.34;0.99]	0.046	0.53	0.59	0.89[0.58;1.37]	0.597	0.36	0.22	1.76[1.23;2.52]	0.002
rs6845818	-	intergenic	C	T	0.31	0.23	2.01[1.14;3.54]	0.016	0.42	0.35	1.17[0.77;1.78]	0.450	0.5	0.50	1.08[0.79;1.48]	0.635
rs62286326	*AC006499.9*	upstream	G	A	0.14	0.11	2.40[1.09;5.32]	0.030	0.27	0.21	1.42[0.86;2.34]	0.166	0.25	0.23	1.20[0.82;1.77]	0.351
rs62286327	*AC006499.9*	upstream	A	G	0.21	0.15	2.10[1.08;4.10]	0.029	0.31	0.24	1.33[0.83;2.13]	0.234	0.25	0.23	1.19[0.81;1.75]	0.375
rs13126279	-	intergenic	T	C	0.18	0.31	0.48[0.26;0.87]	0.016	0.11	0.18	0.51[0.26;0.99]	0.046	0.11	0.04	2.18[1.13;4.21]	0.020
rs4698017	*AC006499.2*	upstream	A	G	0.62	0.69	0.58[0.35;0.99]	0.044	0.52	0.56	0.98[0.64;1.51]	0.939	0.36	0.22	1.71[1.20;2.45]	0.003
rs4697744	*AC006499.1*	upstream	G	A	0.62	0.69	0.58[0.35;0.99]	0.044	0.48	0.44	1.02[0.66;1.56]	0.939	0.36	0.22	1.71[1.20;2.45]	0.003
VAR_CHR4_10298641	*AC006499.1*	upstream	G	A	0.01	0.06	0.05[0.00;0.66]	0.023	0.01	0.00	-	-	0.00	0.00	-	-

VARIANT	GENE	TYPE	Ref allele	Alt allele	WEST POLYNESIAN				EAST POLYNESIAN				EUROPEAN			
					HU-freq	NU-freq	OR(95%CI)*	P_{OR}*	HU-freq	NU-freq	OR(95%CI)*	P_{OR}*	HU-freq	NU-freq	OR(95%CI)#	P_{OR}#
rs11940728	*AC006499.2*	upstream	A	T	0.21	0.15	2.10[1.08;4.10]	0.029	0.32	0.25	1.31[0.82;2.10]	0.263	0.25	0.22	1.19[0.81;1.74]	0.376
rs28798076	*AC006499.1*	upstream	C	A	0.35	0.24	2.06[1.19;3.56]	0.010	0.43	0.38	1.07[0.71;1.63]	0.738	0.46	0.47	1.01[0.74;1.38]	0.941
rs1860905	-	intergenic	C	G	0.62	0.69	0.58[0.35;0.99]	0.044	0.53	0.56	0.99[0.65;1.53]	0.974	0.40	0.22	2.08[1.44;3.02]	0.0001
rs10012795	-	intergenic	G	C	0.21	0.15	2.10[1.08;4.10]	0.029	0.32	0.25	1.31[0.82;2.10]	0.263	0.26	0.22	1.24[0.84;1.81]	0.276
rs28733364	*RP11-136I13.1*	downstream	T	C	0.35	0.26	1.70[1.02;2.84]	0.044	0.46	0.40	1.09[0.71;1.67]	0.696	0.44	0.47	0.96[0.70;1.31]	0.774
rs373311989	*RP11-136I13.1*	downstream	A	G	0.01	0.05	0.04[0.00;0.40]	0.006	0.02	0.03	1.03[0.25;4.27]	0.966	0.00	0.00	-	-
VAR_CHR4_10457448	*ZNF518B*	intronic	A	C	0.01	0.04	0.10[0.02;0.57]	0.010	0.01	0.01	0.27[0.02;3.98]	0.343	0.00	0.00	-	-
rs76917885	*ZNF518B*	intronic	A	C	0.14	0.10	2.72[1.16;6.36]	0.021	0.24	0.19	1.44[0.84;2.48]	0.187	0.069	0.08	0.82[0.45;1.48]	0.515

*The significance threshold was set at 0.05. Variants in LD with each other are highlighted with the same color. HU-freq: minor allele frequency (MAF) in hyperuricemic cases. NU-freq: MAF in normouricemic controls. OR: odds ratio for the alternate (minor) allele. 95% CI: 95% confidence interval. P_{OR}: p-value for odds ratio. *: Odds ratio adjusted for age, sex and PCA1-10, #: Odds ratio adjusted for sex.*

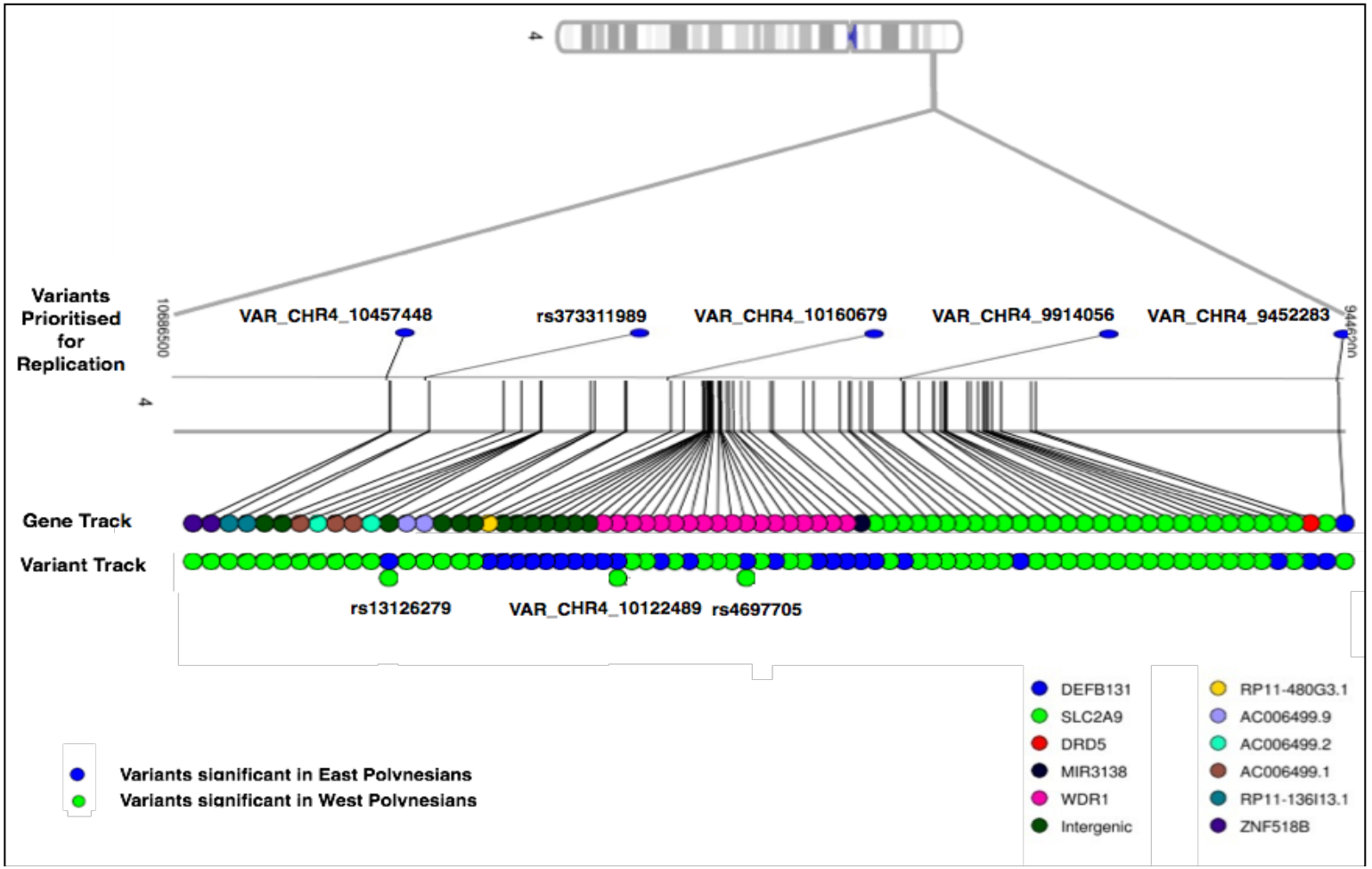


FIG 3.15 GENE ANNOTATIONS OF SIGNIFICANT SIGNALS IN EAST AND WEST POLYNESIANS AND THE VARIANTS PRIORITIZED FOR REPLICATION. *The gene annotations for the variants are provided in the gene track. Variants significant in the East Polynesians and West Polynesians are represented in the variant track as blue and green circles, respectively. The significance threshold was set at 0.05. Three variants were significant in both populations (rs13126279, VAR_CHR4_10122489 and rs4697705). Five variants were chosen for replication (VAR_CHR4_9914056, rs373311989, VAR_CHR4_9452283, VAR_CHR4_10160679 and VAR_CHR4_10457448).*

3.3 LWAS - REPLICATION-PHASE

3.3.1 VARIANTS PRIORITISED

Based on the criteria outlined in section 2.5.1, five Polynesian-specific variants (VAR_CHR4_9914056, rs373311989, VAR_CHR4_9452283, VAR_CHR4_10160679 and VAR_CHR4_10457448) were prioritised for replication in a larger independent Polynesian cohort (table 3.5). Figure 3.16 illustrates the functional prediction of these five variants.

NOTE: VAR_CHR4_10122489 was preferred over VAR_CHR4_9914056 for replication (both variants were in LD) as it was found to be significant in both East and West Polynesian groups. This novel variant had to be genotyped using the Taqman® methodology with customised probes. However, custom probes could not be successfully designed over the region containing this variant because of the presence of multiple polymorphic sites in the vicinity. Therefore, VAR_CHR4_9914056 was chosen for replication.

Firstly, the markers in the Core Exome dataset were screened to identify if any of the variants prioritized (or variants in strong/complete LD with them) were previously genotyped on this platform. However, none of the prioritized variants were genotyped on this platform.

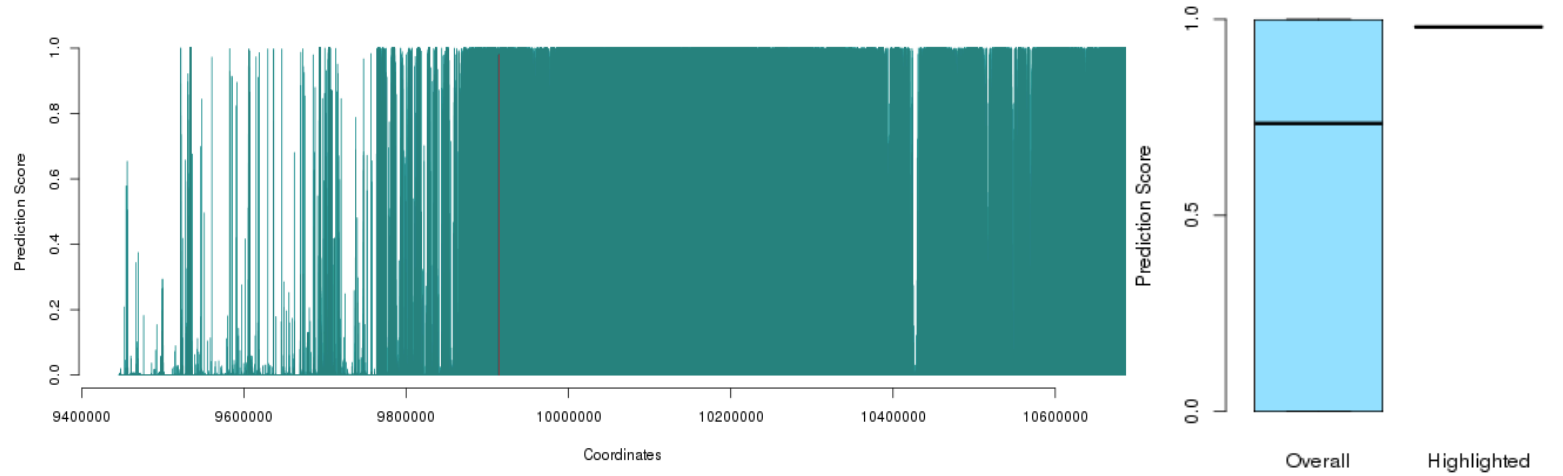
All markers genotyped on the Sequenom MassARRAY platform were screened to identify if any of the prioritized variants were genotyped on this platform. Two of the prioritized variants (VAR_CHR4_10160679 and VAR_CHR4_10457448) were previously genotyped on this platform. Therefore, the corresponding genotype and phenotype data were used for replicating associations of these variants with hyperuricemia followed by analysing association with gout. The remaining three variants (VAR_CHR4_9914056, rs373311989 and VAR_CHR4_9452283) were genotyped using the Taqman® methodology with custom probes. The data obtained were used to replicate association of the variants with hyperuricemia and gout.

TABLE 3.5 VARIANTS PRIORITISED FOR REPLICATION

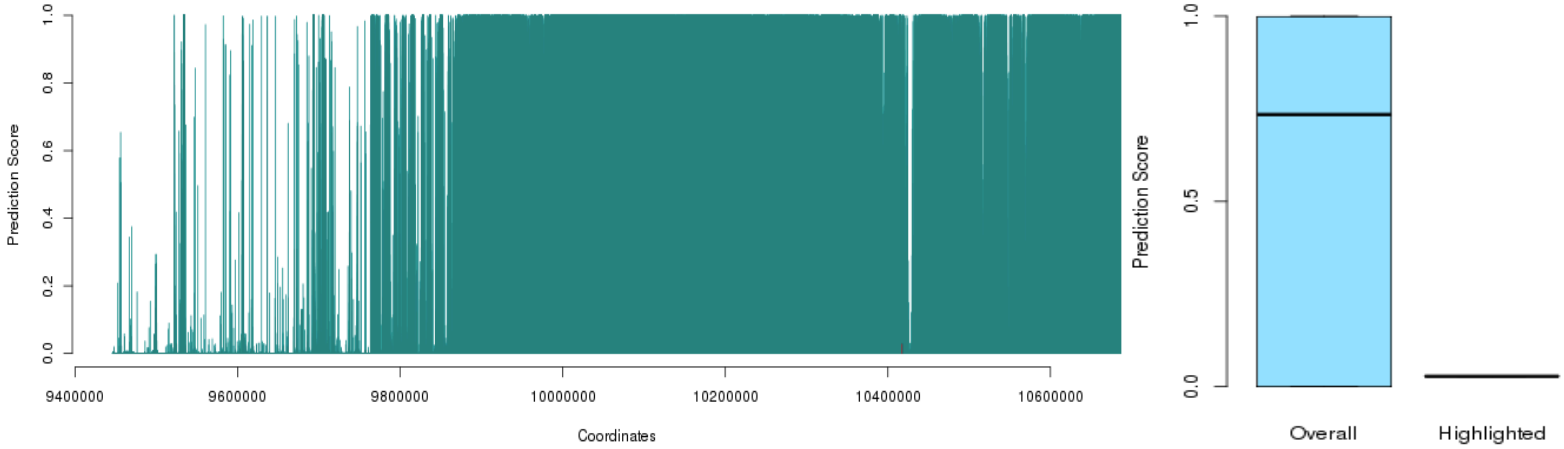
Variant	Genomic position	Gene	Location	CADD score	Ref allele	Alt allele
VAR_CHR4_9914056*	4:9914056	*SLC2A9*	Intronic	5.51	G	A
rs373311989*	4:10417458	*RP11-136I13.1*	Downstream	5.05	A	G
VAR_CHR4_9452283*	4:9452283	*DEFB131A*	Downstream	0.29	T	A
VAR_CHR4_10160679#	4:10160679	intergenic	intergenic	1.51	A	G
VAR_CHR4_10457448#	4:10457448	*ZNF518B*	Intronic	0.192	A	C

Ref: reference. Alt: alternate. indicates that the variant was genotyped using Taqman® methodology to replicate association. # indicates that the variant was genotyped in the Sequenom MassARRAY platform.*

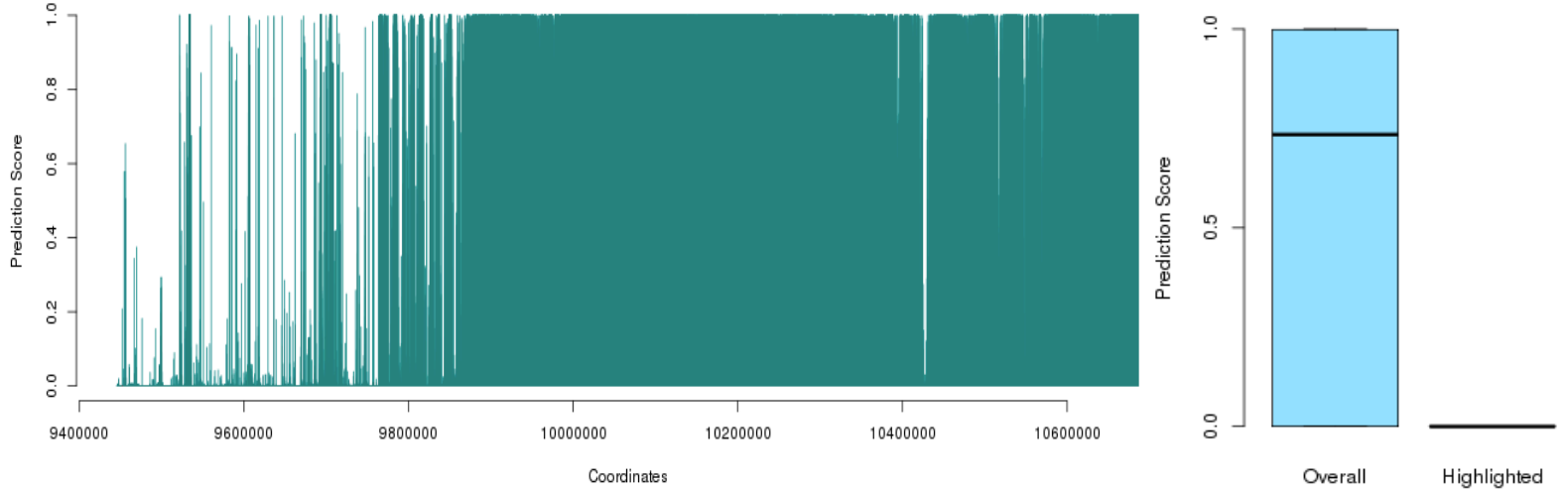
1. Var_CHR4_9914056



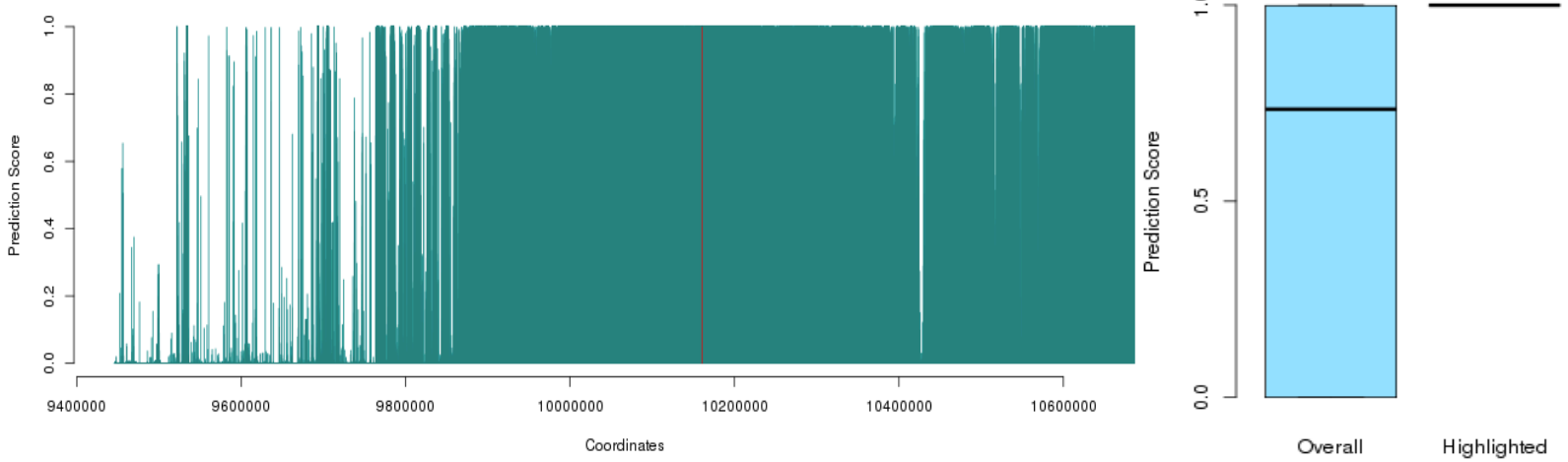
2. rs373311989



3. VAR_CHR4_9452283



4. VAR_CHR4_10160679



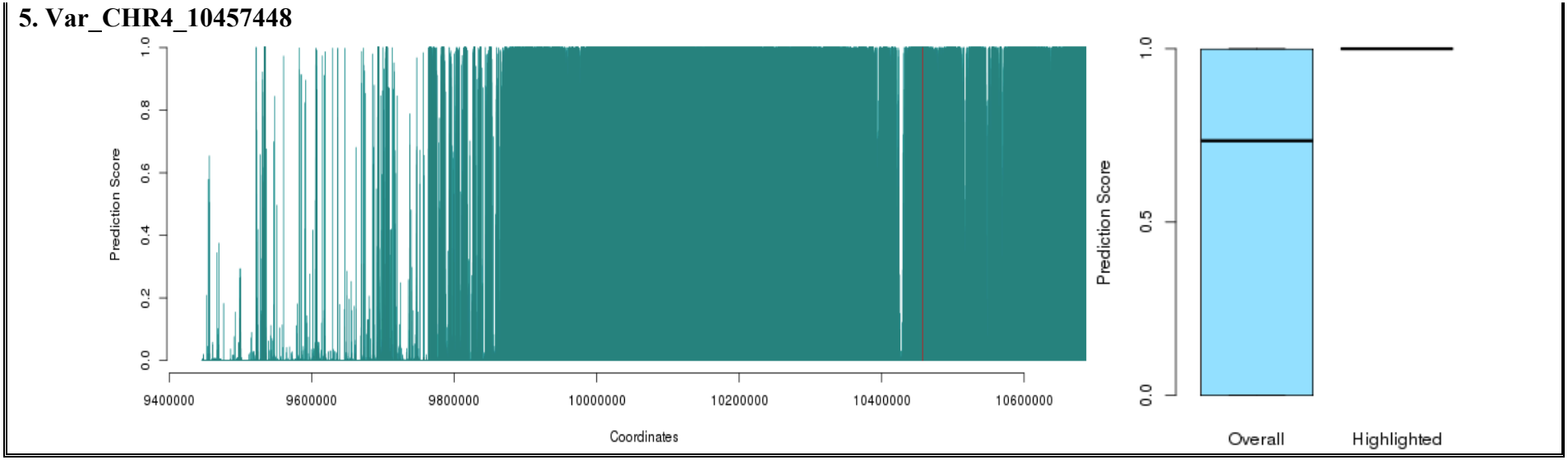


FIGURE 3.16 PLOTS SHOWING THE FUNCTIONAL PREDICTION OF THE FIVE VARIANTS PRIORITIZED FOR REPLICATION. IN EACH PLOT, *the red peak represents the prediction values for the specified variant. The height of the peak is proportional to the functional potential at that genomic location. Tall peaks represent conserved regions with higher predicted functional potential. The boxplots on the right hand side of each plot represent the deleteriousness prediction value for the variant in comparison to that of the overall region. The plots were generated using the GenoCanyon function prediction software.*

3.3.2 POWER OF STUDY

The detection power was calculated for the Replication Cohorts A (Polynesian individuals genotyped on the Sequenom MassARRAY platform) and B (Polynesian individuals genotyped using the TaqMan® SNP Genotyping platform). Detection power ≥ 80% was considered adequate.

The Replication Cohort A consisted of 623 cases (318 East Polynesians and 305 West Polynesians) and 598 controls (389 East Polynesians and 209 West Polynesians) and the Replication Cohort B consisted of 712 cases (367 East Polynesians and 345 West Polynesians) and 865 controls (565 East Polynesians and 300 West Polynesians). The power calculations indicated both datasets to be 100% powered to detect effect sizes of variants with OR ≥ 2.0 having a minor allele frequency (MAF) ≥ 0.05 and adequately powered (≥ 80%) to detect significant associations for variants with OR ≥ 1.5 and MAF ≥ 0.1 (figures 3.17 A and B).

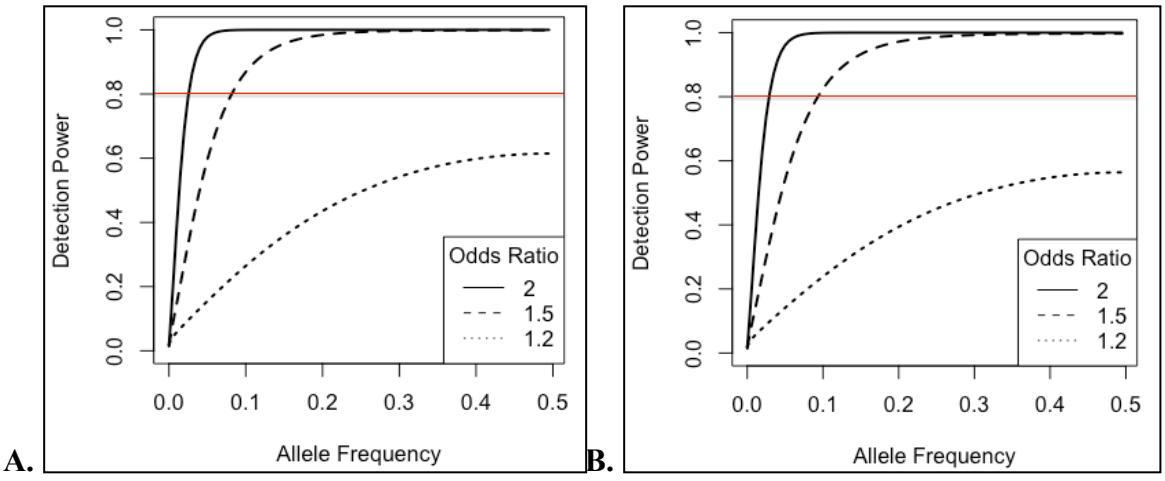


FIGURE 3.17 THE POWER OF STUDY FOR THE REPLICATION COHORTS A AND B, CALCULATED OVER A RANGE OF EFFECT SIZES (LOW EFFECT SIZE- OR = 1.2, MODERATE EFFECT SIZE- OR = 1.5, HIGH EFFECT SIZE- OR = 2) AND MINOR ALLELE FREQUENCIES. *The red line indicates detection power that was considered adequate for this study. A: The power of study for the Replication Cohort A. B: The power of study for the Replication Cohort B. Power calculations were done using R version 3.4.1.*

3.3.3 REPLICATION-PHASE SIGNALS

The complete results are tabulated in table 3.6.

VAR_CHR4_9914056 is a novel Polynesian-specific variant. The A allele of VAR_CHR4_9914056 was significantly associated with risk of hyperuricemia in East Polynesians in the Discovery Cohort with a large effect size (adjusted OR = 28.30, P_{OR} = 0.003). The association was successfully replicated in the larger independent Replication Cohort, although with a relatively smaller effect size (adjusted OR = 2.93, P_{OR} = 0.004). In West Polynesians, the variant did not show up as a significant signal in both the Discovery and Replication Cohorts. However, when meta-analysed using combined East and West Polynesian subgroups, the altered (A) allele of VAR_CHR4_9914056 indicated a strong risk association for hyperuricemia in the Discovery Cohort (OR = 5.01, P_{OR} = 0.003, P_{Het} = 0.07) (figure 3.18 A), but not in the Replication Cohort: OR = 1.76, P_{OR} = 0.23, P_{Het} = 0.04) (figure 3.18 B).

The discovery-phase association of rs373311989 with hyperuricemia could not be replicated. In the Discovery Cohort, the G allele of rs373311989 showed a protective association with hyperuricemia in West Polynesians (adjusted OR = 0.04, P_{OR} = 0.006). However in the Replication Cohort, the association was insignificant with an opposite direction of effect (adjusted OR = 1.25, P_{OR} = 0.56).

Similar results were obtained for VAR_CHR4_9452283 and VAR_CHR4_10160679. The A allele of VAR_CHR4_9452283 showed a significant protective association during discovery (adjusted OR = 0.05, P_{OR} = 0.01) but an insignificant risk association during replication (adjusted OR = 4.57, P_{OR} = 0.17) in West Polynesians.

For VAR_CHR4_10160679, in the Discovery Cohort, the G allele showed a protective association with hyperuricemia in West Polynesians (adjusted OR = 0.05, P_{OR} = 0.02). However in the Replication Cohort, the association was insignificant with an opposite direction of efffect (adjusted OR = 1.48, P_{OR} = 0.29).

The C allele of VAR_CHR4_10457448 which showed a protective association with hyperuricemia in West Polynesians during the discovery-phase (adjusted OR = 0.10, P_{OR} = 0.01) failed to show any association with hyperuricemia in the replication-phase (adjusted OR = 1.12, P_{OR} = 0.88).

TABLE 3.6 REPLICATION OF ASSOCIATION OF VARIANTS WITH HYPERURICEMIA IN EAST AND WEST POLYNESIANS

VARIANT 1							
Variant	**VAR_CHR4_9914056**		Novelty	**Novel**			
Gene	***SLC2A9***		Population specificity	**Polynesian**			
Ref allele	**G**		Alt allele	**A**			
POPULATION	**MAF_{NU}**	**MAF_{HU}**		**P_{OR}**	**OR (95%CI)**	**P_{HWE} (cases)**	**P_{HWE} (controls)**
DISCOVERY COHORT							
EP	**0.01**	**0.06**	**U**	**0.006**	**17.64[1.98;157.23]**	**0.47**	**0.96**
			A*	**0.003**	**28.30[3.17;252.31]**		
WP	0.04	0.07	U	0.14	2.08[0.60;7.20]	0.4	0.72
			A*	0.09	2.86[0.82;9.93]		
REPLICATION COHORT B							
EP	**0.02**	**0.03**	**U**	**0.008**	**2.52[1.29;5.16]**	**0.49**	**0.68**
			A#	**0.004**	**2.93[1.43;6.29]**		
WP	0.05	0.06	U	0.34	1.28[0.78;2.17]	0.68	0.87
			A#	0.64	1.14[0.67;1.98]		
VARIANT 2							
Variant	**rs373311989**		Novelty	**Known**			
Gene	***RP11-136I13.1***		Population specificity	**Polynesian**			
Ref allele	**A**		Alt allele	**G**			
POPULATION	**MAF_{NU}**	**MAF_{HU}**		**P_{OR}**	**OR (95%CI)**	**P_{HWE} (cases)**	**P_{HWE} (controls)**
DISCOVERY COHORT							
EP	0.03	0.02	U	0.89	0.92[0.27;3.09]	0.8	0.78
			A*	0.97	1.03[0.25;4.27]		
WP	0.05	0.01	U	0.03	0.09[0.01;0.79]	0.96	0.68
			A*	0.01	0.04[0.00;0.40]		
REPLICATION COHORT B							
EP	0.02	0.02	U	0.42	1.36[0.63;2.91]	0.7	0.72
			A#	0.67	1.19[0.53;2.66]		
WP	0.03	0.04	U	0.42	1.36[0.66;2.89]	0.54	0.66
			A#	0.56	1.25[0.60;2.69]		

VARIANT 3							
Variant	VAR_CHR4_9452283		Novelty	Novel			
Gene	*DEFB131A*		Population specificity	Polynesian			
Ref allele	T		Alt allele	A			
POPULATION	**MAF_{NU}**	**MAF_{HU}**		**P_{OR}**	**OR (95%CI)**	**P_{HWE} (cases)**	**P_{HWE} (controls)**
DISCOVERY COHORT							
EP	0.02	0.01	U	0.61	0.71[0.19;2.64]	0	0.81
			A*	0.67	0.72[0.16;3.22]		
WP	0.04	0.01	U	0.04	0.11[0.01;0.95]	0.96	0.72
			A*	0.01	0.05[0.01;0.50]		
REPLICATION COHORT B							
EP	0.00	0.01	U	0.34	2.38[0.39;18.14]	0.93	0.96
			A#	0.63	1.57[0.25;12.43]		
WP	0.00	0.01	U	0.16	4.72[0.75;90.85]	0.88	0.95
			A#	0.17	4.57[0.70;90.0]		
VARIANT 4							
Variant	VAR_CHR4_10160679		Novelty	Novel			
Gene	Intergenic		Population specificity	Polynesian			
Ref allele	A		Alt allele	G			
POPULATION	**MAF_{NU}**	**MAF_{HU}**		**P_{OR}**	**OR (95%CI)**	**P_{HWE} (cases)**	**P_{HWE} (controls)**
DISCOVERY COHORT							
EP	0	0.01	U	0.99	--	0.96	--
			A*	0.97	--		
WP	0.06	0.01	U	0.02	0.09[0.01;0.73]	0.96	0.12
			A*	0.02	0.05[0.00;0.66]		
REPLICATION COHORT A							
EP	0.00	0.00	U	0.69	1.75[0.07;44.40]	0.97	0.98
			A#	0.93	1.12[0.04;29.51]		
WP	0.04	0.04	U	0.42	1.32[0.67;2.68]	0	0.16
			A#	0.29	1.48[0.73;3.13]		
VARIANT 5							
Variant	VAR_CHR4_10457448		Novelty	Novel			
Gene	*ZNF518B*		Population specificity	Polynesian			
Ref allele	A		Alt allele	C			
POPULATION	**MAF_{NU}**	**MAF_{HU}**		**P_{OR}**	**OR (95%CI)**	**P_{HWE} (cases)**	**P_{HWE} (controls)**
DISCOVERY COHORT							
EP	0.01	0.01	U	0.38	0.36[0.04;3.53]	0.96	0.89

			A*	0.34	0.27[0.02;3.98]		
WP	0.04	0.01	U	0.07	0.23[0.04;1.15]	0.92	0.72
			A*	0.01	0.10[0.02;0.57]		
REPLICATION COHORT A							
EP	0	0.01	U	0.98	--	0.94	--
			A#	0.98	--		
WP	0.01	0.01	U	0.99	0.99[0.23;4.26]	0.89	0.88
			A#	0.88	1.12[0.25;5.16]		

Ref: reference. Alt: alternate. U: Model unadjusted for confounders. A: Model adjusted for age, sex and PCA 1-10. A#: Model adjusted for age, sex and grandparental ancestry. MAF_{HU}: minor allele frequency in hyperuricemic cases. MAF_{NU}: minor allele frequency in normouricemic controls. OR: odds ratio for the alternate (minor) allele. 95% CI: 95% confidence interval. P_{OR}: p-value for odds ratio. P_{HWE}: P-value for Hardy-Weinberg equilibrium.*

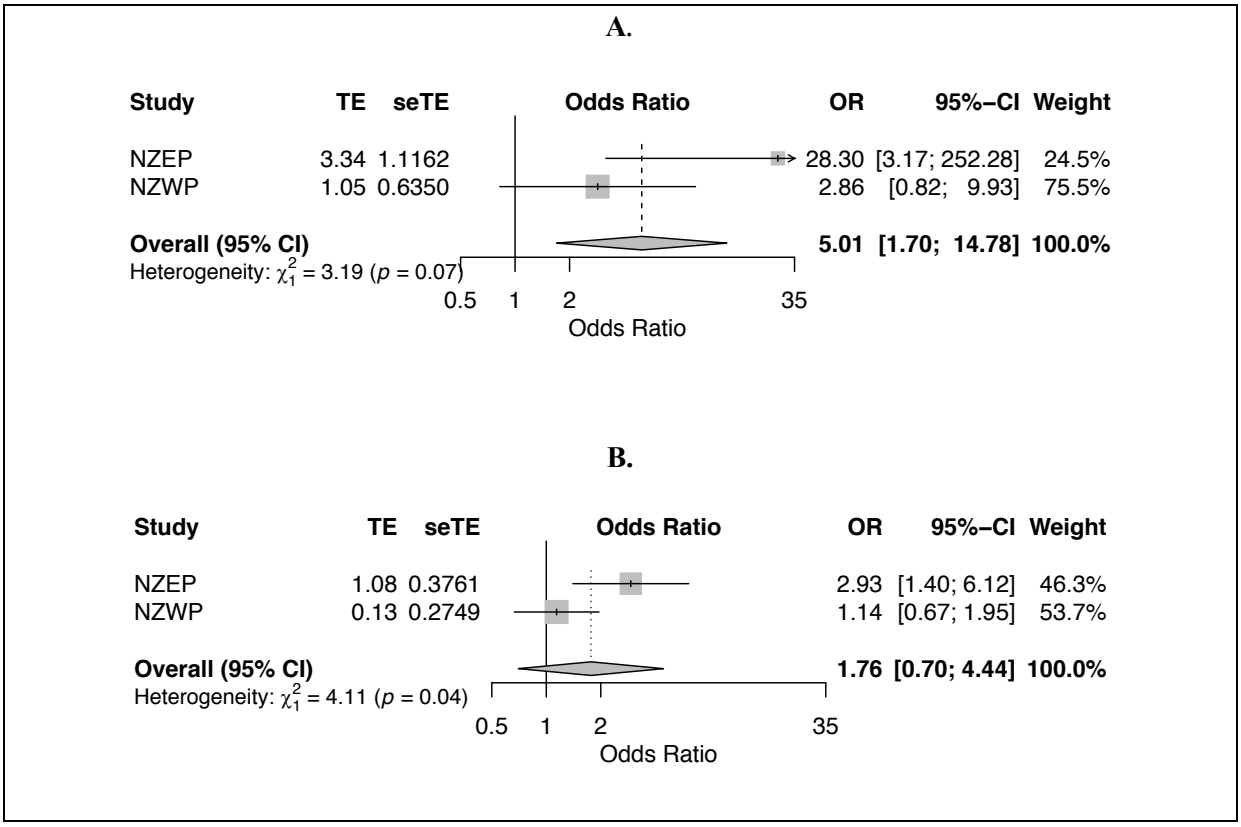


Figure 3.18 Forest plots of SLC2A9 : VAR_CHR4_9914056 and risk of hyperuricemia in combined Polynesian datasets. A. Discovery Cohort B. Replication Cohort. NZEP: New Zealand East Polynesians. NZWP: New Zealand West Polynesians. OR: adjusted odds ratio. 95% CI: 95% confidence interval. TE: natural log of OR. seTE: standard error, P: adjusted p-value. Weight: weight of the study population. The vertical line at the center of the graph represents null effect between the variant and the phenotype. X-axis represents OR calculated after adjusting for confounders. Horizontal lines on the graph represent the study populations, the size of each square being proportional to the size of the study population. The diamond indicates the point estimate and 95% confidence interval (CI) for the summary results. X_2^2 : Heterogeneity between sample sets (P <0.05).

3.4 ASSOCIATION OF VARIANTS WITH GOUT

The five variants chosen for replicating association with hyperuricemia (VAR_CHR4_9914056, rs373311989, VAR_CHR4_9452283, VAR_CHR4_10160679 and VAR_CHR4_10457448) were also tested for their association with gout.

3.4.1 POWER OF STUDY

The detection power was calculated for the Gout Discovery Cohort (Polynesian individuals sequenced by targeted resequencing) and the Gout Replication Cohorts A (Polynesian individuals genotyped on the Sequenom MassARRAY platform) and B (Polynesian individuals genotyped using the TaqMan® SNP Genotyping platform). Detection power ≥ 80% was considered adequate.

The Gout Discovery Cohort consisted of 161 cases (71 East Polynesians and 90 West Polynesians) and 248 controls (152 East Polynesians and 96 West Polynesians). The power calculations indicated the dataset to be adequately powered (≥ 80%) to detect significant associations for variants with OR ≥ 2.0 and MAF ≥ 0.1 (figures 3.19 A).

The Gout Replication Cohort A consisted of 603 cases (312 East Polynesians and 291 West Polynesians) and 618 controls (395 East Polynesians and 223 West Polynesians) and the Gout Replication Cohort B, consisted of 734 cases (400 East Polynesians and 334 West Polynesians) and 815 controls (515 East Polynesians and 300 West Polynesians). The power calculations indicated both datasets to be 100% powered to detect effect sizes of variants with OR ≥ 2.0 having a minor allele frequency (MAF) ≥ 0.05 and adequately powered (≥ 80%) to detect significant associations for variants with OR ≥ 1.5 and MAF ≥ 0.05 (figures 3.19 B and C).

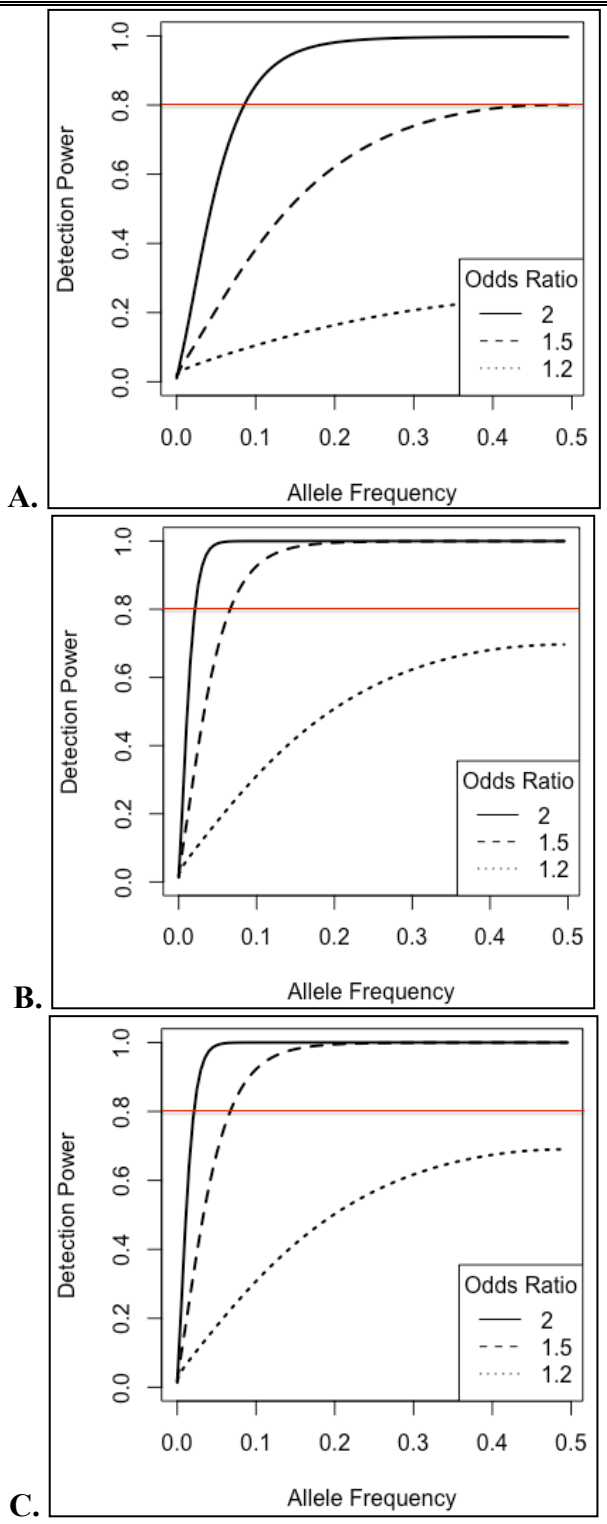


Figure 3.19 The power of study for the Gout Discovery and Gout Replication Cohorts A and B, calculated over a range of effect sizes (low effect size- OR = 1.2, moderate effect size- OR = 1.5, high effect size- OR = 2) and minor allele frequencies. The red line indicates detection power that was considered adequate for this study. A: Discovery Cohort B: Replication Cohort A. C: Replication Cohort B. Power calculations were done using R version 3.4.1.

3.4.2 THE ASSOCIATION OF PRIORITISED VARIANTS WITH GOUT

The complete results are tabulated in table 3.7.

Only one variant, VAR_CHR4_10160679, showed association with gout in both the Discovery and Replication Cohorts. The A allele of VAR_CHR4_10160679 showed a significant protective association both during discovery (adjusted OR = 0.04, P_{OR} = 0.03) and replication (adjusted OR = 0.32, P_{OR} = 0.01) in West Polynesians.

The A allele of VAR_CHR4_9914056 was significantly associated with the risk of gout in East Polynesians in the Discovery Cohort (adjusted OR = 6.08, P_{OR} = 0.01) but the association could not be successfully replicated (adjusted OR = 0.66, P_{OR} = 0.32).

The A allele of VAR_CHR4_9452283 indicated to be protective against gout in West Polynesians in the Discovery Cohort (adjusted OR = 0.09, P_{OR} = 0.04). Again, the result could not be replicated. In fact, the direction of effect was opposite for the altered allele of this variant in the Replication Cohort (adjusted OR = 2.64, P_{OR} = 0.32).

The G allele of rs373311989 did not show any association with gout risk in either of the two populations, both in the discovery and replication datasets. The C allele of VAR_CHR4_10457448 showed a protective association with risk of gout in West Polynesians during the discovery-phase (adjusted OR = 0.16, P_{OR} = 0.05) but failed to show similar association with the trait in the replication phase (adjusted OR = 4.01, P_{OR} = 0.12) (table 3.7).

TABLE 3.7 THE ASSOCIATION OF PRIORITISED VARIANTS WITH GOUT IN EAST AND WEST POLYNESIANS

VARIANT 1							
Variant	VAR_CHR4_9914056		Novelty		Novel		
Gene	*SLC2A9*		Population specificity		Polynesian		
Ref allele	G		Alt allele		A		
POPULATION	**MAF_{NU}**	**MAF_{HU}**		**P_{OR}**	**OR (95%CI)**	**P_{HWE}**	**P_{HWE}**
GOUT DISCOVERY COHORT							
EP	0.02	0.07	U	0.01	4.59[1.48;14.28]	0.56	0.84
			A*	0.01	6.08[1.42;26.04]		
WP	0.05	0.07	U	0.54	1.32[0.54;3.23]	0.5	0.59
			A*	0.52	1.46[0.46;4.62]		
GOUT REPLICATION COHORT B							
EP	0.02	0.02	U	0.75	0.90[0.47;1.72]	0.68	0.6
			A#	0.32	0.66[0.28;1.51]		
WP	0.05	0.07	U	0.35	1.28[0.76;2.16]	0.8	0.66
			A#	0.74	1.11[0.60;2.06]		
VARIANT 2							
Variant	rs373311989		Novelty		Known		
Gene	*RP11-136I13.1*		Population specificity		Polynesian		
Ref allele	A		Alt allele		G		
POPULATION	**MAF_{NU}**	**MAF_{HU}**		**P_{OR}**	**OR (95%CI)**	**P_{HWE}**	**P_{HWE}**
GOUT DISCOVERY COHORT							
EP	0.03	0.02	U	0.82	0.85[0.22;3.31]	0.85	0.74
			A*	0.69	0.70[0.12;4.03]		
WP	0.04	0.00	U	0.98	--	--	0.67
			A*	0.98	--		
GOUT REPLICATION COHORT B							
EP	0.01	0.02	U	0.28	1.48[0.73;3.00]	0.66	0.74
			A#	0.82	1.10[0.48;2.54]		
WP	0.03	0.03	U	0.49	0.78[0.38;1.59]	0.63	0.59
			A#	0.33	0.66[0.29;1.52]		
VARIANT 3							
Variant	VAR_CHR4_9452283		Novelty		Novel		
Gene	*DEFB131A*		Population specificity		Polynesian		
Ref allele	T		Alt allele		A		
POPULATION	**MAF_{NU}**	**MAF_{HU}**		**P_{OR}**	**OR (95%CI)**	**P_{HWE}**	**P_{HWE}**
GOUT DISCOVERY COHORT							
EP	0.02	0.02	U	0.7	1.30[0.35;4.74]	0	0.84
			A*	0.84	1.20[0.22;6.59]		
WP	0.03	0.01	U	0.1	0.17[0.02;1.43]	0.96	0.75
			A*	0.04	0.09[0.01;0.92]		
GOUT REPLICATION COHORT B							
EP	0.00	0.01	U	0.97	--	0.92	--
			A#	0.97	--		
WP	0.00	0.01	U	0.58	2.39[0.43;13.15]	0.91	0.95
			A#	0.32	2.64[0.40;17.60]		
VARIANT 4							

Variant	VAR_CHR4_10160679			Novelty		Novel	
Gene	Intergenic			Population specificity		Polynesian	
Ref allele	A			Alt allele		G	
POPULATION	**MAF_{NU}**	**MAF_{HU}**		**P_{OR}**	**OR (95%CI)**	**P_{HWE}**	**P_{HWE}**
GOUT DISCOVERY COHORT							
EP	~0.00	~0.00	U	0.99	--	--	0.97
			A*	0.98	--		
WP	**0.05**	**0.01**	**U**	**0.06**	**0.14[0.02;1.07]**	**0.96**	**0.07**
			A*	**0.03**	**0.04[0.00;0.75]**		
GOUT REPLICATION COHORT A							
EP	~0.00	~0.00	U	0.81	1.41[0.09;22.69]	0.98	0.98
			A#	0.7	1.98[0.06;61.58]		
WP	**0.05**	**0.01**	**U**	**0.004**	**0.32[0.15;0.70]**	**0**	**0.07**
			A#	**0.01**	**0.32[0.14;0.76]**		
VARIANT 5							
Variant	VAR_CHR4_10457448			Novelty		Novel	
Gene	*ZNF518B*			Population specificity		Polynesian	
Ref allele	A			Alt allele		C	
POPULATION	**MAF_{NU}**	**MAF_{HU}**		**P_{OR}**	**OR (95%CI)**	**P_{HWE}**	**P_{HWE}**
GOUT DISCOVERY COHORT							
EP	0.01	0.01	U	0.81	0.76[0.08;7.42]	0.95	0.9
			A*	0.54	0.41[0.02;7.23]		
WP	0.03	0.01	U	0.19	0.34[0.07;1.73]	0.92	0.75
			A*	0.05	0.16[0.02;1.00]		
GOUT REPLICATION COHORT A							
EP	~0.00	~0.00	U	0.77	0.70[0.06;7.76]	0.98	0.97
			A#	0.7	0.60[0.05;7.57]		
WP	0.01	0.01	U	0.65	1.40[0.33;5.92]	0.88	0.92
			A#	0.12	4.01[0.71;22.54]		

Ref: reference. Alt: alternate. U: Model unadjusted for confounders. A: Model adjusted for age, sex and PCA 1-10. A#: Model adjusted for age, sex and grandparental ancestry. MAF_{HU}: minor allele frequency in hyperuricemic cases. MAF_{NU}: minor allele frequency in normouricemic controls. OR: odds ratio for the alternate (minor) allele. 95% CI: 95% confidence interval. P_{OR}: p-value for odds ratio. P_{HWE}: P-value for Hardy-Weinberg equilibrium.*

Chapter 4

Discussion

CHAPTER 4

DISCUSSION

4.1 RECAPITULATING THE RATIONALE BEHIND THIS STUDY

This project was driven by the hypothesis that the Polynesian genome may contain genetic variants that are specific to the population within the *SLC2A9* locus, a region that has been implicated in the control of serum urate at a genome-wide significance level (Kottgen et al., 2013). The main focus of the study was, therefore, to identify Polynesian-specific hyperuricemia-associated genetic variants, if any, within the *SLC2A9* locus. Single variant association analysis using logistic regression was employed to study associations, using Polynesian individuals sequenced by the targeted resequencing approach. Associations discovered were replicated in a larger independent Polynesian cohort. A significant amount of time was also dedicated towards visualizing the data. The overall rationale to carry out this project is outlined below.

Why -----?	**Rationale**
Hyperuricemia and gout	Hyperuricemia has several roles to play in health and disease. Gout, an excruciatingly painful form of inflammatory arthritis, is the most common manifestation of symptomatic hyperuricemia (VanItallie et al., 2010).
Polynesian	The Polynesian population displays inherent hyperuricemia and a higher predisposition to gout (Gosling et al., 2014).
SLC2A9	The *SLC2A9* gene is one of the most influential genes in the context of urate genetics (Vitart et al., 2008; Doring et al., 2008).
Targeted resequencing approach	Targeted resequencing captures all variants within a target region of interest by scanning the genomes of a given sample set, rather than detecting a limited number of

	predetermined genotypes. It is a method of choice while trying to identify population-specific genetic variants (Keller et al., 2011).
Population-specific variants	Variants in *SLC2A9* have been reported to have population-specific effects (Hollis-Moffatt et al., 2009).
The entire locus rather than the *SLC2A9* gene/exons	Intronic and intergenic variants and epistatic interactions have been reported for this genetic locus (Doring et al., 2008, Wei et al., 2014).
Data visualization methods	Visualization tools help view and understand polymorphic loci such as the *SLC2A9*.

4.2 DATA VISUALIZATION

While handling large information sets, data visualization tools and techniques help us understand the overall distribution of data points and identify data patterns that are hidden or difficult to identify *per se*. Visual presentation makes data interpretation easier.

The circos plot provided with a clear idea of the distribution of the variants across the locus (figure 3.2). For example, it could be easily interpreted that the distribution of variants within the locus was uneven. While a large number of variants mapped to the *SLC2A9* gene, only one variant mapped to the *CLNK* gene. Annotation revealed 97% of the variants to be located within noncoding regions of the locus (introns (~70%), untranslated, regulatory and intergenic). *SLC2A9* is a highly polymorphic gene. Over 970 variants have been reported for this gene in the Exome Aggregation Consortium database (ExAC), comprising exome sequence information for 60,706 unrelated individuals sequenced in various large-scale sequencing projects (http://exac.broadinstitute.org/gene/ENSG00000109667). Of note, a large number of noncoding variants have been reported for this gene. For example, about 1700 *SLC2A9* variants have been deposited in the Genome Aggregation Database (gnomAD, http://gnomad.broadinstitute.org/gene/ENSG00000109667). Unlike the ExAC database, the gnomAD database contains both exome and genome sequence data from unrelated individuals including 123136 exomes and 15496 genomes. Findings from this study reiterate that the *SLC2A9* gene is very rich in polymorphisms, both coding and noncoding.

The function prediction regional plot predicted most parts of the locus to be functionally relevant except for the region (4:9446200 – 4:9750000) which was predicted to display a relatively low functional potential (figure 3.3).

Differentiating haplotypes between populations can at least partly explain the contribution of genetic variations towards the differences in population susceptibility to a particular disease/phenotype. By comparing samples from different populations, genomic regions with significant genetic variation between these populations can be identified (Clark et al., 1998). The impact of genetic variations can be better understood by including the phase information for the haplotypes (for which both the paternal and maternal alleles are known) (Jager et al., 2014).

Europeans have a lower prevalence of gout when compared to Polynesians (Kuo et al., 2015), attributable to the inherent hyperuricemia observed in Polynesians (Merriman, 2011). A comparison of phased haplotypes between these two populations was carried out with the intention of exploring any obvious differences in the haplotype structure between the two populations, which could in turn give some clues about specific regions contributing to the greater incidence of hyperuricemia in the Polynesians. The results indicated two sub regions within the *SLC2A9* locus displaying variation in the haplotype structure between the populations (figures 3.5 and 3.6). The variable region 1 (4:9446207 - 4:9823478) overlaps with the region that was predicted to display a low functional potential (described earlier in this section). This result is in line with the well accepted concept that functionally important regions are more conserved in genomes unlike the regions that lack much functional significance (Warren et al., 2013). The variable region 2 (4:10120364 - 4:10494666) is predominantly intergenic. However, it covers the VAR_CHR4_10160679 variant, which was found to be associated with gout in Polynesians, in both the Discovery and the Replication Cohorts. This could mean that this region is in fact important for urate control in Polynesians, possibly through epistatic interactions. Such interactions have been reported previously for his locus (Wei et al., 2014).

4.3 ASSOCIATION ANALYSIS

GWASs have proven to be incredibly valuable in dissecting the genetic architecture of complex phenotypes and have identified a large number of common genetic variants associated with complex traits. However, a large percentage of heritability remains unexplained, termed missing heritability (Goldstein et al., 2009, Pritchard et al., 2001). Analysing the association of uncommon variants (defined as variants with ≤ 0.5% frequency of occurrence) with complex traits was suggested as a strategy to explain the missing heritability of complex traits (Manolio et al., 2009). Variants that are uncommon or occur infrequently and are specific to a population can be identified by the targeted resequencing approach (Keller et al., 2011), followed by association studies in order to provide important genetic clues about the disease/phenotype.

While interpreting the results of logistic regression, both the statistical significance (p-value) and the effect size are important statistical estimates to consider. Statistical significance (p-value) is the likelihood that an observation is owing to chance. In this study, the significance threshold was set at alpha = 0.05 (equivalent to 95% confidence interval, i.e., 5% risk of a false positive result). Any variant with a p-value ≤ 0.05 was considered to display an nominally significant association between its minor allele and hyperuricemia (or gout, as applicable).

Although the p-value is informative to say whether or not a nominally significant association exists between a variant and the phenotype, it does not reveal the effect size of the variant. "Effect size is the magnitude of the difference between groups" (Sullivan et al., 2012). Computing the effect sizes helps us understand the magnitude of the differences observed. A common effect size index used in epidemiological studies is the odds ratio (OR). "An odds ratio (OR) is a measure of association between an exposure and an outcome. The OR represents the odds that an outcome will occur given a particular exposure, compared to the odds of the outcome occurring in the absence of that exposure" (Szumilas et al., 2010). In this study, the minor allele of a genetic variant was treated as an exposure and hyperuricemia as the outcome in comparison to normouricemia. The allelic odds ratios were therefore predictive of the association of the variant's minor allele and hyperuricemia (or gout, as

applicable). An OR of 1 means that the exposure has no effect on the odds of the outcome. In other words, the variant in discussion is not associated with hyperuricemia. An OR > 1 (not including 1) indicates that the exposure is associated with higher odds of the outcome; that is, the minor allele of the variant is associated with an increased risk of developing hyperuricemia. An OR < 1 (not including 1) is indicative of a protective association between the exposure (variant's minor allele) and the outcome (hyperuricemia). The value of the OR is indicative of the magnitude of association (effect size of the variant) in either direction.

Adjusted logistic regression analysis revealed a large number of variants in the locus displaying nominally significant association with hyperuricemia in the Europeans (multiple testing was not accounted for) (appendix 3). This is consistent with existing scientific reports that illustrate a very strong association of *SLC2A9* genetic variants with serum urate in the European population (Kottgen et al., 2013, Kolz et al., 2009). However, in the Polynesians, a relatively lesser number of associations reached significance (53 variants in West Polynesians and 25 variants in East Polynesians). Notably, many of the significant signals were population-specific, being either monomorphic for the major allele or not reaching statistical significance even if present in the other populations. In either case, these results highlight the population-specific effects of the *SLC2A9* variants that are likely associated with urate. Variants in *SLC2A9* have been previously reported to have population-specific effects. For instance, the variant rs11942223 has been reported to play an important role in conferring susceptibility to gout in both Caucasians (odds ratio (OR = 2) and NZ Polynesians (OR = 5) but with different effect sizes (Hollis-Moffatt et al., 2009). Similarly, some of the intronic variants associated with urate in Europeans have been reported to not associate with the trait in Asians (Okada et al., 2012).

Some of the interesting Polynesian-specific signals identified in the initial discovery-phase association analysis that displayed nominal statistical significance (p-value ≤ 0.05) and high effect size (OR ≤ 0.1 where the direction of association was protective or OR ≥ 2 where the direction of association was risk) were prioritised for replication (table 3.5). Since replication was part of the study design, Bonferroni correction was not applied.

The markers genotyped on the CoreExome bead chip platform were screened to check if any of the prioritized variants were previously genotyped on this platform. It was found that none

of the them were genotyped on this platform. Of the 3963 variants identified by targeted sequencing and the 391 variants in the locus that were genotyped on the CoreExome bead chip platform, only 220 variants were found to overlap. This was because the CoreExome-24 v1.2 bead chip genotyping covered variants in the coding regions of *SLC2A9* and the neighbouring genes, while the targeted resequencing approach pulled out common and uncommon variants in both coding and noncoding regions of the *SLC2A9* locus.

The variant, VAR_CHR4_10122489, located upstream of *WDR1*, appeared to be an important signal with its A allele (alternate allele) conferring risk for hyperuricemia (OR = 4.2, P_{OR} = 0.02) in the West Polynesians. Of note, this variant was also found to be associated with hyperuricemia in he East Polynesians with a larger effect size (OR = 23.96, P_{OR} = 0.004). Since custom probes could not be successfully designed over the region containing this variant (due to the presence of multiple polymorphic sites in the vicinity), the results for this variant could not be directly replicated. However, VAR_CHR4_9914056, which was found to be in 93% LD with VAR_CHR4_10122489 in the East Polynesians, was chosen for replication.

The A allele of VAR_CHR4_9914056 was significantly associated with the risk of hyperuricemia in East Polynesians in the Discovery Cohort with a large effect size (adjusted OR = 28.30, P_{OR} = 0.004) as well as the Replication Cohort, although with a relatively smaller effect size (adjusted OR = 2.93, P_{OR} = 0.003) (table 3.6). The smaller effect size observed during replication may be because of the larger sample size of the replication cohort. Moreover, the Polynesians selected for resequencing were the ones with either very high or very low serum urate levels versus the replication cohort having less extreme urate values. This could be a second potential reason for the relatively smaller effect size observed for the variant during replication.

Although the variant did not show up as a significant signal in the West Polynesians, meta-analysis using combined East and West Polynesian subgroups indicated a strong risk association for the altered (A) allele of the variant with hyperuricemia in the Discovery Cohort (OR = 5.01, P_{OR} = 0.003, P_{Het} = 0.07), which could not be replicated although the direction of association remained consistent (Replication Cohort: OR = 1.76, P_{OR} = 0.23, P_{Het} = 0.04).

VAR_CHR4_9914056 is located in intron 7 of the *SLC2A9* gene (http://grch37.ensembl.org/), has a CADD Phred score = 5.51) and an overall MAF of 5% (including both Discovery and Replication Cohorts) in Polynesians. *SLC2A9* variants associated with serum urate have been reported to reside within introns (Doring et al., 2008). Moreover, variants located within introns 3-7 of the *SLC2A9* gene have been reported to be associated with blood urate levels in Europeans, attaining genome-wide level significance (Kottgen et al., 2013). Therefore results of this project are consistent with earlier reports.

The variant resides within a nuclease accessible region, as shown in figure 4.1 (UCSC Genome Browser GRCh37/hg19). Nuclease accessible/hypersensitive sites (genomic regions that are sensitive to cleavage by nucleases such as deoxyribonuclease I) are potential sites for the binding of factors responsible for transcriptional regulation in eukaryotes. Therefore, nuclease accessible regions are regarded as potentially functional. Variations in such regions may result in epigenetic changes that accompany disease development (Tsompana et al., 2014).

Given that the *SLC2A9*-encoded voltage-dependent urate transporter is responsible for urate reabsorption, it is likely that the risk allele for VAR_CHR4_9914056 contributes to an increased activity of the SLC2A9 protein, resulting in an increased risk of hyperuricemia in those individuals who harbour the risk allele. However, this variant was not associated with gout. These results may be interpreted in the following ways:

- It is possible that the variant is indeed not associated with gout. Such an observation would support the concept that there are different genetic mechanisms and checkpoints that operate during the development of hyperuricemia and the progression to gout (Dalbeth et al., 2014).
- It is also possible that VAR_CHR4_9914056 is associated with the risk for gout but is in LD with another variant exerting a protective effect against gout and thereby nullifying the gout risk effect of VAR_CHR4_9914056 in the East Polynesians.
- A potential reason for this observation could be that the study was inadequately powered, giving rise to a false negative result.

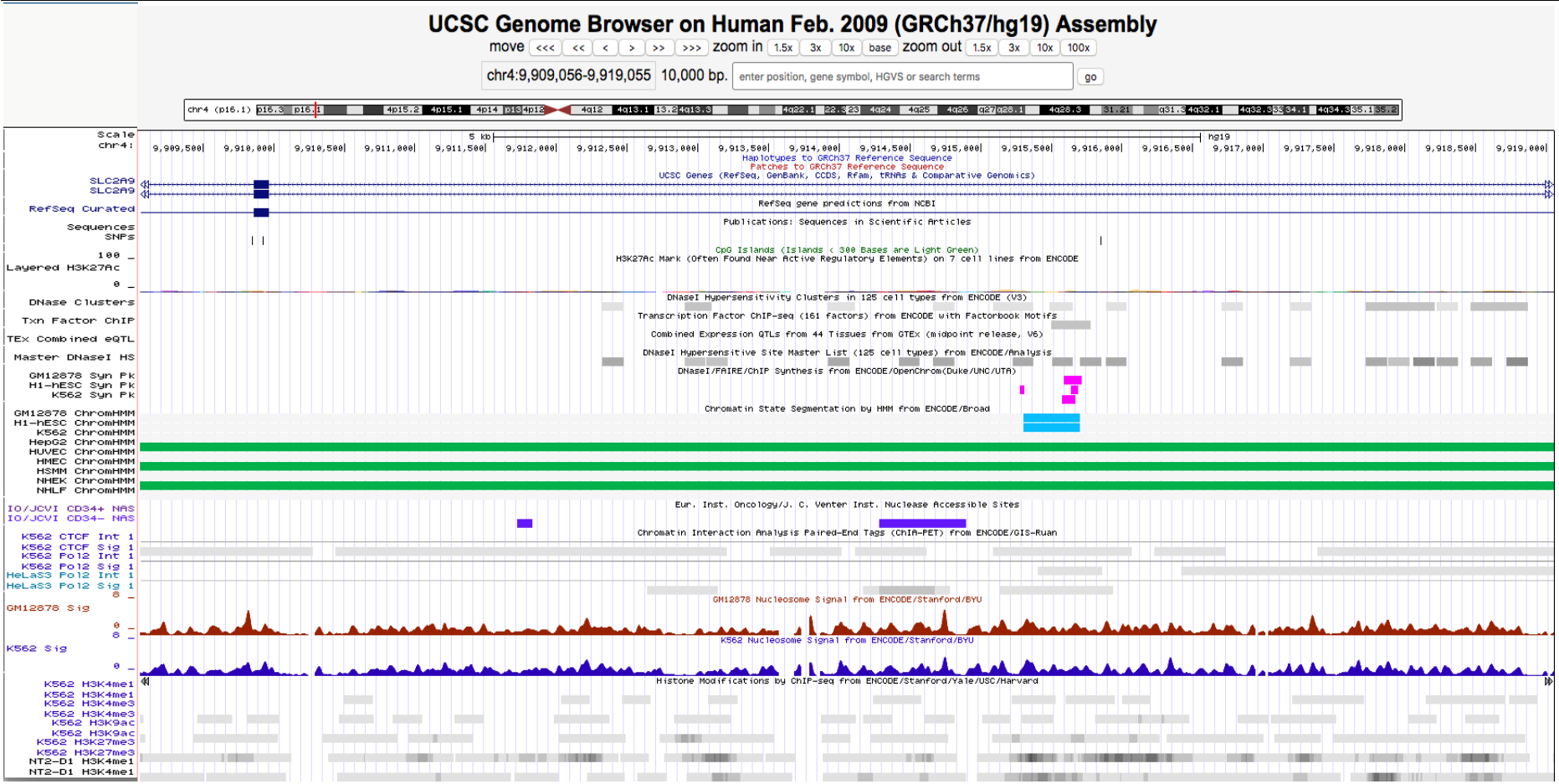


Fig 4.1: Image From The Ucsc Genome Browser Displaying The Variant, Var_Chr4_9914056, In The Genomic Context. *VAR_CHR4_9914056 resides within a nuclease accessible site in the genome, shown as a purple bar in the 'nuclease accessible sites' track. The green bars in the chromatin state segmentation track shows that the region is well transcribed . The red and blue peaks in the GM12676 and K562 nucleosome signal tracks, respectively, represent nucleosome signals in the regions.*

The only other association discovered, that could be successfully replicated, was the association of the variant, VAR_CHR4_10160679, with gout. The A allele of VAR_CHR4_10160679 showed a nominally significant protective association both during discovery (adjusted OR = 0.04, P_{OR} = 0.03) and replication (adjusted OR = 0.32, P_{OR} = 0.01) in West Polynesians. This variant, located in the intergenic region of the locus, was found to be highly specific to the West Polynesians, the minor allele being overrepresented in West Polynesian normouricemic controls (MAF_{HU} = 1% vs MAF_{NU} = 5%). The allele was negligibly prevalent in East Polynesian cases or controls (MAF ~0). The CADD score for the variant was low (CADD Phred score = 1.51). However, inter-genic variants and epistatic interactions within the *SLC2A9* locus have been reported (Wei et al., 2014).

4.4 STRENGTHS AND LIMITATIONS OF THE STUDY

One of the biggest strengths of this study was the use of high throughput resequencing technology, which is an ideal approach in discovering population-specific genetic variants associated with a phenotype. Secondly, locus-wide association analysis, without limiting to the exons of *SLC2A9*, was ideal. As can be seen, all significant signals mapped to non-coding regions of the locus. Thirdly, analysis carried out in a population-stratified manner aided in the identification of alleles having strong population-specific effects. Further, identifying and adjusting for the principal components heightened the possibility of finding true independent associations between genetic variants and the phenotype. Genotyping to replicate the outcomes of the initial analysis helped distinguishing true associations from those obtained by chance.

However, the study had a number of limitations. Firstly, the unavailability of PCA data for the replication cohorts compelled that the regression model be adjusted for grandparental ancestry rather than PCA during the replication phase. Owing to the presence of most extreme hyperuricemic/normouricemic samples in the Discovery Cohort and the small sizes of the sample sets, most discovery-phase associations could not be replicated. Since replication was built into the study design, Bonferroni correction was not applied. However, none of the variants showed extremely low p-values. Therefore, it is highly likely that none

of the variants would have remained significant had correction been applied. By virtue of the time-bound nature of this project, burden analysis could not be performed. Also, gene-gene or epistatic interactions were not considered in this study.

The study also had some intrinsic limitations. Firstly, the resequencing approach has an inherent disadvantage that high or low GC-content can affect probe hybridization and thereby impact sequencing (Samorodnitsky et al., 2015). Secondly, the uncommonness of variants by itself adds a layer of complexity to the identification and replication of such variants and their associations with the phenotype. Thirdly, there are only a limited amount of tools available to annotate non coding variants. Establishing the functional and pathological relevance of non-coding variants is challenging.

4.5 FUTURE DIRECTIONS

There is a scope for further analysis in this project. As a continuum of this study, sex-stratified analysis, burden analysis, fine-mapping studies and the study of epistatic interactions can be performed. Association of variants with fractional excretion of urate, other kidney-related traits and drug response can also be analysed.

VAR_CHR4_9914056 may be clinically relevant in the context of hyperuricemia in the Polynesian population. However, the functional role of this variant needs to be established. It is possible that the variant's risk allele causes aberrant mRNA splicing and thereby affects protein expression, either qualitatively or quantitatively. This hypothesis could be validated by analysing the mRNAs from individuals carrying the risk allele (Cooper, 2010). Mini-gene construct or splicing-specific-PCR technique could be used to determine the effect of the variant on splicing efficiency (Hull et al., 2007; Nascimbeni et al., 2010). Alternatively, the risk allele can be expressed in a model organism like the Xenopus oocyte in order to evaluate the effect of the variant. Once the functional effect of the variant is established, antisense oligonucleotide therapeutic approach may be used to restore the normal splicing pattern (Matos et al., 2018). This approach may be employed as a strategy for personalized treatment of symptomatic hyperuricemic individuals carrying the risk allele for the variant.

4.6 CONCLUSION

This work signifies the usefulness of targeted resequencing, especially in a bespoke fashion, in studying the genetic basis of a trait/disease that is highly prevalent in a particular population and further evinces the association of non-coding variants in the *SLC2A9* locus, mapping to the human 4p16.1 chromosomal region, with hyperuricemia and gout in Polynesians. The study also demonstrates the utility of data visualization tools and techniques in exploratory big data analysis.

The discovery of the Polynesian-specific variant, located in intron 7 of *SLC2A9* at the genomic location 4:9914056, and its association with hyperuricemia is promising, owing to the prominent overrepresentation of its alternate allele in hyperuricemic individuals. Further genetic and functional analyses can plausibly prove the relevance of the variant in the Polynesian population and support the 'no more junk DNA' concept.

The association of the intronic variant, VAR_CHR4_9914056, with hyperuricemia but not gout, on one hand, and the association of the inter-genic variant, VAR_CHR4_10160679, with gout but not hyperuricemia points to the genetic complexity involved in the development of hyperuricemia and its progression to gout, although the low power of study could also provide an explanation for this observation.

However, the identification of only a limited number of variants in the *SLC2A9* locus significantly associated with serum urate in Polynesians, unlike what has been reported for the Europeans, throws light on the missing heritability of this complex trait and gives an inkling that there are more important genes/loci yet to be identified in the context of urate genetics, especially in this population.

REFERENCES

Adzhubei, I.A., Schmidt, S., Peshkin, L., Ramensky, V.E., Gerasimova, A., Bork, P., Kondrashov, A.S., and Sunyaev, S.R. (2010a). A method and server for predicting damaging missense mutations. Nat. Methods 7, 248-249.

Adzhubei, I.A., Schmidt, S., Peshkin, L., Ramensky, V.E., Gerasimova, A., Bork, P., Kondrashov, A.S., and Sunyaev, S.R. (2010b). A method and server for predicting damaging missense mutations. Nat. Methods 7, 248-249.

Alvarez-Hern‡ndez, E., Pel‡ez-Ballestas, I., V‡zquez-Mellado, J., Ter‡n-Estrada, L., Bernard-Medina, A.G., Espinoza, J., Aceves-Avila, F.J., Goycochea-Robles, M.V., Garza, M., Ventura, L., et al. (2008). Validation of the Health Assessment Questionnaire disability index in patients with gout. Arthritis Rheum. 59, 665-669.

Amaral, K.B., Silva, T.P., Malta, K.K., Carmo, L.A.S., Dias, F.F., Almeida, M.R., Andrade, G.F.S., Martins, J.S., Pinho, R.R., Costa-Neto, S.F., et al. (2016). Natural Schistosoma mansoni Infection in the Wild Reservoir Nectomys squamipes Leads to Excessive Lipid Droplet Accumulation in Hepatocytes in the Absence of Liver Functional Impairment. PLoS ONE 11, e0166979.

Ames, B.N., Cathcart, R., Schwiers, E., and Hochstein, P. (1981). Uric acid provides an antioxidant defense in humans against oxidant- and radical-caused aging and cancer: a hypothesis. Proc. Natl. Acad. Sci. U.S.A. 78, 6858-6862.

Anzai, N., Ichida, K., Jutabha, P., Kimura, T., Babu, E., Jin, C.J., Srivastava, S., Kitamura, K., Hisatome, I., Endou, H., et al. (2008). Plasma urate level is directly regulated by a voltage-driven urate efflux transporter URATv1 (SLC2A9) in humans. J. Biol. Chem. 283, 26834-26838.

Anzai, N., Miyazaki, H., Noshiro, R., Khamdang, S., Chairoungdua, A., Shin, H.-J., Enomoto, A., Sakamoto, S., Hirata, T., Tomita, K., et al. (2004). The multivalent PDZ domain-containing protein PDZK1 regulates transport activity of renal urate-anion exchanger URAT1 via its C terminus. J. Biol. Chem. 279, 45942-45950.

Augustin, R., Carayannopoulos, M.O., Dowd, L.O., Phay, J.E., Moley, J.F., and Moley, K.H. (2004). Identification and characterization of human glucose transporter-like protein-9 (GLUT9): alternative splicing alters trafficking. J. Biol. Chem. 279, 16229-16236.

Bahn, A., Hagos, Y., Reuter, S., Balen, D., Brzica, H., Krick, W., Burckhardt, B.C., Sabolic, I., and Burckhardt, G. (2008). Identification of a new urate and high affinity nicotinate transporter, hOAT10 (SLC22A13). J. Biol. Chem. 283, 16332-16341.

Bakhiya, A., Bahn, A., Burckhardt, G., and Wolff, N. (2003). Human organic anion transporter 3 (hOAT3) can operate as an exchanger and mediate secretory urate flux. Cell. Physiol. Biochem. 13, 249-256.

Barrett, J.C., Fry, B., Maller, J., and Daly, M.J. (2005). Haploview: analysis and visualization of LD and haplotype maps. Bioinformatics 21, 263-265.

Batt, C., Phipps-Green, A.J., Black, M.A., Cadzow, M., Merriman, M.E., Topless, R., Gow, P., Harrison, A., Highton, J., Jones, P., et al. (2014). Sugar-sweetened beverage consumption: a risk factor for prevalent gout with SLC2A9 genotype-specific effects on serum urate and risk of gout. Ann. Rheum. Dis. 73, 2101-2106.

Baum, M., Quigley, R., and Satlin, L. (2003). Maturational changes in renal tubular transport. Curr. Opin. Nephrol. Hypertens. 12, 521-526.

Beck, L.H. (1986). Requiem for gouty nephropathy. Kidney Int. 30, 280-287.

Bianchi, M.E. (2007). DAMPs, PAMPs and alarmins: all we need to know about danger. J. Leukoc. Biol. 81, 1-5.

Bien, E.J., and Zucker, M. (1955). Uricolysis in normal and gouty individuals. Ann. Rheum. Dis. 14, 409-411.

Bobulescu, I.A., and Moe, O.W. (2012). Renal transport of uric acid: evolving concepts and uncertainties. Adv Chronic Kidney Dis 19, 358-371.

Bonora, E., Targher, G., Zenere, M.B., Saggiani, F., Cacciatori, V., Tosi, F., Travia, D., Zenti, M.G., Branzi, P., Santi, L., et al. (1996). Relationship of uric acid concentration to cardiovascular risk factors in young men. Role of obesity and central fat distribution. The Verona Young Men Atherosclerosis Risk Factors Study. Int. J. Obes. Relat. Metab. Disord. 20, 975-980.

Bos, M.J., Koudstaal, P.J., Hofman, A., Witteman, J.C.M., and Breteler, M.M.B. (2006). Uric acid is a risk factor for myocardial infarction and stroke: the Rotterdam study. Stroke 37, 1503-1507.

Bowman, G.L., Shannon, J., Frei, B., Kaye, J.A., and Quinn, J.F. (2010). Uric Acid as a CNS Antioxidant. J Alzheimers Dis 19, 1331-1336.

BrandstŠtter, A., Kiechl, S., Kollerits, B., Hunt, S.C., Heid, I.M., Coassin, S., Willeit, J., Adams, T.D., Illig, T., Hopkins, P.N., et al. (2008). Sex-specific association of the putative fructose transporter SLC2A9 variants with uric acid levels is modified by BMI. Diabetes Care 31, 1662-1667.

Brauer, G.W., and Prior, I.A. (1978). A prospective study of gout in New Zealand Maoris. Ann. Rheum. Dis. 37, 466-472.

Braun, E.J., and Campbell, C.E. (1989). Uric acid decomposition in the lower gastrointestinal tract. J Exp Zool Suppl 3, 70-74.

Buckley, H.R. (2007). Possible Gouty Arthritis in Lapita_Associated Skeletons from Teouma, Efate Island, Central Vanuatu. Current Anthropology 48, 741-749.

Caulfield, M.J., Munroe, P.B., O'Neill, D., Witkowska, K., Charchar, F.J., Doblado, M., Evans, S., Eyheramendy, S., Onipinla, A., Howard, P., et al. (2008). SLC2A9 is a high-capacity urate transporter in humans. PLoS Med. 5, e197.

Charles, B.A., Shriner, D., Doumatey, A., Chen, G., Zhou, J., Huang, H., Herbert, A., Gerry, N.P., Christman, M.F., Adeyemo, A., et al. (2011). A genome-wide association study of serum uric acid in African Americans. BMC Med Genomics 4, 17.

Chen, L., Zhu, W., Chen, Z., Dai, H., Ren, J., Chen, J., Chen, L., and Fang, L. (2007).

Relationship between hyperuricemia and metabolic syndrome. J Zhejiang Univ Sci B 8, 593-598.

Chiba, T., Matsuo, H., Kawamura, Y., Nagamori, S., Nishiyama, T., Wei, L., Nakayama, A., Nakamura, T., Sakiyama, M., Takada, T., et al. (2015). NPT1/SLC17A1 is a renal urate exporter in humans and its common gain-of-function variant decreases the risk of renal underexcretion gout. Arthritis & Rheumatology (Hoboken, N.J.) 67, 281-287.

Choi, H.K., Atkinson, K., Karlson, E.W., and Curhan, G. (2005). Obesity, weight change, hypertension, diuretic use, and risk of gout in men: the health professionals follow-up study. Arch. Intern. Med. 165, 742-748.

Choi, H.K., Atkinson, K., Karlson, E.W., Willett, W., and Curhan, G. (2004). Alcohol intake and risk of incident gout in men: a prospective study. Lancet 363, 1277-1281.

Choi, H.K., Soriano, L.C., Zhang, Y., and Rodr'guez, L.A.G. (2012). Antihypertensive drugs and risk of incident gout among patients with hypertension: population based case-control study. BMJ 344, d8190.

Chonchol, M., Shlipak, M.G., Katz, R., Sarnak, M.J., Newman, A.B., Siscovick, D.S., Kestenbaum, B., Carney, J.K., and Fried, L.F. (2007). Relationship of uric acid with progression of kidney disease. Am. J. Kidney Dis. 50, 239-247.

Cingolani, P., Platts, A., Wang, L.L., Coon, M., Nguyen, T., Wang, L., Land, S.J., Lu, X., and Ruden, D.M. (2012). A program for annotating and predicting the effects of single nucleotide polymorphisms, SnpEff: SNPs in the genome of Drosophila melanogaster strain w1118; iso-2; iso-3. Fly (Austin) 6, 80-92.

Clark, A.G., Weiss, K.M., Nickerson, D.A., Taylor, S.L., Buchanan, A., StengŒrd, J., Salomaa, V., Vartiainen, E., Perola, M., Boerwinkle, E., et al. (1998). Haplotype structure and population genetic inferences from nucleotide-sequence variation in human lipoprotein lipase. Am. J. Hum. Genet. 63, 595-612.

Conen, D., Wietlisbach, V., Bovet, P., Shamlaye, C., Riesen, W., Paccaud, F., and Burnier, M. (2004). Prevalence of hyperuricemia and relation of serum uric acid with cardiovascular risk factors in a developing country. BMC Public Health 4, 9.

Cooper, G.M., and Shendure, J. (2011). Needles in stacks of needles: finding disease-causal variants in a wealth of genomic data. Nat. Rev. Genet. 12, 628-640.

Cummings, N., Dyer, T.D., Kotea, N., Kowlessur, S., Chitson, P., Zimmet, P., Blangero, J., and Jowett, J.B.M. (2010). Genome-wide scan identifies a quantitative trait locus at 4p15.3 for serum urate. Eur. J. Hum. Genet. 18, 1243-1247.

Dalbeth, N., and Stamp, L. (2014). Hyperuricaemia and gout: time for a new staging system? Ann. Rheum. Dis. 73, 1598-1600.

Dalbeth, N., Pool, B., Gamble, G.D., Smith, T., Callon, K.E., McQueen, F.M., and Cornish, J. (2010b). Cellular characterization of the gouty tophus: a quantitative analysis. Arthritis Rheum. 62, 1549-1556.

Dalbeth, N., Wong, S., Gamble, G.D., Horne, A., Mason, B., Pool, B., Fairbanks, L., McQueen, F.M., Cornish, J., Reid, I.R., et al. (2010a). Acute effect of milk on serum urate concentrations: a randomised controlled crossover trial. Ann. Rheum. Dis. 69, 1677-1682.

Dehghan, A., Kšttgen, A., Yang, Q., Hwang, S.-J., Kao, W.L., Rivadeneira, F., Boerwinkle, E., Levy, D., Hofman, A., Astor, B.C., et al. (2008a). Association of three genetic loci with uric acid concentration and risk of gout: a genome-wide association study. Lancet 372, 1953-1961.

Dehghan, A., van Hoek, M., Sijbrands, E.J.G., Hofman, A., and Witteman, J.C.M. (2008b). High serum uric acid as a novel risk factor for type 2 diabetes. Diabetes Care 31, 361-362.

Delaneau, O., Marchini, J., Consortium, T. 1000 G.P., McVean, G.A., Donnelly, P., Lunter, G., Marchini, J.L., Myers, S., Gupta-Hinch, A., Iqbal, Z., et al. (2014). Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. Nature Communications 5, 3934.

DePristo, M.A., Banks, E., Poplin, R.E., Garimella, K.V., Maguire, J.R., Hartl, C., Philippakis, A.A., del Angel, G., Rivas, M.., Hanna, M., et al. (2011). A framework for variation discovery and genotyping using next-generation DNA sequencing data. Nat Genet 43, 491-498.

Desideri, G., Castaldo, G., Lombardi, A., Mussap, M., Testa, A., Pontremoli, R., Punzi, L., and Borghi, C. (2014). Is it time to revise the normal range of serum uric acid levels? Eur Rev Med Pharmacol Sci 18, 1295-1306.

Dinour, D., Gray, N.K., Campbell, S., Shu, X., Sawyer, L., Richardson, W., Rechavi, G., Amariglio, N., Ganon, L., Sela, B.-A., et al. (2010). Homozygous SLC2A9 mutations cause severe renal hypouricemia.

J. Am. Soc. Nephrol. 21, 64-72.

Dinour, D., Gray, N.K., Ganon, L., Knox, A.J.S., Shalev, H., Sela, B.-A., Campbell, S., Sawyer, L., Shu, X., Valsamidou, E., et al. (2012). Two novel homozygous SLC2A9 mutations cause renal hypouricemia type 2. Nephrol. Dial. Transplant. 27, 1035-1041.

Dorwart, B.B. (2004). Thomas sydenham (1624-1689), on gout: 1717. J Clin Rheumatol 10, 227.

Drenick, E.J. (1965). Hyperuricemia, acute gout, renal insufficiency and urate nephrolithiasis due to starvation. Arthritis Rheum. 8, 988-997.

Drubay, D., Gautheret, D., and Michiels, S. (2018). A benchmark study of scoring methods for non-coding mutations. Bioinformatics 34, 1635-1641.

Drubay, D., Gautheret, D., and Michiels, S. (2018). A benchmark study of scoring methods for non-coding mutations. Bioinformatics 34, 1635-1641.

Dšring, A., Gieger, C., Mehta, D., Gohlke, H., Prokisch, H., Coassin, S., Fischer, G., Henke, K., Klopp, N., Kronenberg, F., et al. (2008). SLC2A9 influences uric acid concentrations with pronounced sex-specific effects. Nat. Genet. 40, 430-436.

Ekundayo, O.J., Dell'Italia, L.J., Sanders, P.W., Arnett, D., Aban, I., Love, T.E., Filippatos, G., Anker, S.D., Lloyd-Jones, D.M., Bakris, G., et al. (2010). Association between hyperuricemia and incident heart failure among older adults: a propensity-matched study. Int. J. Cardiol. 142, 279-287.

Enomoto, A., Kimura, H., Chairoungdua, A., Shigeta, Y., Jutabha, P., Cha, S.H., Hosoyamada, M., Takeda, M., Sekine, T., Igarashi, T., et al. (2002). Molecular identification of a renal urate anion exchanger that regulates blood urate levels. Nature 417, 447-452.

Eraly, S.A., Vallon, V., Rieg, T., Gangoiti, J.A., Wikoff, W.R., Siuzdak, G., Barshop, B.A., and Nigam, S.K. (2008). Multiple organic anion transporters contribute to net renal excretion of uric acid. Physiol. Genomics 33, 180-192.

Facchini, F., Chen, Y.D., Hollenbeck, C.B., and Reaven, G.M. (1991). Relationship between resistance to insulin-mediated glucose uptake, urinary uric acid clearance, and plasma uric acid concentration. JAMA 266, 3008-3011.

Fathallah-Shaykh, S.A., and Cramer, M.T. (2014). Uric acid and the kidney. Pediatr. Nephrol. 29, 999-1008.

Feig, D.I., Soletsky, B., and Johnson, R.J. (2008). Effect of allopurinol on blood pressure of adolescents with newly diagnosed essential hypertension: a randomized trial. JAMA 300, 924-932.

Finau, S.A., Stanhope, J.M., Prior, I.A., Joseph, J.G., Puloka, S.T., and Leslie, P.N. (1983). The Tonga cardiovascular and metabolic study: design, demographic aspects and medical findings. Community Health Stud 7, 67-77.

Flynn, T.J., Cadzow, M., Dalbeth, N., Jones, P.B., Stamp, L.K., Hindmarsh, J.H., Todd, A.S., Walker, R.J., Topless, R., and Merriman, T.R. (2015). Positive association of tomato consumption with serum urate: support for tomato consumption as an anecdotal trigger of gout flares. BMC Musculoskelet Disord 16, 196.

Gagliardi, A.C.M., Miname, M.H., and Santos, R.D. (2009). Uric acid: A marker of increased cardiovascular risk. Atherosclerosis 202, 11-17.

Gershon, S.L., and Fox, I.H. (1974). Pharmacologic effects of nicotinic acid on human purine metabolism. J. Lab. Clin. Med. 84, 179-186.

Goldstein, D.B. (2009). Common genetic variation and human traits. N. Engl. J. Med. 360, 1696-1698.

Gosling, A.L., Matisoo-Smith, E., and Merriman, T.R. (2014). Hyperuricaemia in the Pacific: why the elevated serum urate levels? Rheumatol. Int. 34, 743-757.

Grandvuinet, A.S., Vestergaard, H.T., Rapin, N., and Steffansen, B. (2012). Intestinal transporters for endogenic and pharmaceutical organic anions: the challenges of deriving in-vitro kinetic parameters for the prediction of clinically relevant drug-drug interactions. J. Pharm. Pharmacol. 64, 1523-1548.

Gutman, A.B. (1965). Renal excretion of uric acid in normal and gouty man. Arthritis Rheum. 8, 665-670.

Gutman, A.B., and YŸ, T.F. (1968). Uric acid nephrolithiasis. Am. J. Med. 45, 756-779.
Hagos, Y., Stein, D., Ugele, B., Burckhardt, G., and Bahn, A. (2007). Human renal organic anion transporter 4 operates as an asymmetric urate transporter. J. Am. Soc. Nephrol. 18, 430-439.

Haidich, A.B. (2010). Meta-analysis in medical research. Hippokratia 14, 29-37.

Hak, A.E., and Choi, H.K. (2008). Menopause, postmenopausal hormone use and serum uric acid levels in US women--the Third National Health and Nutrition Examination Survey. Arthritis Res. Ther. 10, R116.

Halestrap, A.P., and Price, N.T. (1999). The proton-linked monocarboxylate transporter (MCT) family: structure, function and regulation. Biochem. J. 343 Pt 2, 281-299.

Hare, J.M., and Johnson, R.J. (2003). Uric acid predicts clinical outcomes in heart failure: insights regarding the role of xanthine oxidase and uric acid in disease pathophysiology. Circulation 107, 1951-1953.

Hayden, M.R., and Tyagi, S.C. (2004). Uric acid: A new look at an old risk marker for cardiovascular disease, metabolic syndrome, and type 2 diabetes mellitus: The urate redox shuttle. Nutr Metab (Lond) 1, 10.

Hindorff, L.A., Sethupathy, P., Junkins, H.A., Ramos, E.M., Mehta, J.P., Collins, F.S., and Manolio, T.A. (2009). Potential etiologic and functional implications of genome-wide association loci for human diseases and traits. Proc. Natl. Acad. Sci. U.S.A. 106, 9362-9367.

Ho, H.T.B., Ko, B.C.B., Cheung, A.K.H., Lam, A.K.M., Tam, S., Chung, S.K., and Chung, S.S.M. (2007). Generation and characterization of sodium-dicarboxylate cotransporter-deficient mice. Kidney Int. 72, 63-71.

Hollis-Moffatt, J.E., Xu, X., Dalbeth, N., Merriman, M.E., Topless, R., Waddell, C., Gow, P.J., Harrison, A.A., Highton, J., Jones, P.B.B., et al. (2009). Role of the urate transporter SLC2A9 gene in susceptibility to gout in New Zealand M_ori, Pacific Island, and Caucasian case-control sample sets. Arthritis Rheum. 60, 3485-3492.

Hooper, D.C., Spitsin, S., Kean, R.B., Champion, J.M., Dickson, G.M., Chaudhry, I., and Koprowski, H. (1998). Uric acid, a natural scavenger of peroxynitrite, in experimental allergic encephalomyelitis and multiple_sclerosis. Proc Natl Acad Sci U S A 95, 675-680.

Hsu, C., Iribarren, C., McCulloch, C.E., Darbinian, J., and Go, A.S. (2009). Risk factors for end-stage renal disease: 25-year follow-up. Arch. Intern. Med. 169, 342-350.

Hyink, D.P., Rappoport, J.Z., Wilson, P.D., and Abramson, R.G. (2001). Expression of the urate transporter/channel is developmentally regulated in human kidneys. Am. J. Physiol. Renal Physiol. 281, F875-886.

Hyndman, D., Liu, S., and Miner, J.N. (2016). Urate Handling in the Human Body. Curr Rheumatol Rep

18, 34.

Ichida, K., Hosoyamada, M., Hisatome, I., Enomoto, A., Hikita, M., Endou, H., and Hosoya, T. (2004). Clinical and molecular analysis of patients with renal hypouricemia in Japan-influence of URAT1 gene on urinary urate excretion. J. Am. Soc. Nephrol. 15, 164-173.

Ichida, K., Hosoyamada, M., Kimura, H., Takeda, M., Utsunomiya, Y., Hosoya, T., and Endou, H. (2003). Urate transport via human PAH transporter hOAT1 and its gene structure. Kidney Int. 63, 143-155.

Ichida, K., Matsuo, H., Takada, T., Nakayama, A., Murakami, K., Shimizu, T., Yamanashi, Y., Kasuga, H., Nakashima, H., Nakamura, T., et al. (2012). Decreased extra-renal urate excretion is a common cause of hyperuricemia. Nat Commun 3, 764.

Jackson, L., Taylor, R., Faaiuso, S., Ainuu, S.P., Whitehouse, S., and Zimmet, P. (1981). Hyperuricaemia and gout in Western Samoans. J Chronic Dis 34, 65-75.

Jackson, L., Taylor, R., Whitehouse, S., and Zimmet, P. (1980). THE HIGH PREVALENCE OF HYPERURICAEMIA IN A POLYNESIAN POPULATION. Community Health Studies 4, 175-179.

Jalal, D.I., Rivard, C.J., Johnson, R.J., Maahs, D.M., McFann, K., Rewers, M., and Snell-Bergeon, J.K. (2010). Serum uric acid levels predict the development of albuminuria over 6 years in patients with type 1 diabetes: findings from the Coronary Artery Calcification in Type 1 Diabetes study. Nephrol. Dial. Transplant. 25, 1865-1869.

Jiri, M., Zhang, L., Lan, B., He, N., Feng, T., Liu, K., Jin, T., and Kang, L. (2016). Genetic variation in the ABCG2 gene is associated with gout risk in the Chinese Han population. Clin. Rheumatol. 35, 159-163.

Johnson, G.C., Esposito, L., Barratt, B.J., Smith, A.N., Heward, J., Di Genova, G., Ueda, H., Cordell, H.J., Eaves, I.A., Dudbridge, F., et al. (2001). Haplotype tagging for the identification of common disease genes. Nat. Genet. 29, 233-237.

Johnson, R.J. (2015). Why focus on uric acid? Curr Med Res Opin 31 Suppl 2, 3-7.
JŠger, G., Peltzer, A., and Nieselt, K. (2014). inPHAP: Interactive visualization of genotype and phased haplotype data. BMC Bioinformatics 15, 200.

Jutabha, P., Anzai, N., Wempe, M.F., Wakui, S., Endou, H., and Sakurai, H. (2011). Apical voltage-driven urate efflux transporter NPT4 in renal proximal tubule. Nucleosides Nucleotides Nucleic Acids 30, 1302-1311.

Keller, A., Harz, C., Matzas, M., Meder, B., Katus, H.A., Ludwig, N., Fischer, U., and Meese, E. (2011). Identification of Novel SNPs in Glioblastoma Using Targeted Resequencing. PLoS One 6.

Khanna, D., FitzGerald, J.D., Khanna, P.P., Bae, S., Singh, M., Neogi, T., Pillinger, M.H., Merill, J., Lee, S., Prakash, S., et al. (2012a). 2012 American College of Rheumatology Guidelines for Management of Gout Part I: Systematic Non-pharmacologic and Pharmacologic Therapeutic Approaches to Hyperuricemia. Arthritis Care Res (Hoboken) 64, 1431-1446.

Khanna, D., Khanna, P.P., FitzGerald, J.D., Singh, M.K., Bae, S., Neogi, T., Pillinger, M.H., Merill, J., Lee, S., Prakash, S., et al. (2012b). 2012 American College of Rheumatology Guidelines for Management of Gout Part II: Therapy and Anti-inflammatory Prophylaxis of Acute Gouty Arthritis. Arthritis Care Res (Hoboken) 64, 1447-1461.

Khosla, U.M., Zharikov, S., Finch, J.L., Nakagawa, T., Roncal, C., Mu, W., Krotova, K., Block, E.R., Prabhakar, S., and Johnson, R.J. (2005). Hyperuricemia induces endothelial dysfunction. Kidney Int. 67, 1739-1742.

Kimura, T., Takahashi, M., Yan, K., and Sakurai, H. (2014). Expression of SLC2A9 isoforms in the kidney and their localization in polarized epithelial cells. PLoS ONE 9, e84996.

Kircher, M., Witten, D.M., Jain, P., O'Roak, B.J., Cooper, G.M., and Shendure, J. (2014). A general framework for estimating the relative pathogenicity of human genetic variants. Nat. Genet. 46, 310-315.

Klein, B.E.K., Klein, R., and Lee, K.E. (2002). Components of the metabolic syndrome and risk of cardiovascular disease and diabetes in Beaver Dam. Diabetes Care 25, 1790-1794.

Klemp, P., Stansfield, S.A., Castle, B., and Robertson, M.C. (1997). Gout is on the increase in New Zealand. Ann. Rheum. Dis. 56, 22-26.

Kolz, M., Johnson, T., Sanna, S., Teumer, A., Vitart, V., Perola, M., Mangino, M., Albrecht, E., Wallace, C., Farrall, M., et al. (2009). Meta-analysis of 28,141 individuals identifies common variants within five new loci that influence uric acid concentrations. PLoS Genet. 5, e1000504.

Kraft, P., Zeggini, E., and Ioannidis, J.P.A. (2009). Replication in genome-wide association studies. Stat Sci 24, 561-573.

Krishnan, E., Lessov-Schlaggar, C.N., Krasnow, R.E., and Swan, G.E. (2012). Nature versus nurture in gout: a twin study. Am. J. Med. 125, 499-504.

Krzywinski, M., Schein, J., Birol, I., Connors, J., Gascoyne, R., Horsman, D., Jones, S.J., and Marra, M.A. (2009). Circos: an information aesthetic for comparative genomics. Genome Res. 19, 1639-1645.

Kšttgen, A., Albrecht, E., Teumer, A., Vitart, V., Krumsiek, J., Hundertmark, C., Pistis, G., Ruggiero, D., O'Seaghdha, C.M., Haller, T., et al. (2013). Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nat. Genet. 45, 145-154.

Kuo, C.-F., Grainge, M.J., Mallen, C., Zhang, W., and Doherty, M. (2016). Comorbidities in patients with gout prior to and following diagnosis: case-control study. Ann. Rheum. Dis. 75, 210-217.

Kuo, C.-F., Grainge, M.J., Zhang, W., and Doherty, M. (2015). Global epidemiology of gout: prevalence, incidence and risk factors. Nat Rev Rheumatol 11, 649-662.

Kuzkaya, N., Weissmann, N., Harrison, D.G., and Dikalov, S. (2005). Interactions of peroxynitrite with uric acid in the presence of ascorbate and thiols: implications for uncoupling endothelial nitric oxide synthase. Biochem. Pharmacol. 70, 343-354.

Le, M.T., Shafiu, M., Mu, W., and Johnson, R.J. (2008). SLC2A9--a fructose transporter identified as a novel uric acid transporter. Nephrol. Dial. Transplant. 23, 2746-2749.

Lee, I.R., Yang, L., Sebetso, G., Allen, R., Doan, T.H.N., Blundell, R., Lui, E.Y.L., Morrow, C.A., and Fraser, J.A. (2013). Characterization of the Complete Uric Acid Degradation Pathway in the Fungal Pathogen Cryptococcus neoformans. PLOS ONE 8, e64292.

Lee, K., Belinsky, M.G., Bell, D.W., Testa, J.R., and Kruh, G.D. (1998). Isolation of MOAT-B, a widely expressed multidrug resistance-associated protein/canalicular multispecific organic anion transporter-related transporter. Cancer Res. 58, 2741-2747.

Levinson, D.J., and Sorensen, L.B. (1980). Renal handling of uric acid in normal and gouty subject: evidence for a 4-component system. Ann. Rheum. Dis. 39, 173-179.

Li, C., Chu, N., Wang, B., Wang, J., Luan, J., Han, L., Meng, D., Wang, Y., Suo, P., Cheng, L., et al. (2012). Polymorphisms in the presumptive promoter region of the SLC2A9 gene are associated with gout in a Chinese male population. PLoS ONE 7, e24561.

Li, H., and Durbin, R. (2009). Fast and accurate short read alignment with Burrows-Wheeler transform. Bioinformatics 25, 1754-1760.

Li, S., Sanna, S., Maschio, A., Busonero, F., Usala, G., Mulas, A., Lai, S., Dei, M., Orr□, M., Albai, G., et al. (2007). The GLUT9 gene is associated with serum uric acid levels in Sardinia and Chianti cohorts. PLoS Genet. 3, e194.

Li, Z., Zhou, Z., Hou, X., Lu, D., Yuan, X., Lu, J., Wang, C., Han, L., Cui, L., Liu, Z., et al. (2017). Replication of Gout/Urate Concentrations GWAS Susceptibility Loci Associated with Gout in a Han Chinese Population. Sci Rep 7, 4094.

Lin, J.-D., Chiou, W.-K., Chang, H.-Y., Liu, F.-H., and Weng, H.-F. (2007). Serum uric acid and leptin levels in metabolic syndrome: a quandary over the role of uric acid. Metab. Clin. Exp. 56, 751-756.

Lipkowitz, M.S., Leal-Pinto, E., Rappoport, J.Z., Najfeld, V., and Abramson, R.G. (2001). Functional reconstitution, membrane targeting, genomic structure, and chromosomal localization of a human urate transporter. J Clin Invest 107, 1103-1115.

Loeb, J.N. (1972). The influence of temperature on the solubility of monosodium urate. Arthritis Rheum. 15, 189-192.

Long, J.C. (1991). The genetic structure of admixed populations. Genetics 127, 417-428.

Lu, Q., Hu, Y., Sun, J., Cheng, Y., Cheung, K.-H., and Zhao, H. (2015). A statistical framework to predict functional non-coding regions in the human genome through integrated analysis of annotation data. Sci Rep 5, 10576.

Maekawa, M., Tomida, H., Aoki, T., Hishida, M., Morinaga, T., and Tamai, H. (2014). Successful treatment of refractory gout using combined therapy consisting of febuxostat and allopurinol in a patient with chronic renal failure. Intern. Med. 53, 609-612.

Manolio, T.A., Collins, F.S., Cox, N.J., Goldstein, D.B., Hindorff, L.A., Hunter, D.J., McCarthy, M.I., Ramos, E.M., Cardon, L.R., Chakravarti, A., et al. (2009). Finding the missing heritability of complex diseases. Nature 461, 747-753.

Manolio, T.A., Collins, F.S., Cox, N.J., Goldstein, D.B., Hindorff, L.A., Hunter, D.J., McCarthy, M.I., Ramos, E.M., Cardon, L.R., Chakravarti, A., et al. (2009). Finding the missing heritability of complex diseases. Nature 461, 747-753.

Martillo, M.A., Nazzal, L., and Crittenden, D.B. (2014). The crystallization of monosodium urate. Curr Rheumatol Rep 16, 400.

Martinon, F., PŽtrilli, V., Mayor, A., Tardivel, A., and Tschopp, J. (2006). Gout-associated uric acid crystals activate the NALP3 inflammasome. Nature 440, 237-241.

Matsuo, H., Chiba, T., Nagamori, S., Nakayama, A., Domoto, H., Phetdee, K., Wiriyasermkul, P., Kikuchi, Y., Oda, T., Nishiyama, J., et al. (2008). Mutations in glucose transporter 9 gene SLC2A9 cause renal hypouricemia. Am. J. Hum. Genet. 83, 744-751.

Matsuo, H., Yamamoto, K., Nakaoka, H., Nakayama, A., Sakiyama, M., Chiba, T., Takahashi, A., Nakamura, T., Nakashima, H., Takada, Y., et al. (2016). Genome-wide association study of clinically defined gout identifies multiple risk loci and its association with clinical subtypes. Ann. Rheum. Dis. 75, 652-659.

Matsuura, F., Yamashita, S., Nakamura, T., Nishida, M., Nozaki, S., Funahashi, T., and Matsuzawa, Y. (1998). Effect of visceral fat accumulation on uric acid metabolism in male obese subjects: visceral fat obesity is linked more closely to overproduction of uric acid than subcutaneous fat obesity. Metab. Clin. Exp. 47, 929-933.

Mazzali, M., Kanellis, J., Han, L., Feng, L., Xia, Y.-Y., Chen, Q., Kang, D.-H., Gordon, K.L., Watanabe, S., Nakagawa, T., et al. (2002). Hyperuricemia induces a primary renal arteriolopathy in rats by a blood pressure-independent mechanism. Am. J. Physiol. Renal Physiol. 282, F991-997.

McAdams-DeMarco, M.A., Maynard, J.W., Baer, A.N., Kao, L.W., Kottgen, A., and Coresh, J. (2013). A urate gene-by-diuretic interaction and gout risk in participants with hypertension: results from the ARIC study. Ann. Rheum. Dis. 72, 701-706.

McKenna, A., Hanna, M., Banks, E., Sivachenko, A., Cibulskis, K., Kernytsky, A., Garimella, K., Altshuler, D., Gabriel, S., Daly, M., et al. (2010). The Genome Analysis Toolkit: a MapReduce framework for analyzing next-generation DNA sequencing data. Genome Res. 20, 1297-1303.

McLaren, W., Gil, L., Hunt, S.E., Riat, H.S., Ritchie, G.R.S., Thormann, A., Flicek, P., and Cunningham, F. (2016). The Ensembl Variant Effect Predictor. Genome Biol. 17, 122.

Merriman, T.R. (2011). Population heterogeneity in the genetic control of serum urate. Semin. Nephrol. 31, 420-425.

Miyazaki, H., Anzai, N., Ekaratanawong, S., Sakata, T., Shin, H.J., Jutabha, P., Hirata, T., He, X., Nonoguchi, H., Tomita, K., et al. (2005). Modulation of renal apical organic anion transporter 4 function by two PDZ domain-containing proteins. J. Am. Soc. Nephrol. 16, 3498-3506.

Mount, D.B., Kwon, C.Y., and Zandi-Nejad, K. (2006). Renal urate transport. Rheum. Dis. Clin. North Am. 32, 313-331, vi.

Nakayama, A., Matsuo, H., Shimizu, T., Ogata, H., Takada, Y., Nakashima, H., Nakamura, T., Shimizu, S., Chiba, T., Sakiyama, M., et al. (2013). Common missense variant of monocarboxylate transporter 9 (MCT9/SLC16A9) gene is associated with renal overload gout, but not with all gout susceptibility. Hum. Cell 26, 133-136.

Nath, S.D., Voruganti, V.S., Arar, N.H., Thameem, F., Lopez-Alvarenga, J.C., Bauer, R., Blangero, J., MacCluer, J.W., Comuzzie, A.G., and Abboud, H.E. (2007). Genome scan for determinants of serum uric acid variability. J. Am. Soc. Nephrol. 18, 3156-3163.

Neogi, T., Ellison, R.C., Hunt, S., Terkeltaub, R., Felson, D.T., and Zhang, Y. (2009). Serum uric acid is associated with carotid plaques: the National Heart, Lung, and Blood Institute Family Heart Study. J. Rheumatol. 36, 378-384.

Nuki, G., and Simkin, P.A. (2006). A concise history of gout and hyperuricemia and their treatment. Arthritis Res. Ther. 8 Suppl 1, S1.

O'Connell, J., Gurdasani, D., Delaneau, O., Pirastu, N., Ulivi, S., Cocca, M., Traglia, M., Huang, J., Huffman, J.E., Rudan, I., et al. (2014). A General Approach for Haplotype Phasing across the Full Spectrum of Relatedness. PLOS Genetics 10, e1004234.

Obermayr, R.P., Temml, C., Gutjahr, G., Knechtelsdorfer, M., Oberbauer, R., and Klauser-Braun, R. (2008). Elevated uric acid increases the risk for kidney disease. J. Am. Soc. Nephrol. 19, 2407-2413.

Oda, M., Satta, Y., Takenaka, O., and Takahata, N. (2002). Loss of urate oxidase activity in hominoids and its evolutionary implications. Mol. Biol. Evol. 19, 640-653.

Okada, Y., Sim, X., Go, M.J., Wu, J.-Y., Gu, D., Takeuchi, F., Takahashi, A., Maeda, S., Tsunoda, T., Chen, P., et al. (2012). Meta-analysis identifies multiple loci associated with kidney function-related traits in east Asian populations. Nat. Genet. 44, 904-909.

Ostbye, T., Welby, T.J., Prior, I. a. M., Salmond, C.E., and Stokes, Y.M. (1989). Type 2 (non-insulin-dependent) diabetes mellitus, migration and westernisation: The Tokelau Island Migrant study. Diabetologia 32, 585-590.

Pascal, Z., Valcov, R., Fabreguet, I., Dumusc, A., Omoumi, P., and So, A. (2015). A prospective evaluation of ultrasound as a diagnostic tool in acute microcrystalline arthritis. Arthritis Res Ther 17.

Pascual, E., and Perdiguero, M. (2006). Gout, diuretics and the kidney. Ann. Rheum. Dis. 65, 981-982.

Passwell, J.H., Modan, M., Brish, M., Orda, S., and Boichis, H. (1974). Fractional excretion of uric acid in infancy and childhood. Index of tubular maturation. Arch. Dis. Child. 49, 878-882.

Patschan, D., Patschan, S., Gobe, G.G., Chintala, S., and Goligorsky, M.S. (2007). Uric acid heralds ischemic tissue injury to mobilize endothelial progenitor cells. J. Am. Soc. Nephrol. 18, 1516-1524.

Peden, D.B., Hohman, R., Brown, M.E., Mason, R.T., Berkebile, C., Fales, H.M., and Kaliner, M.A. (1990). Uric acid is a major antioxidant in human nasal airway secretions. Proc. Natl. Acad. Sci. U.S.A. 87, 7638-7642.

Peden, D.B., Swiersz, M., Ohkubo, K., Hahn, B., Emery, B., and Kaliner, M.A. (1993). Nasal secretion of the ozone scavenger uric acid. Am. Rev. Respir. Dis. 148, 455-461.

Perez-Ruiz, F., and Naredo, E. (2007). Imaging modalities and monitoring measures of gout. Curr Opin Rheumatol 19, 128-133.

Perez-Ruiz, F., Calabozo, M., Erauskin, G.G., Ruibal, A., and Herrero-Beites, A.M. (2002). Renal underexcretion of uric acid is present in patients with apparent high urinary uric acid output. Arthritis Rheum. 47, 610-613.

Phay, J.E., Hussain, H.B., and Moley, J.F. (2000a). Cloning and expression analysis of a novel member of the facilitative glucose transporter family, SLC2A9 (GLUT9). Genomics 66, 217-220.

Phay, J.E., Hussain, H.B., and Moley, J.F. (2000b). Cloning and expression analysis of a novel member of the facilitative glucose transporter family, SLC2A9 (GLUT9). Genomics 66, 217-220.

Popovich, I., Lee, A.C.L., Doyle, A., McHaffie, A., Clarke, A., Reeves, Q., Dalbeth, N., and McQueen, F.M. (2015). A comparative MRI study of cartilage damage in gout versus rheumatoid arthritis. J Med Imaging Radiat Oncol 59, 431-435.

Price, A.L., Patterson, N.J., Plenge, R.M., Weinblatt, M.E., Shadick, N.A., and Reich, D. (2006). Principal components analysis corrects for stratification in genome-wide association studies. Nat. Genet. 38, 904-909.

Prior, I.A., and Rose, B.S. (1966). Uric acid, gout and public health in the South Pacific. N. Z. Med. J. 65, 295-300.

Pritchard, J.K. (2001). Are rare variants responsible for susceptibility to complex diseases? Am. J. Hum. Genet. 69, 124-137.

Pritchard, J.K., and Rosenberg, N.A. (1999). Use of unlinked genetic markers to detect population stratification in association studies. Am. J. Hum. Genet. 65, 220-228.

Pruim, R.J., Welch, R.P., Sanna, S., Teslovich, T.M., Chines, P.S., Gliedt, T.P., Boehnke, M., Abecasis, G.R., and Willer, C.J. (2010). LocusZoom: regional visualization of genome-wide association scan results. Bioinformatics 26, 2336-2337.

Puig, J.G., Torres, R.J., de Miguel, E., S‡nchez, A., BailŽn, R., and Banegas, J.R. (2012). Uric acid excretion in healthy subjects: a nomogram to assess the mechanisms underlying purine metabolic disorders. Metab. Clin. Exp. 61, 512-518.

Reimer, R.J., and Edwards, R.H. (2004). Organic anion transport is the primary function of the SLC17/type I phosphate transporter family. Pflugers Arch. 447, 629-635.

Richet, G. (1995). The chemistry of urinary stones around 1800: a first in clinical chemistry. Kidney Int. 48, 876-886.

Ritchie, G.R.S., Dunham, I., Zeggini, E., and Flicek, P. (2014a). Functional annotation of noncoding sequence variants. Nat. Methods 11, 294-296.

Ritchie, G.R.S., Dunham, I., Zeggini, E., and Flicek, P. (2014b). Functional annotation of noncoding sequence variants. Nat. Methods 11, 294-296.

Roddy, E., Zhang, W., and Doherty, M. (2007). Are joints affected by gout also affected by osteoarthritis? Ann. Rheum. Dis. 66, 1374-1377.

Rosolowsky, E.T., Ficociello, L.H., Maselli, N.J., Niewczas, M.A., Binns, A.L., Roshan, B., Warram, J.H., and Krolewski, A.S. (2008). High-normal serum uric acid is associated with impaired glomerular filtration rate in nonproteinuric patients with type 1 diabetes. Clin J Am Soc Nephrol 3, 706-713.

S‡nchez-Lozada, L.G., Soto, V., Tapia, E., Avila-Casado, C., Sautin, Y.Y., Nakagawa, T., Franco, M., Rodr'guez-Iturbe, B., and Johnson, R.J. (2008). Role of oxidative stress in the renal abnormalities induced by experimental hyperuricemia. Am. J. Physiol. Renal Physiol. 295, F1134-1141.

S‡nchez-Lozada, L.G., Tapia, E., L—pez-Molina, R., Nepomuceno, T., Soto, V., Avila-Casado, C., Nakagawa, T., Johnson, R.J., Herrera-Acosta, J., and Franco, M. (2007). Effects of acute and chronic L-arginine treatment in experimental hyperuricemia. Am. J. Physiol. Renal Physiol. 292, F1238-1244.

Sakiyama, M., Matsuo, H., Shimizu, S., Nakashima, H., Nakayama, A., Chiba, T., Naito, M., Takada, T., Suzuki, H., Hamajima, N., et al. (2014). A common variant of organic anion transporter 4 (OAT4/SLC22A11) gene is associated with renal underexcretion type gout. Drug Metab. Pharmacokinet. 29, 208-210.

Sato, M., Mamada, H., Anzai, N., Shirasaka, Y., Nakanishi, T., and Tamai, I. (2010). Renal secretion of uric acid by organic anion transporter 2 (OAT2/SLC22A7) in human. Biol. Pharm. Bull. 33, 498-503.

Scharpf, R.B., Mireles, L., Yang, Q., Kšttgen, A., Ruczinski, I., Susztak, K., Halper-Stromberg, E., Tin, A., Cristiano, S., Chakravarti, A., et al. (2014). Copy number polymorphisms near SLC2A9 are associated with serum uric acid concentrations. BMC Genet. 15, 81.

Schumacher, H.R., Becker, M.A., Palo, W.A., Streit, J., MacDonald, P.A., and Joseph-Ridge, N. (2005). Tophaceous gout: quantitative evaluation by direct physical measurement. J. Rheumatol. 32, 2368-2372.

Schwarzschild, M.A., Schwid, S.R., Marek, K., Watts, A., Lang, A.E., Oakes, D., Shoulson, I., and Ascherio, A. (2008). 1!Serum urate as a predictor of clinical and radiographic progression in Parkinson's disease. Arch Neurol 65, 716-723.

Shah, P., and Isley, W.L. (2006). Ketoacidosis during a low-carbohydrate diet. N. Engl. J. Med. 354, 97-98.

Shankar, A., Klein, B.E.K., Nieto, F.J., and Klein, R. (2008). Association between serum uric acid level and peripheral arterial disease. Atherosclerosis 196, 749-755.

Shi, Y., Evans, J.E., and Rock, K.L. (2003). Molecular identification of a danger signal that alerts the immune system to dying cells. Nature 425, 516-521.

Shihab, H.A., Rogers, M.F., Gough, J., Mort, M., Cooper, D.N., Day, I.N.M., Gaunt, T.R., and Campbell, C. (2015). An integrative approach to predicting the functional effects of non-coding and coding sequence variation. Bioinformatics 31, 1536-1543.

Shin, H.J., Takeda, M., Enomoto, A., Fujimura, M., Miyazaki, H., Anzai, N., and Endou, H. (2011). Interactions of urate transporter URAT1 in human kidney with uricosuric drugs. Nephrology (Carlton) 16, 156-162.

Sim, N.-L., Kumar, P., Hu, J., Henikoff, S., Schneider, G., and Ng, P.C. (2012). SIFT web server: predicting effects of amino acid substitutions on proteins. Nucleic Acids Res. 40, W452-457.

Skelly, A.C., Dettori, J.R., and Brodt, E.D. (2012). Assessing bias: the importance of considering confounding. Evid Based Spine Care J 3, 9-12.

Slatkin, M. (2008). Linkage disequilibrium--understanding the evolutionary past and mapping the medical future. Nat. Rev. Genet. 9, 477-485.

Smith, E., Hoy, D., Cross, M., Merriman, T.R., Vos, T., Buchbinder, R., Woolf, A., and March, L. (2014). The global burden of gout: estimates from the Global Burden of Disease 2010 study. Ann. Rheum. Dis. 73, 1470-1476.

So, A., and Thorens, B. (2010). Uric acid transport and disease. J. Clin. Invest. 120, 1791-1799.

Sorensen, L.B. (1959). Degradation of uric acid in man. Metab. Clin. Exp. 8, 687-703.
Sorensen, L.B., and Levinson, D.J. (1975). Origin and extrarenal elimination of uric acid in man. Nephron 14, 7-20.

Sperandei, S. (2014). Understanding logistic regression analysis. Biochem Med (Zagreb) 24, 12-18.

Stark, K., Reinhard, W., Grassl, M., Erdmann, J., Schunkert, H., Illig, T., and Hengstenberg, C. (2009). Common polymorphisms influencing serum uric acid levels contribute to susceptibility to gout, but not to coronary artery disease. PLoS ONE 4, e7729.

Stiburkova, B., Miyata, H., Z‡vada, J., Tom_'k, M., Pavelka, K., Storkanova, G., Toyoda, Y., Takada, T., and Suzuki, H. (2016). Novel dysfunctional variant in ABCG2 as a cause of severe tophaceous gout: biochemical, molecular genetics and functional analysis. Rheumatology (Oxford) 55, 191-194.

Strasak, A.M., Kelleher, C.C., Brant, L.J., Rapp, K., Ruttmann, E., Concin, H., Diem, G., Pfeiffer, K.P., Ulmer, H., and VHM&PP Study Group (2008). Serum uric acid is an independent predictor for all major forms of cardiovascular death in 28,613 elderly women: a prospective 21-year follow-up study. Int. J. Cardiol. 125, 232-239.

Sullivan, G.M., and Feinn, R. (2012). Using Effect Size-or Why the P Value Is Not Enough. J Grad Med Educ 4, 279-282.

Szumilas, M. (2010). Explaining odds ratios. J Can Acad Child Adolesc Psychiatry 19, 227-229.

Tange, O. (2011). GNU Parallel: The Command-Line Power Tool | USENIX.
Terkeltaub, R.A. (2003). Clinical practice. Gout. N. Engl. J. Med. 349, 1647-1655.

Thangaraju, M., Ananth, S., Martin, P.M., Roon, P., Smith, S.B., Sterneck, E., Prasad, P.D., and Ganapathy, V. (2006). c/ebpdelta Null mouse as a model for the double knock-out of slc5a8 and slc5a12 in kidney. J. Biol. Chem. 281, 26769-26773.

Tin, A., Woodward, O.M., Kao, W.H.L., Liu, C.-T., Lu, X., Nalls, M.A., Shriner, D., Semmo, M., Akylbekova, E.L., Wyatt, S.B., et al. (2011). Genome-wide association study for serum urate concentrations and gout among African Americans identifies genomic risk loci and a novel URAT1 loss-of-function allele. Hum. Mol. Genet. 20, 4056-4068.

van Aubel, R.A.M.H., Smeets, P.H.E., Peters, J.G.P., Bindels, R.J.M., and Russel, F.G.M. (2002). The MRP4/ABCC4 gene encodes a novel apical organic anion transporter in human kidney proximal tubules: putative efflux pump for urinary cAMP and cGMP. J. Am. Soc. Nephrol. 13, 595-603.

VanItallie, T.B. (2010). Gout: epitome of painful arthritis. Metab. Clin. Exp. 59 Suppl 1, S32-36.

Veronese, N., Carraro, S., Bano, G., Trevisan, C., Solmi, M., Luchini, C., Manzato, E., Caccialanza, R., Sergi, G., Nicetto, D., et al. (2016). Hyperuricemia protects against low bone mineral density, osteoporosis and fractures: a systematic review and meta-analysis. Eur. J. Clin. Invest. 46, 920-930.

Vitart, V., Rudan, I., Hayward, C., Gray, N.K., Floyd, J., Palmer, C.N.A., Knott, S.A., Kolcic, I., Polasek, O., Graessler, J., et al. (2008). SLC2A9 is a newly identified urate transporter influencing serum urate concentration, urate excretion and gout. Nat. Genet. 40, 437-442.

Voruganti, V.S., Franceschini, N., Haack, K., Laston, S., MacCluer, J.W., Umans, J.G., Comuzzie, A.G., North, K.E., and Cole, S.A. (2014). Replication of the effect of SLC2A9 genetic variation on serum uric acid levels in American Indians. Eur. J. Hum. Genet. 22, 938-943.

Voruganti, V.S., Kent, J.W., Debnath, S., Cole, S.A., Haack, K., Gšring, H.H.H., Carless, M.A., Curran, J.E., Johnson, M.P., Almasy, L., et al. (2013). Genome-wide association analysis confirms and extends the association of SLC2A9 with serum uric acid levels to Mexican Americans. Front Genet 4, 279.

Voruganti, V.S., Laston, S., Haack, K., Mehta, N.R., Cole, S.A., Butte, N.F., and Comuzzie, A.G. (2015). Serum uric acid concentrations and SLC2A9 genetic variation in Hispanic children: the Viva La Familia Study. Am. J. Clin. Nutr. 101, 725-732.

Vylet'al, P., Kublov‡, M., Kalb‡cov‡, M., Hodanov‡, K., Baresov‡, V., Stib_rkov‡, B., Sikora, J., H_lkov‡, H., Zivn_, J., Majewski, J., et al. (2006). Alterations of uromodulin biology: a common denominator of the genetically heterogeneous FJHN/MCKD syndrome. Kidney Int. 70, 1155-1169.

Wallace, C., Newhouse, S.J., Braund, P., Zhang, F., Tobin, M., Falchi, M., Ahmadi, K., Dobson, R.J., Mar□ano, A.C.B., Hajat, C., et al. (2008). Genome-wide association study identifies genes for biomarkers of cardiovascular disease: serum urate and dyslipidemia. Am. J. Hum. Genet. 82, 139-149.

Wannamethee, S.G., Shaper, A.G., and Whincup, P.H. (1997). Serum urate and the risk of major coronary heart disease events. Heart 78, 147-153.

Warren, S., Wan, X.-F., Conant, G., and Korkin, D. (2013). Extreme evolutionary conservation of functionally important regions in H1N1 influenza proteome. PLoS ONE 8, e81027.

Watanabe, S., Kang, D.-H., Feng, L., Nakagawa, T., Kanellis, J., Lan, H., Mazzali, M., and Johnson, R.J. (2002). Uric acid, hominoid evolution, and the pathogenesis of salt-sensitivity. Hypertension 40, 355-360.

Wei, W.-H., Guo, Y., Kindt, A.S.D., Merriman, T.R., Semple, C.A., Wang, K., and Haley, C.S. (2014). Abundant local interactions in the 4p16.1 region suggest functional mechanisms underlying SLC2A9 associations with human serum uric acid. Hum. Mol. Genet. 23, 5061-5068.

Wei, W.-H., Guo, Y., Kindt, A.S.D., Merriman, T.R., Semple, C.A., Wang, K., and Haley, C.S. (2014). Abundant local interactions in the 4p16.1 region suggest functional mechanisms underlying SLC2A9 associations with human serum uric acid. Hum. Mol. Genet. 23, 5061-5068.

Weiner, D.E., Tighiouart, H., Elsayed, E.F., Griffith, J.L., Salem, D.N., and Levey, A.S. (2008). Uric acid and incident kidney disease in the community. J. Am. Soc. Nephrol. 19, 1204-1211.

Weisskopf, M.G., O'Reilly, E., Chen, H., Schwarzschild, M.A., and Ascherio, A. (2007). Plasma urate and risk of Parkinson's disease. Am J Epidemiol 166, 561-567.

Witkowska, K., Smith, K.M., Yao, S.Y.M., Ng, A.M.L., O'Neill, D., Karpinski, E., Young, J.D., and Cheeseman, C.I. (2012). Human SLC2A9a and SLC2A9b isoforms mediate electrogenic transport of urate with different characteristics in the presence of hexoses. Am. J. Physiol. Renal Physiol. 303, F527-539.

Woodward, O.M., Kšttgen, A., Coresh, J., Boerwinkle, E., Guggino, W.B., and Kšttgen, M. (2009). Identification of a urate transporter, ABCG2, with a common functional polymorphism causing gout. Proc. Natl. Acad. Sci. U.S.A. 106, 10338-10342.

Wu, X., Wakamiya, M., Vaishnav, S., Geske, R., Montgomery, C., Jones, P., Bradley, A., and Caskey, C.T. (1994). Hyperuricemia and urate nephropathy in urate oxidase-deficient mice. Proc. Natl. Acad. Sci. U.S.A. 91, 742-746.

Wu, X.W., Muzny, D.M., Lee, C.C., and Caskey, C.T. (1992). Two independent mutational events in the loss of urate oxidase during hominoid evolution. J. Mol. Evol. 34, 78-84.

Xu, X., Li, C., Zhou, P., and Jiang, T. (2016). Uric acid transporters hiding in the intestine. Pharm Biol 54, 3151-3155.

Yang, D., Weng, Y., Lin, H., Xie, F., Yin, F., Lou, K., Zhou, X., Han, Y., Li, X., and Zhang, X. (2016). Serum uric acid levels in patients with myasthenia gravis are inversely correlated with disability. Neuroreport 27, 301-305.

Yang, Q., Guo, C.-Y., Cupples, L.A., Levy, D., Wilson, P.W.F., and Fox, C.S. (2005). Genome-wide search for genes affecting serum uric acid levels: the Framingham Heart Study.

Metab. Clin. Exp. 54, 1435-1441.

Yang, Q., Kšttgen, A., Dehghan, A., Smith, A.V., Glazer, N.L., Chen, M.-H., Chasman, D.I., Aspelund, T., Eiriksdottir, G., Harris, T.B., et al. (2010). Multiple genetic loci influence serum urate levels and their relationship with gout and cardiovascular disease risk factors. Circ Cardiovasc Genet 3, 523-530.

Yoo, T.W., Sung, K.C., Shin, H.S., Kim, B.J., Kim, B.S., Kang, J.H., Lee, M.H., Park, J.R., Kim, H., Rhee, E.J., et al. (2005). Relationship between serum uric acid concentration and insulin resistance and metabolic syndrome. Circ. J. 69, 928-933.

Zhou, F., Zhu, L., Cui, P.H., Church, W.B., and Murray, M. (2010). Functional characterization of nonsynonymous single nucleotide polymorphisms in the human organic anion transporter 4 (hOAT4). Br. J. Pharmacol. 159, 419-427.

Zoccolella, S., Tortorella, C., Iaffaldano, P., Direnzo, V., D'Onghia, M., Luciannatelli, E., Paolicelli, D., Livrea, P., and Trojano, M. (2012). Low Serum Urate Levels Are Associated to Female Gender in Multiple Sclerosis Patients. PLoS One 7.

Ahola, A.J., Sandholm, N., Forsblom, C., Harjutsalo, V., Dahlström, E., Groop, P.-H., and FinnDiane Study Group (2017). The serum uric acid concentration is not causally linked to diabetic nephropathy in type 1 diabetes. Kidney Int. *91*, 1178–1185.

Bowden, J., Del Greco M, F., Minelli, C., Davey Smith, G., Sheehan, N., and Thompson, J. (2017). A framework for the investigation of pleiotropy in two-sample summary data Mendelian randomization. Stat Med *36*, 1783–1802.

Choi, H.K., Atkinson, K., Karlson, E.W., Willett, W., and Curhan, G. (2004). Purine-rich foods, dairy and protein intake, and the risk of gout in men. N. Engl. J. Med. *350*, 1093–1103.

Dalbeth, N., Topless, R., Flynn, T., Cadzow, M., Bolland, M.J., and Merriman, T.R. (2015). Mendelian randomization analysis to examine for a causal effect of urate on bone mineral density. J. Bone Miner. Res. *30*, 985–991.

Davey Smith, G., and Hemani, G. (2014). Mendelian randomization: genetic anchors for causal inference in epidemiological studies. Hum. Mol. Genet. *23*, R89-98.

ENCODE Project Consortium (2004). The ENCODE (ENCyclopedia Of DNA Elements) Project. Science *306*, 636–640.

Flynn, T.J., Phipps-Green, A., Hollis-Moffatt, J.E., Merriman, M.E., Topless, R., Montgomery, G., Chapman, B., Stamp, L.K., Dalbeth, N., and Merriman, T.R. (2013). Association analysis of the SLC22A11 (organic anion transporter 4) and SLC22A12 (urate transporter 1) urate transporter locus with gout in New Zealand case-control sample sets reveals multiple ancestral-specific effects. Arthritis Res. Ther. *15*, R220.

Flynn, T.J., Cadzow, M., Dalbeth, N., Jones, P.B., Stamp, L.K., Hindmarsh, J.H., Todd, A.S., Walker, R.J., Topless, R., and Merriman, T.R. (2015). Positive association of tomato consumption with serum urate: support for tomato consumption as an anecdotal trigger of gout flares. BMC Musculoskelet Disord *16*, 196.

Gul, A., Harford, A., and Zager, P. (2017). Mendelian randomization to establish the causality of uric acid with diabetic nephropathy in type 1 diabetics. Kidney Int. *91*, 1005–1007.

Hollis-Moffatt, J.E., Phipps-Green, A.J., Chapman, B., Jones, G.T., van Rij, A., Gow, P.J., Harrison, A.A., Highton, J., Jones, P.B., Montgomery, G.W., et al. (2012). The renal urate transporter SLC17A1 locus: confirmation of association with gout. Arthritis Res. Ther. *14*, R92.

Ishii, S., Miyao, M., Mizuno, Y., Tanaka-Ishikawa, M., Akishita, M., and Ouchi, Y. (2014). Association between serum uric acid and lumbar spine bone mineral density in peri- and postmenopausal Japanese women. Osteoporos Int *25*, 1099–1105.

Keenan, T., Zhao, W., Rasheed, A., Ho, W.K., Malik, R., Felix, J.F., Young, R., Shah, N., Samuel, M., Sheikh, N., et al. (2016). Causal Assessment of Serum Urate Levels in Cardiometabolic Diseases Through a Mendelian Randomization Study. J. Am. Coll. Cardiol. *67*, 407–416.

Lyngdoh, T., Vuistiner, P., Marques-Vidal, P., Rousson, V., Waeber, G., Vollenweider, P., and Bochud, M. (2012). Serum uric acid and adiposity: deciphering causality using a bidirectional Mendelian randomization approach. PLoS ONE *7*, e39321.

Öztürk, M.A., Kaya, A., Şenel, S., Dönmez, S., Balkarlı, A., Çobankara, V., Erhan, Ç., Sayarlıoğlu, M., Ugan, Y., Tunç, Ş.E., et al. (2013). Demographic and clinical features of gout patients in Turkey: a multicenter study. Rheumatol. Int. *33*, 847–852.

Palmer, T.M., Nordestgaard, B.G., Benn, M., Tybjærg-Hansen, A., Davey Smith, G., Lawlor, D.A., and Timpson, N.J. (2013a). Association of plasma uric acid with ischaemic heart disease and blood pressure: mendelian randomisation analysis of two large cohorts. BMJ *347*, f4262.

Palmer, T.M., Nordestgaard, B.G., Benn, M., Tybjærg-Hansen, A., Davey Smith, G., Lawlor, D.A., and Timpson, N.J. (2013b). Association of plasma uric acid with ischaemic heart disease and blood pressure: mendelian randomisation analysis of two large cohorts. BMJ *347*, f4262.

Pfister, R., Barnes, D., Luben, R., Forouhi, N.G., Bochud, M., Khaw, K.-T., Wareham, N.J., and Langenberg, C. (2011). No evidence for a causal link between uric acid and type 2 diabetes: a Mendelian randomisation approach. Diabetologia *54*, 2561–2569.

Phipps-Green, A.J., Hollis-Moffatt, J.E., Dalbeth, N., Merriman, M.E., Topless, R., Gow, P.J., Harrison, A.A., Highton, J., Jones, P.B.B., Stamp, L.K., et al. (2010). A strong role for the ABCG2 gene in susceptibility to gout in New Zealand Pacific Island and Caucasian, but not Māori, case and control sample sets. Hum. Mol. Genet. *19*, 4813–4819.

Rasheed, H., Hughes, K., Flynn, T.J., and Merriman, T.R. (2014). Mendelian randomization provides no evidence for a causal role of serum urate in increasing serum triglyceride levels. Circ Cardiovasc Genet *7*, 830–837.

Robinson, P.C., Choi, H.K., Do, R., and Merriman, T.R. (2016). Insight into rheumatological cause and effect through the use of Mendelian randomization. Nat Rev Rheumatol *12*, 486–496.

White, J., Sofat, R., Hemani, G., Shah, T., Engmann, J., Dale, C., Shah, S., Kruger, F.A., Giambartolomei, C., Swerdlow, D.I., et al. (2016). Plasma urate concentration and risk of coronary heart disease: a Mendelian randomisation analysis. Lancet Diabetes Endocrinol *4*, 327–336.

Williams, P.T. (2008). Effects of diet, physical activity and performance, and body weight on incident gout in ostensibly healthy, vigorously active men. Am. J. Clin. Nutr. *87*, 1480–1487.

Xiong, A., Yao, Q., He, J., Fu, W., Yu, J., and Zhang, Z. (2016). No causal effect of serum urate on bone-related outcomes among a population of postmenopausal women and elderly men of Chinese Han ethnicity--a Mendelian randomization study. Osteoporos Int *27*, 1031–1039.

Cooper, D.N. (2010). Functional intronic polymorphisms: Buried treasure awaiting discovery within our genes. Hum Genomics *4*, 284–288.

Hull, J., Campino, S., Rowlands, K., Chan, M.-S., Copley, R.R., Taylor, M.S., Rockett, K., Elvidge, G., Keating, B., Knight, J., et al. (2007). Identification of common genetic variation that modulates alternative splicing. PLoS Genet. *3*, e99.

Matos, L., Duarte, A.J., Ribeiro, D., Chaves, J., Amaral, O., and Alves, S. (2018). Correction of a Splicing Mutation Affecting an Unverricht-Lundborg Disease Patient by Antisense Therapy. Genes (Basel) *9*.

Nascimbeni, A.C., Fanin, M., Tasca, E., and Angelini, C. (2010). Transcriptional and Translational Effects of Intronic CAPN3 Gene Mutations. Hum Mutat *31*, e1658–e1669.

Samorodnitsky, E., Datta, J., Jewell, B.M., Hagopian, R., Miya, J., Wing, M.R., Damodaran, S., Lippus, J.M., Reeser, J.W., Bhatt, D., et al. (2015). Comparison of Custom Capture for Targeted Next-Generation DNA Sequencing. J Mol Diagn *17*, 64–75.

Tsompana, M., and Buck, M.J. (2014). Chromatin accessibility: a window into the genome. Epigenetics Chromatin *7*.

APPENDIX

Appendix 1

List of SNPs identified in the SLC2A9 locus

rs10000983	rs10023068	rs10939608	rs112215724	rs114056737	rs114852474	rs115952815	rs117154942	rs11732054	rs11933838
rs10001006	rs10024152	rs10939614	rs112222722	rs114069885	rs114919407	rs116003078	rs117212874	rs11732681	rs11934050
rs10001964	rs10025644	rs10939620	rs112255785	rs114104836	rs114949385	rs116006100	rs11721988	rs11732818	rs11934363
rs10002519	rs10025968	rs10939637	rs1122966	rs114110578	rs115037002	rs116021881	rs11722228	rs11734375	rs11935405
rs10002562	rs10026434	rs10939638	rs112298408	rs114163284	rs115037048	rs116050058	rs11722229	rs11734554	rs11936395
rs10003001	rs10027276	rs10939650	rs112359089	rs114197051	rs115048086	rs116108158	rs11722522	rs11734623	rs11937310
rs10003673	rs10029311	rs10939654	rs112389844	rs114214457	rs115066640	rs116115337	rs11722614	rs11734786	rs11938128
rs10004947	rs10030570	rs10939655	rs112395808	rs114337273	rs115099116	rs116142041	rs11722930	rs117348803	rs11938866
rs10005226	rs10031303	rs10939656	rs112404957	rs114361719	rs115145962	rs116147875	rs11722946	rs11734893	rs11940661
rs10005326	rs10033286	rs10939663	rs112469934	rs114372106	rs115184754	rs116227902	rs11722989	rs11735831	rs11940728
rs10006397	rs10033424	rs10939665	rs112540012	rs114407557	rs115190002	rs116242274	rs11723016	rs11735883	rs11941148
rs10006833	rs10033612	rs10939669	rs112574087	rs114435427	rs115217731	rs116243766	rs11723024	rs11736410	rs11942223
rs10007352	rs10033951	rs10939671	rs112674844	rs114489981	rs115272825	rs116244514	rs11723250	rs11736479	rs11943372
rs10007416	rs10034405	rs10939672	rs112724359	rs114506235	rs115281176	rs116274461	rs11723382	rs11737588	rs11946054
rs10008035	rs1007872	rs10939679	rs112787794	rs114525330	rs115301551	rs116284607	rs11723439	rs11737685	rs11947336
rs10009657	rs1014290	rs10939680	rs112851767	rs114529821	rs115318424	rs116288685	rs11723591	rs11737821	rs11947634
rs10009838	rs10155429	rs10939681	rs112939969	rs114532436	rs115323030	rs116305437	rs11723970	rs117405573	rs12108388
rs10010582	rs1048252	rs10939691	rs112961298	rs114536276	rs115359730	rs116316144	rs11724234	rs117443909	rs12374229
rs10010635	rs10516194	rs10939702	rs112967961	rs114540580	rs115360140	rs116388124	rs11724510	rs117535295	rs12374294
rs10010656	rs10516195	rs10939710	rs113006138	rs114557276	rs115404519	rs116449637	rs11724641	rs117540324	rs12374320
rs10010907	rs10516196	rs1106058	rs113017836	rs114584694	rs115417172	rs116533216	rs11726102	rs117606401	rs12498150
rs10011206	rs10516197	rs1106059	rs113058127	rs114597845	rs115453215	rs116585088	rs11726271	rs117657217	rs12498474
rs10012516	rs10516198	rs1107710	rs113063781	rs114602281	rs115464061	rs116602069	rs11726423	rs117670209	rs12498742
rs10012779	rs10516201	rs1107911	rs113133542	rs114614628	rs115490582	rs116628257	rs11726471	rs117694798	rs12498927
rs10012795	rs10516202	rs1107912	rs113181369	rs114656953	rs115490896	rs116658755	rs11727087	rs117822964	rs12498956
rs10012880	rs1071988	rs111297105	rs113188799	rs114663735	rs115502819	rs116687792	rs11727199	rs117861080	rs12499734
rs10016022	rs1079128	rs111338560	rs113216760	rs114664540	rs115537618	rs116694479	rs11727818	rs117867203	rs12499857
rs10016075	rs10805342	rs1114199	rs113254846	rs114670878	rs11557743	rs116710881	rs11728377	rs118033084	rs12500086
rs10016702	rs10805343	rs111445952	rs113310882	rs114688202	rs115588006	rs116796391	rs11729318	rs118034359	rs12500653
rs10017447	rs10805346	rs111459781	rs113401797	rs114693474	rs115662655	rs116804408	rs117296899	rs118072948	rs12500805
rs10017674	rs10938799	rs111599809	rs113451098	rs114727892	rs115764731	rs116839315	rs117301982	rs118085234	rs12500810

rs10017945	rs10939514	rs111928356	rs113565634	rs114731059	rs115770226	rs116859645	rs117309606	rs118093098	rs12501855
rs10018204	rs10939515	rs111935504	rs113674589	rs114734117	rs115787217	rs116882299	rs11731110	rs118123197	rs12502958
rs10018663	rs10939552	rs111953533	rs113816574	rs114748506	rs115793604	rs116913486	rs11731339	rs118137999	rs12503122
rs10018666	rs10939558	rs112061366	rs113888816	rs114750793	rs115809382	rs116956085	rs117315041	rs11930077	rs12504565
rs10020053	rs10939561	rs112172557	rs113995040	rs114751739	rs115847025	rs116968042	rs11731597	rs11930098	rs12505056
rs10021506	rs10939599	rs112183422	rs113995811	rs114756544	rs115848729	rs117005844	rs11731759	rs11930388	rs12505312
rs10022499	rs10939600	rs112202007	rs114021909	rs114772240	rs115861646	rs117023033	rs117318662	rs11930870	rs12505366
rs10022660	rs10939602	rs1122141	rs114026351	rs114837129	rs115940493	rs117076318	rs117319367	rs11932607	rs12506122
rs10022923	rs10939605	rs1122142	rs114047413	rs114847096	rs115945847	rs117095092	rs11732042	rs11933731	rs12506364
rs12506455	rs13105954	rs13124563	rs13145758	rs138550267	rs139979601	rs141354936	rs142989755	rs144428359	rs145911075
rs12506562	rs13106539	rs13125029	rs13146686	rs138553440	rs140023275	rs141392062	rs143009869	rs144431047	rs145945471
rs12506893	rs13106922	rs13125209	rs13147600	rs138554449	rs140057997	rs141419440	rs143022050	rs144448091	rs146017173
rs12506932	rs13106991	rs13125476	rs13148356	rs138558177	rs1401437	rs141443452	rs143024417	rs144499258	rs146017478
rs12507050	rs13107466	rs13125646	rs13148371	rs138584318	rs1401438	rs141494666	rs143025215	rs144569572	rs146123527
rs12507330	rs13107656	rs13125855	rs13148445	rs138605713	rs1401439	rs141516970	rs143104850	rs144582637	rs146158632
rs12507606	rs13108825	rs13126279	rs13148476	rs138627925	rs1401440	rs141562596	rs143154707	rs144651801	rs146186799
rs12507861	rs13110307	rs13126729	rs13148571	rs138633352	rs1401441	rs141566828	rs143175986	rs144652081	rs146190843
rs12508854	rs13111638	rs13127090	rs13149985	rs138640667	rs1401442	rs141578715	rs143194815	rs144708782	rs146242682
rs12508991	rs13112015	rs13127630	rs13150928	rs138678760	rs140148860	rs141596931	rs143250861	rs144742400	rs146292965
rs12509609	rs13112782	rs13128214	rs13151113	rs138755756	rs140176097	rs141626416	rs143321041	rs144752705	rs146310357
rs12509674	rs13113546	rs13128385	rs13151331	rs138757270	rs140186219	rs141720595	rs143334639	rs144757629	rs146322815
rs12509713	rs13113730	rs13129080	rs13151822	rs138811051	rs140253713	rs141767347	rs143364659	rs144868267	rs146327126
rs12509714	rs13113918	rs13129453	rs13152172	rs138828651	rs140280208	rs141769569	rs143368624	rs144876877	rs146345207
rs12509955	rs13114090	rs13129697	rs1320054	rs138866566	rs140307922	rs141780701	rs143440569	rs144878664	rs146357305
rs12511989	rs13114106	rs13129868	rs13328050	rs138891244	rs140319372	rs141794302	rs143442126	rs144929860	rs146364149
rs12641340	rs13114702	rs13129974	rs13435427	rs138940331	rs140334704	rs141833488	rs143466055	rs144974033	rs1464258
rs12642114	rs13115121	rs13131257	rs13435674	rs138949074	rs140346523	rs141846487	rs143484897	rs144996132	rs1464259
rs12642431	rs13115193	rs13132625	rs13441	rs139007297	rs140411445	rs141899745	rs143530991	rs145038256	rs146436740
rs12642537	rs13115469	rs13133766	rs1356643	rs139180190	rs140477370	rs141899952	rs143605952	rs145058214	rs146473160
rs12643296	rs13115661	rs13135351	rs137880042	rs139204497	rs140530586	rs141946400	rs143608834	rs145097501	rs146488248
rs12644047	rs13115776	rs13136962	rs137912718	rs139291984	rs140568661	rs142021630	rs143727065	rs145097623	rs146526473
rs12644471	rs13116337	rs13137069	rs137926524	rs139292069	rs140693556	rs142048822	rs143745354	rs145154883	rs146537115
rs12644592	rs13116446	rs13137074	rs137942938	rs139294906	rs140694008	rs142068085	rs143758325	rs145160523	rs146546936
rs12646099	rs13117275	rs13137343	rs137996170	rs139299672	rs140726714	rs142141871	rs143772489	rs145190091	rs146658616
rs12646380	rs13118112	rs13137795	rs138038869	rs139311846	rs140746050	rs142164246	rs143790062	rs145193830	rs146679712
rs12647117	rs13118272	rs13139055	rs138041093	rs139350408	rs140762331	rs142391721	rs143862618	rs145242845	rs146760627
rs12647883	rs13118801	rs13139970	rs138052838	rs139458641	rs140866200	rs142490971	rs143885121	rs145256735	rs146784455

rs12649245	rs13119059	rs13140718	rs138073909	rs139535718	rs140873488	rs142512695	rs143897850	rs145275096	rs146808983
rs12650373	rs13119731	rs13141233	rs138102553	rs139613826	rs140972700	rs142562622	rs143903193	rs145299659	rs146855072
rs12696844	rs13120348	rs13141629	rs138121361	rs139711307	rs141019279	rs142603647	rs143972829	rs145329462	rs146868066
rs13101683	rs13121211	rs13141635	rs138229174	rs139721393	rs141037145	rs142669794	rs144081055	rs145364569	rs146876703
rs13101688	rs13121355	rs13141706	rs138323944	rs139729941	rs141052822	rs142677291	rs144151269	rs145375160	rs146914131
rs13101772	rs13122026	rs13142238	rs138327996	rs139768772	rs141072456	rs142699433	rs144208664	rs145464632	rs146930596
rs13101785	rs13122112	rs13142273	rs138339252	rs139788797	rs141090791	rs142771591	rs144215444	rs145477423	rs146985372
rs13102085	rs13122290	rs13144709	rs138416405	rs139854873	rs141208648	rs142796555	rs144314662	rs145497708	rs147002127
rs13103429	rs13122689	rs13144899	rs138437679	rs139906968	rs141224249	rs142819777	rs144338226	rs145613518	rs147002367
rs13103497	rs13124007	rs13145108	rs138440736	rs139913518	rs141239529	rs142856421	rs144356708	rs145665522	rs147018551
rs13103690	rs13124141	rs13145442	rs138475000	rs139928301	rs141241707	rs142869655	rs144393783	rs145772196	rs147031819
rs13103879	rs13124305	rs13145554	rs138547806	rs139966035	rs141346944	rs142956580	rs144402103	rs145878854	rs147123083
rs147170567	rs148714209	rs150266109	rs16868246	rs17246745	rs182414296	rs184493584	rs185849919	rs188356704	rs190567713
rs147171965	rs148747594	rs150317722	rs16868271	rs17247314	rs182556362	rs184598209	rs185854976	rs188401313	rs190578816
rs147258783	rs148782913	rs150349587	rs16888725	rs17385001	rs182571761	rs184652935	rs185855785	rs188428223	rs190593177
rs147263130	rs148791554	rs150359939	rs16888747	rs17391280	rs182589584	rs184730016	rs185886938	rs188587273	rs190603187
rs147305766	rs148875253	rs150363708	rs16888799	rs17419612	rs182592473	rs184808273	rs186014393	rs188657256	rs190798554
rs147338898	rs148889786	rs150441658	rs16889260	rs1800762	rs182603736	rs184843205	rs1860905	rs188908273	rs190841282
rs147350938	rs148903910	rs150445552	rs16889264	rs180730877	rs182611868	rs184866950	rs186239844	rs188941768	rs190861676
rs147439739	rs148907062	rs150504446	rs16889270	rs180833011	rs182640566	rs184993936	rs186278403	rs189072747	rs190876865
rs147456393	rs148922822	rs150659411	rs16889496	rs180853490	rs182664578	rs185021027	rs186289358	rs189073544	rs191041567
rs147506185	rs148934813	rs150665766	rs16889509	rs180881388	rs182701836	rs185069208	rs186581711	rs189114089	rs191054451
rs147514517	rs148951726	rs150706987	rs16889519	rs180890841	rs182846929	rs1850732	rs186682810	rs189114622	rs191058500
rs147532156	rs148968285	rs150707370	rs16889691	rs180905771	rs1829413	rs1850733	rs186704661	rs189130002	rs191258712
rs147534794	rs148984563	rs150709642	rs16889842	rs180936488	rs182996926	rs1850737	rs186727677	rs189206645	rs191268745
rs147548493	rs149022308	rs150823559	rs16889932	rs180951075	rs183004032	rs1850739	rs186762677	rs189232743	rs191322243
rs147563048	rs149028152	rs150828093	rs16890590	rs180989473	rs183004276	rs1850740	rs186850997	rs189291952	rs191385164
rs147608456	rs149166425	rs150833841	rs16890728	rs181030592	rs183006594	rs1850744	rs186855576	rs189326238	rs191394302
rs147639097	rs149187442	rs150962779	rs16890905	rs181095964	rs183021241	rs185076494	rs186889066	rs189331504	rs191409840
rs147716199	rs149192460	rs150984370	rs16890979	rs181130991	rs183046178	rs185146232	rs186927203	rs189350135	rs191474189
rs147774694	rs149236596	rs151054437	rs16891020	rs181232702	rs183047359	rs185167073	rs186942366	rs189358732	rs191475275
rs147804285	rs149271942	rs151104273	rs16891234	rs181315906	rs183077226	rs185175605	rs186970316	rs189365277	rs1914874
rs147805997	rs149279261	rs151104857	rs16891285	rs181417171	rs183110868	rs185213646	rs187024415	rs189377152	rs191513628
rs147819274	rs149285862	rs151119440	rs16891489	rs181420478	rs183203239	rs185248830	rs187132080	rs189516145	rs191580578
rs147875823	rs149341985	rs151128040	rs16891746	rs181452327	rs183254695	rs185256774	rs187135408	rs189576127	rs191586435
rs147912672	rs149390450	rs151135364	rs16891923	rs181467183	rs183300357	rs185278846	rs187215218	rs189596279	rs191622025
rs147973376	rs149455738	rs151139969	rs16891926	rs181517438	rs183382473	rs185415458	rs187257950	rs189690296	rs191675521

rs147999868	rs149561889	rs151156660	rs16891971	rs181519830	rs183417303	rs185447022	rs187365313	rs189718883	rs191837179
rs148022027	rs149628125	rs151186539	rs16892069	rs181580893	rs183535279	rs185455331	rs187386256	rs189741361	rs191999259
rs148228110	rs149636792	rs151232397	rs16892419	rs181623671	rs183640684	rs185512663	rs187409592	rs189745455	rs192057509
rs148269664	rs149644486	rs151282040	rs16892420	rs181658363	rs183659377	rs185568946	rs187463212	rs189746790	rs192076740
rs148317100	rs149660051	rs151325127	rs16892449	rs181755864	rs183854319	rs185586853	rs187708863	rs189839379	rs192084120
rs148442170	rs149752397	rs1519092	rs16892474	rs181817180	rs184033171	rs185587884	rs187789518	rs189875791	rs192118297
rs148450134	rs149781747	rs1519093	rs16892475	rs181844636	rs184065097	rs185599792	rs187804802	rs189902533	rs192132756
rs148471487	rs149807407	rs1519094	rs16892493	rs181870973	rs184094798	rs185629831	rs1878276	rs190162322	rs192186455
rs148476605	rs149815051	rs1519095	rs17185835	rs181872225	rs184241396	rs185646091	rs1878277	rs190278491	rs192261037
rs148513455	rs149878055	rs1519096	rs17185870	rs181882156	rs184261910	rs185677474	rs1878278	rs190321252	rs192344071
rs148539010	rs149955569	rs1519097	rs17187075	rs181900390	rs184288806	rs185686223	rs187998726	rs190338030	rs192368924
rs148545499	rs150039611	rs1519098	rs17242364	rs181990502	rs184297548	rs185720419	rs188047000	rs190347592	rs192489364
rs148610844	rs150045473	rs1519099	rs17245436	rs182179248	rs184387875	rs185731129	rs188139530	rs190351940	rs192585541
rs148662327	rs150138969	rs1533615	rs17245723	rs182222566	rs184396578	rs185776752	rs188213035	rs190373654	rs192585916
rs148679448	rs150233577	rs1568318	rs17246501	rs182392177	rs184460416	rs185780638	rs188311840	rs190373872	rs192823699
rs192839949	rs2139242	rs2292916	rs28649726	rs34651105	rs36058283	rs3733584	rs376875409	rs3796838	rs4292332
rs192862502	rs2139243	rs2292917	rs28650494	rs34658962	rs36075927	rs3733585	rs376904135	rs3796839	rs4292333
rs192874676	rs2176644	rs2303401	rs28660321	rs34707376	rs36084205	rs3733586	rs376929668	rs3796840	rs4306953
rs192891241	rs2215693	rs28373109	rs2867383	rs34709913	rs367692082	rs3733587	rs377426881	rs3796841	rs4311315
rs192893054	rs2240720	rs28373658	rs2867388	rs34752819	rs367769397	rs3733588	rs377565288	rs3796842	rs4311316
rs192930761	rs2240721	rs28380210	rs2867393	rs34768406	rs367788933	rs3733589	rs3775930	rs3806816	rs4312756
rs192936490	rs2240722	rs28392795	rs2867394	rs34788376	rs367964588	rs3733590	rs3775931	rs3806817	rs4312757
rs192979816	rs2240723	rs28407807	rs28677023	rs35076540	rs368171065	rs3733591	rs3775932	rs3822236	rs4314284
rs192985502	rs2240724	rs28413933	rs28682539	rs35099040	rs368251638	rs373697506	rs3775933	rs3822239	rs4318649
rs193015978	rs2241464	rs28427256	rs28688686	rs35110076	rs368261141	rs374015639	rs3775935	rs3822241	rs4318650
rs193066246	rs2241465	rs28429694	rs28713317	rs35150828	rs368341354	rs374243364	rs3775936	rs3822242	rs4333184
rs193101331	rs2241466	rs28449404	rs28714541	rs35201034	rs368534990	rs374891992	rs3775939	rs3822243	rs4336225
rs193123110	rs2241467	rs28460143	rs28715627	rs35249656	rs368727336	rs3749558	rs3775940	rs3822245	rs4337733
rs193289149	rs2241469	rs28462017	rs28730480	rs35250962	rs368778860	rs375121720	rs3775941	rs3822246	rs4339203
rs193293531	rs2241472	rs28468399	rs28733364	rs35271694	rs369702220	rs375526781	rs3775942	rs3822247	rs4339211
rs1967550	rs2241473	rs28480661	rs28735365	rs35276762	rs369731453	rs3756215	rs3775943	rs3822250	rs4345181
rs1967551	rs2241474	rs28489733	rs28798076	rs35289776	rs369796563	rs3756217	rs3775944	rs3822259	rs4348091
rs1976792	rs2241475	rs28490259	rs28831091	rs35334203	rs369965226	rs3756218	rs3775945	rs3886038	rs4364264
rs1980219	rs2241476	rs28496610	rs28837683	rs35371429	rs370387533	rs3756219	rs3775946	rs3960679	rs4376135
rs1980220	rs2241477	rs28502637	rs28868569	rs35380388	rs370769581	rs3756220	rs3775947	rs3973946	rs4382035
rs1996335	rs2241480	rs28504140	rs2903564	rs35411989	rs370833528	rs3756222	rs3775948	rs4075869	rs4383618
rs200061806	rs2241484	rs28507715	rs2903827	rs35438220	rs370891760	rs3756223	rs3775949	rs4077362	rs4385059

rs200180059	rs2276961	rs28513781	rs3217	rs35501905	rs370935468	rs3756224	rs3775950	rs41268375	rs4389579
rs200270677	rs2276962	rs28519672	rs34088729	rs35512765	rs370990960	rs3756225	rs377615729	rs41268387	rs4391034
rs200496396	rs2276963	rs28523967	rs34145578	rs35523212	rs371440376	rs3756226	rs3796818	rs41268389	rs4393996
rs200525851	rs2276964	rs28526383	rs34160786	rs35565862	rs371721351	rs3756231	rs3796820	rs4128494	rs4407505
rs200677384	rs2276965	rs28528381	rs34193855	rs35582635	rs371746690	rs3756233	rs3796821	rs4144	rs4408959
rs200699063	rs2278119	rs28553891	rs34208161	rs35629527	rs371897323	rs3756234	rs3796822	rs4235345	rs4422413
rs2012177	rs2278120	rs28558552	rs34213329	rs35750364	rs371899886	rs3756235	rs3796823	rs4235346	rs4428284
rs2013714	rs2278121	rs28571073	rs34245354	rs35758343	rs372000442	rs3756236	rs3796825	rs4235347	rs4444830
rs2018643	rs2278122	rs28583524	rs34297373	rs35782952	rs372021642	rs3756237	rs3796826	rs4235348	rs4447861
rs201988226	rs2278123	rs28591077	rs34325511	rs35782983	rs372300250	rs3756238	rs3796829	rs4235353	rs4447862
rs202000076	rs2280202	rs28592748	rs34407859	rs35865690	rs372346996	rs375676428	rs3796830	rs4235354	rs4447863
rs202097102	rs2280203	rs28602527	rs34422255	rs35866697	rs372420151	rs3762933	rs3796831	rs4235355	rs4455410
rs202170447	rs2280204	rs28607048	rs34426660	rs35922993	rs372494279	rs376405315	rs3796832	rs4235356	rs4456954
rs2030287	rs2280205	rs28610447	rs34501273	rs35933067	rs372496138	rs376564894	rs3796833	rs4276278	rs4459990
rs2066	rs2280206	rs28613263	rs34517659	rs35933336	rs372497976	rs376626145	rs3796834	rs4280729	rs4467563
rs2076907	rs2280207	rs28624182	rs34560968	rs35954357	rs372620891	rs376641818	rs3796835	rs4289442	rs4467564
rs2139238	rs2280208	rs28636428	rs34567300	rs35955619	rs372641102	rs376685079	rs3796836	rs4292327	rs4467565
rs2139240	rs2280333	rs28643326	rs34644460	rs36036984	rs373311989	rs376831433	rs3796837	rs4292328	rs4473653
rs4475146	rs4697696	rs4697925	rs56149009	rs59035374	rs62293226	rs62295971	rs6449213	rs6825888	rs6842853
rs4476596	rs4697697	rs4697926	rs56158923	rs59077355	rs62293240	rs62296002	rs6449217	rs6826185	rs6843873
rs4481233	rs4697698	rs4697932	rs56169830	rs59234705	rs62293270	rs6281	rs6449218	rs6826450	rs6844216
rs4484299	rs4697699	rs4697933	rs56170676	rs59319978	rs62293272	rs6283	rs6449237	rs6826764	rs6844316
rs4485819	rs4697700	rs4697939	rs56178126	rs59518418	rs62293275	rs6414766	rs6449238	rs6826806	rs6844329
rs4495037	rs4697701	rs4697940	rs56190921	rs59574200	rs62293276	rs6448996	rs6449286	rs6827401	rs6844369
rs4502681	rs4697703	rs4697953	rs56202030	rs59707854	rs62293282	rs6449000	rs6449339	rs6827754	rs6844787
rs4505821	rs4697704	rs4697954	rs56205495	rs59815647	rs62293283	rs6449009	rs66538112	rs6827785	rs6845554
rs4511996	rs4697705	rs4697955	rs56223908	rs59871456	rs62293284	rs6449026	rs66647240	rs6828040	rs6845818
rs4515163	rs4697706	rs4697983	rs56239136	rs59924619	rs62293285	rs6449027	rs67523049	rs6829727	rs6846692
rs4516717	rs4697707	rs4698017	rs56253435	rs60045583	rs62293286	rs6449028	rs67820465	rs6829755	rs6847019
rs4518244	rs4697708	rs5028371	rs56275585	rs60125439	rs62293287	rs6449049	rs67968745	rs6831580	rs6847858
rs4519796	rs4697709	rs5028843	rs56278885	rs60285303	rs62293289	rs6449051	rs68013308	rs6831796	rs6847871
rs4525975	rs4697710	rs55668232	rs56288911	rs60445736	rs62293290	rs6449052	rs6810736	rs6832439	rs6847887
rs4529048	rs4697715	rs55670339	rs56322912	rs60599851	rs62293291	rs6449089	rs6811809	rs6832456	rs6848100
rs4529049	rs4697718	rs55686745	rs56351177	rs60715294	rs62293294	rs6449090	rs6812007	rs6832792	rs6848689
rs4543113	rs4697719	rs55721900	rs56358669	rs60956448	rs62293295	rs6449097	rs6812563	rs6833878	rs6849717
rs4546242	rs4697720	rs55723889	rs56393964	rs61121804	rs62293296	rs6449100	rs6812759	rs6834540	rs6849729
rs4547795	rs4697721	rs55760253	rs56396145	rs61154897	rs62293297	rs6449110	rs6812780	rs6834893	rs6849736

rs4560411	rs4697744	rs55801162	rs56399359	rs61166583	rs62293298	rs6449137	rs6812851	rs6834978	rs6849962
rs4572881	rs4697891	rs55811736	rs56402960	rs61209374	rs62293300	rs6449139	rs6814664	rs6835741	rs6850143
rs4575993	rs4697892	rs55816202	rs56826562	rs61233382	rs62293301	rs6449144	rs6815001	rs6836200	rs6850166
rs4575994	rs4697893	rs55817941	rs56970526	rs61312541	rs62293329	rs6449154	rs6815039	rs6836706	rs6850684
rs4579113	rs4697895	rs55858763	rs57136958	rs61338451	rs62293330	rs6449156	rs6815895	rs6836878	rs6851365
rs4580649	rs4697896	rs55864719	rs57235613	rs61446121	rs62293387	rs6449157	rs6816053	rs6836961	rs6852425
rs4591605	rs4697898	rs55916827	rs57250714	rs61476037	rs62293415	rs6449158	rs6817564	rs6837224	rs6852441
rs4608811	rs4697899	rs55921149	rs57574512	rs61691299	rs62294288	rs6449159	rs6818572	rs6837273	rs6853056
rs4613568	rs4697900	rs55943327	rs57723486	rs62286326	rs62294289	rs6449171	rs6819833	rs6837336	rs6853437
rs4621429	rs4697901	rs55959038	rs57731161	rs62286327	rs62294290	rs6449172	rs6820009	rs6837659	rs6853922
rs4621431	rs4697902	rs55959894	rs57757169	rs62286328	rs62294293	rs6449173	rs6820188	rs6838021	rs6855095
rs4622999	rs4697903	rs55962381	rs57897925	rs62286562	rs62294331	rs6449174	rs6820230	rs6838317	rs6855911
rs4637402	rs4697904	rs55973727	rs57904542	rs62286563	rs62294332	rs6449175	rs6820616	rs6838850	rs6856012
rs4639072	rs4697905	rs56003345	rs57905135	rs62286568	rs62294334	rs6449176	rs6821843	rs6838891	rs6856127
rs4639073	rs4697908	rs56036138	rs58130873	rs62286569	rs62295669	rs6449177	rs6822023	rs6838986	rs6856396
rs4640670	rs4697909	rs56038393	rs58380370	rs62287542	rs62295672	rs6449178	rs6822889	rs6839302	rs6857001
rs4697690	rs4697910	rs56095448	rs58693849	rs62287543	rs62295690	rs6449179	rs6822988	rs6839490	rs6857693
rs4697692	rs4697911	rs56113653	rs58769709	rs62288489	rs62295694	rs6449183	rs6823129	rs6840802	rs6858614
rs4697693	rs4697913	rs56123633	rs58782826	rs62288519	rs62295695	rs6449196	rs6823324	rs6840999	rs714871
rs4697694	rs4697923	rs56136402	rs58847608	rs62288891	rs62295697	rs6449201	rs6824636	rs6841397	rs714872
rs4697695	rs4697924	rs56139970	rs58981012	rs62293224	rs62295967	rs6449202	rs6825187	rs6842850	rs714873
rs715979	rs73221597	rs7376948	rs74970122	rs76257144	rs7669444	rs7686538	rs77265107	rs78491056	rs79679425
rs71603975	rs73221599	rs7376960	rs75015234	rs76275868	rs7669607	rs7687896	rs77269347	rs78507984	rs79704809
rs71603976	rs73223775	rs7377578	rs75024060	rs76367047	rs7669742	rs7688167	rs77275218	rs78533886	rs79707209
rs71603977	rs73223785	rs7377625	rs75044083	rs76388621	rs76698299	rs7688629	rs77304661	rs78549292	rs79756119
rs71603978	rs73223786	rs7378305	rs75101489	rs76411769	rs7670751	rs76903922	rs77326183	rs78570464	rs79765234
rs71603981	rs73223788	rs7378340	rs751092	rs76421184	rs7671266	rs76917885	rs77356241	rs78589581	rs79785876
rs71603992	rs73224474	rs73804393	rs75110348	rs76457286	rs7672947	rs76920131	rs77376600	rs78594917	rs79824251
rs72648876	rs73224492	rs73804455	rs75137127	rs76466354	rs7674156	rs76943656	rs77388911	rs78698809	rs79835095
rs73090004	rs73224493	rs73805439	rs75164297	rs76552410	rs76743293	rs7694496	rs77414593	rs78755014	rs79876692
rs73090005	rs73224496	rs73805487	rs75181558	rs7656342	rs7674711	rs7694997	rs77434921	rs78757705	rs79888997
rs73092479	rs73224498	rs73805488	rs75234256	rs7656624	rs7674723	rs7695113	rs77459722	rs78785836	rs79931771
rs73092500	rs73225806	rs73805489	rs75241535	rs7657096	rs7675964	rs7695555	rs77554178	rs78801470	rs79996818
rs73094598	rs73225810	rs73805490	rs75245044	rs7657127	rs7676605	rs76958015	rs77564396	rs78876648	rs80059751
rs73096620	rs73225811	rs73805847	rs75245155	rs7657340	rs7676733	rs7695879	rs77666919	rs78882332	rs80061611
rs73096626	rs73225812	rs73806483	rs75375980	rs7658170	rs7677710	rs7696092	rs77671965	rs78892247	rs80081453
rs73096634	rs73225813	rs741075	rs75389148	rs7659717	rs7677939	rs7696536	rs77684901	rs78917351	rs80116299

rs73096647	rs73225827	rs74285646	rs75468543	rs7659924	rs76779802	rs7696895	rs77759711	rs78921276	rs80119233
rs73100621	rs73225831	rs7434391	rs75487798	rs76606104	rs7678012	rs7696971	rs77859955	rs78946091	rs80180400
rs73100632	rs73225835	rs7435196	rs75488049	rs7660895	rs7678287	rs7696983	rs77862592	rs78963587	rs80204783
rs73104537	rs73225881	rs7437120	rs75521345	rs7661701	rs7678346	rs7697004	rs77870747	rs79043019	rs80224261
rs73104539	rs73225891	rs74377900	rs75599884	rs76617398	rs7679464	rs7697416	rs77882555	rs79048870	rs80268248
rs731069	rs73225893	rs7439210	rs75604947	rs76617595	rs7679724	rs76978600	rs77895782	rs79063585	rs80331485
rs731070	rs73227853	rs7442295	rs75620494	rs7661796	rs7679916	rs76985474	rs77935410	rs79095673	rs874432
rs73212808	rs73227873	rs7442336	rs75690580	rs7662439	rs76800309	rs7698858	rs77957927	rs79107516	rs882222
rs73212817	rs73227883	rs74433158	rs75708958	rs76624494	rs7680126	rs7699512	rs77963917	rs79113604	rs882223
rs73212828	rs73229818	rs74472339	rs75805865	rs7663032	rs7680554	rs7699609	rs78002041	rs79133792	rs883041
rs73212830	rs73229828	rs74510990	rs75871043	rs7663044	rs7680896	rs7699671	rs78028161	rs79146062	rs884573
rs73212848	rs73229836	rs74527798	rs75896783	rs7663079	rs76813200	rs7700047	rs78061800	rs79197118	rs9291640
rs73212853	rs73229842	rs74544177	rs75964023	rs7663097	rs7683059	rs77026746	rs78087789	rs79226847	rs9291641
rs73212886	rs733175	rs74561581	rs75968456	rs76632978	rs7683253	rs77093467	rs78126175	rs79234071	rs9291642
rs73212889	rs734122	rs74606663	rs75987279	rs7663448	rs7683283	rs77101951	rs78153443	rs79323395	rs9291645
rs73212890	rs734553	rs74623241	rs76038859	rs7663670	rs7683792	rs77105911	rs78203288	rs79380329	rs938552
rs73212891	rs7349721	rs74642414	rs76056379	rs76640365	rs7683831	rs77130163	rs78284941	rs79422384	rs938553
rs73212895	rs735527	rs74651202	rs76065252	rs7664572	rs7683832	rs77138280	rs78301913	rs79437705	rs938554
rs73212898	rs737267	rs74706199	rs76069034	rs7665666	rs7683856	rs77140241	rs78310306	rs79501171	rs938555
rs73212899	rs7375587	rs74778870	rs76098280	rs7666545	rs7683948	rs77152814	rs78319160	rs79526919	rs938556
rs73212900	rs7375599	rs74794351	rs76099163	rs7668175	rs7684245	rs77165435	rs78389225	rs79568191	rs938557
rs73215003	rs7375642	rs74812044	rs76138462	rs76689568	rs7684306	rs77203987	rs78403883	rs79598790	rs938558
rs73215005	rs7375643	rs74838002	rs76139601	rs7669090	rs7685396	rs77223742	rs78432726	rs79652759	rs938562
rs73218792	rs7376505	rs74915949	rs76156864	rs7669296	rs7685958	rs77251997	rs78441715	rs79673783	rs938563

rs938564	VAR_CHR4_10002504	VAR_CHR4_10011580	VAR_CHR4_10021637	VAR_CHR4_10030938	VAR_CHR4_10038001	VAR_CHR4_10048770	VAR_CHR4_10070612
rs939131	VAR_CHR4_10002535	VAR_CHR4_10012005	VAR_CHR4_10021709	VAR_CHR4_10030987	VAR_CHR4_10038018	VAR_CHR4_10049655	VAR_CHR4_10070694
rs939132	VAR_CHR4_10002537	VAR_CHR4_10012061	VAR_CHR4_10022272	VAR_CHR4_10032096	VAR_CHR4_10038070	VAR_CHR4_10050012	VAR_CHR4_10070873
rs939134	VAR_CHR4_10002587	VAR_CHR4_10012078	VAR_CHR4_10022598	VAR_CHR4_10032292	VAR_CHR4_10038481	VAR_CHR4_10050181	VAR_CHR4_10075174
rs950309	VAR_CHR4_10002611	VAR_CHR4_10012105	VAR_CHR4_10023840	VAR_CHR4_10032359	VAR_CHR4_10038560	VAR_CHR4_10051050	VAR_CHR4_10075310
rs950310	VAR_CHR4_10002666	VAR_CHR4_10012590	VAR_CHR4_10024169	VAR_CHR4_10032439	VAR_CHR4_10038956	VAR_CHR4_10051422	VAR_CHR4_10075365
rs9684002	VAR_CHR4_10002893	VAR_CHR4_10012720	VAR_CHR4_10024740	VAR_CHR4_10032680	VAR_CHR4_10039930	VAR_CHR4_10051439	VAR_CHR4_10075423
rs9684729	VAR_CHR4_10002908	VAR_CHR4_10012872	VAR_CHR4_10024885	VAR_CHR4_10033275	VAR_CHR4_10040062	VAR_CHR4_10051504	VAR_CHR4_10075775
rs9685427	VAR_CHR4_10003582	VAR_CHR4_10013037	VAR_CHR4_10024911	VAR_CHR4_10033416	VAR_CHR4_10040390	VAR_CHR4_10051568	VAR_CHR4_10076235
rs9685502	VAR_CHR4_10003729	VAR_CHR4_10013450	VAR_CHR4_10024940	VAR_CHR4_10033630	VAR_CHR4_10040522	VAR_CHR4_10052084	VAR_CHR4_10076430
rs9732	VAR_CHR4_10004006	VAR_CHR4_10013631	VAR_CHR4_10025326	VAR_CHR4_10033646	VAR_CHR4_10040586	VAR_CHR4_10052153	VAR_CHR4_10076666
rs978465	VAR_CHR4_10004039	VAR_CHR4_10014719	VAR_CHR4_10025537	VAR_CHR4_10033794	VAR_CHR4_10040622	VAR_CHR4_10052411	VAR_CHR4_10076680
rs978466	VAR_CHR4_10004164	VAR_CHR4_10015600	VAR_CHR4_10025855	VAR_CHR4_10033892	VAR_CHR4_10041212	VAR_CHR4_10052488	VAR_CHR4_10076873

rs9884416	VAR_CHR4_10004517	VAR_CHR4_10016055	VAR_CHR4_10026104	VAR_CHR4_10034103	VAR_CHR4_10042306	VAR_CHR4_10052578	VAR_CHR4_10077133
rs9926	VAR_CHR4_10004785	VAR_CHR4_10016076	VAR_CHR4_10026105	VAR_CHR4_10034318	VAR_CHR4_10042453	VAR_CHR4_10053472	VAR_CHR4_10077356
rs993173	VAR_CHR4_10004788	VAR_CHR4_10016201	VAR_CHR4_10026132	VAR_CHR4_10034830	VAR_CHR4_10042692	VAR_CHR4_10054033	VAR_CHR4_10077447
rs998675	VAR_CHR4_10005785	VAR_CHR4_10016444	VAR_CHR4_10026910	VAR_CHR4_10034867	VAR_CHR4_10043133	VAR_CHR4_10054835	VAR_CHR4_10077821
rs998676	VAR_CHR4_10005875	VAR_CHR4_10016652	VAR_CHR4_10027024	VAR_CHR4_10034958	VAR_CHR4_10043549	VAR_CHR4_10055028	VAR_CHR4_10077834
rs9990770	VAR_CHR4_10005965	VAR_CHR4_10016870	VAR_CHR4_10027126	VAR_CHR4_10035233	VAR_CHR4_10043631	VAR_CHR4_10055116	VAR_CHR4_10078201
rs9991278	VAR_CHR4_10006072	VAR_CHR4_10016937	VAR_CHR4_10027691	VAR_CHR4_10035319	VAR_CHR4_10043645	VAR_CHR4_10055757	VAR_CHR4_10078219
rs9992406	VAR_CHR4_10006555	VAR_CHR4_10017153	VAR_CHR4_10027769	VAR_CHR4_10035337	VAR_CHR4_10043649	VAR_CHR4_10055812	VAR_CHR4_10078308
rs9992815	VAR_CHR4_10006592	VAR_CHR4_10017318	VAR_CHR4_10027795	VAR_CHR4_10035353	VAR_CHR4_10043689	VAR_CHR4_10055978	VAR_CHR4_10078458
rs9993410	VAR_CHR4_10006761	VAR_CHR4_10017334	VAR_CHR4_10027922	VAR_CHR4_10035366	VAR_CHR4_10044266	VAR_CHR4_10056069	VAR_CHR4_10078527
rs9993652	VAR_CHR4_10007357	VAR_CHR4_10017454	VAR_CHR4_10028062	VAR_CHR4_10035630	VAR_CHR4_10044515	VAR_CHR4_10056211	VAR_CHR4_10078631
rs9994216	VAR_CHR4_10007772	VAR_CHR4_10017660	VAR_CHR4_10028127	VAR_CHR4_10035637	VAR_CHR4_10044689	VAR_CHR4_10056248	VAR_CHR4_10078649
rs9994266	VAR_CHR4_10008178	VAR_CHR4_10017698	VAR_CHR4_10028159	VAR_CHR4_10035961	VAR_CHR4_10045184	VAR_CHR4_10058246	VAR_CHR4_10078746
rs9994937	VAR_CHR4_10008194	VAR_CHR4_10017740	VAR_CHR4_10028415	VAR_CHR4_10036061	VAR_CHR4_10045363	VAR_CHR4_10058329	VAR_CHR4_10078946
rs9996799	VAR_CHR4_10008328	VAR_CHR4_10018166	VAR_CHR4_10028775	VAR_CHR4_10036700	VAR_CHR4_10045619	VAR_CHR4_10058411	VAR_CHR4_10079442
rs9998739	VAR_CHR4_10008485	VAR_CHR4_10018364	VAR_CHR4_10028792	VAR_CHR4_10036917	VAR_CHR4_10045871	VAR_CHR4_10058529	VAR_CHR4_10079670
rs9998811	VAR_CHR4_10008637	VAR_CHR4_10018420	VAR_CHR4_10029217	VAR_CHR4_10036949	VAR_CHR4_10046071	VAR_CHR4_10058812	VAR_CHR4_10079775
VAR_CHR4_10000372	VAR_CHR4_10008687	VAR_CHR4_10018514	VAR_CHR4_10029420	VAR_CHR4_10036995	VAR_CHR4_10046551	VAR_CHR4_10059286	VAR_CHR4_10079891
VAR_CHR4_10000672	VAR_CHR4_10008732	VAR_CHR4_10018555	VAR_CHR4_10029546	VAR_CHR4_10037052	VAR_CHR4_10046649	VAR_CHR4_10064032	VAR_CHR4_10083014
VAR_CHR4_10000731	VAR_CHR4_10008938	VAR_CHR4_10018806	VAR_CHR4_10029629	VAR_CHR4_10037210	VAR_CHR4_10046992	VAR_CHR4_10064151	VAR_CHR4_10083028
VAR_CHR4_10000886	VAR_CHR4_10009112	VAR_CHR4_10020358	VAR_CHR4_10029927	VAR_CHR4_10037265	VAR_CHR4_10047075	VAR_CHR4_10064766	VAR_CHR4_10083077
VAR_CHR4_10001025	VAR_CHR4_10009179	VAR_CHR4_10020755	VAR_CHR4_10030015	VAR_CHR4_10037288	VAR_CHR4_10047361	VAR_CHR4_10065005	VAR_CHR4_10084604
VAR_CHR4_10001421	VAR_CHR4_10009267	VAR_CHR4_10021017	VAR_CHR4_10030108	VAR_CHR4_10037328	VAR_CHR4_10047533	VAR_CHR4_10065121	VAR_CHR4_10085541
VAR_CHR4_10001735	VAR_CHR4_10009391	VAR_CHR4_10021026	VAR_CHR4_10030283	VAR_CHR4_10037457	VAR_CHR4_10048187	VAR_CHR4_10065355	VAR_CHR4_10085673
VAR_CHR4_10002254	VAR_CHR4_10010030	VAR_CHR4_10021028	VAR_CHR4_10030366	VAR_CHR4_10037563	VAR_CHR4_10048233	VAR_CHR4_10065399	VAR_CHR4_10085750
VAR_CHR4_10002318	VAR_CHR4_10010651	VAR_CHR4_10021323	VAR_CHR4_10030437	VAR_CHR4_10037934	VAR_CHR4_10048635	VAR_CHR4_10065474	VAR_CHR4_10085771
VAR_CHR4_10002457	VAR_CHR4_10011367	VAR_CHR4_10021460	VAR_CHR4_10030519	VAR_CHR4_10037956	VAR_CHR4_10048705	VAR_CHR4_10065769	VAR_CHR4_10085886
VAR_CHR4_10086323	VAR_CHR4_10094319	VAR_CHR4_10108688	VAR_CHR4_10119117	VAR_CHR4_10121607	VAR_CHR4_10124890	VAR_CHR4_10159975	VAR_CHR4_10175698
VAR_CHR4_10086328	VAR_CHR4_10094363	VAR_CHR4_10108728	VAR_CHR4_10119171	VAR_CHR4_10121625	VAR_CHR4_10125011	VAR_CHR4_10160135	VAR_CHR4_10175708
VAR_CHR4_10086329	VAR_CHR4_10094790	VAR_CHR4_10108951	VAR_CHR4_10119183	VAR_CHR4_10121719	VAR_CHR4_10125110	VAR_CHR4_10160221	VAR_CHR4_10175736
VAR_CHR4_10086525	VAR_CHR4_10094981	VAR_CHR4_10109053	VAR_CHR4_10119290	VAR_CHR4_10121801	VAR_CHR4_10125127	VAR_CHR4_10160449	VAR_CHR4_10175982
VAR_CHR4_10086586	VAR_CHR4_10095292	VAR_CHR4_10109070	VAR_CHR4_10119309	VAR_CHR4_10121803	VAR_CHR4_10125290	VAR_CHR4_10160529	VAR_CHR4_10176136
VAR_CHR4_10086608	VAR_CHR4_10095439	VAR_CHR4_10109185	VAR_CHR4_10119332	VAR_CHR4_10121811	VAR_CHR4_10125357	VAR_CHR4_10160679	VAR_CHR4_10176355
VAR_CHR4_10089721	VAR_CHR4_10095790	VAR_CHR4_10109590	VAR_CHR4_10119356	VAR_CHR4_10121906	VAR_CHR4_10126049	VAR_CHR4_10161969	VAR_CHR4_10176508
VAR_CHR4_10089801	VAR_CHR4_10095806	VAR_CHR4_10109685	VAR_CHR4_10119521	VAR_CHR4_10121962	VAR_CHR4_10126148	VAR_CHR4_10162180	VAR_CHR4_10176595
VAR_CHR4_10089949	VAR_CHR4_10096014	VAR_CHR4_10109687	VAR_CHR4_10119556	VAR_CHR4_10122007	VAR_CHR4_10126324	VAR_CHR4_10162183	VAR_CHR4_10207992
VAR_CHR4_10090075	VAR_CHR4_10096146	VAR_CHR4_10109801	VAR_CHR4_10119577	VAR_CHR4_10122031	VAR_CHR4_10126355	VAR_CHR4_10166475	VAR_CHR4_10208077

VAR_CHR4_10090359	VAR_CHR4_10096318	VAR_CHR4_10110270	VAR_CHR4_10119620	VAR_CHR4_10122052	VAR_CHR4_10126506	VAR_CHR4_10166533	VAR_CHR4_10208114
VAR_CHR4_10090385	VAR_CHR4_10096346	VAR_CHR4_10110342	VAR_CHR4_10119665	VAR_CHR4_10122145	VAR_CHR4_10126520	VAR_CHR4_10166734	VAR_CHR4_10208399
VAR_CHR4_10090574	VAR_CHR4_10096349	VAR_CHR4_10110362	VAR_CHR4_10119672	VAR_CHR4_10122195	VAR_CHR4_10126714	VAR_CHR4_10166794	VAR_CHR4_10208427
VAR_CHR4_10090840	VAR_CHR4_10096691	VAR_CHR4_10110374	VAR_CHR4_10119680	VAR_CHR4_10122248	VAR_CHR4_10126738	VAR_CHR4_10166804	VAR_CHR4_10208797
VAR_CHR4_10091163	VAR_CHR4_10096785	VAR_CHR4_10115424	VAR_CHR4_10119717	VAR_CHR4_10122450	VAR_CHR4_10126826	VAR_CHR4_10166817	VAR_CHR4_10208805
VAR_CHR4_10091205	VAR_CHR4_10096869	VAR_CHR4_10115473	VAR_CHR4_10119781	VAR_CHR4_10122489	VAR_CHR4_10146741	VAR_CHR4_10166829	VAR_CHR4_10241757
VAR_CHR4_10091270	VAR_CHR4_10097380	VAR_CHR4_10115710	VAR_CHR4_10119808	VAR_CHR4_10122496	VAR_CHR4_10146815	VAR_CHR4_10166830	VAR_CHR4_10241938
VAR_CHR4_10091339	VAR_CHR4_10097586	VAR_CHR4_10115771	VAR_CHR4_10119960	VAR_CHR4_10122523	VAR_CHR4_10146845	VAR_CHR4_10167052	VAR_CHR4_10242058
VAR_CHR4_10091387	VAR_CHR4_10098507	VAR_CHR4_10116167	VAR_CHR4_10119974	VAR_CHR4_10122595	VAR_CHR4_10147087	VAR_CHR4_10167245	VAR_CHR4_10242309
VAR_CHR4_10091424	VAR_CHR4_10098618	VAR_CHR4_10116511	VAR_CHR4_10120142	VAR_CHR4_10122613	VAR_CHR4_10147093	VAR_CHR4_10173433	VAR_CHR4_10242476
VAR_CHR4_10091515	VAR_CHR4_10098840	VAR_CHR4_10116516	VAR_CHR4_10120144	VAR_CHR4_10122642	VAR_CHR4_10147094	VAR_CHR4_10173461	VAR_CHR4_10245633
VAR_CHR4_10091789	VAR_CHR4_10100814	VAR_CHR4_10116567	VAR_CHR4_10120177	VAR_CHR4_10122715	VAR_CHR4_10151894	VAR_CHR4_10173502	VAR_CHR4_10245641
VAR_CHR4_10091897	VAR_CHR4_10100820	VAR_CHR4_10116764	VAR_CHR4_10120197	VAR_CHR4_10122751	VAR_CHR4_10151964	VAR_CHR4_10173503	VAR_CHR4_10245759
VAR_CHR4_10092098	VAR_CHR4_10105476	VAR_CHR4_10116853	VAR_CHR4_10120218	VAR_CHR4_10122936	VAR_CHR4_10152036	VAR_CHR4_10173619	VAR_CHR4_10246107
VAR_CHR4_10092795	VAR_CHR4_10105980	VAR_CHR4_10116864	VAR_CHR4_10120264	VAR_CHR4_10122938	VAR_CHR4_10152133	VAR_CHR4_10173746	VAR_CHR4_10246152
VAR_CHR4_10092796	VAR_CHR4_10106072	VAR_CHR4_10116931	VAR_CHR4_10120395	VAR_CHR4_10122946	VAR_CHR4_10152139	VAR_CHR4_10173802	VAR_CHR4_10246155
VAR_CHR4_10092829	VAR_CHR4_10106147	VAR_CHR4_10116942	VAR_CHR4_10120439	VAR_CHR4_10122992	VAR_CHR4_10152277	VAR_CHR4_10173934	VAR_CHR4_10246279
VAR_CHR4_10093084	VAR_CHR4_10107101	VAR_CHR4_10116999	VAR_CHR4_10120485	VAR_CHR4_10123047	VAR_CHR4_10152680	VAR_CHR4_10173984	VAR_CHR4_10246344
VAR_CHR4_10093333	VAR_CHR4_10107289	VAR_CHR4_10117136	VAR_CHR4_10120559	VAR_CHR4_10123129	VAR_CHR4_10159232	VAR_CHR4_10173991	VAR_CHR4_10246667
VAR_CHR4_10093370	VAR_CHR4_10107475	VAR_CHR4_10117634	VAR_CHR4_10120688	VAR_CHR4_10123549	VAR_CHR4_10159286	VAR_CHR4_10174239	VAR_CHR4_10246861
VAR_CHR4_10093384	VAR_CHR4_10107760	VAR_CHR4_10117655	VAR_CHR4_10120782	VAR_CHR4_10123874	VAR_CHR4_10159328	VAR_CHR4_10174272	VAR_CHR4_10247089
VAR_CHR4_10093469	VAR_CHR4_10108096	VAR_CHR4_10117737	VAR_CHR4_10120852	VAR_CHR4_10123931	VAR_CHR4_10159347	VAR_CHR4_10174433	VAR_CHR4_10247171
VAR_CHR4_10093550	VAR_CHR4_10108159	VAR_CHR4_10117939	VAR_CHR4_10120962	VAR_CHR4_10123983	VAR_CHR4_10159448	VAR_CHR4_10174604	VAR_CHR4_10298118
VAR_CHR4_10093617	VAR_CHR4_10108163	VAR_CHR4_10118628	VAR_CHR4_10121018	VAR_CHR4_10124003	VAR_CHR4_10159481	VAR_CHR4_10174717	VAR_CHR4_10298197
VAR_CHR4_10093867	VAR_CHR4_10108210	VAR_CHR4_10118676	VAR_CHR4_10121130	VAR_CHR4_10124107	VAR_CHR4_10159537	VAR_CHR4_10174816	VAR_CHR4_10298307
VAR_CHR4_10093908	VAR_CHR4_10108315	VAR_CHR4_10118731	VAR_CHR4_10121186	VAR_CHR4_10124120	VAR_CHR4_10159643	VAR_CHR4_10174883	VAR_CHR4_10298357
VAR_CHR4_10093943	VAR_CHR4_10108385	VAR_CHR4_10118742	VAR_CHR4_10121450	VAR_CHR4_10124275	VAR_CHR4_10159687	VAR_CHR4_10174945	VAR_CHR4_10298394
VAR_CHR4_10094106	VAR_CHR4_10108441	VAR_CHR4_10118748	VAR_CHR4_10121474	VAR_CHR4_10124293	VAR_CHR4_10159766	VAR_CHR4_10175237	VAR_CHR4_10298473
VAR_CHR4_10094155	VAR_CHR4_10108449	VAR_CHR4_10118942	VAR_CHR4_10121493	VAR_CHR4_10124390	VAR_CHR4_10159801	VAR_CHR4_10175358	VAR_CHR4_10298492
VAR_CHR4_10094251	VAR_CHR4_10108569	VAR_CHR4_10119009	VAR_CHR4_10121515	VAR_CHR4_10124403	VAR_CHR4_10159858	VAR_CHR4_10175434	VAR_CHR4_10298641
VAR_CHR4_10298712	VAR_CHR4_10443264	VAR_CHR4_10458194	VAR_CHR4_9776029	VAR_CHR4_9783597	VAR_CHR4_9793118	VAR_CHR4_9804714	VAR_CHR4_9813105
VAR_CHR4_10299180	VAR_CHR4_10443318	VAR_CHR4_10458530	VAR_CHR4_9776141	VAR_CHR4_9783870	VAR_CHR4_9793287	VAR_CHR4_9804730	VAR_CHR4_9813252
VAR_CHR4_10299216	VAR_CHR4_10443491	VAR_CHR4_10458942	VAR_CHR4_9776301	VAR_CHR4_9784934	VAR_CHR4_9793397	VAR_CHR4_9804860	VAR_CHR4_9813275
VAR_CHR4_10318970	VAR_CHR4_10443534	VAR_CHR4_10458959	VAR_CHR4_9776417	VAR_CHR4_9785144	VAR_CHR4_9793430	VAR_CHR4_9805132	VAR_CHR4_9813935
VAR_CHR4_10319025	VAR_CHR4_10443677	VAR_CHR4_10459137	VAR_CHR4_9776494	VAR_CHR4_9785203	VAR_CHR4_9793644	VAR_CHR4_9806027	VAR_CHR4_9814169
VAR_CHR4_10319449	VAR_CHR4_10443775	VAR_CHR4_10459434	VAR_CHR4_9776538	VAR_CHR4_9785240	VAR_CHR4_9793795	VAR_CHR4_9806044	VAR_CHR4_9814640
VAR_CHR4_10319467	VAR_CHR4_10443808	VAR_CHR4_10459500	VAR_CHR4_9776972	VAR_CHR4_9785249	VAR_CHR4_9794647	VAR_CHR4_9806305	VAR_CHR4_9815107

VAR_CHR4_10319500	VAR_CHR4_10443922	VAR_CHR4_10459538	VAR_CHR4_9777182	VAR_CHR4_9785350	VAR_CHR4_9794851	VAR_CHR4_9806373	VAR_CHR4_9815320
VAR_CHR4_10323546	VAR_CHR4_10444032	VAR_CHR4_10459633	VAR_CHR4_9777922	VAR_CHR4_9785375	VAR_CHR4_9794979	VAR_CHR4_9806375	VAR_CHR4_9815417
VAR_CHR4_10323559	VAR_CHR4_10444058	VAR_CHR4_10459831	VAR_CHR4_9778122	VAR_CHR4_9785539	VAR_CHR4_9795166	VAR_CHR4_9806406	VAR_CHR4_9815904
VAR_CHR4_10323592	VAR_CHR4_10444176	VAR_CHR4_10462045	VAR_CHR4_9778272	VAR_CHR4_9785577	VAR_CHR4_9795245	VAR_CHR4_9806442	VAR_CHR4_9816670
VAR_CHR4_10323798	VAR_CHR4_10444469	VAR_CHR4_10462649	VAR_CHR4_9778338	VAR_CHR4_9786343	VAR_CHR4_9795356	VAR_CHR4_9806939	VAR_CHR4_9816836
VAR_CHR4_10323834	VAR_CHR4_10444870	VAR_CHR4_10462684	VAR_CHR4_9778431	VAR_CHR4_9786464	VAR_CHR4_9795599	VAR_CHR4_9806958	VAR_CHR4_9816977
VAR_CHR4_10336853	VAR_CHR4_10445509	VAR_CHR4_10462934	VAR_CHR4_9778565	VAR_CHR4_9786673	VAR_CHR4_9796101	VAR_CHR4_9806991	VAR_CHR4_9817002
VAR_CHR4_10336890	VAR_CHR4_10445650	VAR_CHR4_10463022	VAR_CHR4_9778719	VAR_CHR4_9786723	VAR_CHR4_9797652	VAR_CHR4_9807602	VAR_CHR4_9817114
VAR_CHR4_10336998	VAR_CHR4_10446358	VAR_CHR4_10463131	VAR_CHR4_9779148	VAR_CHR4_9786800	VAR_CHR4_9797750	VAR_CHR4_9807903	VAR_CHR4_9817310
VAR_CHR4_10337019	VAR_CHR4_10446436	VAR_CHR4_10463353	VAR_CHR4_9779258	VAR_CHR4_9786955	VAR_CHR4_9797778	VAR_CHR4_9807904	VAR_CHR4_9817468
VAR_CHR4_10337084	VAR_CHR4_10447663	VAR_CHR4_10463494	VAR_CHR4_9779986	VAR_CHR4_9787595	VAR_CHR4_9797965	VAR_CHR4_9808303	VAR_CHR4_9817483
VAR_CHR4_10337090	VAR_CHR4_10448038	VAR_CHR4_10464141	VAR_CHR4_9780010	VAR_CHR4_9787748	VAR_CHR4_9798476	VAR_CHR4_9808575	VAR_CHR4_9817546
VAR_CHR4_10337212	VAR_CHR4_10448890	VAR_CHR4_10494005	VAR_CHR4_9780038	VAR_CHR4_9788390	VAR_CHR4_9798487	VAR_CHR4_9809044	VAR_CHR4_9818215
VAR_CHR4_10405136	VAR_CHR4_10449194	VAR_CHR4_10494255	VAR_CHR4_9780254	VAR_CHR4_9788415	VAR_CHR4_9799396	VAR_CHR4_9809214	VAR_CHR4_9818354
VAR_CHR4_10405173	VAR_CHR4_10450401	VAR_CHR4_10494411	VAR_CHR4_9780426	VAR_CHR4_9788426	VAR_CHR4_9799421	VAR_CHR4_9809257	VAR_CHR4_9818891
VAR_CHR4_10405517	VAR_CHR4_10452338	VAR_CHR4_9452283	VAR_CHR4_9780736	VAR_CHR4_9788572	VAR_CHR4_9800131	VAR_CHR4_9809634	VAR_CHR4_9819000
VAR_CHR4_10406139	VAR_CHR4_10452407	VAR_CHR4_9772858	VAR_CHR4_9780762	VAR_CHR4_9788597	VAR_CHR4_9800445	VAR_CHR4_9809891	VAR_CHR4_9819301
VAR_CHR4_10417237	VAR_CHR4_10453269	VAR_CHR4_9773205	VAR_CHR4_9781428	VAR_CHR4_9788642	VAR_CHR4_9800514	VAR_CHR4_9810265	VAR_CHR4_9819361
VAR_CHR4_10417345	VAR_CHR4_10453388	VAR_CHR4_9773445	VAR_CHR4_9781498	VAR_CHR4_9789019	VAR_CHR4_9800539	VAR_CHR4_9810620	VAR_CHR4_9819397
VAR_CHR4_10417361	VAR_CHR4_10453670	VAR_CHR4_9773451	VAR_CHR4_9781524	VAR_CHR4_9789484	VAR_CHR4_9800697	VAR_CHR4_9810630	VAR_CHR4_9819765
VAR_CHR4_10417909	VAR_CHR4_10453772	VAR_CHR4_9773648	VAR_CHR4_9781557	VAR_CHR4_9789756	VAR_CHR4_9801071	VAR_CHR4_9810636	VAR_CHR4_9819831
VAR_CHR4_10418059	VAR_CHR4_10453952	VAR_CHR4_9773780	VAR_CHR4_9781574	VAR_CHR4_9790201	VAR_CHR4_9801099	VAR_CHR4_9810893	VAR_CHR4_9820085
VAR_CHR4_10418250	VAR_CHR4_10454160	VAR_CHR4_9773989	VAR_CHR4_9781596	VAR_CHR4_9790297	VAR_CHR4_9801308	VAR_CHR4_9811097	VAR_CHR4_9820217
VAR_CHR4_10419685	VAR_CHR4_10454161	VAR_CHR4_9774015	VAR_CHR4_9781708	VAR_CHR4_9790849	VAR_CHR4_9801311	VAR_CHR4_9811132	VAR_CHR4_9820317
VAR_CHR4_10419694	VAR_CHR4_10454329	VAR_CHR4_9774080	VAR_CHR4_9781971	VAR_CHR4_9791090	VAR_CHR4_9801485	VAR_CHR4_9811531	VAR_CHR4_9820440
VAR_CHR4_10419831	VAR_CHR4_10456357	VAR_CHR4_9774158	VAR_CHR4_9782087	VAR_CHR4_9791175	VAR_CHR4_9801915	VAR_CHR4_9811999	VAR_CHR4_9820768
VAR_CHR4_10423845	VAR_CHR4_10456489	VAR_CHR4_9774305	VAR_CHR4_9782173	VAR_CHR4_9791312	VAR_CHR4_9801949	VAR_CHR4_9812199	VAR_CHR4_9820931
VAR_CHR4_10424123	VAR_CHR4_10456614	VAR_CHR4_9774381	VAR_CHR4_9782250	VAR_CHR4_9791672	VAR_CHR4_9802572	VAR_CHR4_9812284	VAR_CHR4_9821265
VAR_CHR4_10424177	VAR_CHR4_10456669	VAR_CHR4_9774453	VAR_CHR4_9782587	VAR_CHR4_9791696	VAR_CHR4_9802829	VAR_CHR4_9812331	VAR_CHR4_9821517
VAR_CHR4_10441131	VAR_CHR4_10457389	VAR_CHR4_9774859	VAR_CHR4_9782641	VAR_CHR4_9791907	VAR_CHR4_9803145	VAR_CHR4_9812425	VAR_CHR4_9821667
VAR_CHR4_10441853	VAR_CHR4_10457448	VAR_CHR4_9775144	VAR_CHR4_9782858	VAR_CHR4_9792384	VAR_CHR4_9803240	VAR_CHR4_9812494	VAR_CHR4_9821801
VAR_CHR4_10442363	VAR_CHR4_10457866	VAR_CHR4_9775280	VAR_CHR4_9782860	VAR_CHR4_9792397	VAR_CHR4_9803372	VAR_CHR4_9812857	VAR_CHR4_9821866
VAR_CHR4_10443042	VAR_CHR4_10458085	VAR_CHR4_9775910	VAR_CHR4_9783410	VAR_CHR4_9792990	VAR_CHR4_9803905	VAR_CHR4_9812935	VAR_CHR4_9822078
VAR_CHR4_9822342	VAR_CHR4_9835189	VAR_CHR4_9845218	VAR_CHR4_9857040	VAR_CHR4_9868674	VAR_CHR4_9878824	VAR_CHR4_9890105	VAR_CHR4_9900625
VAR_CHR4_9822546	VAR_CHR4_9835331	VAR_CHR4_9845416	VAR_CHR4_9858711	VAR_CHR4_9868703	VAR_CHR4_9878889	VAR_CHR4_9890126	VAR_CHR4_9900703
VAR_CHR4_9822599	VAR_CHR4_9835429	VAR_CHR4_9845810	VAR_CHR4_9858951	VAR_CHR4_9869240	VAR_CHR4_9878969	VAR_CHR4_9890504	VAR_CHR4_9900708
VAR_CHR4_9822768	VAR_CHR4_9835881	VAR_CHR4_9845920	VAR_CHR4_9859586	VAR_CHR4_9869363	VAR_CHR4_9879333	VAR_CHR4_9890807	VAR_CHR4_9900829

VAR_CHR4_9822949	VAR_CHR4_9836154	VAR_CHR4_9846069	VAR_CHR4_9860342	VAR_CHR4_9869371	VAR_CHR4_9879480	VAR_CHR4_9891209	VAR_CHR4_9901020
VAR_CHR4_9823497	VAR_CHR4_9836187	VAR_CHR4_9846302	VAR_CHR4_9860397	VAR_CHR4_9869452	VAR_CHR4_9879706	VAR_CHR4_9891341	VAR_CHR4_9901322
VAR_CHR4_9823832	VAR_CHR4_9836725	VAR_CHR4_9846358	VAR_CHR4_9861350	VAR_CHR4_9869688	VAR_CHR4_9879725	VAR_CHR4_9891391	VAR_CHR4_9901756
VAR_CHR4_9824612	VAR_CHR4_9836811	VAR_CHR4_9847617	VAR_CHR4_9861511	VAR_CHR4_9869792	VAR_CHR4_9879765	VAR_CHR4_9892112	VAR_CHR4_9902078
VAR_CHR4_9824801	VAR_CHR4_9836850	VAR_CHR4_9848077	VAR_CHR4_9861969	VAR_CHR4_9869793	VAR_CHR4_9880329	VAR_CHR4_9892341	VAR_CHR4_9902136
VAR_CHR4_9826725	VAR_CHR4_9837110	VAR_CHR4_9848486	VAR_CHR4_9862293	VAR_CHR4_9870323	VAR_CHR4_9880350	VAR_CHR4_9892557	VAR_CHR4_9902284
VAR_CHR4_9826893	VAR_CHR4_9837290	VAR_CHR4_9849153	VAR_CHR4_9862531	VAR_CHR4_9870375	VAR_CHR4_9880434	VAR_CHR4_9893294	VAR_CHR4_9903086
VAR_CHR4_9827024	VAR_CHR4_9837975	VAR_CHR4_9849158	VAR_CHR4_9862769	VAR_CHR4_9870703	VAR_CHR4_9880475	VAR_CHR4_9893455	VAR_CHR4_9903160
VAR_CHR4_9827025	VAR_CHR4_9838322	VAR_CHR4_9849201	VAR_CHR4_9862770	VAR_CHR4_9870875	VAR_CHR4_9881090	VAR_CHR4_9893519	VAR_CHR4_9903385
VAR_CHR4_9827300	VAR_CHR4_9838332	VAR_CHR4_9849507	VAR_CHR4_9862847	VAR_CHR4_9871094	VAR_CHR4_9881258	VAR_CHR4_9893569	VAR_CHR4_9903441
VAR_CHR4_9827387	VAR_CHR4_9838463	VAR_CHR4_9849767	VAR_CHR4_9862934	VAR_CHR4_9871225	VAR_CHR4_9881520	VAR_CHR4_9893794	VAR_CHR4_9903519
VAR_CHR4_9827885	VAR_CHR4_9838487	VAR_CHR4_9849913	VAR_CHR4_9863414	VAR_CHR4_9871637	VAR_CHR4_9881663	VAR_CHR4_9894041	VAR_CHR4_9903619
VAR_CHR4_9828379	VAR_CHR4_9838531	VAR_CHR4_9850318	VAR_CHR4_9864212	VAR_CHR4_9871779	VAR_CHR4_9881815	VAR_CHR4_9894638	VAR_CHR4_9903894
VAR_CHR4_9829400	VAR_CHR4_9838642	VAR_CHR4_9850347	VAR_CHR4_9864318	VAR_CHR4_9872108	VAR_CHR4_9881972	VAR_CHR4_9894773	VAR_CHR4_9903964
VAR_CHR4_9829624	VAR_CHR4_9838673	VAR_CHR4_9850380	VAR_CHR4_9864633	VAR_CHR4_9872400	VAR_CHR4_9882111	VAR_CHR4_9895032	VAR_CHR4_9904012
VAR_CHR4_9829755	VAR_CHR4_9838948	VAR_CHR4_9850578	VAR_CHR4_9865038	VAR_CHR4_9872474	VAR_CHR4_9882284	VAR_CHR4_9895163	VAR_CHR4_9904197
VAR_CHR4_9830007	VAR_CHR4_9838966	VAR_CHR4_9850673	VAR_CHR4_9865290	VAR_CHR4_9872518	VAR_CHR4_9882545	VAR_CHR4_9895378	VAR_CHR4_9904572
VAR_CHR4_9830150	VAR_CHR4_9839412	VAR_CHR4_9850902	VAR_CHR4_9865321	VAR_CHR4_9872881	VAR_CHR4_9882591	VAR_CHR4_9895586	VAR_CHR4_9905184
VAR_CHR4_9830364	VAR_CHR4_9839976	VAR_CHR4_9850978	VAR_CHR4_9865827	VAR_CHR4_9873058	VAR_CHR4_9882651	VAR_CHR4_9895868	VAR_CHR4_9905356
VAR_CHR4_9830433	VAR_CHR4_9839977	VAR_CHR4_9851548	VAR_CHR4_9865924	VAR_CHR4_9873341	VAR_CHR4_9882885	VAR_CHR4_9895935	VAR_CHR4_9905869
VAR_CHR4_9830475	VAR_CHR4_9841533	VAR_CHR4_9851551	VAR_CHR4_9866183	VAR_CHR4_9873494	VAR_CHR4_9884450	VAR_CHR4_9896752	VAR_CHR4_9906000
VAR_CHR4_9830556	VAR_CHR4_9841568	VAR_CHR4_9851651	VAR_CHR4_9866481	VAR_CHR4_9873542	VAR_CHR4_9884477	VAR_CHR4_9896762	VAR_CHR4_9907381
VAR_CHR4_9830596	VAR_CHR4_9841760	VAR_CHR4_9852167	VAR_CHR4_9866509	VAR_CHR4_9873782	VAR_CHR4_9884985	VAR_CHR4_9897112	VAR_CHR4_9907574
VAR_CHR4_9832351	VAR_CHR4_9842036	VAR_CHR4_9852703	VAR_CHR4_9866514	VAR_CHR4_9873997	VAR_CHR4_9885139	VAR_CHR4_9897304	VAR_CHR4_9907823
VAR_CHR4_9832475	VAR_CHR4_9842089	VAR_CHR4_9852735	VAR_CHR4_9866553	VAR_CHR4_9874509	VAR_CHR4_9885978	VAR_CHR4_9897390	VAR_CHR4_9907872
VAR_CHR4_9832858	VAR_CHR4_9842261	VAR_CHR4_9852768	VAR_CHR4_9867245	VAR_CHR4_9874890	VAR_CHR4_9887385	VAR_CHR4_9897526	VAR_CHR4_9907897
VAR_CHR4_9832954	VAR_CHR4_9842490	VAR_CHR4_9852829	VAR_CHR4_9867318	VAR_CHR4_9875526	VAR_CHR4_9887517	VAR_CHR4_9897630	VAR_CHR4_9908332
VAR_CHR4_9833092	VAR_CHR4_9842934	VAR_CHR4_9853675	VAR_CHR4_9867329	VAR_CHR4_9875710	VAR_CHR4_9887739	VAR_CHR4_9898455	VAR_CHR4_9909251
VAR_CHR4_9833308	VAR_CHR4_9843168	VAR_CHR4_9855182	VAR_CHR4_9867433	VAR_CHR4_9875994	VAR_CHR4_9887904	VAR_CHR4_9898608	VAR_CHR4_9909425
VAR_CHR4_9833322	VAR_CHR4_9843432	VAR_CHR4_9855799	VAR_CHR4_9867456	VAR_CHR4_9876107	VAR_CHR4_9887935	VAR_CHR4_9898665	VAR_CHR4_9909434
VAR_CHR4_9833565	VAR_CHR4_9843585	VAR_CHR4_9855919	VAR_CHR4_9867498	VAR_CHR4_9876360	VAR_CHR4_9888444	VAR_CHR4_9899429	VAR_CHR4_9909581
VAR_CHR4_9833833	VAR_CHR4_9843809	VAR_CHR4_9855954	VAR_CHR4_9867758	VAR_CHR4_9877686	VAR_CHR4_9888765	VAR_CHR4_9899660	VAR_CHR4_9910575
VAR_CHR4_9833913	VAR_CHR4_9844131	VAR_CHR4_9855973	VAR_CHR4_9868026	VAR_CHR4_9877721	VAR_CHR4_9889065	VAR_CHR4_9899749	VAR_CHR4_9910717
VAR_CHR4_9834226	VAR_CHR4_9844345	VAR_CHR4_9856370	VAR_CHR4_9868079	VAR_CHR4_9878048	VAR_CHR4_9889420	VAR_CHR4_9900157	VAR_CHR4_9910733
VAR_CHR4_9834424	VAR_CHR4_9844688	VAR_CHR4_9856788	VAR_CHR4_9868194	VAR_CHR4_9878436	VAR_CHR4_9889900	VAR_CHR4_9900342	VAR_CHR4_9911525
VAR_CHR4_9835156	VAR_CHR4_9845082	VAR_CHR4_9856797	VAR_CHR4_9868615	VAR_CHR4_9878726	VAR_CHR4_9890046	VAR_CHR4_9900526	VAR_CHR4_9911543
VAR_CHR4_9911595	VAR_CHR4_9924430	VAR_CHR4_9936141	VAR_CHR4_9947406	VAR_CHR4_9958761	VAR_CHR4_9971939	VAR_CHR4_9983747	VAR_CHR4_9999412

VAR_CHR4_9911720	VAR_CHR4_9924780	VAR_CHR4_9937429	VAR_CHR4_9947625	VAR_CHR4_9958986	VAR_CHR4_9972281	VAR_CHR4_9983888	VAR_CHR4_9999449
VAR_CHR4_9912036	VAR_CHR4_9925280	VAR_CHR4_9937774	VAR_CHR4_9947693	VAR_CHR4_9959310	VAR_CHR4_9973684	VAR_CHR4_9983996	VAR_CHR4_9999978
VAR_CHR4_9912397	VAR_CHR4_9925436	VAR_CHR4_9938021	VAR_CHR4_9947728	VAR_CHR4_9960394	VAR_CHR4_9973695	VAR_CHR4_9984415	
VAR_CHR4_9912605	VAR_CHR4_9925784	VAR_CHR4_9938424	VAR_CHR4_9947838	VAR_CHR4_9960643	VAR_CHR4_9974002	VAR_CHR4_9984495	
VAR_CHR4_9912897	VAR_CHR4_9925944	VAR_CHR4_9938551	VAR_CHR4_9948140	VAR_CHR4_9960707	VAR_CHR4_9974022	VAR_CHR4_9984543	
VAR_CHR4_9913311	VAR_CHR4_9926218	VAR_CHR4_9938599	VAR_CHR4_9948358	VAR_CHR4_9960762	VAR_CHR4_9974178	VAR_CHR4_9984788	
VAR_CHR4_9913353	VAR_CHR4_9926480	VAR_CHR4_9938713	VAR_CHR4_9949014	VAR_CHR4_9961958	VAR_CHR4_9974329	VAR_CHR4_9984843	
VAR_CHR4_9913557	VAR_CHR4_9926525	VAR_CHR4_9938866	VAR_CHR4_9949140	VAR_CHR4_9961960	VAR_CHR4_9974584	VAR_CHR4_9984889	
VAR_CHR4_9914056	VAR_CHR4_9927317	VAR_CHR4_9938997	VAR_CHR4_9949563	VAR_CHR4_9962079	VAR_CHR4_9977628	VAR_CHR4_9984971	
VAR_CHR4_9914631	VAR_CHR4_9927949	VAR_CHR4_9939553	VAR_CHR4_9949633	VAR_CHR4_9962592	VAR_CHR4_9977748	VAR_CHR4_9985652	
VAR_CHR4_9915389	VAR_CHR4_9928106	VAR_CHR4_9939574	VAR_CHR4_9950247	VAR_CHR4_9962807	VAR_CHR4_9977797	VAR_CHR4_9986164	
VAR_CHR4_9915532	VAR_CHR4_9928560	VAR_CHR4_9940175	VAR_CHR4_9950432	VAR_CHR4_9962831	VAR_CHR4_9978151	VAR_CHR4_9986597	
VAR_CHR4_9915853	VAR_CHR4_9928582	VAR_CHR4_9940567	VAR_CHR4_9950527	VAR_CHR4_9964348	VAR_CHR4_9978225	VAR_CHR4_9988213	
VAR_CHR4_9915880	VAR_CHR4_9929036	VAR_CHR4_9940859	VAR_CHR4_9951069	VAR_CHR4_9965134	VAR_CHR4_9978283	VAR_CHR4_9989486	
VAR_CHR4_9916249	VAR_CHR4_9929476	VAR_CHR4_9941195	VAR_CHR4_9951547	VAR_CHR4_9965721	VAR_CHR4_9978293	VAR_CHR4_9989861	
VAR_CHR4_9916451	VAR_CHR4_9929726	VAR_CHR4_9941301	VAR_CHR4_9951779	VAR_CHR4_9965736	VAR_CHR4_9978395	VAR_CHR4_9990575	
VAR_CHR4_9916712	VAR_CHR4_9930137	VAR_CHR4_9941689	VAR_CHR4_9951821	VAR_CHR4_9965826	VAR_CHR4_9978702	VAR_CHR4_9990810	
VAR_CHR4_9916833	VAR_CHR4_9930171	VAR_CHR4_9942352	VAR_CHR4_9951999	VAR_CHR4_9965912	VAR_CHR4_9979148	VAR_CHR4_9991236	
VAR_CHR4_9917208	VAR_CHR4_9930208	VAR_CHR4_9942538	VAR_CHR4_9952001	VAR_CHR4_9966361	VAR_CHR4_9979570	VAR_CHR4_9991626	
VAR_CHR4_9917336	VAR_CHR4_9930328	VAR_CHR4_9942578	VAR_CHR4_9952982	VAR_CHR4_9966448	VAR_CHR4_9979807	VAR_CHR4_9992098	
VAR_CHR4_9917489	VAR_CHR4_9930620	VAR_CHR4_9942665	VAR_CHR4_9954426	VAR_CHR4_9967330	VAR_CHR4_9979938	VAR_CHR4_9992359	
VAR_CHR4_9917672	VAR_CHR4_9930717	VAR_CHR4_9942691	VAR_CHR4_9954919	VAR_CHR4_9967568	VAR_CHR4_9979995	VAR_CHR4_9992478	
VAR_CHR4_9917789	VAR_CHR4_9931480	VAR_CHR4_9943064	VAR_CHR4_9954931	VAR_CHR4_9967589	VAR_CHR4_9980539	VAR_CHR4_9992735	
VAR_CHR4_9917944	VAR_CHR4_9931512	VAR_CHR4_9943262	VAR_CHR4_9954973	VAR_CHR4_9967695	VAR_CHR4_9980942	VAR_CHR4_9992808	
VAR_CHR4_9918331	VAR_CHR4_9932301	VAR_CHR4_9943306	VAR_CHR4_9955130	VAR_CHR4_9968774	VAR_CHR4_9981025	VAR_CHR4_9993138	
VAR_CHR4_9918424	VAR_CHR4_9932565	VAR_CHR4_9943731	VAR_CHR4_9955248	VAR_CHR4_9969043	VAR_CHR4_9981113	VAR_CHR4_9993326	
VAR_CHR4_9918678	VAR_CHR4_9932738	VAR_CHR4_9944094	VAR_CHR4_9955750	VAR_CHR4_9969156	VAR_CHR4_9981135	VAR_CHR4_9995119	
VAR_CHR4_9918968	VAR_CHR4_9932840	VAR_CHR4_9944374	VAR_CHR4_9955857	VAR_CHR4_9969218	VAR_CHR4_9981262	VAR_CHR4_9995139	
VAR_CHR4_9920278	VAR_CHR4_9932951	VAR_CHR4_9944414	VAR_CHR4_9956093	VAR_CHR4_9969230	VAR_CHR4_9981302	VAR_CHR4_9995520	
VAR_CHR4_9920579	VAR_CHR4_9932979	VAR_CHR4_9944535	VAR_CHR4_9956210	VAR_CHR4_9970123	VAR_CHR4_9981322	VAR_CHR4_9995999	
VAR_CHR4_9921175	VAR_CHR4_9933501	VAR_CHR4_9945179	VAR_CHR4_9956249	VAR_CHR4_9970562	VAR_CHR4_9981412	VAR_CHR4_9996140	
VAR_CHR4_9921310	VAR_CHR4_9933877	VAR_CHR4_9946259	VAR_CHR4_9956572	VAR_CHR4_9970825	VAR_CHR4_9981457	VAR_CHR4_9996377	
VAR_CHR4_9921328	VAR_CHR4_9934112	VAR_CHR4_9946407	VAR_CHR4_9957248	VAR_CHR4_9970860	VAR_CHR4_9981528	VAR_CHR4_9996737	
VAR_CHR4_9921348	VAR_CHR4_9934731	VAR_CHR4_9946797	VAR_CHR4_9957376	VAR_CHR4_9970941	VAR_CHR4_9981647	VAR_CHR4_9997215	
VAR_CHR4_9921368	VAR_CHR4_9935236	VAR_CHR4_9946890	VAR_CHR4_9958239	VAR_CHR4_9971133	VAR_CHR4_9981924	VAR_CHR4_9997579	
VAR_CHR4_9922053	VAR_CHR4_9935896	VAR_CHR4_9946949	VAR_CHR4_9958340	VAR_CHR4_9971141	VAR_CHR4_9982643	VAR_CHR4_9997757	
VAR_CHR4_9922730	VAR_CHR4_9935948	VAR_CHR4_9946960	VAR_CHR4_9958357	VAR_CHR4_9971179	VAR_CHR4_9983219	VAR_CHR4_9997820	

VAR_CHR4_9922796	VAR_CHR4_9936024	VAR_CHR4_9947167	VAR_CHR4_9958380	VAR_CHR4_9971567	VAR_CHR4_9983310	VAR_CHR4_9998103
VAR_CHR4_9924200	VAR_CHR4_9936139	VAR_CHR4_9947201	VAR_CHR4_9958526	VAR_CHR4_9971846	VAR_CHR4_9983694	VAR_CHR4_9998194

APPENDIX 2
VARIANT ANNOTATIONS

VARIANT	CHROMOSOME	POSITION	ALLELE	GENE	PREDICTED CONSEQUENCE	IMPACT	CADD_RAW	CADD_PHRED	GWAVA SCORE
RS28650494	4	9446207	A	DEFB131A	upstream_gene_variant	MODIFIER	0.038262	2.963	0.52
RS187463212	4	9446234	C	DEFB131A	upstream_gene_variant	MODIFIER	-	-	0.54
RS28373658	4	9452222	T	DEFB131A	synonymous_variant	LOW	0.003625	2.621	0.25
RS369702220	4	9452223	T	DEFB131A	stop_gained	HIGH	7.400551	34	-
RS28583524	4	9452272	T	DEFB131A	downstream_gene_variant	MODIFIER	-0.156186	1.348	0.32
VAR_CHR4_9452283	4	9452283	T	DEFB131A	downstream_gene_variant	MODIFIER	-	-	-
VAR_CHR4_9772858	4	9772858	T	-	regulatory_region_variant	MODIFIER	-0.470092	0.261	-
RS182846929	4	9773013	C	-	regulatory_region_variant	MODIFIER	-0.270248	0.775	0.11
RS10939514	4	9773196	G	-	regulatory_region_variant	MODIFIER	-0.345543	0.521	0.18
VAR_CHR4_9773205	4	9773205	C	-	intergenic_variant	MODIFIER	-0.368046	0.461	-
RS13124141	4	9773237	C	-	intergenic_variant	MODIFIER	-0.276654	0.75	0.26
RS13124305	4	9773273	C	-	intergenic_variant	MODIFIER	-0.528775	0.187	0.23
RS10939515	4	9773296	T	-	intergenic_variant	MODIFIER	-0.523556	0.192	0.22
RS73221597	4	9773354	T	-	intergenic_variant	MODIFIER	-0.184661	1.181	0.16
RS10022923	4	9773438	C	-	intergenic_variant	MODIFIER	-0.517925	0.198	0.12
VAR_CHR4_9773445	4	9773445	C	-	intergenic_variant	MODIFIER	-	-	-
RS58847608	4	9773449	G	-	intergenic_variant	MODIFIER	-0.304695	0.648	0.14
VAR_CHR4_9773451	4	9773451	T	-	intergenic_variant	MODIFIER	-0.045541	2.17	-
RS374015639	4	9773484	T	-	intergenic_variant	MODIFIER	0.674878	8.662	-

RS149628125	4	9773594	C	-	intergenic_variant	MODIFIER	-0.258522	0.822	0.2
VAR_CHR4_9773648	4	9773648	A	-	intergenic_variant	MODIFIER	-0.3276	0.574	-
VAR_CHR4_9773780	4	9773780	T	-	intergenic_variant	MODIFIER	-0.499202	0.221	-
VAR_CHR4_9773989	4	9773989	A	-	intergenic_variant	MODIFIER	0.140367	4.042	-
VAR_CHR4_9774015	4	9774015	T	-	intergenic_variant	MODIFIER	-0.181368	1.2	-
VAR_CHR4_9774080	4	9774080	G	-	intergenic_variant	MODIFIER	-	-	-
RS62293224	4	9774138	C	-	intergenic_variant	MODIFIER	-0.908961	0.025	0.32
VAR_CHR4_9774158	4	9774158	T	-	intergenic_variant	MODIFIER	-0.177478	1.222	-
VAR_CHR4_9774305	4	9774305	G	-	intergenic_variant	MODIFIER	-0.255757	0.834	-
RS189350135	4	9774329	C	-	intergenic_variant	MODIFIER	-	-	0.33
RS28523967	4	9774354	T	-	intergenic_variant	MODIFIER	-0.317845	0.605	0.35
VAR_CHR4_9774381	4	9774381	T	-	intergenic_variant	MODIFIER	-0.37068	0.455	-
VAR_CHR4_9774453	4	9774453	T	-	intergenic_variant	MODIFIER	-	-	-
RS376685079	4	9774537	T	-	intergenic_variant	MODIFIER	-0.468297	0.263	-
RS3973946	4	9774688	C	-	intergenic_variant	MODIFIER	-0.328035	0.573	0.22
VAR_CHR4_9774859	4	9774859	G	-	intergenic_variant	MODIFIER	-	-	-
RS191394302	4	9774929	G	-	intergenic_variant	MODIFIER	0.173862	4.402	0.23
RS146473160	4	9774995	T	-	intergenic_variant	MODIFIER	-0.211495	1.038	0.41
VAR_CHR4_9775144	4	9775144	C	-	intergenic_variant	MODIFIER	-0.475024	0.253	-
VAR_CHR4_9775280	4	9775280	G	-	intergenic_variant	MODIFIER	-	-	-
RS183659377	4	9775562	A	-	intergenic_variant	MODIFIER	0.083919	3.437	0.48
RS76617595	4	9775585	A	-	intergenic_variant	MODIFIER	0.094132	3.545	0.37
VAR_CHR4_9775910	4	9775910	G	-	intergenic_variant	MODIFIER	-0.070156	1.962	-
RS112183422	4	9775977	C	-	intergenic_variant	MODIFIER	-0.572712	0.146	0.44
RS28413933	4	9775991	G	-	intergenic_variant	MODIFIER	-0.603651	0.122	0.37
RS368251638	4	9776006	A	-	intergenic_variant	MODIFIER	0.712765	8.91	-

VAR_CHR4_9776029	4	9776029	C	-	intergenic_variant	MODIFIER	-0.248095	0.867	-
VAR_CHR4_9776141	4	9776141	T	-	intergenic_variant	MODIFIER	-0.519812	0.196	-
VAR_CHR4_9776301	4	9776301	G	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_9776417	4	9776417	C	-	intergenic_variant	MODIFIER	-0.583562	0.137	-
RS184808273	4	9776444	G	-	intergenic_variant	MODIFIER	-0.671689	0.084	0.37
VAR_CHR4_9776494	4	9776494	A	-	intergenic_variant	MODIFIER	0.221496	4.904	-
RS369731453	4	9776509	A	-	intergenic_variant	MODIFIER	0.045786	3.04	-
VAR_CHR4_9776538	4	9776538	G	-	intergenic_variant	MODIFIER	-0.090071	1.805	-
RS4516717	4	9776653	C	-	intergenic_variant	MODIFIER	-0.386914	0.416	0.34
RS142021630	4	9776684	A	-	intergenic_variant	MODIFIER	-0.187589	1.165	0.39
RS55723889	4	9776966	G	-	intergenic_variant	MODIFIER	-0.150619	1.383	0.37
RS56095448	4	9776967	G	-	intergenic_variant	MODIFIER	-0.151968	1.375	0.41
VAR_CHR4_9776972	4	9776972	C	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_9777182	4	9777182	C	-	intergenic_variant	MODIFIER	-	-	-
RS12507861	4	9777590	C	-	intergenic_variant	MODIFIER	-0.584444	0.136	0.16
RS62293226	4	9777660	T	-	intergenic_variant	MODIFIER	-0.741178	0.058	0.14
RS6815039	4	9777809	A	-	intergenic_variant	MODIFIER	0.052514	3.109	0.4
VAR_CHR4_9777922	4	9777922	G	-	intergenic_variant	MODIFIER	-0.139754	1.453	-
RS73221599	4	9777970	C	-	intergenic_variant	MODIFIER	-	-	0.32
RS57136958	4	9777971	T	-	intergenic_variant	MODIFIER	-0.693366	0.075	0.29
RS191474189	4	9778059	A	-	intergenic_variant	MODIFIER	-0.143064	1.431	0.17
VAR_CHR4_9778122	4	9778122	T	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_9778272	4	9778272	G	DRD5	upstream_gene_variant	MODIFIER	-0.24204	0.893	-
RS2030287	4	9778301	C	DRD5	upstream_gene_variant	MODIFIER	-0.552957	0.163	0.31
RS187804802	4	9778337	C	DRD5	upstream_gene_variant	MODIFIER	-0.117291	1.605	0.42
VAR_CHR4_9778338	4	9778338	A	DRD5	upstream_gene_variant	MODIFIER	0.216799	4.855	-

VAR_CHR4_9778431	4	9778431	T	DRD5	upstream_gene_variant	MODIFIER	-0.152223	1.373	-
RS139180190	4	9778503	A	DRD5	upstream_gene_variant	MODIFIER	0.265264	5.351	0.29
RS61166583	4	9778530	T	DRD5	upstream_gene_variant	MODIFIER	0.508019	7.492	0.2
VAR_CHR4_9778565	4	9778565	G	DRD5	upstream_gene_variant	MODIFIER	0.339002	6.065	-
VAR_CHR4_9778719	4	9778719	G	DRD5	upstream_gene_variant	MODIFIER	0.012191	2.704	-
RS185256774	4	9778722	A	DRD5	upstream_gene_variant	MODIFIER	0.167306	4.332	0.37
RS114688202	4	9778815	T	DRD5	upstream_gene_variant	MODIFIER	-0.676438	0.082	0.27
RS6835741	4	9778911	C	DRD5	upstream_gene_variant	MODIFIER	-0.751946	0.055	0.43
RS115490896	4	9779072	A	DRD5	upstream_gene_variant	MODIFIER	0.129618	3.926	0.36
RS192874676	4	9779118	A	DRD5	upstream_gene_variant	MODIFIER	-0.099924	1.731	0.31
VAR_CHR4_9779148	4	9779148	T	DRD5	upstream_gene_variant	MODIFIER	-0.246235	0.875	-
VAR_CHR4_9779258	4	9779258	A	DRD5	upstream_gene_variant	MODIFIER	-0.375838	0.442	-
RS114407557	4	9779357	G	DRD5	upstream_gene_variant	MODIFIER	-	-	0.29
RS13129974	4	9779526	C	DRD5	upstream_gene_variant	MODIFIER	-0.324096	0.585	0.25
RS181030592	4	9779579	A	DRD5	upstream_gene_variant	MODIFIER	0.267304	5.371	0.28
RS10033951	4	9779580	A	DRD5	upstream_gene_variant	MODIFIER	0.288409	5.581	0.28
RS9685502	4	9779636	C	DRD5	upstream_gene_variant	MODIFIER	-0.681911	0.079	0.19
VAR_CHR4_9779986	4	9779986	A	DRD5	upstream_gene_variant	MODIFIER	-0.051046	2.122	-
VAR_CHR4_9780010	4	9780010	T	DRD5	upstream_gene_variant	MODIFIER	-0.037526	2.24	-
VAR_CHR4_9780038	4	9780038	T	DRD5	upstream_gene_variant	MODIFIER	-0.072344	1.945	-
RS7657127	4	9780078	G	DRD5	upstream_gene_variant	MODIFIER	-0.444195	0.302	0.22
VAR_CHR4_9780254	4	9780254	A	DRD5	upstream_gene_variant	MODIFIER	0.496586	7.405	-
RS182222566	4	9780321	A	DRD5	upstream_gene_variant	MODIFIER	0.079953	3.395	0.33
VAR_CHR4_9780426	4	9780426	T	DRD5	upstream_gene_variant	MODIFIER	-0.414429	0.357	-
VAR_CHR4_9780736	4	9780736	A	DRD5	upstream_gene_variant	MODIFIER	-	-	-
VAR_CHR4_9780762	4	9780762	T	DRD5	upstream_gene_variant	MODIFIER	-0.002763	2.56	-

VAR_CHR4_9781428	4	9781428	G	DRD5	upstream_gene_variant	MODIFIER	0.208609	4.77	-
VAR_CHR4_9781498	4	9781498	C	DRD5	upstream_gene_variant	MODIFIER	-0.049105	2.139	-
RS78876648	4	9781516	A	DRD5	upstream_gene_variant	MODIFIER	-0.102224	1.714	0.32
VAR_CHR4_9781524	4	9781524	G	DRD5	upstream_gene_variant	MODIFIER	0.168498	4.344	-
VAR_CHR4_9781557	4	9781557	G	DRD5	upstream_gene_variant	MODIFIER	-	-	-
VAR_CHR4_9781574	4	9781574	A	DRD5	upstream_gene_variant	MODIFIER	0.205752	4.74	-
RS144974033	4	9781594	G	DRD5	upstream_gene_variant	MODIFIER	-0.153525	1.365	0.28
VAR_CHR4_9781596	4	9781596	T	DRD5	upstream_gene_variant	MODIFIER	-0.285845	0.715	-
RS181580893	4	9781625	T	DRD5	upstream_gene_variant	MODIFIER	-0.298807	0.668	0.38
VAR_CHR4_9781708	4	9781708	T	DRD5	upstream_gene_variant	MODIFIER	-0.112909	1.636	-
VAR_CHR4_9781971	4	9781971	G	DRD5	upstream_gene_variant	MODIFIER	-	-	-
RS34145578	4	9782030	A	DRD5	upstream_gene_variant	MODIFIER	0.383953	6.473	0.47
VAR_CHR4_9782087	4	9782087	T	DRD5	upstream_gene_variant	MODIFIER	-0.197591	1.111	-
RS182414296	4	9782134	T	DRD5	upstream_gene_variant	MODIFIER	-0.471783	0.258	0.44
RS77434921	4	9782163	T	DRD5	upstream_gene_variant	MODIFIER	-0.461073	0.274	0.47
VAR_CHR4_9782173	4	9782173	A	DRD5	upstream_gene_variant	MODIFIER	1.301046	12.27	-
VAR_CHR4_9782250	4	9782250	T	DRD5	upstream_gene_variant	MODIFIER	-0.06551	2.001	-
VAR_CHR4_9782587	4	9782587	A	DRD5	upstream_gene_variant	MODIFIER	-	-	-
VAR_CHR4_9782641	4	9782641	G	DRD5	upstream_gene_variant	MODIFIER	-	-	-
RS182556362	4	9782676	T	DRD5	upstream_gene_variant	MODIFIER	-0.483662	0.241	0.46
RS141443452	4	9782804	A	DRD5	upstream_gene_variant	MODIFIER	-	-	0.46
VAR_CHR4_9782858	4	9782858	G	DRD5	upstream_gene_variant	MODIFIER	-	-	-
VAR_CHR4_9782860	4	9782860	T	DRD5	upstream_gene_variant	MODIFIER	0.31075	5.797	-
RS183047359	4	9783060	T	DRD5	upstream_gene_variant	MODIFIER	0.122166	3.846	0.52
VAR_CHR4_9783410	4	9783410	A	DRD5	5_prime_UTR_variant	MODIFIER	0.520207	7.584	-
RS2076907	4	9783428	C	DRD5	5_prime_UTR_variant	MODIFIER	-0.340106	0.537	0.57

VAR_CHR4_9783597	4	9783597	T	DRD5	5_prime_UTR_variant	MODIFIER	-0.318666	0.602	-
VAR_CHR4_9783870	4	9783870	A	DRD5	missense_variant	MODERATE	2.288521	18.09	-
RS151282040	4	9783877	G	DRD5	missense_variant	MODERATE	4.417374	24.2	0.31
RS184288806	4	9783977	C	DRD5	synonymous_variant	LOW	-	-	0.43
RS6283	4	9784631	A	DRD5	synonymous_variant	LOW	1.407526	12.83	0.23
RS1800762	4	9784642	T	DRD5	missense_variant	MODERATE	-0.346965	0.518	0.18
RS145497708	4	9784658	T	DRD5	synonymous_variant	LOW	1.106392	11.25	0.21
RS6281	4	9784889	A	DRD5	missense_variant	MODERATE	-0.292398	0.691	0.16
VAR_CHR4_9784934	4	9784934	C	DRD5	synonymous_variant	LOW	-	-	-
RS1967551	4	9785134	A	DRD5	3_prime_UTR_variant	MODIFIER	-0.098016	1.745	0.25
VAR_CHR4_9785144	4	9785144	C	DRD5	3_prime_UTR_variant	MODIFIER	-	-	-
VAR_CHR4_9785203	4	9785203	T	DRD5	3_prime_UTR_variant	MODIFIER	0.023868	2.819	-
RS189072747	4	9785207	C	DRD5	3_prime_UTR_variant	MODIFIER	-0.111285	1.648	0.3
RS181467183	4	9785213	G	DRD5	3_prime_UTR_variant	MODIFIER	-	-	0.36
VAR_CHR4_9785240	4	9785240	T	DRD5	3_prime_UTR_variant	MODIFIER	-	-	-
VAR_CHR4_9785249	4	9785249	A	DRD5	3_prime_UTR_variant	MODIFIER	0.072666	3.318	-
RS1967550	4	9785265	C	DRD5	3_prime_UTR_variant	MODIFIER	0.078339	3.378	0.32
VAR_CHR4_9785350	4	9785350	T	DRD5	3_prime_UTR_variant	MODIFIER	-	-	-
VAR_CHR4_9785375	4	9785375	G	DRD5	3_prime_UTR_variant	MODIFIER	-	-	-
VAR_CHR4_9785539	4	9785539	T	DRD5	3_prime_UTR_variant	MODIFIER	-0.133	1.497	-
RS180936488	4	9785549	C	DRD5	3_prime_UTR_variant	MODIFIER	-	-	0.35
VAR_CHR4_9785577	4	9785577	G	DRD5	3_prime_UTR_variant	MODIFIER	0.138689	4.024	-
RS115323030	4	9786041	C	DRD5	downstream_gene_variant	MODIFIER	-0.248646	0.864	0.29
VAR_CHR4_9786343	4	9786343	C	DRD5	downstream_gene_variant	MODIFIER	-	-	-
VAR_CHR4_9786464	4	9786464	C	DRD5	downstream_gene_variant	MODIFIER	2.221357	17.65	-
RS62293240	4	9786486	A	DRD5	downstream_gene_variant	MODIFIER	0.733296	9.044	0.34

RS73805847	4	9786549	G	DRD5	downstream_gene_variant	MODIFIER	1.511828	13.38	0.32
VAR_CHR4_9786673	4	9786673	T	DRD5	downstream_gene_variant	MODIFIER	0.253773	5.235	-
VAR_CHR4_9786723	4	9786723	G	DRD5	downstream_gene_variant	MODIFIER	-	-	-
RS11726471	4	9786732	A	DRD5	downstream_gene_variant	MODIFIER	0.257293	5.271	0.35
VAR_CHR4_9786800	4	9786800	G	DRD5	downstream_gene_variant	MODIFIER	0.22641	4.955	-
VAR_CHR4_9786955	4	9786955	A	DRD5	downstream_gene_variant	MODIFIER	0.052973	3.113	-
RS146546936	4	9787290	A	DRD5	downstream_gene_variant	MODIFIER	0.200606	4.686	0.28
RS371721351	4	9787452	A	DRD5	downstream_gene_variant	MODIFIER	0.160821	4.262	-
VAR_CHR4_9787595	4	9787595	A	DRD5	downstream_gene_variant	MODIFIER	-0.550962	0.165	-
RS77269347	4	9787659	C	DRD5	downstream_gene_variant	MODIFIER	0.00356	2.62	0.2
VAR_CHR4_9787748	4	9787748	G	DRD5	downstream_gene_variant	MODIFIER	0.056743	3.152	-
RS116142041	4	9787836	T	DRD5	downstream_gene_variant	MODIFIER	-1.104129	0.01	0.27
RS141794302	4	9787859	A	DRD5	downstream_gene_variant	MODIFIER	0.093184	3.535	0.3
RS2867383	4	9787935	C	DRD5	downstream_gene_variant	MODIFIER	-0.21327	1.03	0.2
RS2903564	4	9787937	C	DRD5	downstream_gene_variant	MODIFIER	-0.323198	0.588	0.17
VAR_CHR4_9788390	4	9788390	A	DRD5	downstream_gene_variant	MODIFIER	-0.028944	2.317	-
VAR_CHR4_9788415	4	9788415	A	DRD5	downstream_gene_variant	MODIFIER	0.348465	6.152	-
VAR_CHR4_9788426	4	9788426	T	DRD5	downstream_gene_variant	MODIFIER	0.051693	3.1	-
RS10001006	4	9788498	A	DRD5	downstream_gene_variant	MODIFIER	-0.293094	0.689	0.19
RS186581711	4	9788553	T	DRD5	downstream_gene_variant	MODIFIER	-0.134061	1.49	0.17
VAR_CHR4_9788572	4	9788572	A	DRD5	downstream_gene_variant	MODIFIER	0.001214	2.598	-
VAR_CHR4_9788597	4	9788597	C	DRD5	downstream_gene_variant	MODIFIER	-	-	-
RS6842850	4	9788598	T	DRD5	downstream_gene_variant	MODIFIER	-0.147463	1.403	0.2
VAR_CHR4_9788642	4	9788642	C	DRD5	downstream_gene_variant	MODIFIER	-	-	-
RS115359730	4	9788894	A	DRD5	downstream_gene_variant	MODIFIER	-0.074025	1.931	0.25
VAR_CHR4_9789019	4	9789019	C	DRD5	downstream_gene_variant	MODIFIER	-0.731393	0.061	-

RS186927203	4	9789367	T	DRD5	downstream_gene_variant	MODIFIER	-0.255478	0.835	0.29
VAR_CHR4_9789484	4	9789484	T	DRD5	downstream_gene_variant	MODIFIER	-0.162489	1.31	-
RS56205495	4	9789501	A	DRD5	downstream_gene_variant	MODIFIER	-0.070418	1.96	0.3
RS146436740	4	9789568	G	DRD5	downstream_gene_variant	MODIFIER	0.303051	5.723	0.22
RS182179248	4	9789706	A	DRD5	downstream_gene_variant	MODIFIER	-	-	0.31
VAR_CHR4_9789756	4	9789756	T	DRD5	downstream_gene_variant	MODIFIER	-0.408137	0.37	-
RS138038869	4	9790199	A	DRD5	downstream_gene_variant	MODIFIER	1.014081	10.74	0.36
VAR_CHR4_9790201	4	9790201	T	DRD5	downstream_gene_variant	MODIFIER	0.721112	8.965	-
RS144876877	4	9790220	T	DRD5	downstream_gene_variant	MODIFIER	-	-	0.28
VAR_CHR4_9790297	4	9790297	T	DRD5	downstream_gene_variant	MODIFIER	0.547255	7.783	-
RS114734117	4	9790428	C	DRD5	downstream_gene_variant	MODIFIER	-0.154285	1.36	0.39
RS117005844	4	9790572	T	DRD5	downstream_gene_variant	MODIFIER	-0.232875	0.935	0.39
RS1850744	4	9790712	A	-	intergenic_variant	MODIFIER	-0.027566	2.329	0.28
VAR_CHR4_9790849	4	9790849	T	-	intergenic_variant	MODIFIER	0.818677	9.579	-
VAR_CHR4_9791090	4	9791090	T	-	intergenic_variant	MODIFIER	-0.205894	1.067	-
VAR_CHR4_9791175	4	9791175	G	-	intergenic_variant	MODIFIER	0.659612	8.56	-
RS6448996	4	9791254	C	-	intergenic_variant	MODIFIER	-0.445699	0.299	0.27
RS146190843	4	9791282	T	-	intergenic_variant	MODIFIER	-0.148175	1.398	0.31
VAR_CHR4_9791312	4	9791312	T	-	intergenic_variant	MODIFIER	0.216546	4.853	-
RS147999868	4	9791423	G	-	intergenic_variant	MODIFIER	-	-	0.46
RS188657256	4	9791467	T	-	intergenic_variant	MODIFIER	-	-	0.33
VAR_CHR4_9791672	4	9791672	C	-	intergenic_variant	MODIFIER	0.046066	3.042	-
VAR_CHR4_9791696	4	9791696	G	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_9791907	4	9791907	A	-	intergenic_variant	MODIFIER	0.37694	6.411	-
RS113017836	4	9792231	T	-	intergenic_variant	MODIFIER	-0.163003	1.307	0.21
RS1829413	4	9792339	C	-	intergenic_variant	MODIFIER	-0.389894	0.409	0.22

VAR_CHR4_9792384	4	9792384	T	-	intergenic_variant	MODIFIER	-0.143459	1.429	-
VAR_CHR4_9792397	4	9792397	A	-	intergenic_variant	MODIFIER	-	-	-
RS375121720	4	9792551	A	-	intergenic_variant	MODIFIER	-0.609985	0.118	-
VAR_CHR4_9792990	4	9792990	G	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_9793118	4	9793118	G	-	intergenic_variant	MODIFIER	-0.949795	0.02	-
RS28407807	4	9793241	A	-	intergenic_variant	MODIFIER	0.356579	6.227	0.24
VAR_CHR4_9793287	4	9793287	G	-	intergenic_variant	MODIFIER	0.005889	2.643	-
RS9685427	4	9793380	A	-	intergenic_variant	MODIFIER	0.400976	6.623	0.26
VAR_CHR4_9793397	4	9793397	T	-	intergenic_variant	MODIFIER	0.089002	3.491	-
VAR_CHR4_9793430	4	9793430	T	-	intergenic_variant	MODIFIER	-0.261683	0.809	-
RS143972829	4	9793515	T	-	intergenic_variant	MODIFIER	-0.088628	1.816	0.28
RS147305766	4	9793603	T	-	intergenic_variant	MODIFIER	-0.05116	2.121	0.19
VAR_CHR4_9793644	4	9793644	T	-	intergenic_variant	MODIFIER	0.700188	8.828	-
VAR_CHR4_9793795	4	9793795	G	-	intergenic_variant	MODIFIER	-0.331228	0.563	-
RS13118112	4	9794580	A	-	intergenic_variant	MODIFIER	0.138662	4.023	0.4
VAR_CHR4_9794647	4	9794647	A	-	intergenic_variant	MODIFIER	0.096564	3.571	-
RS7685396	4	9794724	G	-	intergenic_variant	MODIFIER	-0.079415	1.888	0.23
RS181755864	4	9794844	A	-	intergenic_variant	MODIFIER	-	-	0.25
VAR_CHR4_9794851	4	9794851	A	-	intergenic_variant	MODIFIER	0.943676	10.33	-
RS185677474	4	9794900	T	-	intergenic_variant	MODIFIER	-0.792008	0.045	0.24
VAR_CHR4_9794979	4	9794979	A	-	intergenic_variant	MODIFIER	-0.541662	0.173	-
VAR_CHR4_9795166	4	9795166	G	-	regulatory_region_variant	MODIFIER	0.136246	3.997	-
RS375526781	4	9795174	T	-	regulatory_region_variant	MODIFIER	-	-	-
VAR_CHR4_9795245	4	9795245	G	-	regulatory_region_variant	MODIFIER	0.255423	5.252	-
RS368534990	4	9795329	A	-	regulatory_region_variant	MODIFIER	-0.088069	1.82	-
VAR_CHR4_9795356	4	9795356	C	-	regulatory_region_variant	MODIFIER	-0.035288	2.26	-

VAR_CHR4_9795599	4	9795599	G	-	intergenic_variant	MODIFIER	0.362927	6.285	-
RS200496396	4	9795788	A	-	intergenic_variant	MODIFIER	-0.218727	1.002	0.4
VAR_CHR4_9796101	4	9796101	A	-	intergenic_variant	MODIFIER	-0.045234	2.172	-
RS2867388	4	9796495	G	-	intergenic_variant	MODIFIER	0.039134	2.972	0.49
RS10012516	4	9797178	G	-	intergenic_variant	MODIFIER	0.149722	4.143	0.35
RS1850740	4	9797258	C	-	intergenic_variant	MODIFIER	-0.252086	0.849	0.38
RS1850739	4	9797343	A	-	intergenic_variant	MODIFIER	0.137667	4.013	0.37
RS143009869	4	9797362	T	-	intergenic_variant	MODIFIER	-0.216336	1.014	0.4
RS192489364	4	9797364	A	-	intergenic_variant	MODIFIER	-0.86837	0.03	0.42
RS147774694	4	9797466	T	-	intergenic_variant	MODIFIER	-0.300718	0.662	0.36
VAR_CHR4_9797652	4	9797652	A	-	intergenic_variant	MODIFIER	-0.144096	1.424	-
RS13106539	4	9797703	G	-	intergenic_variant	MODIFIER	-0.055034	2.088	0.45
VAR_CHR4_9797750	4	9797750	C	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_9797778	4	9797778	C	-	intergenic_variant	MODIFIER	-0.133365	1.495	-
RS184387875	4	9797919	C	-	intergenic_variant	MODIFIER	-0.168809	1.272	0.45
VAR_CHR4_9797965	4	9797965	A	-	intergenic_variant	MODIFIER	0.202558	4.706	-
RS2139240	4	9798092	A	-	intergenic_variant	MODIFIER	-0.027944	2.326	0.34
RS138052838	4	9798126	C	-	intergenic_variant	MODIFIER	-0.058776	2.057	0.38
RS185646091	4	9798257	C	-	intergenic_variant	MODIFIER	-0.032806	2.282	0.31
VAR_CHR4_9798476	4	9798476	A	-	regulatory_region_variant	MODIFIER	0.431078	6.88	-
VAR_CHR4_9798487	4	9798487	A	-	regulatory_region_variant	MODIFIER	0.521159	7.591	-
RS149644486	4	9798566	A	-	regulatory_region_variant	MODIFIER	0.132754	3.96	0.43
RS6449000	4	9798612	C	-	regulatory_region_variant	MODIFIER	-0.430157	0.327	0.41
RS140023275	4	9798750	C	-	intergenic_variant	MODIFIER	-0.503117	0.216	0.38
RS61121804	4	9798777	A	-	intergenic_variant	MODIFIER	0.184337	4.513	0.53
RS2280206	4	9799237	T	-	intergenic_variant	MODIFIER	-0.688559	0.077	0.36

RS1850737	4	9799287	C	-	intergenic_variant	MODIFIER	-0.474656	0.254	0.36
RS372497976	4	9799343	A	-	intergenic_variant	MODIFIER	0.124868	3.875	-
VAR_CHR4_9799396	4	9799396	C	-	intergenic_variant	MODIFIER	-0.502736	0.216	-
VAR_CHR4_9799421	4	9799421	C	-	intergenic_variant	MODIFIER	-0.287941	0.707	-
RS183006594	4	9799607	T	-	intergenic_variant	MODIFIER	-0.317265	0.607	0.17
RS2280207	4	9799776	A	-	intergenic_variant	MODIFIER	0.035934	2.939	0.39
RS192823699	4	9799810	T	-	intergenic_variant	MODIFIER	-0.307245	0.64	0.4
RS2280208	4	9800043	T	-	intergenic_variant	MODIFIER	0.339283	6.067	0.33
VAR_CHR4_9800131	4	9800131	A	-	intergenic_variant	MODIFIER	-0.163531	1.304	-
RS79931771	4	9800431	T	-	intergenic_variant	MODIFIER	-0.084906	1.845	0.38
VAR_CHR4_9800445	4	9800445	G	-	intergenic_variant	MODIFIER	-	-	-
RS16888725	4	9800450	A	-	intergenic_variant	MODIFIER	0.156015	4.21	0.37
VAR_CHR4_9800514	4	9800514	A	-	intergenic_variant	MODIFIER	-0.113107	1.635	-
VAR_CHR4_9800539	4	9800539	T	-	intergenic_variant	MODIFIER	0.687841	8.747	-
VAR_CHR4_9800697	4	9800697	G	-	intergenic_variant	MODIFIER	-0.773306	0.049	-
VAR_CHR4_9801071	4	9801071	T	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_9801099	4	9801099	A	-	intergenic_variant	MODIFIER	-0.253987	0.841	-
RS114529821	4	9801269	A	-	intergenic_variant	MODIFIER	-0.166916	1.283	0.39
RS7679464	4	9801283	G	-	intergenic_variant	MODIFIER	-0.186628	1.17	0.37
VAR_CHR4_9801308	4	9801308	T	-	intergenic_variant	MODIFIER	0.03248	2.905	-
VAR_CHR4_9801311	4	9801311	C	-	intergenic_variant	MODIFIER	-0.214567	1.023	-
RS114021909	4	9801360	C	-	intergenic_variant	MODIFIER	-0.764392	0.051	0.33
VAR_CHR4_9801485	4	9801485	T	-	intergenic_variant	MODIFIER	-0.330304	0.566	-
RS16888747	4	9801553	G	-	intergenic_variant	MODIFIER	-	-	0.35
RS141072456	4	9801620	G	-	intergenic_variant	MODIFIER	-0.189388	1.155	0.32
RS180881388	4	9801787	G	-	intergenic_variant	MODIFIER	-0.127042	1.537	0.42

VAR_CHR4_9801915	4	9801915	T	-	intergenic_variant	MODIFIER	-0.353453	0.5	-
VAR_CHR4_9801949	4	9801949	A	-	intergenic_variant	MODIFIER	0.262943	5.328	-
RS56139970	4	9802272	G	-	intergenic_variant	MODIFIER	-0.507396	0.211	0.31
RS938556	4	9802366	T	-	intergenic_variant	MODIFIER	-0.548505	0.167	0.25
VAR_CHR4_9802572	4	9802572	T	-	intergenic_variant	MODIFIER	-0.127767	1.532	-
RS186850997	4	9802725	G	-	intergenic_variant	MODIFIER	1.5377	13.51	0.34
VAR_CHR4_9802829	4	9802829	C	-	intergenic_variant	MODIFIER	-0.124056	1.558	-
RS1519097	4	9802853	C	-	intergenic_variant	MODIFIER	-0.225224	0.971	0.33
RS116533216	4	9803107	G	-	intergenic_variant	MODIFIER	-0.031877	2.29	0.27
VAR_CHR4_9803145	4	9803145	G	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_9803240	4	9803240	A	-	intergenic_variant	MODIFIER	0.012601	2.708	-
RS187789518	4	9803241	T	-	intergenic_variant	MODIFIER	-0.317615	0.606	0.36
VAR_CHR4_9803372	4	9803372	C	-	intergenic_variant	MODIFIER	0.213639	4.822	-
RS77138280	4	9803665	T	-	intergenic_variant	MODIFIER	-0.108741	1.666	0.33
VAR_CHR4_9803905	4	9803905	T	-	intergenic_variant	MODIFIER	-	-	-
RS57904542	4	9804013	A	-	intergenic_variant	MODIFIER	0.453175	7.062	0.27
RS370990960	4	9804189	A	-	intergenic_variant	MODIFIER	-0.36666	0.465	-
RS28528381	4	9804225	C	-	intergenic_variant	MODIFIER	-1.108087	0.01	0.18
RS1533615	4	9804524	A	-	intergenic_variant	MODIFIER	0.340457	6.078	0.37
RS16888799	4	9804556	A	-	intergenic_variant	MODIFIER	0.232784	5.021	0.39
RS59518418	4	9804559	A	-	intergenic_variant	MODIFIER	-0.301512	0.659	0.39
VAR_CHR4_9804714	4	9804714	A	-	intergenic_variant	MODIFIER	0.881888	9.96	-
VAR_CHR4_9804730	4	9804730	T	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_9804860	4	9804860	T	-	intergenic_variant	MODIFIER	0.397616	6.593	-
VAR_CHR4_9805132	4	9805132	T	-	intergenic_variant	MODIFIER	2.060157	16.6	-
RS149187442	4	9805397	C	-	intergenic_variant	MODIFIER	-0.103291	1.706	0.36

RS6844369	4	9805562	T	-	intergenic_variant	MODIFIER	-	-	0.26
RS76257144	4	9805733	T	-	intergenic_variant	MODIFIER	0.011968	2.702	0.29
RS1519096	4	9805872	G	-	intergenic_variant	MODIFIER	0.122364	3.848	0.4
VAR_CHR4_9806027	4	9806027	G	-	intergenic_variant	MODIFIER	0.010277	2.685	-
VAR_CHR4_9806044	4	9806044	C	-	intergenic_variant	MODIFIER	-	-	-
RS185021027	4	9806247	A	-	intergenic_variant	MODIFIER	-0.317846	0.605	0.26
VAR_CHR4_9806305	4	9806305	C	-	intergenic_variant	MODIFIER	-	-	-
RS140726714	4	9806364	A	-	intergenic_variant	MODIFIER	-0.240267	0.901	0.29
VAR_CHR4_9806373	4	9806373	T	-	intergenic_variant	MODIFIER	-0.211884	1.037	-
VAR_CHR4_9806375	4	9806375	A	-	intergenic_variant	MODIFIER	0.038492	2.965	-
VAR_CHR4_9806406	4	9806406	T	-	intergenic_variant	MODIFIER	-0.533805	0.181	-
RS77759711	4	9806411	A	-	intergenic_variant	MODIFIER	0.274512	5.443	0.37
VAR_CHR4_9806442	4	9806442	T	-	intergenic_variant	MODIFIER	-0.115987	1.614	-
VAR_CHR4_9806939	4	9806939	A	-	intergenic_variant	MODIFIER	0.050932	3.092	-
VAR_CHR4_9806958	4	9806958	A	-	intergenic_variant	MODIFIER	-0.608315	0.119	-
VAR_CHR4_9806991	4	9806991	A	-	intergenic_variant	MODIFIER	0.039242	2.973	-
RS139729941	4	9807574	A	-	intergenic_variant	MODIFIER	0.265127	5.35	0.3
VAR_CHR4_9807602	4	9807602	T	-	intergenic_variant	MODIFIER	-0.717059	0.066	-
RS77026746	4	9807632	C	-	intergenic_variant	MODIFIER	-0.702206	0.071	0.3
RS190347592	4	9807855	A	-	intergenic_variant	MODIFIER	-0.065846	1.998	0.27
RS74706199	4	9807857	G	-	intergenic_variant	MODIFIER	-	-	0.25
VAR_CHR4_9807903	4	9807903	A	-	intergenic_variant	MODIFIER	-0.119998	1.586	-
VAR_CHR4_9807904	4	9807904	T	-	intergenic_variant	MODIFIER	-0.741086	0.058	-
RS148610844	4	9807925	T	-	intergenic_variant	MODIFIER	-0.807403	0.041	0.25
RS112674844	4	9807999	A	-	intergenic_variant	MODIFIER	-0.258942	0.82	0.23
RS1850733	4	9808018	C	-	intergenic_variant	MODIFIER	-0.598846	0.126	0.27

RS1850732	4	9808134	C	-	intergenic_variant	MODIFIER	-0.147526	1.403	0.28
RS58693849	4	9808255	G	-	intergenic_variant	MODIFIER	-0.369737	0.457	0.32
VAR_CHR4_9808303	4	9808303	T	-	intergenic_variant	MODIFIER	-0.423329	0.34	-
RS80119233	4	9808347	T	-	intergenic_variant	MODIFIER	-	-	0.31
RS140693556	4	9808505	T	-	intergenic_variant	MODIFIER	-0.526342	0.189	0.4
RS189902533	4	9808536	A	-	intergenic_variant	MODIFIER	0.184636	4.516	0.3
VAR_CHR4_9808575	4	9808575	A	-	intergenic_variant	MODIFIER	-0.017663	2.42	-
RS7664572	4	9808709	A	-	intergenic_variant	MODIFIER	0.210227	4.787	0.31
RS75164297	4	9808717	A	-	intergenic_variant	MODIFIER	0.14052	4.044	0.31
RS79707209	4	9808830	A	-	intergenic_variant	MODIFIER	-0.184577	1.182	0.37
RS143250861	4	9808861	C	-	intergenic_variant	MODIFIER	-0.272372	0.766	0.33
VAR_CHR4_9809044	4	9809044	C	-	intergenic_variant	MODIFIER	-	-	-
RS118072948	4	9809149	T	-	intergenic_variant	MODIFIER	-0.056693	2.074	0.28
VAR_CHR4_9809214	4	9809214	G	-	intergenic_variant	MODIFIER	-0.175821	1.231	-
RS148317100	4	9809224	C	-	intergenic_variant	MODIFIER	-	-	0.36
VAR_CHR4_9809257	4	9809257	G	-	intergenic_variant	MODIFIER	0.124184	3.867	-
RS77326183	4	9809542	T	-	intergenic_variant	MODIFIER	-1.161646	0.008	0.4
RS187135408	4	9809587	G	-	intergenic_variant	MODIFIER	0.029722	2.877	0.36
VAR_CHR4_9809634	4	9809634	C	-	intergenic_variant	MODIFIER	-	-	-
RS77859955	4	9809837	G	-	intergenic_variant	MODIFIER	0.510138	7.508	0.32
RS12500086	4	9809859	C	-	intergenic_variant	MODIFIER	0.061897	3.206	0.36
VAR_CHR4_9809891	4	9809891	A	-	TF_binding_site_variant	MODIFIER	0.289242	5.589	-
RS6842853	4	9810124	T	-	intergenic_variant	MODIFIER	-0.296466	0.677	0.3
RS78549292	4	9810197	C	-	intergenic_variant	MODIFIER	-	-	0.35
VAR_CHR4_9810265	4	9810265	A	-	intergenic_variant	MODIFIER	0.048733	3.07	-
VAR_CHR4_9810620	4	9810620	G	-	intergenic_variant	MODIFIER	-0.05635	2.077	-

VAR_CHR4_9810630	4	9810630	G	-	intergenic_variant	MODIFIER	0.051757	3.101	-
VAR_CHR4_9810636	4	9810636	T	-	intergenic_variant	MODIFIER	-	-	-
RS73223775	4	9810714	C	-	intergenic_variant	MODIFIER	0.145986	4.102	0.39
VAR_CHR4_9810893	4	9810893	A	-	intergenic_variant	MODIFIER	0.225793	4.949	-
RS1519095	4	9810931	C	-	intergenic_variant	MODIFIER	-0.656337	0.091	0.46
VAR_CHR4_9811097	4	9811097	T	-	intergenic_variant	MODIFIER	-0.286949	0.711	-
VAR_CHR4_9811132	4	9811132	A	-	intergenic_variant	MODIFIER	-0.191557	1.143	-
RS2280333	4	9811133	C	-	intergenic_variant	MODIFIER	-0.681575	0.079	0.44
VAR_CHR4_9811531	4	9811531	C	-	intergenic_variant	MODIFIER	-	-	-
RS185849919	4	9811705	C	-	intergenic_variant	MODIFIER	-0.037359	2.241	0.37
RS10005226	4	9811805	A	-	intergenic_variant	MODIFIER	0.364673	6.301	0.44
RS184033171	4	9811841	T	-	intergenic_variant	MODIFIER	-0.245903	0.876	0.34
RS115809382	4	9811873	C	-	intergenic_variant	MODIFIER	-0.008789	2.503	0.4
VAR_CHR4_9811999	4	9811999	C	-	intergenic_variant	MODIFIER	-	-	-
RS116305437	4	9812078	C	-	intergenic_variant	MODIFIER	-0.241528	0.896	0.41
RS181872225	4	9812188	G	-	intergenic_variant	MODIFIER	-0.391567	0.405	0.45
VAR_CHR4_9812199	4	9812199	A	-	intergenic_variant	MODIFIER	-0.056954	2.072	-
VAR_CHR4_9812284	4	9812284	C	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_9812331	4	9812331	G	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_9812425	4	9812425	G	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_9812494	4	9812494	A	-	intergenic_variant	MODIFIER	0.297317	5.668	-
RS1356643	4	9812741	G	-	intergenic_variant	MODIFIER	0.206241	4.745	0.44
RS115490582	4	9812777	A	-	intergenic_variant	MODIFIER	0.150707	4.153	0.52
VAR_CHR4_9812857	4	9812857	T	-	intergenic_variant	MODIFIER	-0.26779	0.784	-
RS117095092	4	9812898	G	-	intergenic_variant	MODIFIER	0.368909	6.339	0.34
VAR_CHR4_9812935	4	9812935	A	-	intergenic_variant	MODIFIER	0.071928	3.31	-

VAR_CHR4_9813105	4	9813105	A	-	intergenic_variant	MODIFIER	-0.367533	0.463	-
VAR_CHR4_9813252	4	9813252	G	-	intergenic_variant	MODIFIER	0.083096	3.428	-
VAR_CHR4_9813275	4	9813275	T	-	intergenic_variant	MODIFIER	-0.067531	1.984	-
VAR_CHR4_9813935	4	9813935	T	-	intergenic_variant	MODIFIER	-0.221912	0.987	-
VAR_CHR4_9814169	4	9814169	A	-	intergenic_variant	MODIFIER	0.216766	4.855	-
RS143605952	4	9814388	T	-	intergenic_variant	MODIFIER	2.096268	16.83	0.47
RS1401438	4	9814456	T	-	intergenic_variant	MODIFIER	2.258723	17.89	0.56
VAR_CHR4_9814640	4	9814640	T	-	intergenic_variant	MODIFIER	0.070072	3.291	-
RS78061800	4	9814663	C	-	intergenic_variant	MODIFIER	0.152513	4.173	0.5
RS150706987	4	9815081	A	-	intergenic_variant	MODIFIER	-0.017506	2.421	0.41
VAR_CHR4_9815107	4	9815107	C	-	intergenic_variant	MODIFIER	-0.385209	0.42	-
VAR_CHR4_9815320	4	9815320	G	-	intergenic_variant	MODIFIER	-0.142246	1.436	-
RS6841397	4	9815402	C	-	intergenic_variant	MODIFIER	-0.338134	0.543	0.24
VAR_CHR4_9815417	4	9815417	A	-	intergenic_variant	MODIFIER	-0.138926	1.458	-
RS11735883	4	9815762	T	-	intergenic_variant	MODIFIER	-1.042448	0.013	0.2
RS11722614	4	9815824	A	-	intergenic_variant	MODIFIER	-0.083803	1.854	0.2
RS11724234	4	9815825	A	-	intergenic_variant	MODIFIER	-	-	0.18
VAR_CHR4_9815904	4	9815904	T	-	intergenic_variant	MODIFIER	-	-	-
RS76069034	4	9815968	T	-	intergenic_variant	MODIFIER	-0.34081	0.535	0.24
RS190861676	4	9816336	G	-	intergenic_variant	MODIFIER	0.051128	3.094	0.39
RS36075927	4	9816408	G	-	intergenic_variant	MODIFIER	0.082447	3.421	0.3
RS35582635	4	9816409	T	-	intergenic_variant	MODIFIER	-0.490854	0.231	0.35
RS55686745	4	9816531	A	-	intergenic_variant	MODIFIER	0.064126	3.229	0.33
RS78589581	4	9816556	C	-	intergenic_variant	MODIFIER	-0.129678	1.519	0.41
RS183046178	4	9816642	A	-	intergenic_variant	MODIFIER	-	-	0.29
VAR_CHR4_9816670	4	9816670	T	-	intergenic_variant	MODIFIER	-0.120311	1.584	-

RS76689568	4	9816766	C	-	intergenic_variant	MODIFIER	0.06922	3.282	0.32
RS80224261	4	9816781	T	-	intergenic_variant	MODIFIER	-0.345362	0.522	0.36
RS28468399	4	9816806	T	-	intergenic_variant	MODIFIER	-0.167041	1.283	0.26
VAR_CHR4_9816836	4	9816836	T	-	intergenic_variant	MODIFIER	-0.135235	1.482	-
VAR_CHR4_9816977	4	9816977	G	-	intergenic_variant	MODIFIER	0.079429	3.389	-
VAR_CHR4_9817002	4	9817002	A	-	intergenic_variant	MODIFIER	-	-	-
RS13148356	4	9817070	C	-	intergenic_variant	MODIFIER	-0.148675	1.395	0.28
VAR_CHR4_9817114	4	9817114	T	-	intergenic_variant	MODIFIER	-0.338857	0.541	-
RS1519094	4	9817286	A	-	intergenic_variant	MODIFIER	0.062585	3.213	0.4
RS116242274	4	9817290	T	-	intergenic_variant	MODIFIER	-0.312125	0.623	0.39
VAR_CHR4_9817310	4	9817310	T	-	intergenic_variant	MODIFIER	-0.339585	0.539	-
VAR_CHR4_9817468	4	9817468	C	-	intergenic_variant	MODIFIER	0.063745	3.225	-
VAR_CHR4_9817483	4	9817483	A	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_9817546	4	9817546	C	-	intergenic_variant	MODIFIER	-	-	-
RS7656342	4	9818116	T	-	intergenic_variant	MODIFIER	-0.161852	1.314	0.3
RS79888997	4	9818167	G	-	intergenic_variant	MODIFIER	-0.253895	0.842	0.22
VAR_CHR4_9818215	4	9818215	C	-	intergenic_variant	MODIFIER	-0.290348	0.699	-
RS13141706	4	9818345	A	-	intergenic_variant	MODIFIER	0.306195	5.754	0.18
VAR_CHR4_9818354	4	9818354	C	-	intergenic_variant	MODIFIER	-0.322303	0.591	-
RS184396578	4	9818450	G	-	intergenic_variant	MODIFIER	-0.778734	0.048	0.18
RS2139238	4	9818655	T	-	intergenic_variant	MODIFIER	-0.632714	0.104	0.21
RS148889786	4	9818810	A	-	intergenic_variant	MODIFIER	0.112936	3.746	0.24
VAR_CHR4_9818891	4	9818891	T	-	intergenic_variant	MODIFIER	-0.385436	0.419	-
VAR_CHR4_9819000	4	9819000	T	-	intergenic_variant	MODIFIER	-0.60166	0.124	-
RS6449009	4	9819094	C	-	intergenic_variant	MODIFIER	-0.253211	0.845	0.32
RS181817180	4	9819247	A	-	intergenic_variant	MODIFIER	-	-	0.28

VAR_CHR4_9819301	4	9819301	G	-	intergenic_variant	MODIFIER	-0.166803	1.284	-
VAR_CHR4_9819361	4	9819361	G	-	intergenic_variant	MODIFIER	0.188945	4.562	-
VAR_CHR4_9819397	4	9819397	C	-	intergenic_variant	MODIFIER	-0.205795	1.068	-
RS11726423	4	9819572	G	-	intergenic_variant	MODIFIER	-0.05728	2.069	0.18
RS145945471	4	9819662	T	-	intergenic_variant	MODIFIER	0.034306	2.923	0.15
RS1401437	4	9819763	C	-	intergenic_variant	MODIFIER	-0.40265	0.381	0.15
VAR_CHR4_9819765	4	9819765	A	-	intergenic_variant	MODIFIER	0.045903	3.041	-
VAR_CHR4_9819831	4	9819831	T	-	intergenic_variant	MODIFIER	-0.140595	1.447	-
RS141208648	4	9819938	T	-	intergenic_variant	MODIFIER	-0.068026	1.98	0.29
RS6855095	4	9819977	T	-	intergenic_variant	MODIFIER	-0.252701	0.847	0.24
RS7687896	4	9820064	G	-	intergenic_variant	MODIFIER	-0.133987	1.491	0.26
VAR_CHR4_9820085	4	9820085	A	-	intergenic_variant	MODIFIER	-0.421831	0.342	-
RS1107912	4	9820179	T	-	intergenic_variant	MODIFIER	-0.348565	0.513	0.14
VAR_CHR4_9820217	4	9820217	G	-	intergenic_variant	MODIFIER	-0.144615	1.421	-
RS1107911	4	9820256	G	-	intergenic_variant	MODIFIER	-	-	0.22
VAR_CHR4_9820317	4	9820317	G	-	intergenic_variant	MODIFIER	-	-	-
RS147532156	4	9820362	G	-	intergenic_variant	MODIFIER	-	-	0.31
VAR_CHR4_9820440	4	9820440	A	-	intergenic_variant	MODIFIER	0.182222	4.491	-
RS369796563	4	9820441	T	-	intergenic_variant	MODIFIER	0.084702	3.445	-
VAR_CHR4_9820768	4	9820768	T	-	intergenic_variant	MODIFIER	-	-	-
RS939132	4	9820883	A	-	intergenic_variant	MODIFIER	-0.026717	2.337	0.4
VAR_CHR4_9820931	4	9820931	T	-	intergenic_variant	MODIFIER	-	-	-
RS939131	4	9820950	T	-	intergenic_variant	MODIFIER	-0.125838	1.546	0.28
RS192979816	4	9821056	C	-	intergenic_variant	MODIFIER	0.029755	2.877	0.18
VAR_CHR4_9821265	4	9821265	A	-	intergenic_variant	MODIFIER	0.128002	3.909	-
RS7663670	4	9821471	A	-	intergenic_variant	MODIFIER	0.371436	6.362	0.18

VAR_CHR4_9821517	4	9821517	A	-	intergenic_variant	MODIFIER	0.133552	3.968	-
RS10020053	4	9821648	G	-	intergenic_variant	MODIFIER	-0.507668	0.21	0.23
VAR_CHR4_9821667	4	9821667	C	-	intergenic_variant	MODIFIER	-0.216778	1.012	-
RS12643296	4	9821752	C	-	intergenic_variant	MODIFIER	-0.15089	1.381	0.23
VAR_CHR4_9821801	4	9821801	T	-	intergenic_variant	MODIFIER	-0.092799	1.784	-
VAR_CHR4_9821866	4	9821866	A	-	intergenic_variant	MODIFIER	-0.075781	1.917	-
RS185720419	4	9822057	C	-	intergenic_variant	MODIFIER	-	-	0.28
VAR_CHR4_9822078	4	9822078	T	-	intergenic_variant	MODIFIER	-	-	-
RS144569572	4	9822081	G	-	intergenic_variant	MODIFIER	-	-	0.27
RS7669742	4	9822205	A	-	intergenic_variant	MODIFIER	0.041624	2.997	0.19
RS77130163	4	9822257	C	-	intergenic_variant	MODIFIER	0.125595	3.883	0.24
RS7683059	4	9822275	C	-	intergenic_variant	MODIFIER	-0.263403	0.802	0.21
RS4697891	4	9822319	C	-	intergenic_variant	MODIFIER	-0.335639	0.55	0.28
VAR_CHR4_9822342	4	9822342	T	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_9822546	4	9822546	G	-	intergenic_variant	MODIFIER	0.43037	6.874	-
VAR_CHR4_9822599	4	9822599	T	-	intergenic_variant	MODIFIER	-0.268427	0.782	-
RS4697690	4	9822674	G	-	intergenic_variant	MODIFIER	0.321622	5.901	0.17
VAR_CHR4_9822768	4	9822768	G	-	intergenic_variant	MODIFIER	0.324178	5.925	-
RS28831091	4	9822845	C	-	intergenic_variant	MODIFIER	0.874297	9.914	0.21
VAR_CHR4_9822949	4	9822949	C	SLC2A9	downstream_gene_variant	MODIFIER	-0.261731	0.809	-
RS114731059	4	9823060	T	SLC2A9	downstream_gene_variant	MODIFIER	-0.397925	0.391	0.14
RS112222722	4	9823312	A	SLC2A9	downstream_gene_variant	MODIFIER	0.253964	5.237	0.32
RS73223785	4	9823335	G	SLC2A9	downstream_gene_variant	MODIFIER	0.678877	8.688	0.3
RS73223786	4	9823348	A	SLC2A9	downstream_gene_variant	MODIFIER	0.913941	10.16	0.22
RS60715294	4	9823478	C	SLC2A9	downstream_gene_variant	MODIFIER	0.116535	3.785	0.16
RS147514517	4	9823493	A	SLC2A9	downstream_gene_variant	MODIFIER	0.911683	10.15	0.18

VAR_CHR4_9823497	4	9823497	G	SLC2A9	downstream_gene_variant	MODIFIER	0.807281	9.509	-
RS140148860	4	9823552	C	SLC2A9	downstream_gene_variant	MODIFIER	0.620223	8.295	0.17
RS145665522	4	9823561	C	SLC2A9	downstream_gene_variant	MODIFIER	0.553294	7.826	0.17
RS147338898	4	9823656	A	SLC2A9	downstream_gene_variant	MODIFIER	0.183113	4.5	0.14
RS149781747	4	9823734	C	SLC2A9	downstream_gene_variant	MODIFIER	-0.074376	1.928	0.15
VAR_CHR4_9823832	4	9823832	G	SLC2A9	downstream_gene_variant	MODIFIER	0.5954	8.124	-
RS4697892	4	9823837	T	SLC2A9	downstream_gene_variant	MODIFIER	0.707478	8.876	0.17
RS148539010	4	9823882	C	SLC2A9	downstream_gene_variant	MODIFIER	0.226721	4.958	0.24
RS2867393	4	9823918	G	SLC2A9	downstream_gene_variant	MODIFIER	-0.081091	1.875	0.2
RS1519093	4	9824019	A	SLC2A9	downstream_gene_variant	MODIFIER	-0.301026	0.661	0.17
RS7695879	4	9824151	C	SLC2A9	downstream_gene_variant	MODIFIER	-0.39107	0.406	0.24
RS146488248	4	9824237	T	SLC2A9	downstream_gene_variant	MODIFIER	-0.222002	0.987	0.18
RS144878664	4	9824340	G	SLC2A9	downstream_gene_variant	MODIFIER	-0.029108	2.315	0.14
VAR_CHR4_9824612	4	9824612	G	SLC2A9	downstream_gene_variant	MODIFIER	-	-	-
RS11938128	4	9824619	C	SLC2A9	downstream_gene_variant	MODIFIER	-0.166638	1.285	0.14
RS1980220	4	9824636	T	SLC2A9	downstream_gene_variant	MODIFIER	-0.769364	0.05	0.9
RS151232397	4	9824708	G	SLC2A9	downstream_gene_variant	MODIFIER	0.05057	3.089	0.1
VAR_CHR4_9824801	4	9824801	A	SLC2A9	downstream_gene_variant	MODIFIER	0.267102	5.369	-
RS2066	4	9824874	T	SLC2A9	downstream_gene_variant	MODIFIER	-0.344486	0.524	0.13
RS1878276	4	9824945	C	SLC2A9	downstream_gene_variant	MODIFIER	-0.511576	0.206	0.16
RS62295669	4	9825002	C	SLC2A9	downstream_gene_variant	MODIFIER	-0.345841	0.521	0.26
RS3762933	4	9825026	G	SLC2A9	downstream_gene_variant	MODIFIER	-0.170615	1.261	0.26
RS1878277	4	9825143	A	SLC2A9	downstream_gene_variant	MODIFIER	-0.295995	0.678	0.21
RS74527798	4	9825514	G	SLC2A9	downstream_gene_variant	MODIFIER	-	-	0.26
RS1996335	4	9825814	T	SLC2A9	downstream_gene_variant	MODIFIER	-0.263265	0.803	0.32
RS57731161	4	9825847	A	SLC2A9	downstream_gene_variant	MODIFIER	-0.076295	1.913	0.3

RS138475000	4	9826050	C	SLC2A9	downstream_gene_variant	MODIFIER	0.680442	8.698	0.27
RS79095673	4	9826077	T	SLC2A9	downstream_gene_variant	MODIFIER	0.081417	3.41	0.31
RS4697893	4	9826183	G	SLC2A9	downstream_gene_variant	MODIFIER	0.026391	2.844	0.33
RS184261910	4	9826235	G	SLC2A9	downstream_gene_variant	MODIFIER	0.171559	4.377	0.38
VAR_CHR4_9826725	4	9826725	A	SLC2A9	downstream_gene_variant	MODIFIER	0.00188	2.604	-
RS117535295	4	9826729	C	SLC2A9	downstream_gene_variant	MODIFIER	-	-	0.23
RS6822889	4	9826757	A	SLC2A9	downstream_gene_variant	MODIFIER	-0.21595	1.016	0.26
RS1519092	4	9826801	A	SLC2A9	downstream_gene_variant	MODIFIER	0.287312	5.57	-
RS4621429	4	9826870	C	SLC2A9	downstream_gene_variant	MODIFIER	-0.237954	0.912	0.21
VAR_CHR4_9826893	4	9826893	G	SLC2A9	downstream_gene_variant	MODIFIER	0.295029	5.645	-
VAR_CHR4_9827024	4	9827024	T	SLC2A9	downstream_gene_variant	MODIFIER	0.082978	3.427	-
VAR_CHR4_9827025	4	9827025	A	SLC2A9	downstream_gene_variant	MODIFIER	0.182237	4.491	-
VAR_CHR4_9827300	4	9827300	G	SLC2A9	downstream_gene_variant	MODIFIER	0.515596	7.549	-
VAR_CHR4_9827387	4	9827387	C	SLC2A9	downstream_gene_variant	MODIFIER	0.049341	3.076	-
RS938557	4	9827556	A	SLC2A9	downstream_gene_variant	MODIFIER	0.20195	4.7	0.34
RS150828093	4	9827730	A	SLC2A9	downstream_gene_variant	MODIFIER	0.301744	5.711	0.37
VAR_CHR4_9827885	4	9827885	G	SLC2A9	3_prime_UTR_variant	MODIFIER	0.226035	4.951	-
RS144428359	4	9828099	T	SLC2A9	synonymous_variant	LOW	0.754395	9.179	0.44
RS371746690	4	9828230	T	SLC2A9	splice_region_variant,intron_variant	LOW	1.532688	13.49	-
VAR_CHR4_9828379	4	9828379	C	SLC2A9	intron_variant	MODIFIER	-0.257648	0.826	-
RS139913518	4	9828391	T	SLC2A9	intron_variant	MODIFIER	-0.033529	2.276	0.35
RS4697895	4	9828484	G	SLC2A9	intron_variant	MODIFIER	0.414166	6.736	0.4
RS73223788	4	9828502	A	SLC2A9	intron_variant	MODIFIER	-0.171812	1.254	0.25
RS148907062	4	9828524	A	SLC2A9	intron_variant	MODIFIER	0.740677	9.091	0.22
RS11930077	4	9828534	C	SLC2A9	intron_variant	MODIFIER	0.859379	9.825	0.19
RS4697896	4	9828569	A	SLC2A9	intron_variant	MODIFIER	0.828941	9.641	0.24

RS6817564	4	9828745	C	SLC2A9	intron_variant	MODIFIER	-0.256044	0.833	0.25
RS56253435	4	9828765	G	SLC2A9	intron_variant	MODIFIER	0.000472	2.59	0.22
RS6837273	4	9829086	G	SLC2A9	intron_variant	MODIFIER	0.322659	5.911	0.24
VAR_CHR4_9829400	4	9829400	T	SLC2A9	intron_variant	MODIFIER	-0.698817	0.072	-
RS7680554	4	9829481	G	SLC2A9	intron_variant	MODIFIER	-0.02144	2.385	0.44
VAR_CHR4_9829624	4	9829624	A	SLC2A9	intron_variant	MODIFIER	0.082129	3.418	-
RS62295672	4	9829658	T	SLC2A9	intron_variant	MODIFIER	-0.408326	0.369	0.38
VAR_CHR4_9829755	4	9829755	G	SLC2A9	intron_variant	MODIFIER	-0.163062	1.306	-
RS11938866	4	9829799	A	SLC2A9	intron_variant	MODIFIER	0.208346	4.767	0.35
RS144652081	4	9829882	G	SLC2A9	intron_variant	MODIFIER	0.18073	4.475	0.38
RS372021642	4	9829956	T	SLC2A9	intron_variant	MODIFIER	0.039792	2.979	-
VAR_CHR4_9830007	4	9830007	T	SLC2A9	intron_variant	MODIFIER	-0.070666	1.958	-
RS28735365	4	9830036	C	SLC2A9	intron_variant	MODIFIER	-0.22966	0.95	0.34
RS112255785	4	9830039	A	SLC2A9	intron_variant	MODIFIER	-0.111469	1.646	0.37
VAR_CHR4_9830150	4	9830150	G	SLC2A9	intron_variant	MODIFIER	-0.379004	0.434	-
RS73804393	4	9830301	T	SLC2A9	intron_variant	MODIFIER	-	-	0.25
VAR_CHR4_9830364	4	9830364	G	SLC2A9	intron_variant	MODIFIER	0.147566	4.119	-
VAR_CHR4_9830433	4	9830433	G	SLC2A9	intron_variant	MODIFIER	0.067772	3.267	-
VAR_CHR4_9830475	4	9830475	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS186289358	4	9830514	A	SLC2A9	intron_variant	MODIFIER	-0.533889	0.181	0.26
RS59574200	4	9830540	C	SLC2A9	intron_variant	MODIFIER	0.064916	3.237	0.26
VAR_CHR4_9830556	4	9830556	C	SLC2A9	intron_variant	MODIFIER	-0.128123	1.53	-
VAR_CHR4_9830596	4	9830596	A	SLC2A9	intron_variant	MODIFIER	0.159021	4.243	-
RS61338451	4	9830614	G	SLC2A9	intron_variant	MODIFIER	-0.220033	0.996	0.3
RS28504140	4	9830761	G	SLC2A9	intron_variant	MODIFIER	-0.148942	1.394	0.29
RS183110868	4	9830785	G	SLC2A9	intron_variant	MODIFIER	0.262025	5.319	0.22

RS141241707	4	9832196	A	SLC2A9	intron_variant	MODIFIER	0.231558	5.008	0.35
RS1401441	4	9832304	A	SLC2A9	intron_variant	MODIFIER	0.529339	7.651	0.23
VAR_CHR4_9832351	4	9832351	T	SLC2A9	intron_variant	MODIFIER	0.041048	2.991	-
VAR_CHR4_9832475	4	9832475	T	SLC2A9	intron_variant	MODIFIER	0.276767	5.466	-
RS1401440	4	9832512	A	SLC2A9	intron_variant	MODIFIER	-0.067012	1.988	0.37
RS1401439	4	9832622	G	SLC2A9	intron_variant	MODIFIER	-	-	0.27
RS75110348	4	9832774	T	SLC2A9	intron_variant	MODIFIER	0.834905	9.677	0.26
RS10022660	4	9832851	A	SLC2A9	intron_variant	MODIFIER	0.406265	6.668	0.19
RS74970122	4	9832857	A	SLC2A9	intron_variant	MODIFIER	-0.180903	1.202	0.12
VAR_CHR4_9832858	4	9832858	T	SLC2A9	intron_variant	MODIFIER	-1.023321	0.014	-
VAR_CHR4_9832954	4	9832954	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS6449026	4	9833042	C	SLC2A9	intron_variant	MODIFIER	-0.249763	0.859	0.22
VAR_CHR4_9833092	4	9833092	T	SLC2A9	intron_variant	MODIFIER	-0.568284	0.149	-
RS6449027	4	9833140	C	SLC2A9	intron_variant	MODIFIER	-0.451391	0.29	0.2
RS6449028	4	9833226	G	SLC2A9	intron_variant	MODIFIER	-0.125347	1.549	0.26
VAR_CHR4_9833308	4	9833308	A	SLC2A9	intron_variant	MODIFIER	-0.050164	2.13	-
VAR_CHR4_9833322	4	9833322	C	SLC2A9	intron_variant	MODIFIER	-0.338572	0.541	-
VAR_CHR4_9833565	4	9833565	G	SLC2A9	intron_variant	MODIFIER	-0.470387	0.26	-
RS10025644	4	9833649	A	SLC2A9	intron_variant	MODIFIER	0.333624	6.014	0.19
RS10009657	4	9833734	C	SLC2A9	intron_variant	MODIFIER	-0.961082	0.019	0.32
RS114532436	4	9833809	T	SLC2A9	intron_variant	MODIFIER	-0.585314	0.136	0.3
VAR_CHR4_9833833	4	9833833	T	SLC2A9	intron_variant	MODIFIER	-0.255981	0.833	-
RS10009838	4	9833882	T	SLC2A9	intron_variant	MODIFIER	0.005653	2.64	0.25
VAR_CHR4_9833913	4	9833913	C	SLC2A9	intron_variant	MODIFIER	0.0777	3.371	-
RS10025968	4	9834003	A	SLC2A9	intron_variant	MODIFIER	0.290535	5.601	0.26
RS1464258	4	9834107	A	SLC2A9	intron_variant	MODIFIER	-0.099534	1.733	0.27

VAR_CHR4_9834226	4	9834226	T	SLC2A9	intron_variant	MODIFIER	-0.873359	0.03	-
RS144757629	4	9834257	G	SLC2A9	intron_variant	MODIFIER	0.087868	3.479	0.33
VAR_CHR4_9834424	4	9834424	A	SLC2A9	intron_variant	MODIFIER	0.070847	3.299	-
RS1464259	4	9834462	T	SLC2A9	intron_variant	MODIFIER	-0.018803	2.409	0.43
RS183382473	4	9834553	T	SLC2A9	intron_variant	MODIFIER	-0.408862	0.368	0.29
RS16889260	4	9834896	A	SLC2A9	intron_variant	MODIFIER	-0.221847	0.987	0.41
RS16889264	4	9834999	G	SLC2A9	intron_variant	MODIFIER	0.059247	3.178	0.38
VAR_CHR4_9835156	4	9835156	T	SLC2A9	intron_variant	MODIFIER	-0.465712	0.267	-
VAR_CHR4_9835189	4	9835189	A	SLC2A9	intron_variant	MODIFIER	-0.047271	2.155	-
VAR_CHR4_9835331	4	9835331	G	SLC2A9	intron_variant	MODIFIER	0.189498	4.568	-
RS114919407	4	9835352	G	SLC2A9	intron_variant	MODIFIER	-0.201879	1.088	0.23
VAR_CHR4_9835429	4	9835429	T	SLC2A9	intron_variant	MODIFIER	0.036555	2.946	-
RS10012880	4	9835480	A	SLC2A9	intron_variant	MODIFIER	-0.266058	0.791	0.29
RS113181369	4	9835517	T	SLC2A9	intron_variant	MODIFIER	0.220887	4.898	0.27
RS138811051	4	9835552	A	SLC2A9	intron_variant	MODIFIER	0.021561	2.796	0.22
RS9996799	4	9835563	C	SLC2A9	intron_variant	MODIFIER	-0.17791	1.219	0.3
RS16889270	4	9835566	T	SLC2A9	intron_variant	MODIFIER	-0.10287	1.709	0.2
RS58782826	4	9835567	C	SLC2A9	intron_variant	MODIFIER	-0.083295	1.858	0.31
VAR_CHR4_9835881	4	9835881	T	SLC2A9	intron_variant	MODIFIER	0.463547	7.146	-
VAR_CHR4_9836154	4	9836154	G	SLC2A9	intron_variant	MODIFIER	0.483017	7.3	-
RS12644471	4	9836164	G	SLC2A9	intron_variant	MODIFIER	-0.052752	2.108	0.35
VAR_CHR4_9836187	4	9836187	C	SLC2A9	intron_variant	MODIFIER	-0.364292	0.471	-
RS12642114	4	9836190	T	SLC2A9	intron_variant	MODIFIER	-0.091507	1.794	0.43
RS77957927	4	9836281	A	SLC2A9	intron_variant	MODIFIER	-0.003782	2.55	0.33
RS3775950	4	9836366	A	SLC2A9	intron_variant	MODIFIER	0.217189	4.859	0.41
RS181882156	4	9836370	G	SLC2A9	intron_variant	MODIFIER	0.388197	6.511	0.39

RS147534794	4	9836625	T	SLC2A9	synonymous_variant	LOW	-0.262577	0.806	0.25
VAR_CHR4_9836725	4	9836725	T	SLC2A9	intron_variant	MODIFIER	0.021143	2.792	-
VAR_CHR4_9836811	4	9836811	A	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9836850	4	9836850	C	SLC2A9	intron_variant	MODIFIER	-0.333488	0.556	-
RS7665666	4	9836861	A	SLC2A9	intron_variant	MODIFIER	0.801027	9.47	0.17
RS10002519	4	9836986	C	SLC2A9	intron_variant	MODIFIER	-0.596558	0.127	0.34
RS12505312	4	9837090	C	SLC2A9	intron_variant	MODIFIER	-	-	0.41
VAR_CHR4_9837110	4	9837110	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS6823129	4	9837206	A	SLC2A9	intron_variant	MODIFIER	0.2812	5.51	0.37
RS6856012	4	9837207	G	SLC2A9	intron_variant	MODIFIER	0.055913	3.144	0.36
VAR_CHR4_9837290	4	9837290	T	SLC2A9	intron_variant	MODIFIER	-0.083186	1.858	-
VAR_CHR4_9837975	4	9837975	G	SLC2A9	intron_variant	MODIFIER	0.261186	5.31	-
VAR_CHR4_9838322	4	9838322	T	SLC2A9	intron_variant	MODIFIER	0.037245	2.953	-
VAR_CHR4_9838332	4	9838332	T	SLC2A9	intron_variant	MODIFIER	0.047451	3.057	-
RS28429694	4	9838335	C	SLC2A9	intron_variant	MODIFIER	0.218411	4.872	0.25
RS6844216	4	9838387	C	SLC2A9	intron_variant	MODIFIER	-0.320574	0.596	0.18
RS78570464	4	9838408	T	SLC2A9	intron_variant	MODIFIER	-0.191088	1.146	0.2
RS148922822	4	9838450	T	SLC2A9	intron_variant	MODIFIER	0.026094	2.841	0.3
VAR_CHR4_9838463	4	9838463	T	SLC2A9	intron_variant	MODIFIER	-0.294757	0.683	-
VAR_CHR4_9838487	4	9838487	T	SLC2A9	intron_variant	MODIFIER	-0.141845	1.439	-
VAR_CHR4_9838531	4	9838531	G	SLC2A9	intron_variant	MODIFIER	0.020733	2.788	-
RS372346996	4	9838535	G	SLC2A9	intron_variant	MODIFIER	0.065792	3.246	-
RS10939552	4	9838548	T	SLC2A9	intron_variant	MODIFIER	0.09511	3.556	0.33
VAR_CHR4_9838642	4	9838642	A	SLC2A9	intron_variant	MODIFIER	0.022987	2.81	-
VAR_CHR4_9838673	4	9838673	A	SLC2A9	intron_variant	MODIFIER	0.38882	6.516	-
RS187132080	4	9838712	T	SLC2A9	intron_variant	MODIFIER	-0.554843	0.161	0.31

RS191475275	4	9838756	A	SLC2A9	intron_variant	MODIFIER	-0.067264	1.986	0.25
RS76139601	4	9838798	A	SLC2A9	intron_variant	MODIFIER	-	-	0.34
RS117606401	4	9838919	C	SLC2A9	intron_variant	MODIFIER	0.105423	3.666	0.36
VAR_CHR4_9838948	4	9838948	C	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9838966	4	9838966	C	SLC2A9	intron_variant	MODIFIER	0.151198	4.159	-
RS145911075	4	9839165	A	SLC2A9	intron_variant	MODIFIER	-0.380954	0.43	0.39
VAR_CHR4_9839412	4	9839412	T	SLC2A9	intron_variant	MODIFIER	-0.295717	0.679	-
RS1401442	4	9839447	G	SLC2A9	intron_variant	MODIFIER	-0.121158	1.578	0.35
RS1914874	4	9839490	G	SLC2A9	intron_variant	MODIFIER	0.01676	2.748	0.41
RS1114199	4	9839687	A	SLC2A9	intron_variant	MODIFIER	0.117897	3.8	0.25
RS185629831	4	9839948	A	SLC2A9	intron_variant	MODIFIER	-0.430988	0.325	0.42
VAR_CHR4_9839976	4	9839976	T	SLC2A9	intron_variant	MODIFIER	0.381238	6.449	-
VAR_CHR4_9839977	4	9839977	A	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9841533	4	9841533	A	SLC2A9	intron_variant	MODIFIER	0.674276	8.658	-
VAR_CHR4_9841568	4	9841568	G	SLC2A9	intron_variant	MODIFIER	0.219564	4.884	-
RS191675521	4	9841625	A	SLC2A9	intron_variant	MODIFIER	-0.308621	0.635	0.41
RS10031303	4	9841690	A	SLC2A9	intron_variant	MODIFIER	-	-	0.41
VAR_CHR4_9841760	4	9841760	G	SLC2A9	intron_variant	MODIFIER	0.48997	7.354	-
RS34088729	4	9841979	A	SLC2A9	intron_variant	MODIFIER	-	-	0.33
RS368341354	4	9842027	T	SLC2A9	intron_variant	MODIFIER	-0.167334	1.281	-
VAR_CHR4_9842036	4	9842036	A	SLC2A9	intron_variant	MODIFIER	-0.259799	0.817	-
VAR_CHR4_9842089	4	9842089	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS77388911	4	9842207	T	SLC2A9	intron_variant	MODIFIER	-	-	0.34
VAR_CHR4_9842261	4	9842261	G	SLC2A9	intron_variant	MODIFIER	-0.094657	1.77	-
RS192132756	4	9842486	A	SLC2A9	intron_variant	MODIFIER	-0.34413	0.525	0.35
VAR_CHR4_9842490	4	9842490	A	SLC2A9	intron_variant	MODIFIER	0.032068	2.901	-

RS950309	4	9842754	G	SLC2A9	intron_variant	MODIFIER	-0.080266	1.881	0.35
RS950310	4	9842850	T	SLC2A9	intron_variant	MODIFIER	-	-	0.26
RS376831433	4	9842878	G	SLC2A9	intron_variant	MODIFIER	0.759692	9.212	-
VAR_CHR4_9842934	4	9842934	T	SLC2A9	intron_variant	MODIFIER	1.044968	10.91	-
RS13435427	4	9843024	T	SLC2A9	intron_variant	MODIFIER	1.289365	12.21	0.35
VAR_CHR4_9843168	4	9843168	C	SLC2A9	intron_variant	MODIFIER	0.720604	8.961	-
RS146537115	4	9843203	G	SLC2A9	intron_variant	MODIFIER	0.632893	8.381	0.29
VAR_CHR4_9843432	4	9843432	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS62295690	4	9843518	G	SLC2A9	intron_variant	MODIFIER	0.03355	2.915	0.45
VAR_CHR4_9843585	4	9843585	T	SLC2A9	intron_variant	MODIFIER	-0.069678	1.966	-
RS141566828	4	9843601	G	SLC2A9	intron_variant	MODIFIER	0.575306	7.983	0.43
RS79785876	4	9843620	G	SLC2A9	intron_variant	MODIFIER	-	-	0.44
RS181417171	4	9843798	A	SLC2A9	intron_variant	MODIFIER	1.698932	14.4	0.38
VAR_CHR4_9843809	4	9843809	T	SLC2A9	intron_variant	MODIFIER	1.124364	11.35	-
RS116006100	4	9843848	C	SLC2A9	intron_variant	MODIFIER	-0.186873	1.169	0.44
RS116316144	4	9843947	T	SLC2A9	intron_variant	MODIFIER	-0.109492	1.66	0.44
VAR_CHR4_9844131	4	9844131	T	SLC2A9	intron_variant	MODIFIER	0.984189	10.57	-
RS10939558	4	9844162	A	SLC2A9	intron_variant	MODIFIER	1.175191	11.62	0.33
VAR_CHR4_9844345	4	9844345	A	SLC2A9	intron_variant	MODIFIER	0.095214	3.557	-
RS6449049	4	9844514	G	SLC2A9	intron_variant	MODIFIER	0.134277	3.976	0.28
RS151128040	4	9844518	T	SLC2A9	intron_variant	MODIFIER	-0.006769	2.522	0.29
VAR_CHR4_9844688	4	9844688	A	SLC2A9	intron_variant	MODIFIER	0.122621	3.851	-
RS6449051	4	9844711	A	SLC2A9	intron_variant	MODIFIER	0.188619	4.559	0.26
RS6449052	4	9844732	C	SLC2A9	intron_variant	MODIFIER	-0.158768	1.332	0.34
RS189365277	4	9844760	T	SLC2A9	intron_variant	MODIFIER	-0.257241	0.828	0.23
RS78785836	4	9844767	A	SLC2A9	intron_variant	MODIFIER	0.081683	3.413	0.3

RS7683831	4	9845079	A	SLC2A9	intron_variant	MODIFIER	0.11393	3.757	0.34
VAR_CHR4_9845082	4	9845082	G	SLC2A9	intron_variant	MODIFIER	0.133693	3.97	-
VAR_CHR4_9845218	4	9845218	C	SLC2A9	intron_variant	MODIFIER	-0.321584	0.593	-
VAR_CHR4_9845416	4	9845416	G	SLC2A9	intron_variant	MODIFIER	-0.221196	0.99	-
RS16889496	4	9845597	T	SLC2A9	intron_variant	MODIFIER	-0.328618	0.571	0.45
RS150659411	4	9845787	A	SLC2A9	intron_variant	MODIFIER	0.090484	3.506	0.26
VAR_CHR4_9845810	4	9845810	G	SLC2A9	intron_variant	MODIFIER	-0.029447	2.312	-
VAR_CHR4_9845920	4	9845920	A	SLC2A9	intron_variant	MODIFIER	0.025663	2.837	-
RS77895782	4	9845942	A	SLC2A9	intron_variant	MODIFIER	0.390192	6.528	0.35
RS75620494	4	9845943	T	SLC2A9	intron_variant	MODIFIER	0.448494	7.024	0.34
RS13141635	4	9845985	A	SLC2A9	intron_variant	MODIFIER	-0.153597	1.364	0.35
VAR_CHR4_9846069	4	9846069	C	SLC2A9	intron_variant	MODIFIER	-0.078035	1.899	-
RS13142238	4	9846244	A	SLC2A9	intron_variant	MODIFIER	0.810426	9.528	0.35
RS11946054	4	9846247	A	SLC2A9	intron_variant	MODIFIER	0.789259	9.398	0.35
VAR_CHR4_9846302	4	9846302	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS1976792	4	9846309	T	SLC2A9	intron_variant	MODIFIER	-0.738838	0.059	0.12
VAR_CHR4_9846358	4	9846358	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS190567713	4	9846475	G	SLC2A9	intron_variant	MODIFIER	-	-	0.25
RS28624182	4	9846625	T	SLC2A9	intron_variant	MODIFIER	-0.631209	0.105	0.29
VAR_CHR4_9847617	4	9847617	C	SLC2A9	intron_variant	MODIFIER	-0.038979	2.227	-
RS146186799	4	9847736	A	SLC2A9	intron_variant	MODIFIER	-0.198155	1.108	0.18
RS55864719	4	9847766	A	SLC2A9	intron_variant	MODIFIER	0.360596	6.264	0.32
RS13119059	4	9847860	C	SLC2A9	intron_variant	MODIFIER	-0.594423	0.129	0.38
VAR_CHR4_9848077	4	9848077	T	SLC2A9	intron_variant	MODIFIER	-0.385963	0.418	-
RS185213646	4	9848325	G	SLC2A9	intron_variant	MODIFIER	-0.285011	0.718	0.32
RS16889509	4	9848326	A	SLC2A9	intron_variant	MODIFIER	-0.018806	2.409	0.35

RS75024060	4	9848374	G	SLC2A9	intron_variant	MODIFIER	-0.290522	0.698	0.28
RS150045473	4	9848433	C	SLC2A9	intron_variant	MODIFIER	0.09559	3.561	0.35
VAR_CHR4_9848486	4	9848486	A	SLC2A9	intron_variant	MODIFIER	-0.282227	0.729	-
RS189516145	4	9848545	A	SLC2A9	intron_variant	MODIFIER	1.925512	15.75	0.26
RS11723024	4	9848849	T	SLC2A9	intron_variant	MODIFIER	-	-	0.1
RS11721988	4	9848899	C	SLC2A9	intron_variant	MODIFIER	-0.669941	0.085	0.26
VAR_CHR4_9849153	4	9849153	A	SLC2A9	intron_variant	MODIFIER	-0.093317	1.78	-
VAR_CHR4_9849158	4	9849158	A	SLC2A9	intron_variant	MODIFIER	0.042578	3.007	-
RS16889519	4	9849200	G	SLC2A9	intron_variant	MODIFIER	-0.190255	1.15	0.13
VAR_CHR4_9849201	4	9849201	T	SLC2A9	intron_variant	MODIFIER	-0.698765	0.072	-
VAR_CHR4_9849507	4	9849507	A	SLC2A9	intron_variant	MODIFIER	-	-	-
RS2176644	4	9849528	A	SLC2A9	intron_variant	MODIFIER	0.800174	9.465	0.51
RS9992815	4	9849628	T	SLC2A9	intron_variant	MODIFIER	-0.060389	2.043	0.21
VAR_CHR4_9849767	4	9849767	C	SLC2A9	intron_variant	MODIFIER	-0.450732	0.291	-
RS9990770	4	9849800	G	SLC2A9	intron_variant	MODIFIER	-0.515292	0.201	0.39
RS2139242	4	9849864	A	SLC2A9	intron_variant	MODIFIER	0.006132	2.645	0.32
VAR_CHR4_9849913	4	9849913	T	SLC2A9	intron_variant	MODIFIER	-0.03357	2.275	-
RS145190091	4	9850191	A	SLC2A9	intron_variant	MODIFIER	0.369448	6.344	0.12
RS6812007	4	9850220	G	SLC2A9	intron_variant	MODIFIER	0.057044	3.155	0.12
VAR_CHR4_9850318	4	9850318	C	SLC2A9	intron_variant	MODIFIER	0.503375	7.457	-
VAR_CHR4_9850347	4	9850347	C	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9850380	4	9850380	T	SLC2A9	intron_variant	MODIFIER	0.003847	2.623	-
RS6828040	4	9850480	A	SLC2A9	intron_variant	MODIFIER	0.144117	4.082	0.15
VAR_CHR4_9850578	4	9850578	T	SLC2A9	intron_variant	MODIFIER	-0.381771	0.428	-
RS1980219	4	9850621	A	SLC2A9	intron_variant	MODIFIER	-0.211219	1.04	0.13
RS116244514	4	9850624	T	SLC2A9	intron_variant	MODIFIER	0.032288	2.903	0.15

VAR_CHR4_9850673	4	9850673	A	SLC2A9	intron_variant	MODIFIER	-0.2631	0.803	-
RS28392795	4	9850721	T	SLC2A9	intron_variant	MODIFIER	-0.421344	0.343	0.25
RS148228110	4	9850742	T	SLC2A9	intron_variant	MODIFIER	0.068	3.269	0.36
VAR_CHR4_9850902	4	9850902	T	SLC2A9	intron_variant	MODIFIER	-0.465374	0.268	-
VAR_CHR4_9850978	4	9850978	A	SLC2A9	intron_variant	MODIFIER	-	-	-
RS17242364	4	9851200	C	SLC2A9	intron_variant	MODIFIER	-0.615474	0.114	0.36
RS10939561	4	9851542	A	SLC2A9	intron_variant	MODIFIER	0.075997	3.353	0.38
VAR_CHR4_9851548	4	9851548	G	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9851551	4	9851551	G	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9851651	4	9851651	C	SLC2A9	intron_variant	MODIFIER	-0.148791	1.395	-
RS192839949	4	9851785	T	SLC2A9	intron_variant	MODIFIER	-0.028509	2.321	0.24
RS4697898	4	9851827	A	SLC2A9	intron_variant	MODIFIER	-0.440898	0.307	0.22
RS4697899	4	9851875	T	SLC2A9	intron_variant	MODIFIER	0.096465	3.57	0.24
RS184094798	4	9851877	A	SLC2A9	intron_variant	MODIFIER	0.132711	3.959	0.26
RS75690580	4	9852032	A	SLC2A9	intron_variant	MODIFIER	-0.222446	0.984	0.17
RS185069208	4	9852146	A	SLC2A9	intron_variant	MODIFIER	0.306683	5.758	0.23
RS139854873	4	9852155	A	SLC2A9	intron_variant	MODIFIER	0.055438	3.139	0.21
VAR_CHR4_9852167	4	9852167	A	SLC2A9	intron_variant	MODIFIER	0.102687	3.637	-
RS10004947	4	9852392	A	SLC2A9	intron_variant	MODIFIER	0.357941	6.239	0.2
RS35933336	4	9852516	C	SLC2A9	intron_variant	MODIFIER	0.904998	10.11	0.18
RS186855576	4	9852556	A	SLC2A9	intron_variant	MODIFIER	0.835918	9.684	0.23
RS114214457	4	9852649	A	SLC2A9	intron_variant	MODIFIER	-	-	0.18
RS77963917	4	9852696	C	SLC2A9	intron_variant	MODIFIER	-	-	0.16
VAR_CHR4_9852703	4	9852703	C	SLC2A9	intron_variant	MODIFIER	-0.124919	1.552	-
RS11930098	4	9852709	C	SLC2A9	intron_variant	MODIFIER	-0.795481	0.044	0.19
VAR_CHR4_9852735	4	9852735	A	SLC2A9	intron_variant	MODIFIER	0.115708	3.776	-

RS3960679	4	9852745	A	SLC2A9	intron_variant	MODIFIER	0.234697	5.041	0.21
RS6831580	4	9852750	G	SLC2A9	intron_variant	MODIFIER	-0.131572	1.507	0.17
RS6812563	4	9852757	G	SLC2A9	intron_variant	MODIFIER	-	-	0.18
VAR_CHR4_9852768	4	9852768	A	SLC2A9	intron_variant	MODIFIER	0.184882	4.519	-
VAR_CHR4_9852829	4	9852829	T	SLC2A9	intron_variant	MODIFIER	-0.327872	0.573	-
RS6831796	4	9852898	C	SLC2A9	intron_variant	MODIFIER	-	-	0.26
RS116859645	4	9852913	A	SLC2A9	intron_variant	MODIFIER	0.906028	10.11	0.22
RS11933838	4	9852920	G	SLC2A9	intron_variant	MODIFIER	0.631381	8.371	0.21
RS6847858	4	9853059	A	SLC2A9	intron_variant	MODIFIER	0.606168	8.199	0.25
RS6847871	4	9853074	A	SLC2A9	intron_variant	MODIFIER	-0.304545	0.649	0.25
RS74623241	4	9853193	A	SLC2A9	intron_variant	MODIFIER	0.328649	5.968	0.28
RS373697506	4	9853306	C	SLC2A9	intron_variant	MODIFIER	0.266056	5.359	-
RS6832792	4	9853350	T	SLC2A9	intron_variant	MODIFIER	0.25618	5.26	0.34
RS148747594	4	9853368	G	SLC2A9	intron_variant	MODIFIER	-	-	0.29
VAR_CHR4_9853675	4	9853675	A	SLC2A9	intron_variant	MODIFIER	-	-	-
RS73092479	4	9854410	C	SLC2A9	intron_variant	MODIFIER	-0.140173	1.45	0.3
RS13152172	4	9855141	G	SLC2A9	intron_variant	MODIFIER	-0.067029	1.988	0.33
VAR_CHR4_9855182	4	9855182	G	SLC2A9	intron_variant	MODIFIER	-0.383935	0.423	-
RS11933731	4	9855712	A	SLC2A9	intron_variant	MODIFIER	1.860514	15.35	0.24
VAR_CHR4_9855799	4	9855799	G	SLC2A9	intron_variant	MODIFIER	1.340442	12.48	-
RS11932607	4	9855878	T	SLC2A9	intron_variant	MODIFIER	0.734448	9.051	0.38
VAR_CHR4_9855919	4	9855919	T	SLC2A9	intron_variant	MODIFIER	-0.158455	1.334	-
VAR_CHR4_9855954	4	9855954	G	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9855973	4	9855973	C	SLC2A9	intron_variant	MODIFIER	-0.082678	1.862	-
VAR_CHR4_9856370	4	9856370	G	SLC2A9	intron_variant	MODIFIER	0.179862	4.466	-
RS6826806	4	9856469	C	SLC2A9	intron_variant	MODIFIER	0.20276	4.708	0.28

RS11934050	4	9856485	A	SLC2A9	intron_variant	MODIFIER	0.464163	7.151	0.32
RS28868569	4	9856515	T	SLC2A9	intron_variant	MODIFIER	-0.305789	0.645	0.29
VAR_CHR4_9856788	4	9856788	A	SLC2A9	intron_variant	MODIFIER	0.778017	9.328	-
VAR_CHR4_9856797	4	9856797	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS6852425	4	9856859	C	SLC2A9	intron_variant	MODIFIER	-0.32288	0.589	0.24
RS139292069	4	9857039	A	SLC2A9	intron_variant	MODIFIER	-0.07055	1.959	0.32
VAR_CHR4_9857040	4	9857040	T	SLC2A9	intron_variant	MODIFIER	-0.417061	0.352	-
RS11728377	4	9858701	T	SLC2A9	intron_variant	MODIFIER	-	-	0.15
VAR_CHR4_9858711	4	9858711	C	SLC2A9	intron_variant	MODIFIER	0.083933	3.437	-
RS4575993	4	9858744	T	SLC2A9	intron_variant	MODIFIER	-0.28336	0.724	0.18
VAR_CHR4_9858951	4	9858951	T	SLC2A9	intron_variant	MODIFIER	-0.19221	1.139	-
RS138041093	4	9858956	A	SLC2A9	intron_variant	MODIFIER	-0.351112	0.506	0.19
RS141720595	4	9858984	A	SLC2A9	intron_variant	MODIFIER	0.202032	4.701	0.23
RS181315906	4	9859141	T	SLC2A9	intron_variant	MODIFIER	-0.037771	2.238	0.22
RS61209374	4	9859160	G	SLC2A9	intron_variant	MODIFIER	-	-	0.27
RS56970526	4	9859557	G	SLC2A9	intron_variant	MODIFIER	-0.135879	1.478	0.23
VAR_CHR4_9859586	4	9859586	T	SLC2A9	intron_variant	MODIFIER	-0.06882	1.973	-
RS16889691	4	9859763	T	SLC2A9	intron_variant	MODIFIER	0.387315	6.503	0.26
RS13116446	4	9859897	C	SLC2A9	intron_variant	MODIFIER	-0.348188	0.514	0.29
RS4697900	4	9859976	T	SLC2A9	intron_variant	MODIFIER	-0.080282	1.881	0.23
RS146327126	4	9860151	A	SLC2A9	intron_variant	MODIFIER	-0.35644	0.492	0.29
RS62295694	4	9860327	C	SLC2A9	intron_variant	MODIFIER	0.985573	10.58	0.24
VAR_CHR4_9860342	4	9860342	G	SLC2A9	intron_variant	MODIFIER	0.789746	9.401	-
VAR_CHR4_9860397	4	9860397	A	SLC2A9	intron_variant	MODIFIER	-0.635185	0.103	-
RS62295695	4	9860434	T	SLC2A9	intron_variant	MODIFIER	-0.263628	0.801	0.17
RS112851767	4	9860882	G	SLC2A9	intron_variant	MODIFIER	-	-	0.34

RS181420478	4	9860904	C	SLC2A9	intron_variant	MODIFIER	0.049379	3.076	0.29
RS192368924	4	9861236	G	SLC2A9	intron_variant	MODIFIER	0.07594	3.353	0.33
RS73225806	4	9861237	T	SLC2A9	intron_variant	MODIFIER	-0.360489	0.481	0.36
RS56136402	4	9861300	A	SLC2A9	intron_variant	MODIFIER	0.469967	7.197	0.32
VAR_CHR4_9861350	4	9861350	G	SLC2A9	intron_variant	MODIFIER	1.08007	11.11	-
RS116968042	4	9861461	C	SLC2A9	intron_variant	MODIFIER	0.00013	2.587	0.21
VAR_CHR4_9861511	4	9861511	A	SLC2A9	intron_variant	MODIFIER	0.047348	3.055	-
RS1106059	4	9861512	T	SLC2A9	intron_variant	MODIFIER	-0.367313	0.463	0.31
RS1106058	4	9861524	T	SLC2A9	intron_variant	MODIFIER	0.213753	4.823	0.35
RS28462017	4	9861630	T	SLC2A9	intron_variant	MODIFIER	-0.104204	1.699	0.24
RS192891241	4	9861758	G	SLC2A9	intron_variant	MODIFIER	-	-	0.31
VAR_CHR4_9861969	4	9861969	A	SLC2A9	intron_variant	MODIFIER	0.369902	6.348	-
RS9684729	4	9862036	G	SLC2A9	intron_variant	MODIFIER	-0.016702	2.429	0.23
RS142856421	4	9862134	G	SLC2A9	intron_variant	MODIFIER	-	-	0.35
RS118033084	4	9862180	A	SLC2A9	intron_variant	MODIFIER	0.232816	5.021	0.24
RS116243766	4	9862208	G	SLC2A9	intron_variant	MODIFIER	0.183222	4.501	0.25
VAR_CHR4_9862293	4	9862293	A	SLC2A9	intron_variant	MODIFIER	-0.042573	2.196	-
RS10003673	4	9862300	C	SLC2A9	intron_variant	MODIFIER	-0.171621	1.256	0.3
RS148662327	4	9862367	C	SLC2A9	intron_variant	MODIFIER	-0.319529	0.599	0.25
RS376904135	4	9862380	A	SLC2A9	intron_variant	MODIFIER	-0.092541	1.786	-
RS62295697	4	9862456	C	SLC2A9	intron_variant	MODIFIER	-0.379496	0.433	0.24
VAR_CHR4_9862531	4	9862531	T	SLC2A9	intron_variant	MODIFIER	-0.25199	0.85	-
RS117540324	4	9862685	C	SLC2A9	intron_variant	MODIFIER	-	-	0.27
VAR_CHR4_9862769	4	9862769	T	SLC2A9	intron_variant	MODIFIER	0.011601	2.698	-
VAR_CHR4_9862770	4	9862770	T	SLC2A9	intron_variant	MODIFIER	0.106078	3.673	-
VAR_CHR4_9862847	4	9862847	A	SLC2A9	intron_variant	MODIFIER	0.538688	7.72	-

RS4613568	4	9862902	A	SLC2A9	intron_variant	MODIFIER	0.385672	6.488	0.3
VAR_CHR4_9862934	4	9862934	A	SLC2A9	intron_variant	MODIFIER	-0.306227	0.643	-
RS114693474	4	9863033	A	SLC2A9	intron_variant	MODIFIER	0.095855	3.564	0.22
RS79048870	4	9863145	C	SLC2A9	intron_variant	MODIFIER	1.034245	10.85	0.38
VAR_CHR4_9863414	4	9863414	G	SLC2A9	intron_variant	MODIFIER	0.30744	5.766	-
RS61233382	4	9863443	T	SLC2A9	intron_variant	MODIFIER	-	-	0.28
RS28591077	4	9863678	T	SLC2A9	intron_variant	MODIFIER	-0.24295	0.889	0.23
RS4697901	4	9863698	C	SLC2A9	intron_variant	MODIFIER	-0.211789	1.037	0.28
RS4697902	4	9863936	A	SLC2A9	intron_variant	MODIFIER	0.020078	2.781	0.2
RS147563048	4	9863976	T	SLC2A9	intron_variant	MODIFIER	-0.270413	0.774	0.23
RS376405315	4	9863997	G	SLC2A9	intron_variant	MODIFIER	-0.119809	1.587	-
RS7680896	4	9864065	G	SLC2A9	intron_variant	MODIFIER	-0.063576	2.017	0.22
VAR_CHR4_9864212	4	9864212	T	SLC2A9	intron_variant	MODIFIER	-0.12456	1.554	-
RS35629527	4	9864232	G	SLC2A9	intron_variant	MODIFIER	0.082823	3.425	0.25
VAR_CHR4_9864318	4	9864318	A	SLC2A9	intron_variant	MODIFIER	-0.459969	0.276	-
RS192585541	4	9864454	G	SLC2A9	intron_variant	MODIFIER	-0.563603	0.153	0.41
VAR_CHR4_9864633	4	9864633	A	SLC2A9	intron_variant	MODIFIER	-0.207865	1.057	-
RS114750793	4	9864645	A	SLC2A9	intron_variant	MODIFIER	-0.017642	2.42	0.4
RS115318424	4	9864855	A	SLC2A9	intron_variant	MODIFIER	-0.43582	0.316	0.38
VAR_CHR4_9865038	4	9865038	A	SLC2A9	intron_variant	MODIFIER	-0.210748	1.042	-
VAR_CHR4_9865290	4	9865290	G	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9865321	4	9865321	A	SLC2A9	intron_variant	MODIFIER	-0.043991	2.183	-
RS4697903	4	9865426	T	SLC2A9	intron_variant	MODIFIER	-0.293862	0.686	0.45
RS56288911	4	9865615	A	SLC2A9	intron_variant	MODIFIER	0.108087	3.694	0.35
VAR_CHR4_9865827	4	9865827	A	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9865924	4	9865924	A	SLC2A9	intron_variant	MODIFIER	0.939508	10.31	-

VAR_CHR4_9866183	4	9866183	G	SLC2A9	intron_variant	MODIFIER	0.562172	7.89	-
RS79598790	4	9866480	A	SLC2A9	intron_variant	MODIFIER	-0.008618	2.504	0.32
VAR_CHR4_9866481	4	9866481	A	SLC2A9	intron_variant	MODIFIER	-0.383261	0.424	-
RS9684002	4	9866498	C	SLC2A9	intron_variant	MODIFIER	-0.554023	0.162	0.31
VAR_CHR4_9866509	4	9866509	C	SLC2A9	intron_variant	MODIFIER	-0.188774	1.158	-
VAR_CHR4_9866514	4	9866514	C	SLC2A9	intron_variant	MODIFIER	-0.050663	2.125	-
RS185447022	4	9866537	A	SLC2A9	intron_variant	MODIFIER	0.170272	4.363	0.37
VAR_CHR4_9866553	4	9866553	T	SLC2A9	intron_variant	MODIFIER	-0.109316	1.662	-
RS73092500	4	9866760	T	SLC2A9	intron_variant	MODIFIER	-0.556449	0.16	0.35
VAR_CHR4_9867245	4	9867245	C	SLC2A9	intron_variant	MODIFIER	-0.590443	0.132	-
RS2292917	4	9867277	G	SLC2A9	intron_variant	MODIFIER	-0.179226	1.212	0.17
VAR_CHR4_9867318	4	9867318	G	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9867329	4	9867329	C	SLC2A9	intron_variant	MODIFIER	0.040891	2.99	-
VAR_CHR4_9867433	4	9867433	T	SLC2A9	intron_variant	MODIFIER	-0.93849	0.021	-
VAR_CHR4_9867456	4	9867456	G	SLC2A9	intron_variant	MODIFIER	0.038837	2.969	-
RS75375980	4	9867478	A	SLC2A9	intron_variant	MODIFIER	-0.173707	1.243	0.27
VAR_CHR4_9867498	4	9867498	G	SLC2A9	intron_variant	MODIFIER	0.242483	5.121	-
RS2139243	4	9867502	C	SLC2A9	intron_variant	MODIFIER	-0.273785	0.761	0.21
RS2292916	4	9867515	G	SLC2A9	intron_variant	MODIFIER	-0.10443	1.697	0.24
RS57235613	4	9867708	A	SLC2A9	intron_variant	MODIFIER	0.262148	5.32	0.15
VAR_CHR4_9867758	4	9867758	T	SLC2A9	intron_variant	MODIFIER	-0.174036	1.242	-
VAR_CHR4_9868026	4	9868026	T	SLC2A9	intron_variant	MODIFIER	-0.367134	0.464	-
VAR_CHR4_9868079	4	9868079	G	SLC2A9	intron_variant	MODIFIER	0.009784	2.68	-
VAR_CHR4_9868194	4	9868194	T	SLC2A9	intron_variant	MODIFIER	-0.221528	0.989	-
RS883041	4	9868346	A	SLC2A9	intron_variant	MODIFIER	0.02998	2.88	0.23
RS118137999	4	9868359	T	SLC2A9	intron_variant	MODIFIER	-0.161569	1.315	0.21

RS13105954	4	9868417	G	SLC2A9	intron_variant	MODIFIER	-0.529891	0.185	0.23
RS939134	4	9868593	A	SLC2A9	intron_variant	MODIFIER	-	-	0.25
VAR_CHR4_9868615	4	9868615	A	SLC2A9	intron_variant	MODIFIER	-0.117822	1.601	-
VAR_CHR4_9868674	4	9868674	A	SLC2A9	intron_variant	MODIFIER	-0.279146	0.74	-
VAR_CHR4_9868703	4	9868703	T	SLC2A9	intron_variant	MODIFIER	-0.065367	2.002	-
RS149815051	4	9868904	T	SLC2A9	intron_variant	MODIFIER	-0.302763	0.655	0.31
RS11731339	4	9868930	A	SLC2A9	intron_variant	MODIFIER	-0.012889	2.464	0.24
RS193066246	4	9868977	G	SLC2A9	intron_variant	MODIFIER	-0.368634	0.46	0.33
RS56396145	4	9869215	G	SLC2A9	intron_variant	MODIFIER	-0.188691	1.159	0.32
VAR_CHR4_9869240	4	9869240	A	SLC2A9	intron_variant	MODIFIER	-0.254882	0.837	-
VAR_CHR4_9869363	4	9869363	A	SLC2A9	intron_variant	MODIFIER	1.131441	11.38	-
VAR_CHR4_9869371	4	9869371	A	SLC2A9	intron_variant	MODIFIER	0.759358	9.21	-
VAR_CHR4_9869452	4	9869452	A	SLC2A9	intron_variant	MODIFIER	0.10943	3.709	-
VAR_CHR4_9869688	4	9869688	T	SLC2A9	intron_variant	MODIFIER	-0.076907	1.908	-
RS884573	4	9869734	G	SLC2A9	intron_variant	MODIFIER	-	-	0.21
RS62293270	4	9869738	G	SLC2A9	intron_variant	MODIFIER	-0.070428	1.96	0.18
VAR_CHR4_9869792	4	9869792	A	SLC2A9	intron_variant	MODIFIER	0.372138	6.368	-
VAR_CHR4_9869793	4	9869793	T	SLC2A9	intron_variant	MODIFIER	-0.193573	1.132	-
RS55858763	4	9869970	T	SLC2A9	intron_variant	MODIFIER	-0.690747	0.076	0.2
RS78757705	4	9870119	T	SLC2A9	intron_variant	MODIFIER	0.001446	2.6	0.29
RS1320054	4	9870125	G	SLC2A9	intron_variant	MODIFIER	0.055493	3.139	0.25
VAR_CHR4_9870323	4	9870323	A	SLC2A9	intron_variant	MODIFIER	-0.139265	1.456	-
VAR_CHR4_9870375	4	9870375	A	SLC2A9	intron_variant	MODIFIER	-	-	-
RS150441658	4	9870389	T	SLC2A9	intron_variant	MODIFIER	-0.639422	0.1	0.26
RS138102553	4	9870449	A	SLC2A9	intron_variant	MODIFIER	0.308126	5.772	0.26
RS1048252	4	9870535	A	SLC2A9	intron_variant	MODIFIER	0.06808	3.27	0.25

VAR_CHR4_9870703	4	9870703	T	SLC2A9	intron_variant	MODIFIER	-0.252684	0.847	-
VAR_CHR4_9870875	4	9870875	A	SLC2A9	intron_variant	MODIFIER	-0.327605	0.574	-
RS62293272	4	9871007	A	SLC2A9	intron_variant	MODIFIER	0.372683	6.373	0.39
VAR_CHR4_9871094	4	9871094	C	SLC2A9	intron_variant	MODIFIER	-0.687428	0.077	-
VAR_CHR4_9871225	4	9871225	T	SLC2A9	intron_variant	MODIFIER	-0.405023	0.376	-
RS149236596	4	9871351	C	SLC2A9	intron_variant	MODIFIER	-0.743862	0.057	0.33
RS144448091	4	9871484	G	SLC2A9	intron_variant	MODIFIER	-0.427786	0.331	0.34
RS1568318	4	9871541	G	SLC2A9	intron_variant	MODIFIER	0.040624	2.987	0.42
RS376875409	4	9871592	G	SLC2A9	intron_variant	MODIFIER	0.112921	3.746	-
VAR_CHR4_9871637	4	9871637	A	SLC2A9	intron_variant	MODIFIER	0.269746	5.396	-
RS142562622	4	9871770	T	SLC2A9	intron_variant	MODIFIER	-0.082328	1.865	0.33
VAR_CHR4_9871779	4	9871779	A	SLC2A9	intron_variant	MODIFIER	0.255918	5.257	-
RS16889842	4	9872013	T	SLC2A9	intron_variant	MODIFIER	-0.359612	0.483	0.26
RS11947634	4	9872089	A	SLC2A9	intron_variant	MODIFIER	0.27286	5.427	0.35
VAR_CHR4_9872108	4	9872108	A	SLC2A9	intron_variant	MODIFIER	0.088617	3.487	-
RS11941148	4	9872364	C	SLC2A9	intron_variant	MODIFIER	-0.297985	0.671	0.19
VAR_CHR4_9872400	4	9872400	G	SLC2A9	intron_variant	MODIFIER	-0.054151	2.096	-
RS11731759	4	9872456	G	SLC2A9	intron_variant	MODIFIER	-	-	0.16
VAR_CHR4_9872474	4	9872474	A	SLC2A9	intron_variant	MODIFIER	-0.143039	1.431	-
RS2867394	4	9872475	T	SLC2A9	intron_variant	MODIFIER	-0.405664	0.375	0.13
VAR_CHR4_9872518	4	9872518	A	SLC2A9	intron_variant	MODIFIER	-0.028182	2.324	-
RS56149009	4	9872581	A	SLC2A9	intron_variant	MODIFIER	0.018636	2.767	0.19
RS56351177	4	9872795	A	SLC2A9	intron_variant	MODIFIER	0.42639	6.84	0.22
RS56275585	4	9872878	T	SLC2A9	intron_variant	MODIFIER	-0.035816	2.255	0.22
VAR_CHR4_9872881	4	9872881	C	SLC2A9	intron_variant	MODIFIER	-0.627962	0.107	-
VAR_CHR4_9873058	4	9873058	C	SLC2A9	intron_variant	MODIFIER	-0.287703	0.708	-

VAR_CHR4_9873341	4	9873341	T	SLC2A9	intron_variant	MODIFIER	-0.101337	1.72	-
RS73225810	4	9873370	T	SLC2A9	intron_variant	MODIFIER	-0.09242	1.787	0.18
VAR_CHR4_9873494	4	9873494	T	SLC2A9	intron_variant	MODIFIER	0.215199	4.839	-
VAR_CHR4_9873542	4	9873542	G	SLC2A9	intron_variant	MODIFIER	0.60683	8.203	-
RS372496138	4	9873635	C	SLC2A9	intron_variant	MODIFIER	-0.206333	1.065	-
VAR_CHR4_9873782	4	9873782	C	SLC2A9	intron_variant	MODIFIER	0.675448	8.665	-
RS73225811	4	9873790	A	SLC2A9	intron_variant	MODIFIER	1.173545	11.61	0.23
RS138416405	4	9873822	G	SLC2A9	intron_variant	MODIFIER	-0.281549	0.731	0.21
RS13148571	4	9873855	G	SLC2A9	intron_variant	MODIFIER	-0.143625	1.427	0.28
RS56202030	4	9873858	T	SLC2A9	intron_variant	MODIFIER	-0.004174	2.546	0.22
VAR_CHR4_9873997	4	9873997	A	SLC2A9	intron_variant	MODIFIER	0.121371	3.837	-
RS73225812	4	9873999	A	SLC2A9	intron_variant	MODIFIER	-0.003589	2.552	0.26
RS116658755	4	9874127	A	SLC2A9	intron_variant	MODIFIER	-0.023451	2.367	0.28
RS1519099	4	9874130	A	SLC2A9	intron_variant	MODIFIER	0.254348	5.241	-
RS182611868	4	9874381	C	SLC2A9	intron_variant	MODIFIER	-	-	0.39
VAR_CHR4_9874509	4	9874509	C	SLC2A9	intron_variant	MODIFIER	0.064335	3.231	-
RS141354936	4	9874705	C	SLC2A9	intron_variant	MODIFIER	0.05432	3.127	0.52
VAR_CHR4_9874890	4	9874890	T	SLC2A9	intron_variant	MODIFIER	-0.25272	0.847	-
VAR_CHR4_9875526	4	9875526	G	SLC2A9	intron_variant	MODIFIER	0.505161	7.47	-
VAR_CHR4_9875710	4	9875710	A	SLC2A9	intron_variant	MODIFIER	-0.033895	2.272	-
RS146123527	4	9875751	C	SLC2A9	intron_variant	MODIFIER	-0.448539	0.294	0.31
RS116628257	4	9875798	A	SLC2A9	intron_variant	MODIFIER	0.152748	4.175	0.3
VAR_CHR4_9875994	4	9875994	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS114104836	4	9876035	A	SLC2A9	intron_variant	MODIFIER	-0.095709	1.762	0.3
RS148782913	4	9876104	A	SLC2A9	intron_variant	MODIFIER	-0.203662	1.079	0.33
VAR_CHR4_9876107	4	9876107	C	SLC2A9	intron_variant	MODIFIER	-	-	-

RS62293275	4	9876276	C	SLC2A9	intron_variant	MODIFIER	-0.201794	1.088	0.41
VAR_CHR4_9876360	4	9876360	G	SLC2A9	intron_variant	MODIFIER	-0.227814	0.959	-
RS62293276	4	9876519	G	SLC2A9	intron_variant	MODIFIER	-0.264932	0.796	0.23
RS55916827	4	9876977	G	SLC2A9	intron_variant	MODIFIER	0.29336	5.629	0.22
RS55816202	4	9877014	G	SLC2A9	intron_variant	MODIFIER	-0.251406	0.852	0.14
RS10033286	4	9877040	T	SLC2A9	intron_variant	MODIFIER	-	-	0.29
RS138828651	4	9877081	G	SLC2A9	intron_variant	MODIFIER	1.155397	11.51	0.2
RS367769397	4	9877182	C	SLC2A9	intron_variant	MODIFIER	0.123102	3.856	-
RS62293282	4	9877556	T	SLC2A9	intron_variant	MODIFIER	-0.167868	1.278	0.19
RS73225813	4	9877617	C	SLC2A9	intron_variant	MODIFIER	-	-	0.31
RS16889932	4	9877640	A	SLC2A9	intron_variant	MODIFIER	-0.043479	2.188	0.24
RS138554449	4	9877676	G	SLC2A9	intron_variant	MODIFIER	0.017596	2.757	0.18
VAR_CHR4_9877686	4	9877686	T	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9877721	4	9877721	C	SLC2A9	intron_variant	MODIFIER	0.031357	2.893	-
RS188213035	4	9877779	G	SLC2A9	intron_variant	MODIFIER	0.110073	3.716	0.9
RS62293283	4	9877837	T	SLC2A9	intron_variant	MODIFIER	0.021871	2.799	0.17
RS62293284	4	9877862	T	SLC2A9	intron_variant	MODIFIER	-0.355512	0.494	0.13
RS62293285	4	9877926	C	SLC2A9	intron_variant	MODIFIER	-0.901905	0.026	0.14
RS184652935	4	9877988	T	SLC2A9	intron_variant	MODIFIER	1.243837	11.98	0.17
VAR_CHR4_9878048	4	9878048	T	SLC2A9	intron_variant	MODIFIER	-0.235859	0.921	-
RS192084120	4	9878188	T	SLC2A9	intron_variant	MODIFIER	0.310102	5.791	0.22
RS7688629	4	9878201	G	SLC2A9	intron_variant	MODIFIER	-0.212003	1.036	0.25
VAR_CHR4_9878436	4	9878436	A	SLC2A9	intron_variant	MODIFIER	-0.082548	1.863	-
RS12647883	4	9878464	G	SLC2A9	intron_variant	MODIFIER	-	-	0.29
RS180951075	4	9878684	A	SLC2A9	intron_variant	MODIFIER	0.036818	2.948	0.3
VAR_CHR4_9878726	4	9878726	G	SLC2A9	intron_variant	MODIFIER	0.813828	9.549	-

VAR_CHR4_9878824	4	9878824	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS117296899	4	9878867	T	SLC2A9	intron_variant	MODIFIER	0.219016	4.878	0.3
VAR_CHR4_9878889	4	9878889	T	SLC2A9	intron_variant	MODIFIER	0.215808	4.845	-
VAR_CHR4_9878969	4	9878969	T	SLC2A9	intron_variant	MODIFIER	0.448867	7.027	-
RS78087789	4	9879010	T	SLC2A9	intron_variant	MODIFIER	-0.286514	0.713	0.33
RS145329462	4	9879114	C	SLC2A9	intron_variant	MODIFIER	-0.078905	1.892	0.37
RS62293286	4	9879127	A	SLC2A9	intron_variant	MODIFIER	0.21941	4.883	0.45
RS76606104	4	9879187	G	SLC2A9	intron_variant	MODIFIER	-0.010055	2.491	0.38
VAR_CHR4_9879333	4	9879333	G	SLC2A9	intron_variant	MODIFIER	-0.287376	0.709	-
RS181623671	4	9879342	G	SLC2A9	intron_variant	MODIFIER	-	-	0.26
RS113565634	4	9879410	T	SLC2A9	intron_variant	MODIFIER	-	-	0.3
VAR_CHR4_9879480	4	9879480	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS79146062	4	9879667	T	SLC2A9	intron_variant	MODIFIER	-0.041185	2.208	0.26
VAR_CHR4_9879706	4	9879706	G	SLC2A9	intron_variant	MODIFIER	-0.28885	0.704	-
VAR_CHR4_9879725	4	9879725	A	SLC2A9	intron_variant	MODIFIER	0.070246	3.293	-
RS114069885	4	9879727	G	SLC2A9	intron_variant	MODIFIER	-0.175502	1.233	0.15
RS6810736	4	9879728	G	SLC2A9	intron_variant	MODIFIER	-0.05865	2.058	0.14
VAR_CHR4_9879765	4	9879765	A	SLC2A9	intron_variant	MODIFIER	-0.658806	0.09	-
RS191322243	4	9879766	A	SLC2A9	intron_variant	MODIFIER	-	-	0.17
RS182640566	4	9879771	G	SLC2A9	intron_variant	MODIFIER	-0.125706	1.546	0.19
RS75015234	4	9879924	G	SLC2A9	intron_variant	MODIFIER	-0.106844	1.68	0.17
RS147912672	4	9880160	T	SLC2A9	intron_variant	MODIFIER	-0.130444	1.514	0.22
RS6840999	4	9880169	T	SLC2A9	intron_variant	MODIFIER	-0.159952	1.325	0.25
VAR_CHR4_9880329	4	9880329	C	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9880350	4	9880350	G	SLC2A9	intron_variant	MODIFIER	0.216439	4.852	-
VAR_CHR4_9880434	4	9880434	A	SLC2A9	intron_variant	MODIFIER	-0.120103	1.585	-

VAR_CHR4_9880475	4	9880475	G	SLC2A9	intron_variant	MODIFIER	0.073373	3.326	-
RS62293287	4	9880940	T	SLC2A9	intron_variant	MODIFIER	-0.655875	0.091	0.26
RS145058214	4	9881075	A	SLC2A9	intron_variant	MODIFIER	-0.008505	2.505	0.2
VAR_CHR4_9881090	4	9881090	T	SLC2A9	intron_variant	MODIFIER	-0.30226	0.657	-
RS370891760	4	9881124	A	SLC2A9	intron_variant	MODIFIER	0.115483	3.774	-
RS1519098	4	9881158	G	SLC2A9	intron_variant	MODIFIER	-0.082064	1.867	0.19
VAR_CHR4_9881258	4	9881258	G	SLC2A9	intron_variant	MODIFIER	0.100116	3.609	-
RS367788933	4	9881313	C	SLC2A9	intron_variant	MODIFIER	-0.338292	0.542	-
RS78284941	4	9881418	T	SLC2A9	intron_variant	MODIFIER	-0.454564	0.285	0.22
VAR_CHR4_9881520	4	9881520	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS6834978	4	9881600	A	SLC2A9	intron_variant	MODIFIER	0.457241	7.095	0.21
RS144929860	4	9881605	T	SLC2A9	intron_variant	MODIFIER	-0.039746	2.22	0.25
VAR_CHR4_9881663	4	9881663	G	SLC2A9	intron_variant	MODIFIER	0.026433	2.844	-
RS372000442	4	9881706	C	SLC2A9	intron_variant	MODIFIER	-0.212427	1.034	-
VAR_CHR4_9881815	4	9881815	A	SLC2A9	intron_variant	MODIFIER	0.201754	4.698	-
RS6824636	4	9881851	G	SLC2A9	intron_variant	MODIFIER	-0.54193	0.173	0.23
RS117694798	4	9881919	A	SLC2A9	intron_variant	MODIFIER	0.066937	3.258	0.35
RS180833011	4	9881920	T	SLC2A9	intron_variant	MODIFIER	-0.261017	0.812	0.36
VAR_CHR4_9881972	4	9881972	T	SLC2A9	intron_variant	MODIFIER	-0.151428	1.378	-
VAR_CHR4_9882111	4	9882111	C	SLC2A9	intron_variant	MODIFIER	-0.622177	0.11	-
VAR_CHR4_9882284	4	9882284	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS117076318	4	9882417	G	SLC2A9	intron_variant	MODIFIER	0.159505	4.248	0.8
RS56358669	4	9882470	G	SLC2A9	intron_variant	MODIFIER	-0.188918	1.157	0.5
VAR_CHR4_9882545	4	9882545	T	SLC2A9	intron_variant	MODIFIER	-0.067327	1.986	-
RS62293289	4	9882584	A	SLC2A9	intron_variant	MODIFIER	0.400948	6.622	0.19
VAR_CHR4_9882591	4	9882591	A	SLC2A9	intron_variant	MODIFIER	0.054279	3.127	-

VAR_CHR4_9882651	4	9882651	G	SLC2A9	intron_variant	MODIFIER	0.096089	3.566	-
RS62293290	4	9882662	G	SLC2A9	intron_variant	MODIFIER	-0.332318	0.56	0.31
RS62293291	4	9882687	G	SLC2A9	intron_variant	MODIFIER	-0.051518	2.118	0.32
VAR_CHR4_9882885	4	9882885	G	SLC2A9	intron_variant	MODIFIER	-0.000473	2.581	-
RS181517438	4	9882998	T	SLC2A9	intron_variant	MODIFIER	-0.065885	1.997	0.24
RS189875791	4	9883179	G	SLC2A9	intron_variant	MODIFIER	0.057466	3.16	0.16
RS117861080	4	9883218	A	SLC2A9	intron_variant	MODIFIER	0.193461	4.61	0.19
RS35512765	4	9883233	G	SLC2A9	intron_variant	MODIFIER	0.040531	2.986	0.18
RS55943327	4	9883438	G	SLC2A9	intron_variant	MODIFIER	-0.234487	0.928	0.15
RS55721900	4	9883534	C	SLC2A9	intron_variant	MODIFIER	-0.43502	0.318	0.17
RS6847887	4	9883801	T	SLC2A9	intron_variant	MODIFIER	-0.137323	1.469	0.22
RS6838850	4	9884057	G	SLC2A9	intron_variant	MODIFIER	-0.072316	1.945	0.13
RS6838891	4	9884114	G	SLC2A9	intron_variant	MODIFIER	-0.519611	0.197	0.11
RS6848689	4	9884197	C	SLC2A9	intron_variant	MODIFIER	-0.191916	1.141	0.14
RS6449089	4	9884258	C	SLC2A9	intron_variant	MODIFIER	-0.376768	0.44	0.16
RS6839302	4	9884324	A	SLC2A9	intron_variant	MODIFIER	0.009318	2.676	0.12
VAR_CHR4_9884450	4	9884450	G	SLC2A9	intron_variant	MODIFIER	0.014642	2.728	-
RS141052822	4	9884475	C	SLC2A9	intron_variant	MODIFIER	-	-	0.15
VAR_CHR4_9884477	4	9884477	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS7696971	4	9884528	A	SLC2A9	intron_variant	MODIFIER	0.164178	4.298	0.13
RS6449090	4	9884536	A	SLC2A9	intron_variant	MODIFIER	0.170464	4.365	0.12
RS193289149	4	9884613	G	SLC2A9	intron_variant	MODIFIER	-0.049316	2.137	0.16
RS73225827	4	9884782	G	SLC2A9	intron_variant	MODIFIER	-0.30942	0.632	0.21
RS77105911	4	9884876	T	SLC2A9	intron_variant	MODIFIER	-0.257833	0.825	0.28
RS78028161	4	9884979	T	SLC2A9	intron_variant	MODIFIER	-0.585361	0.136	0.2
VAR_CHR4_9884985	4	9884985	A	SLC2A9	intron_variant	MODIFIER	-0.189615	1.154	-

RS56322912	4	9885083	T	SLC2A9	intron_variant	MODIFIER	0.083701	3.434	0.34
VAR_CHR4_9885139	4	9885139	G	SLC2A9	intron_variant	MODIFIER	-0.361146	0.479	-
RS145256735	4	9885227	T	SLC2A9	intron_variant	MODIFIER	0.40837	6.687	0.25
RS11737821	4	9885245	G	SLC2A9	intron_variant	MODIFIER	0.302354	5.717	0.36
RS185512663	4	9885622	C	SLC2A9	intron_variant	MODIFIER	0.346212	6.132	0.36
RS79043019	4	9885798	T	SLC2A9	intron_variant	MODIFIER	-0.560806	0.156	0.52
VAR_CHR4_9885978	4	9885978	G	SLC2A9	intron_variant	MODIFIER	-0.031708	2.292	-
RS143104850	4	9886009	A	SLC2A9	intron_variant	MODIFIER	0.220173	4.89	0.45
RS10939599	4	9886860	T	SLC2A9	intron_variant	MODIFIER	0.101995	3.629	0.22
RS55670339	4	9886908	T	SLC2A9	intron_variant	MODIFIER	-0.117033	1.607	0.13
RS10939600	4	9886931	T	SLC2A9	intron_variant	MODIFIER	-0.107955	1.672	0.11
RS10805342	4	9887086	A	SLC2A9	intron_variant	MODIFIER	0.133934	3.973	0.26
RS139906968	4	9887250	G	SLC2A9	intron_variant	MODIFIER	-	-	0.18
VAR_CHR4_9887385	4	9887385	T	SLC2A9	intron_variant	MODIFIER	-0.134126	1.49	-
RS62293294	4	9887387	T	SLC2A9	intron_variant	MODIFIER	-0.361955	0.477	0.19
RS62293295	4	9887429	C	SLC2A9	intron_variant	MODIFIER	-0.297103	0.674	0.21
RS62293296	4	9887444	C	SLC2A9	intron_variant	MODIFIER	-0.576777	0.142	0.33
VAR_CHR4_9887517	4	9887517	G	SLC2A9	intron_variant	MODIFIER	0.244346	5.14	-
RS140411445	4	9887605	A	SLC2A9	intron_variant	MODIFIER	-	-	0.33
RS114751739	4	9887657	T	SLC2A9	intron_variant	MODIFIER	-0.151977	1.374	0.39
RS73225831	4	9887710	T	SLC2A9	intron_variant	MODIFIER	0.61728	8.275	0.36
VAR_CHR4_9887739	4	9887739	G	SLC2A9	intron_variant	MODIFIER	2.119663	16.98	-
VAR_CHR4_9887904	4	9887904	A	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9887935	4	9887935	A	SLC2A9	intron_variant	MODIFIER	-0.098045	1.745	-
RS140746050	4	9887938	T	SLC2A9	intron_variant	MODIFIER	-0.424183	0.338	0.34
RS138755756	4	9888026	A	SLC2A9	intron_variant	MODIFIER	-0.206837	1.062	0.29

RS185854976	4	9888385	C	SLC2A9	intron_variant	MODIFIER	-	-	0.27
VAR_CHR4_9888444	4	9888444	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS143321041	4	9888548	A	SLC2A9	intron_variant	MODIFIER	0.366079	6.313	0.12
RS62293297	4	9888579	C	SLC2A9	intron_variant	MODIFIER	0.042768	3.009	0.14
VAR_CHR4_9888765	4	9888765	T	SLC2A9	intron_variant	MODIFIER	-0.215686	1.017	-
RS62293298	4	9888843	T	SLC2A9	intron_variant	MODIFIER	-0.298894	0.668	0.14
RS9993652	4	9888849	C	SLC2A9	intron_variant	MODIFIER	-0.513805	0.203	0.19
RS4697904	4	9888994	G	SLC2A9	intron_variant	MODIFIER	-0.029711	2.31	0.12
RS4697905	4	9889042	A	SLC2A9	intron_variant	MODIFIER	-0.548107	0.167	0.19
VAR_CHR4_9889065	4	9889065	A	SLC2A9	intron_variant	MODIFIER	0.00339	2.618	-
RS6836878	4	9889069	G	SLC2A9	intron_variant	MODIFIER	-0.065236	2.003	0.17
VAR_CHR4_9889420	4	9889420	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS6818572	4	9889448	T	SLC2A9	intron_variant	MODIFIER	-0.244027	0.884	0.15
RS56399359	4	9889487	C	SLC2A9	intron_variant	MODIFIER	-0.257766	0.825	0.15
RS200180059	4	9889492	T	SLC2A9	intron_variant	MODIFIER	-0.104606	1.696	0.13
RS6858614	4	9889740	A	SLC2A9	intron_variant	MODIFIER	-0.078523	1.895	0.18
VAR_CHR4_9889900	4	9889900	G	SLC2A9	intron_variant	MODIFIER	-0.137375	1.468	-
RS113816574	4	9889924	T	SLC2A9	intron_variant	MODIFIER	-0.663804	0.088	0.19
VAR_CHR4_9890046	4	9890046	A	SLC2A9	intron_variant	MODIFIER	0.03127	2.893	-
RS149955569	4	9890047	T	SLC2A9	intron_variant	MODIFIER	-0.019112	2.406	0.32
VAR_CHR4_9890105	4	9890105	T	SLC2A9	intron_variant	MODIFIER	0.350451	6.171	-
VAR_CHR4_9890126	4	9890126	A	SLC2A9	intron_variant	MODIFIER	-0.047408	2.153	-
RS116388124	4	9890133	C	SLC2A9	intron_variant	MODIFIER	0.135842	3.993	0.33
RS62293300	4	9890359	A	SLC2A9	intron_variant	MODIFIER	-0.596667	0.127	0.29
RS149028152	4	9890470	A	SLC2A9	intron_variant	MODIFIER	0.073179	3.323	0.42
VAR_CHR4_9890504	4	9890504	T	SLC2A9	intron_variant	MODIFIER	-0.12499	1.551	-

RS73225835	4	9890535	G	SLC2A9	intron_variant	MODIFIER	0.00582	2.642	0.31
RS1107710	4	9890708	C	SLC2A9	intron_variant	MODIFIER	-0.328703	0.571	0.24
VAR_CHR4_9890807	4	9890807	T	SLC2A9	intron_variant	MODIFIER	1.457358	13.09	-
RS141239529	4	9890822	C	SLC2A9	intron_variant	MODIFIER	-	-	0.12
RS185455331	4	9890913	T	SLC2A9	intron_variant	MODIFIER	-0.449425	0.293	0.21
RS938563	4	9890998	G	SLC2A9	intron_variant	MODIFIER	-	-	0.26
RS59815647	4	9891009	T	SLC2A9	intron_variant	MODIFIER	-	-	0.31
RS938562	4	9891031	A	SLC2A9	intron_variant	MODIFIER	0.028238	2.862	0.35
VAR_CHR4_9891209	4	9891209	T	SLC2A9	intron_variant	MODIFIER	-0.434615	0.319	-
RS58769709	4	9891240	T	SLC2A9	intron_variant	MODIFIER	0.026235	2.842	0.27
VAR_CHR4_9891341	4	9891341	C	SLC2A9	intron_variant	MODIFIER	-0.028718	2.319	-
RS187386256	4	9891345	C	SLC2A9	intron_variant	MODIFIER	-0.096458	1.756	0.28
RS140568661	4	9891386	A	SLC2A9	intron_variant	MODIFIER	-0.064719	2.007	0.34
VAR_CHR4_9891391	4	9891391	A	SLC2A9	intron_variant	MODIFIER	-0.515274	0.201	-
RS138339252	4	9891440	G	SLC2A9	intron_variant	MODIFIER	-0.10332	1.705	0.26
RS62293301	4	9891488	C	SLC2A9	intron_variant	MODIFIER	-0.529414	0.186	0.16
RS114047413	4	9891525	T	SLC2A9	intron_variant	MODIFIER	-0.309203	0.633	0.36
RS186239844	4	9891908	T	SLC2A9	intron_variant	MODIFIER	-0.19235	1.139	0.27
RS113006138	4	9891941	G	SLC2A9	intron_variant	MODIFIER	0.114607	3.764	0.29
RS28489733	4	9892061	T	SLC2A9	intron_variant	MODIFIER	0.069752	3.288	0.34
RS10939602	4	9892102	A	SLC2A9	intron_variant	MODIFIER	0.295431	5.649	0.42
VAR_CHR4_9892112	4	9892112	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS28571073	4	9892139	C	SLC2A9	intron_variant	MODIFIER	-0.000564	2.581	0.52
RS146345207	4	9892152	T	SLC2A9	intron_variant	MODIFIER	0.847603	9.754	0.47
RS139291984	4	9892172	T	SLC2A9	intron_variant	MODIFIER	-0.068309	1.978	0.44
VAR_CHR4_9892341	4	9892341	A	SLC2A9	splice_region_variant,intron_variant	LOW	1.449917	13.05	-

RS114361719	4	9892424	C	SLC2A9	intron_variant	MODIFIER	-	-	0.42
VAR_CHR4_9892557	4	9892557	G	SLC2A9	intron_variant	MODIFIER	0.043532	3.017	-
RS189114089	4	9892591	A	SLC2A9	intron_variant	MODIFIER	-0.156066	1.349	0.39
RS116913486	4	9892743	T	SLC2A9	intron_variant	MODIFIER	-0.301194	0.66	0.38
RS79197118	4	9893020	T	SLC2A9	intron_variant	MODIFIER	-0.427172	0.332	0.14
RS4697692	4	9893197	A	SLC2A9	intron_variant	MODIFIER	-0.079837	1.885	0.33
RS374243364	4	9893249	A	SLC2A9	intron_variant	MODIFIER	-0.255233	0.836	-
RS4697908	4	9893282	A	SLC2A9	intron_variant	MODIFIER	0.107152	3.684	0.21
VAR_CHR4_9893294	4	9893294	G	SLC2A9	intron_variant	MODIFIER	-0.4946	0.227	-
RS12644047	4	9893403	T	SLC2A9	intron_variant	MODIFIER	-0.319	0.601	0.23
VAR_CHR4_9893455	4	9893455	T	SLC2A9	intron_variant	MODIFIER	-0.517425	0.199	-
RS143772489	4	9893498	T	SLC2A9	intron_variant	MODIFIER	0.244505	5.141	0.23
RS7688167	4	9893506	C	SLC2A9	intron_variant	MODIFIER	-0.767344	0.051	0.22
VAR_CHR4_9893519	4	9893519	C	SLC2A9	intron_variant	MODIFIER	-0.462912	0.271	-
VAR_CHR4_9893569	4	9893569	A	SLC2A9	intron_variant	MODIFIER	-0.023083	2.37	-
RS151104857	4	9893570	T	SLC2A9	intron_variant	MODIFIER	-0.545155	0.17	0.19
RS7669444	4	9893577	T	SLC2A9	intron_variant	MODIFIER	-0.537055	0.178	0.21
VAR_CHR4_9893794	4	9893794	A	SLC2A9	intron_variant	MODIFIER	0.089287	3.494	-
VAR_CHR4_9894041	4	9894041	A	SLC2A9	intron_variant	MODIFIER	0.270458	5.403	-
RS117315041	4	9894261	A	SLC2A9	intron_variant	MODIFIER	0.009901	2.681	0.37
RS80204783	4	9894371	A	SLC2A9	intron_variant	MODIFIER	-0.184454	1.182	0.51
VAR_CHR4_9894638	4	9894638	C	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9894773	4	9894773	T	SLC2A9	intron_variant	MODIFIER	-0.207114	1.061	-
RS56036138	4	9894954	T	SLC2A9	intron_variant	MODIFIER	-	-	0.17
VAR_CHR4_9895032	4	9895032	A	SLC2A9	intron_variant	MODIFIER	-0.357373	0.489	-
RS7698858	4	9895070	G	SLC2A9	intron_variant	MODIFIER	0.136007	3.995	0.38

VAR_CHR4_9895163	4	9895163	A	SLC2A9	intron_variant	MODIFIER	-0.257881	0.825	-
RS13114702	4	9895176	C	SLC2A9	intron_variant	MODIFIER	-0.502605	0.216	0.27
RS7684245	4	9895180	A	SLC2A9	intron_variant	MODIFIER	-0.502649	0.216	0.26
RS75521345	4	9895369	T	SLC2A9	intron_variant	MODIFIER	-0.576634	0.142	0.31
VAR_CHR4_9895378	4	9895378	T	SLC2A9	intron_variant	MODIFIER	-0.318879	0.602	-
RS141346944	4	9895518	T	SLC2A9	intron_variant	MODIFIER	-0.330201	0.566	0.33
VAR_CHR4_9895586	4	9895586	G	SLC2A9	intron_variant	MODIFIER	0.115786	3.777	-
RS147439739	4	9895642	G	SLC2A9	intron_variant	MODIFIER	-0.090047	1.805	0.41
RS4697693	4	9895860	G	SLC2A9	intron_variant	MODIFIER	-0.008681	2.504	0.42
VAR_CHR4_9895868	4	9895868	G	SLC2A9	intron_variant	MODIFIER	0.011369	2.696	-
VAR_CHR4_9895935	4	9895935	C	SLC2A9	intron_variant	MODIFIER	-0.11075	1.651	-
RS10939605	4	9896293	T	SLC2A9	intron_variant	MODIFIER	0.723793	8.982	0.27
RS78755014	4	9896571	G	SLC2A9	intron_variant	MODIFIER	-0.036532	2.249	0.28
RS145154883	4	9896609	T	SLC2A9	intron_variant	MODIFIER	-0.399202	0.389	0.27
RS4697694	4	9896642	G	SLC2A9	intron_variant	MODIFIER	-0.057328	2.069	0.27
RS6449097	4	9896734	A	SLC2A9	intron_variant	MODIFIER	0.417282	6.763	0.28
RS113058127	4	9896741	C	SLC2A9	intron_variant	MODIFIER	-0.226885	0.963	0.26
VAR_CHR4_9896752	4	9896752	T	SLC2A9	intron_variant	MODIFIER	-0.511451	0.206	-
RS4697909	4	9896760	T	SLC2A9	intron_variant	MODIFIER	-0.200357	1.096	0.3
VAR_CHR4_9896762	4	9896762	C	SLC2A9	intron_variant	MODIFIER	0.006732	2.651	-
RS13107656	4	9896938	T	SLC2A9	intron_variant	MODIFIER	0.035433	2.934	0.18
VAR_CHR4_9897112	4	9897112	T	SLC2A9	intron_variant	MODIFIER	0.302256	5.716	-
VAR_CHR4_9897304	4	9897304	G	SLC2A9	intron_variant	MODIFIER	0.049396	3.076	-
RS13115121	4	9897342	A	SLC2A9	intron_variant	MODIFIER	-0.138677	1.46	0.22
RS13129868	4	9897372	C	SLC2A9	intron_variant	MODIFIER	-0.546459	0.169	0.21
VAR_CHR4_9897390	4	9897390	G	SLC2A9	intron_variant	MODIFIER	-0.239204	0.906	-

RS138584318	4	9897438	A	SLC2A9	intron_variant	MODIFIER	0.021451	2.795	0.18
RS12505366	4	9897520	T	SLC2A9	intron_variant	MODIFIER	0.130026	3.93	0.29
VAR_CHR4_9897526	4	9897526	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS180853490	4	9897532	G	SLC2A9	intron_variant	MODIFIER	-0.220878	0.992	0.24
VAR_CHR4_9897630	4	9897630	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS56038393	4	9897885	C	SLC2A9	intron_variant	MODIFIER	-1.152691	0.008	0.22
RS56239136	4	9898003	A	SLC2A9	intron_variant	MODIFIER	0.233496	5.028	0.31
RS56113653	4	9898052	T	SLC2A9	intron_variant	MODIFIER	-0.325997	0.579	0.3
RS34567300	4	9898148	G	SLC2A9	intron_variant	MODIFIER	-0.313208	0.62	0.24
RS13122026	4	9898207	A	SLC2A9	intron_variant	MODIFIER	0.464942	7.157	0.25
RS117867203	4	9898376	C	SLC2A9	intron_variant	MODIFIER	-0.389712	0.41	0.26
VAR_CHR4_9898455	4	9898455	T	SLC2A9	intron_variant	MODIFIER	0.13022	3.932	-
VAR_CHR4_9898608	4	9898608	A	SLC2A9	intron_variant	MODIFIER	-0.603684	0.122	-
VAR_CHR4_9898665	4	9898665	T	SLC2A9	intron_variant	MODIFIER	0.055109	3.135	-
RS55962381	4	9898764	A	SLC2A9	intron_variant	MODIFIER	-0.411404	0.363	0.21
RS189741361	4	9898916	G	SLC2A9	intron_variant	MODIFIER	-	-	0.35
RS12644592	4	9899068	C	SLC2A9	intron_variant	MODIFIER	-0.414364	0.357	0.26
RS75599884	4	9899181	A	SLC2A9	intron_variant	MODIFIER	-	-	0.29
RS117318662	4	9899218	C	SLC2A9	intron_variant	MODIFIER	-0.750111	0.055	0.22
VAR_CHR4_9899429	4	9899429	A	SLC2A9	intron_variant	MODIFIER	0.04468	3.028	-
RS146868066	4	9899468	A	SLC2A9	intron_variant	MODIFIER	0.007753	2.661	0.21
VAR_CHR4_9899660	4	9899660	T	SLC2A9	intron_variant	MODIFIER	-0.956135	0.02	-
RS58380370	4	9899727	G	SLC2A9	intron_variant	MODIFIER	0.018541	2.766	0.41
VAR_CHR4_9899749	4	9899749	G	SLC2A9	intron_variant	MODIFIER	0.069662	3.287	-
RS16890590	4	9899855	A	SLC2A9	intron_variant	MODIFIER	-0.136971	1.471	0.3
RS145193830	4	9900007	C	SLC2A9	intron_variant	MODIFIER	-0.259388	0.819	0.23

VAR_CHR4_9900157	4	9900157	A	SLC2A9	intron_variant	MODIFIER	1.025601	10.81	-
RS118034359	4	9900267	A	SLC2A9	intron_variant	MODIFIER	0.194633	4.622	0.26
RS13136962	4	9900314	A	SLC2A9	intron_variant	MODIFIER	0.29657	5.66	0.23
RS55801162	4	9900318	C	SLC2A9	intron_variant	MODIFIER	-0.41708	0.352	0.2
VAR_CHR4_9900342	4	9900342	T	SLC2A9	intron_variant	MODIFIER	-0.487199	0.236	-
VAR_CHR4_9900526	4	9900526	T	SLC2A9	intron_variant	MODIFIER	-0.238921	0.907	-
VAR_CHR4_9900625	4	9900625	C	SLC2A9	intron_variant	MODIFIER	-0.667654	0.086	-
VAR_CHR4_9900703	4	9900703	A	SLC2A9	intron_variant	MODIFIER	-0.23573	0.922	-
VAR_CHR4_9900708	4	9900708	C	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9900829	4	9900829	T	SLC2A9	intron_variant	MODIFIER	-0.381632	0.428	-
VAR_CHR4_9901020	4	9901020	T	SLC2A9	intron_variant	MODIFIER	0.047578	3.058	-
VAR_CHR4_9901322	4	9901322	G	SLC2A9	intron_variant	MODIFIER	0.678152	8.683	-
RS146985372	4	9901373	C	SLC2A9	intron_variant	MODIFIER	-0.244938	0.88	0.45
RS143727065	4	9901556	T	SLC2A9	intron_variant	MODIFIER	-0.420047	0.346	0.38
RS6449100	4	9901563	G	SLC2A9	intron_variant	MODIFIER	0.059212	3.178	0.22
RS116115337	4	9901731	A	SLC2A9	intron_variant	MODIFIER	0.491273	7.364	0.24
VAR_CHR4_9901756	4	9901756	T	SLC2A9	intron_variant	MODIFIER	-0.059245	2.053	-
RS4697910	4	9901874	T	SLC2A9	intron_variant	MODIFIER	-0.786216	0.046	0.21
RS180890841	4	9901929	G	SLC2A9	intron_variant	MODIFIER	0.289773	5.594	0.22
VAR_CHR4_9902078	4	9902078	A	SLC2A9	intron_variant	MODIFIER	0.110889	3.724	-
VAR_CHR4_9902136	4	9902136	T	SLC2A9	intron_variant	MODIFIER	-0.133824	1.492	-
RS10027276	4	9902193	G	SLC2A9	intron_variant	MODIFIER	-0.13532	1.482	0.19
VAR_CHR4_9902284	4	9902284	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS143758325	4	9902321	G	SLC2A9	intron_variant	MODIFIER	0.122606	3.85	0.19
RS4697911	4	9902340	C	SLC2A9	intron_variant	MODIFIER	-0.230828	0.945	-
RS13151822	4	9902562	A	SLC2A9	intron_variant	MODIFIER	0.529269	7.651	0.19

RS144499258	4	9902580	G	SLC2A9	intron_variant	MODIFIER	0.097837	3.585	0.18
RS13140718	4	9902676	G	SLC2A9	intron_variant	MODIFIER	-0.07068	1.958	0.26
RS11732681	4	9902876	C	SLC2A9	intron_variant	MODIFIER	-0.560856	0.156	0.25
RS187365313	4	9903022	G	SLC2A9	intron_variant	MODIFIER	-0.545835	0.169	0.24
VAR_CHR4_9903086	4	9903086	T	SLC2A9	intron_variant	MODIFIER	-0.454962	0.284	-
RS11737685	4	9903121	T	SLC2A9	intron_variant	MODIFIER	0.11781	3.799	0.13
VAR_CHR4_9903160	4	9903160	C	SLC2A9	intron_variant	MODIFIER	-0.240357	0.901	-
VAR_CHR4_9903385	4	9903385	A	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9903441	4	9903441	A	SLC2A9	intron_variant	MODIFIER	0.196117	4.638	-
RS6829755	4	9903518	C	SLC2A9	intron_variant	MODIFIER	0.518474	7.571	0.35
VAR_CHR4_9903519	4	9903519	T	SLC2A9	intron_variant	MODIFIER	0.52398	7.612	-
RS76632978	4	9903603	T	SLC2A9	intron_variant	MODIFIER	0.030364	2.883	0.29
VAR_CHR4_9903619	4	9903619	C	SLC2A9	intron_variant	MODIFIER	-0.072371	1.944	-
VAR_CHR4_9903894	4	9903894	G	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9903964	4	9903964	G	SLC2A9	intron_variant	MODIFIER	-0.766444	0.051	-
VAR_CHR4_9904012	4	9904012	A	SLC2A9	intron_variant	MODIFIER	-0.513899	0.203	-
VAR_CHR4_9904197	4	9904197	T	SLC2A9	intron_variant	MODIFIER	-0.126378	1.542	-
RS13129080	4	9904242	C	SLC2A9	intron_variant	MODIFIER	-0.331553	0.562	0.33
VAR_CHR4_9904572	4	9904572	G	SLC2A9	intron_variant	MODIFIER	0.165014	4.307	-
RS75805865	4	9904600	C	SLC2A9	intron_variant	MODIFIER	-	-	0.34
RS185587884	4	9904773	T	SLC2A9	intron_variant	MODIFIER	-0.25169	0.851	0.41
VAR_CHR4_9905184	4	9905184	A	SLC2A9	intron_variant	MODIFIER	0.26434	5.342	-
RS377615729	4	9905297	A	SLC2A9	intron_variant	MODIFIER	0.102485	3.634	-
VAR_CHR4_9905356	4	9905356	C	SLC2A9	intron_variant	MODIFIER	-0.814638	0.04	-
VAR_CHR4_9905869	4	9905869	G	SLC2A9	intron_variant	MODIFIER	0.024699	2.827	-
VAR_CHR4_9906000	4	9906000	G	SLC2A9	intron_variant	MODIFIER	-	-	-

RS117301982	4	9906016	A	SLC2A9	intron_variant	MODIFIER	0.39979	6.612	0.29
RS56003345	4	9906073	C	SLC2A9	intron_variant	MODIFIER	-	-	0.31
RS147875823	4	9906648	A	SLC2A9	intron_variant	MODIFIER	0.234617	5.04	0.26
RS10805343	4	9907039	A	SLC2A9	intron_variant	MODIFIER	0.2508	5.205	0.24
RS11940661	4	9907202	T	SLC2A9	intron_variant	MODIFIER	-0.122281	1.57	0.25
RS10939608	4	9907336	G	SLC2A9	intron_variant	MODIFIER	-0.196843	1.115	0.17
VAR_CHR4_9907381	4	9907381	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS77671965	4	9907573	A	SLC2A9	intron_variant	MODIFIER	0.120566	3.829	0.15
VAR_CHR4_9907574	4	9907574	G	SLC2A9	intron_variant	MODIFIER	0.197397	4.652	-
RS4389579	4	9907604	G	SLC2A9	intron_variant	MODIFIER	-0.056765	2.074	0.25
RS62293329	4	9907662	T	SLC2A9	intron_variant	MODIFIER	-	-	0.28
VAR_CHR4_9907823	4	9907823	G	SLC2A9	intron_variant	MODIFIER	0.035481	2.935	-
VAR_CHR4_9907872	4	9907872	A	SLC2A9	intron_variant	MODIFIER	-0.060643	2.041	-
VAR_CHR4_9907897	4	9907897	A	SLC2A9	intron_variant	MODIFIER	-0.043856	2.184	-
RS148903910	4	9908141	T	SLC2A9	intron_variant	MODIFIER	-0.405866	0.374	0.35
RS56123633	4	9908185	G	SLC2A9	intron_variant	MODIFIER	0.1472	4.115	0.4
VAR_CHR4_9908332	4	9908332	C	SLC2A9	intron_variant	MODIFIER	-0.015718	2.438	-
RS80268248	4	9908364	T	SLC2A9	intron_variant	MODIFIER	-0.361912	0.477	0.23
RS137880042	4	9908538	C	SLC2A9	intron_variant	MODIFIER	-0.12565	1.547	0.16
RS142391721	4	9908543	T	SLC2A9	intron_variant	MODIFIER	-0.344519	0.524	0.24
RS16890728	4	9908833	T	SLC2A9	intron_variant	MODIFIER	0.199304	4.672	0.22
VAR_CHR4_9909251	4	9909251	G	SLC2A9	intron_variant	MODIFIER	0.089277	3.494	-
RS2280202	4	9909295	A	SLC2A9	intron_variant	MODIFIER	0.325379	5.937	0.27
VAR_CHR4_9909425	4	9909425	G	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9909434	4	9909434	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS2280203	4	9909559	A	SLC2A9	intron_variant	MODIFIER	0.277062	5.469	0.22

RS139928301	4	9909572	G	SLC2A9	intron_variant	MODIFIER	-0.212987	1.031	0.16
VAR_CHR4_9909581	4	9909581	T	SLC2A9	intron_variant	MODIFIER	-0.168234	1.275	-
RS2280204	4	9909850	C	SLC2A9	intron_variant	MODIFIER	-0.074997	1.923	0.24
RS367692082	4	9909887	A	SLC2A9	missense_variant	MODERATE	2.035472	16.44	-
RS2280205	4	9909923	C	SLC2A9	missense_variant	MODERATE	-0.078636	1.894	0.24
RS4518244	4	9910350	A	SLC2A9	intron_variant	MODIFIER	0.053221	3.116	0.13
RS11734893	4	9910441	C	SLC2A9	intron_variant	MODIFIER	-0.811313	0.04	0.2
RS13113546	4	9910467	T	SLC2A9	intron_variant	MODIFIER	-0.033597	2.275	0.26
RS4639072	4	9910468	G	SLC2A9	intron_variant	MODIFIER	-	-	0.24
VAR_CHR4_9910575	4	9910575	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS118093098	4	9910619	G	SLC2A9	intron_variant	MODIFIER	-0.209216	1.05	0.13
RS13103429	4	9910635	G	SLC2A9	intron_variant	MODIFIER	-0.426227	0.334	0.11
RS13108825	4	9910663	G	SLC2A9	intron_variant	MODIFIER	-0.59267	0.13	0.13
VAR_CHR4_9910717	4	9910717	A	SLC2A9	intron_variant	MODIFIER	0.130547	3.936	-
VAR_CHR4_9910733	4	9910733	G	SLC2A9	intron_variant	MODIFIER	0.076537	3.359	-
RS147263130	4	9910770	G	SLC2A9	intron_variant	MODIFIER	-	-	0.25
RS142141871	4	9911048	G	SLC2A9	intron_variant	MODIFIER	-	-	0.33
RS4382035	4	9911396	A	SLC2A9	intron_variant	MODIFIER	0.045939	3.041	0.38
RS4376135	4	9911408	A	SLC2A9	intron_variant	MODIFIER	-	-	0.35
RS146526473	4	9911463	A	SLC2A9	intron_variant	MODIFIER	-0.307905	0.637	0.37
VAR_CHR4_9911525	4	9911525	T	SLC2A9	intron_variant	MODIFIER	-0.98803	0.017	-
VAR_CHR4_9911543	4	9911543	A	SLC2A9	intron_variant	MODIFIER	-0.293389	0.688	-
VAR_CHR4_9911595	4	9911595	G	SLC2A9	intron_variant	MODIFIER	0.155571	4.206	-
RS62293330	4	9911699	C	SLC2A9	intron_variant	MODIFIER	-0.136733	1.472	0.32
VAR_CHR4_9911720	4	9911720	A	SLC2A9	intron_variant	MODIFIER	-0.001081	2.576	-
RS138553440	4	9911796	G	SLC2A9	intron_variant	MODIFIER	-	-	0.32

RS4640670	4	9911809	T	SLC2A9	intron_variant	MODIFIER	-0.551563	0.164	0.32
RS11935405	4	9911843	A	SLC2A9	intron_variant	MODIFIER	0.1955	4.632	0.35
RS4336225	4	9911872	A	SLC2A9	intron_variant	MODIFIER	0.226941	4.961	0.4
VAR_CHR4_9912036	4	9912036	T	SLC2A9	intron_variant	MODIFIER	-0.468968	0.262	-
RS11934363	4	9912101	T	SLC2A9	intron_variant	MODIFIER	-0.136812	1.472	0.31
RS192118297	4	9912136	A	SLC2A9	intron_variant	MODIFIER	-0.187278	1.167	0.43
RS112469934	4	9912137	G	SLC2A9	intron_variant	MODIFIER	-	-	0.35
RS376641818	4	9912349	A	SLC2A9	intron_variant	MODIFIER	-0.191866	1.141	-
VAR_CHR4_9912397	4	9912397	A	SLC2A9	intron_variant	MODIFIER	0.12954	3.925	-
VAR_CHR4_9912605	4	9912605	G	SLC2A9	intron_variant	MODIFIER	-0.094308	1.773	-
RS6449110	4	9912625	A	SLC2A9	intron_variant	MODIFIER	0.215869	4.846	0.22
RS1878278	4	9912648	T	SLC2A9	intron_variant	MODIFIER	-0.003265	2.555	0.16
RS73225881	4	9912825	A	SLC2A9	intron_variant	MODIFIER	-0.076652	1.91	0.32
VAR_CHR4_9912897	4	9912897	T	SLC2A9	intron_variant	MODIFIER	0.466588	7.17	-
RS28643326	4	9912993	A	SLC2A9	intron_variant	MODIFIER	0.000273	2.589	0.3
RS191258712	4	9913212	T	SLC2A9	intron_variant	MODIFIER	-0.229541	0.951	0.42
VAR_CHR4_9913311	4	9913311	T	SLC2A9	intron_variant	MODIFIER	-0.786141	0.046	-
VAR_CHR4_9913353	4	9913353	G	SLC2A9	intron_variant	MODIFIER	0.28355	5.533	-
VAR_CHR4_9913557	4	9913557	G	SLC2A9	intron_variant	MODIFIER	0.109488	3.709	-
VAR_CHR4_9914056	4	9914056	T	SLC2A9	intron_variant	MODIFIER	0.029235	2.872	-
RS79568191	4	9914230	G	SLC2A9	intron_variant	MODIFIER	-0.246228	0.875	0.45
RS144752705	4	9914556	A	SLC2A9	intron_variant	MODIFIER	0.404481	6.653	0.47
VAR_CHR4_9914631	4	9914631	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS117212874	4	9914688	T	SLC2A9	intron_variant	MODIFIER	-0.066128	1.995	0.35
RS148450134	4	9914705	G	SLC2A9	intron_variant	MODIFIER	0.278752	5.485	0.31
RS12649245	4	9915173	G	SLC2A9	intron_variant	MODIFIER	-	-	0.44

RS151139969	4	9915307	A	SLC2A9	intron_variant	MODIFIER	0.571551	7.957	0.41
RS6825187	4	9915325	A	SLC2A9	intron_variant	MODIFIER	0.478384	7.264	0.4
VAR_CHR4_9915389	4	9915389	G	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9915532	4	9915532	A	SLC2A9	intron_variant	MODIFIER	0.211773	4.803	-
RS150317722	4	9915570	A	SLC2A9	intron_variant	MODIFIER	0.354898	6.212	0.34
RS11722228	4	9915741	A	SLC2A9	intron_variant	MODIFIER	-0.035228	2.26	0.16
RS76943656	4	9915761	C	SLC2A9	intron_variant	MODIFIER	-	-	0.22
RS4697695	4	9915850	T	SLC2A9	intron_variant	MODIFIER	-0.306572	0.642	0.22
VAR_CHR4_9915853	4	9915853	A	SLC2A9	intron_variant	MODIFIER	-0.429032	0.329	-
RS4697696	4	9915870	A	SLC2A9	intron_variant	MODIFIER	-0.329177	0.569	0.21
RS4697697	4	9915874	T	SLC2A9	intron_variant	MODIFIER	-0.181967	1.196	0.23
VAR_CHR4_9915880	4	9915880	C	SLC2A9	intron_variant	MODIFIER	-0.680892	0.08	-
RS75181558	4	9916133	C	SLC2A9	intron_variant	MODIFIER	-0.059954	2.047	0.26
RS7674711	4	9916180	G	SLC2A9	intron_variant	MODIFIER	0.293825	5.634	0.17
RS7674723	4	9916202	G	SLC2A9	intron_variant	MODIFIER	0.108717	3.701	0.2
RS74433158	4	9916206	G	SLC2A9	intron_variant	MODIFIER	-0.301755	0.658	0.25
RS10516194	4	9916209	G	SLC2A9	intron_variant	MODIFIER	0.257129	5.269	0.22
VAR_CHR4_9916249	4	9916249	T	SLC2A9	intron_variant	MODIFIER	0.127589	3.904	-
RS191513628	4	9916332	T	SLC2A9	intron_variant	MODIFIER	-0.388461	0.412	0.2
VAR_CHR4_9916451	4	9916451	C	SLC2A9	intron_variant	MODIFIER	-0.524088	0.192	-
RS78301913	4	9916574	G	SLC2A9	intron_variant	MODIFIER	-	-	0.25
RS16890905	4	9916662	A	SLC2A9	intron_variant	MODIFIER	0.093383	3.537	0.21
VAR_CHR4_9916712	4	9916712	T	SLC2A9	intron_variant	MODIFIER	-0.060044	2.046	-
VAR_CHR4_9916833	4	9916833	G	SLC2A9	intron_variant	MODIFIER	-0.356674	0.491	-
RS143466055	4	9916938	C	SLC2A9	intron_variant	MODIFIER	-0.530893	0.184	0.1
RS6838317	4	9916964	A	SLC2A9	intron_variant	MODIFIER	0.303001	5.723	0.12

VAR_CHR4_9917208	4	9917208	T	SLC2A9	intron_variant	MODIFIER	-0.115905	1.615	-
VAR_CHR4_9917336	4	9917336	C	SLC2A9	intron_variant	MODIFIER	-0.194441	1.127	-
RS76640365	4	9917371	G	SLC2A9	intron_variant	MODIFIER	-0.121539	1.575	0.54
RS34213329	4	9917484	C	SLC2A9	intron_variant	MODIFIER	-	-	0.29
VAR_CHR4_9917489	4	9917489	A	SLC2A9	intron_variant	MODIFIER	0.521344	7.592	-
VAR_CHR4_9917672	4	9917672	A	SLC2A9	intron_variant	MODIFIER	0.357429	6.235	-
VAR_CHR4_9917789	4	9917789	T	SLC2A9	intron_variant	MODIFIER	-0.734966	0.06	-
RS114602281	4	9917811	G	SLC2A9	intron_variant	MODIFIER	-	-	0.49
RS6838986	4	9917921	G	SLC2A9	intron_variant	MODIFIER	0.148345	4.128	0.4
VAR_CHR4_9917944	4	9917944	T	SLC2A9	intron_variant	MODIFIER	0.343478	6.106	-
RS13101683	4	9918133	C	SLC2A9	intron_variant	MODIFIER	-0.471095	0.259	0.37
RS150266109	4	9918159	A	SLC2A9	intron_variant	MODIFIER	-	-	0.36
VAR_CHR4_9918331	4	9918331	A	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9918424	4	9918424	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS56223908	4	9918492	G	SLC2A9	intron_variant	MODIFIER	-0.370962	0.454	0.3
RS6811809	4	9918557	C	SLC2A9	intron_variant	MODIFIER	-0.438426	0.312	0.27
VAR_CHR4_9918678	4	9918678	A	SLC2A9	intron_variant	MODIFIER	-0.279951	0.737	-
RS180905771	4	9918771	C	SLC2A9	intron_variant	MODIFIER	-	-	0.42
RS149341985	4	9918810	T	SLC2A9	intron_variant	MODIFIER	0.213942	4.825	0.48
RS113310882	4	9918859	C	SLC2A9	intron_variant	MODIFIER	-0.274371	0.759	0.33
RS34752819	4	9918920	C	SLC2A9	intron_variant	MODIFIER	-0.258186	0.824	0.31
VAR_CHR4_9918968	4	9918968	G	SLC2A9	intron_variant	MODIFIER	-0.097478	1.749	-
RS35955619	4	9918986	A	SLC2A9	intron_variant	MODIFIER	0.001718	2.602	0.21
RS141769569	4	9919280	T	SLC2A9	intron_variant	MODIFIER	-0.756608	0.053	0.38
RS139204497	4	9919421	A	SLC2A9	intron_variant	MODIFIER	0.286058	5.558	0.44
RS112202007	4	9919679	T	SLC2A9	intron_variant	MODIFIER	-0.127765	1.532	0.38

RS371899886	4	9919784	T	SLC2A9	intron_variant	MODIFIER	-0.554524	0.161	-
RS147805997	4	9919939	A	SLC2A9	intron_variant	MODIFIER	-0.19688	1.114	0.41
RS142512695	4	9919984	A	SLC2A9	intron_variant	MODIFIER	0.499945	7.431	0.39
RS73094598	4	9920086	A	SLC2A9	intron_variant	MODIFIER	-0.168007	1.277	0.42
VAR_CHR4_9920278	4	9920278	C	SLC2A9	intron_variant	MODIFIER	0.182076	4.489	-
RS10805346	4	9920347	G	SLC2A9	intron_variant	MODIFIER	-0.154502	1.359	0.25
VAR_CHR4_9920579	4	9920579	T	SLC2A9	intron_variant	MODIFIER	-0.24986	0.859	-
RS874432	4	9920606	T	SLC2A9	intron_variant	MODIFIER	-	-	0.39
RS113401797	4	9920830	T	SLC2A9	intron_variant	MODIFIER	-0.476411	0.251	0.41
RS184241396	4	9921082	A	SLC2A9	intron_variant	MODIFIER	0.051379	3.097	0.48
VAR_CHR4_9921175	4	9921175	C	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9921310	4	9921310	A	SLC2A9	intron_variant	MODIFIER	0.0771	3.365	-
VAR_CHR4_9921328	4	9921328	G	SLC2A9	intron_variant	MODIFIER	-0.021368	2.386	-
VAR_CHR4_9921348	4	9921348	A	SLC2A9	intron_variant	MODIFIER	0.078338	3.378	-
VAR_CHR4_9921368	4	9921368	G	SLC2A9	intron_variant	MODIFIER	0.149359	4.139	-
VAR_CHR4_9922053	4	9922053	A	SLC2A9	missense_variant	MODERATE	4.830909	24.8	-
RS74651202	4	9922113	T	SLC2A9	missense_variant	MODERATE	0.361655	6.273	0.38
RS3733591	4	9922130	A	SLC2A9	missense_variant	MODERATE	4.95859	25	0.3
RS16890979	4	9922167	A	SLC2A9	missense_variant	MODERATE	4.668257	24.5	0.32
RS73225891	4	9922170	C	SLC2A9	synonymous_variant	LOW	-	-	0.33
RS112404957	4	9922187	T	SLC2A9	missense_variant	MODERATE	0.865892	9.864	0.37
RS938564	4	9922573	C	SLC2A9	intron_variant	MODIFIER	0.025987	2.84	0.35
VAR_CHR4_9922730	4	9922730	C	SLC2A9	intron_variant	MODIFIER	0.023089	2.811	-
VAR_CHR4_9922796	4	9922796	C	SLC2A9	intron_variant	MODIFIER	-0.037383	2.241	-
RS113674589	4	9922955	A	SLC2A9	intron_variant	MODIFIER	-0.073912	1.932	0.31
RS185731129	4	9922983	A	SLC2A9	intron_variant	MODIFIER	0.183083	4.5	0.33

RS734553	4	9923004	C	SLC2A9	intron_variant	MODIFIER	0.07122	3.303	0.31
RS77935410	4	9923008	C	SLC2A9	intron_variant	MODIFIER	-0.415135	0.355	0.33
RS144996132	4	9923049	C	SLC2A9	intron_variant	MODIFIER	-0.101141	1.722	0.28
RS6815895	4	9923165	G	SLC2A9	intron_variant	MODIFIER	-0.000242	2.584	0.55
RS142677291	4	9924106	T	SLC2A9	intron_variant	MODIFIER	-0.345494	0.522	0.22
RS114597845	4	9924198	G	SLC2A9	intron_variant	MODIFIER	-0.035729	2.256	0.17
VAR_CHR4_9924200	4	9924200	A	SLC2A9	intron_variant	MODIFIER	0.187611	4.548	-
RS6832439	4	9924319	T	SLC2A9	intron_variant	MODIFIER	-0.142333	1.436	0.26
RS6832456	4	9924336	T	SLC2A9	intron_variant	MODIFIER	1.371533	12.64	0.26
VAR_CHR4_9924430	4	9924430	T	SLC2A9	intron_variant	MODIFIER	-0.541048	0.174	-
RS114372106	4	9924457	C	SLC2A9	intron_variant	MODIFIER	-	-	0.33
RS147350938	4	9924493	A	SLC2A9	intron_variant	MODIFIER	0.356982	6.231	0.32
RS16891020	4	9924563	A	SLC2A9	intron_variant	MODIFIER	0.60227	8.172	0.23
VAR_CHR4_9924780	4	9924780	G	SLC2A9	intron_variant	MODIFIER	0.539782	7.728	-
RS2012177	4	9924877	A	SLC2A9	intron_variant	MODIFIER	-0.047549	2.152	0.35
RS13115469	4	9925145	A	SLC2A9	intron_variant	MODIFIER	0.93852	10.3	0.19
RS73804455	4	9925181	T	SLC2A9	intron_variant	MODIFIER	0.240113	5.096	0.21
RS150039611	4	9925279	T	SLC2A9	intron_variant	MODIFIER	-0.18927	1.156	0.18
VAR_CHR4_9925280	4	9925280	A	SLC2A9	intron_variant	MODIFIER	-0.185652	1.176	-
VAR_CHR4_9925436	4	9925436	G	SLC2A9	intron_variant	MODIFIER	-0.705358	0.07	-
RS138891244	4	9925496	G	SLC2A9	intron_variant	MODIFIER	0.675568	8.666	0.17
RS938552	4	9925524	A	SLC2A9	intron_variant	MODIFIER	0.120074	3.823	0.15
RS938553	4	9925526	G	SLC2A9	intron_variant	MODIFIER	0.009226	2.675	0.17
RS146784455	4	9925583	C	SLC2A9	intron_variant	MODIFIER	0.055086	3.135	0.11
RS73225893	4	9925603	C	SLC2A9	intron_variant	MODIFIER	0.098383	3.591	0.16
RS938554	4	9925692	G	SLC2A9	intron_variant	MODIFIER	0.004448	2.629	0.24

RS112939969	4	9925735	T	SLC2A9	intron_variant	MODIFIER	-0.313506	0.619	0.21
VAR_CHR4_9925784	4	9925784	T	SLC2A9	intron_variant	MODIFIER	0.135237	3.987	-
RS35076540	4	9925835	A	SLC2A9	intron_variant	MODIFIER	0.18756	4.548	0.17
RS35922993	4	9925925	A	SLC2A9	intron_variant	MODIFIER	-0.320375	0.597	0.19
VAR_CHR4_9925944	4	9925944	T	SLC2A9	intron_variant	MODIFIER	0.429154	6.863	-
RS938555	4	9926051	T	SLC2A9	intron_variant	MODIFIER	-0.078555	1.895	0.19
VAR_CHR4_9926218	4	9926218	C	SLC2A9	intron_variant	MODIFIER	-0.240308	0.901	-
VAR_CHR4_9926480	4	9926480	T	SLC2A9	intron_variant	MODIFIER	-0.665864	0.087	-
VAR_CHR4_9926525	4	9926525	G	SLC2A9	intron_variant	MODIFIER	-0.071402	1.952	-
RS10939614	4	9926613	G	SLC2A9	intron_variant	MODIFIER	-0.107326	1.676	0.26
RS187024415	4	9926934	T	SLC2A9	intron_variant	MODIFIER	-0.194933	1.125	0.18
RS13129697	4	9926967	C	SLC2A9	intron_variant	MODIFIER	0.359264	6.251	0.24
RS376564894	4	9927277	T	SLC2A9	intron_variant	MODIFIER	0.090224	3.504	-
VAR_CHR4_9927317	4	9927317	G	SLC2A9	intron_variant	MODIFIER	-0.232223	0.938	-
RS60956448	4	9927498	A	SLC2A9	intron_variant	MODIFIER	-0.171145	1.258	0.13
RS13124563	4	9927553	C	SLC2A9	intron_variant	MODIFIER	-0.455516	0.283	0.14
RS6838021	4	9927620	A	SLC2A9	intron_variant	MODIFIER	-0.209213	1.05	0.2
RS143885121	4	9927648	A	SLC2A9	intron_variant	MODIFIER	-1.178745	0.007	0.12
RS112215724	4	9927690	A	SLC2A9	intron_variant	MODIFIER	-	-	0.15
RS189130002	4	9927749	A	SLC2A9	intron_variant	MODIFIER	0.134538	3.979	0.19
VAR_CHR4_9927949	4	9927949	T	SLC2A9	intron_variant	MODIFIER	0.268428	5.383	-
RS13137069	4	9928017	A	SLC2A9	intron_variant	MODIFIER	0.246945	5.166	0.2
VAR_CHR4_9928106	4	9928106	C	SLC2A9	intron_variant	MODIFIER	-0.056898	2.072	-
RS114949385	4	9928193	A	SLC2A9	intron_variant	MODIFIER	0.870627	9.892	0.31
RS116710881	4	9928314	A	SLC2A9	intron_variant	MODIFIER	0.402174	6.633	0.41
VAR_CHR4_9928560	4	9928560	A	SLC2A9	intron_variant	MODIFIER	-0.021908	2.381	-

VAR_CHR4_9928582	4	9928582	C	SLC2A9	intron_variant	MODIFIER	-0.229872	0.949	-
RS149166425	4	9929001	G	SLC2A9	intron_variant	MODIFIER	-0.023505	2.366	0.28
VAR_CHR4_9929036	4	9929036	A	SLC2A9	intron_variant	MODIFIER	0.020252	2.783	-
RS189358732	4	9929379	G	SLC2A9	intron_variant	MODIFIER	0.095277	3.557	0.31
VAR_CHR4_9929476	4	9929476	A	SLC2A9	intron_variant	MODIFIER	-0.009068	2.5	-
RS11936395	4	9929575	T	SLC2A9	intron_variant	MODIFIER	0.597495	8.139	0.33
RS147819274	4	9929582	G	SLC2A9	intron_variant	MODIFIER	0.419121	6.779	0.37
VAR_CHR4_9929726	4	9929726	T	SLC2A9	intron_variant	MODIFIER	-0.339159	0.54	-
RS11937310	4	9929738	T	SLC2A9	intron_variant	MODIFIER	-1.12077	0.009	0.15
RS147002127	4	9929932	A	SLC2A9	intron_variant	MODIFIER	1.121855	11.33	0.2
VAR_CHR4_9930137	4	9930137	A	SLC2A9	intron_variant	MODIFIER	-0.254156	0.841	-
RS7684306	4	9930139	T	SLC2A9	intron_variant	MODIFIER	-0.288448	0.705	0.23
VAR_CHR4_9930171	4	9930171	A	SLC2A9	intron_variant	MODIFIER	-0.472696	0.257	-
VAR_CHR4_9930208	4	9930208	C	SLC2A9	intron_variant	MODIFIER	-0.213756	1.027	-
RS4235345	4	9930219	T	SLC2A9	intron_variant	MODIFIER	-0.947107	0.02	0.17
VAR_CHR4_9930328	4	9930328	A	SLC2A9	intron_variant	MODIFIER	-0.384109	0.422	-
RS114540580	4	9930366	C	SLC2A9	intron_variant	MODIFIER	-0.761639	0.052	0.35
RS141626416	4	9930395	G	SLC2A9	intron_variant	MODIFIER	-	-	0.25
VAR_CHR4_9930620	4	9930620	T	SLC2A9	intron_variant	MODIFIER	-0.230407	0.946	-
VAR_CHR4_9930717	4	9930717	G	SLC2A9	intron_variant	MODIFIER	0.107052	3.683	-
RS62294288	4	9931173	A	SLC2A9	intron_variant	MODIFIER	-0.522354	0.193	0.18
VAR_CHR4_9931480	4	9931480	A	SLC2A9	intron_variant	MODIFIER	-0.077714	1.902	-
VAR_CHR4_9931512	4	9931512	T	SLC2A9	intron_variant	MODIFIER	-0.209512	1.049	-
RS4447862	4	9931645	C	SLC2A9	intron_variant	MODIFIER	-	-	0.31
RS62294289	4	9931870	C	SLC2A9	intron_variant	MODIFIER	-	-	0.19
RS189326238	4	9931938	A	SLC2A9	intron_variant	MODIFIER	-0.841091	0.035	0.23

VAR_CHR4_9932301	4	9932301	A	SLC2A9	intron_variant	MODIFIER	-0.076607	1.91	-
RS73096620	4	9932341	T	SLC2A9	intron_variant	MODIFIER	-	-	0.19
RS6823324	4	9932359	G	SLC2A9	intron_variant	MODIFIER	0.004298	2.627	0.18
RS6449137	4	9932479	A	SLC2A9	intron_variant	MODIFIER	-	-	0.9
RS6837336	4	9932510	T	SLC2A9	intron_variant	MODIFIER	-0.133217	1.496	0.19
VAR_CHR4_9932565	4	9932565	C	SLC2A9	intron_variant	MODIFIER	0.116636	3.786	-
VAR_CHR4_9932738	4	9932738	C	SLC2A9	intron_variant	MODIFIER	-0.338116	0.543	-
RS181658363	4	9932749	C	SLC2A9	intron_variant	MODIFIER	-	-	0.28
VAR_CHR4_9932840	4	9932840	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS114756544	4	9932882	A	SLC2A9	intron_variant	MODIFIER	0.312217	5.811	0.35
VAR_CHR4_9932951	4	9932951	A	SLC2A9	intron_variant	MODIFIER	0.65327	8.518	-
VAR_CHR4_9932979	4	9932979	G	SLC2A9	intron_variant	MODIFIER	-0.052006	2.114	-
VAR_CHR4_9933501	4	9933501	G	SLC2A9	intron_variant	MODIFIER	1.908105	15.64	-
RS73096626	4	9933514	A	SLC2A9	intron_variant	MODIFIER	1.794382	14.95	0.23
RS13112015	4	9933796	G	SLC2A9	intron_variant	MODIFIER	0.460295	7.12	0.31
RS13122290	4	9933832	T	SLC2A9	intron_variant	MODIFIER	0.140195	4.04	0.21
VAR_CHR4_9933877	4	9933877	A	SLC2A9	intron_variant	MODIFIER	-0.0121	2.472	-
RS6449139	4	9934111	G	SLC2A9	intron_variant	MODIFIER	-0.076541	1.911	0.22
VAR_CHR4_9934112	4	9934112	T	SLC2A9	intron_variant	MODIFIER	-0.315889	0.611	-
RS77356241	4	9934200	C	SLC2A9	intron_variant	MODIFIER	-0.047128	2.156	0.15
RS12507606	4	9934561	A	SLC2A9	intron_variant	MODIFIER	0.646138	8.47	0.22
VAR_CHR4_9934731	4	9934731	A	SLC2A9	intron_variant	MODIFIER	0.12563	3.883	-
RS737267	4	9934744	A	SLC2A9	intron_variant	MODIFIER	-0.245697	0.877	0.73
RS62294290	4	9934894	T	SLC2A9	intron_variant	MODIFIER	-0.594716	0.129	0.46
RS77862592	4	9935234	A	SLC2A9	intron_variant	MODIFIER	-0.355662	0.494	0.25
VAR_CHR4_9935236	4	9935236	G	SLC2A9	intron_variant	MODIFIER	-	-	-

RS115502819	4	9935277	G	SLC2A9	intron_variant	MODIFIER	-0.022494	2.375	0.38
RS73096634	4	9935584	T	SLC2A9	intron_variant	MODIFIER	-0.379032	0.434	0.31
VAR_CHR4_9935896	4	9935896	A	SLC2A9	intron_variant	MODIFIER	0.075059	3.343	-
RS6855911	4	9935910	C	SLC2A9	intron_variant	MODIFIER	-0.097347	1.75	0.27
VAR_CHR4_9935948	4	9935948	A	SLC2A9	intron_variant	MODIFIER	-0.116757	1.609	-
VAR_CHR4_9936024	4	9936024	G	SLC2A9	intron_variant	MODIFIER	0.148348	4.128	-
VAR_CHR4_9936139	4	9936139	G	SLC2A9	intron_variant	MODIFIER	0.021928	2.799	-
VAR_CHR4_9936141	4	9936141	A	SLC2A9	intron_variant	MODIFIER	-0.156668	1.345	-
RS139979601	4	9936232	T	SLC2A9	intron_variant	MODIFIER	-0.097014	1.752	0.23
RS185175605	4	9936979	T	SLC2A9	intron_variant	MODIFIER	-0.449119	0.294	0.38
RS10010582	4	9937085	A	SLC2A9	intron_variant	MODIFIER	0.100562	3.614	0.36
RS116050058	4	9937120	C	SLC2A9	intron_variant	MODIFIER	-0.24732	0.87	0.38
RS137912718	4	9937349	T	SLC2A9	intron_variant	MODIFIER	-1.131992	0.009	0.25
VAR_CHR4_9937429	4	9937429	A	SLC2A9	intron_variant	MODIFIER	-0.329686	0.568	-
RS71603975	4	9937741	A	SLC2A9	intron_variant	MODIFIER	0.005664	2.64	0.28
VAR_CHR4_9937774	4	9937774	T	SLC2A9	intron_variant	MODIFIER	0.183281	4.502	-
RS28480661	4	9937798	C	SLC2A9	intron_variant	MODIFIER	1.853623	15.31	0.25
RS10017945	4	9937852	C	SLC2A9	intron_variant	MODIFIER	-0.186704	1.17	0.25
VAR_CHR4_9938021	4	9938021	A	SLC2A9	intron_variant	MODIFIER	0.276503	5.463	-
RS79704809	4	9938279	T	SLC2A9	intron_variant	MODIFIER	0.139731	4.035	0.17
RS191586435	4	9938289	A	SLC2A9	intron_variant	MODIFIER	-0.051727	2.116	0.24
VAR_CHR4_9938424	4	9938424	A	SLC2A9	intron_variant	MODIFIER	0.01843	2.765	-
VAR_CHR4_9938551	4	9938551	T	SLC2A9	intron_variant	MODIFIER	-0.544155	0.171	-
RS10005326	4	9938591	T	SLC2A9	intron_variant	MODIFIER	-0.374259	0.446	0.29
VAR_CHR4_9938599	4	9938599	G	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9938713	4	9938713	A	SLC2A9	intron_variant	MODIFIER	-0.112508	1.639	-

RS7670751	4	9938773	G	SLC2A9	intron_variant	MODIFIER	0.155666	4.207	0.14
VAR_CHR4_9938866	4	9938866	T	SLC2A9	intron_variant	MODIFIER	-0.204259	1.076	-
RS188047000	4	9938910	T	SLC2A9	intron_variant	MODIFIER	-0.139685	1.453	0.22
RS4447863	4	9938969	A	SLC2A9	intron_variant	MODIFIER	-0.125193	1.55	0.21
VAR_CHR4_9938997	4	9938997	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS938558	4	9939205	C	SLC2A9	intron_variant	MODIFIER	-0.735363	0.06	0.3
VAR_CHR4_9939553	4	9939553	A	SLC2A9	intron_variant	MODIFIER	-0.440855	0.308	-
VAR_CHR4_9939574	4	9939574	T	SLC2A9	intron_variant	MODIFIER	-0.412035	0.362	-
RS185599792	4	9939761	T	SLC2A9	intron_variant	MODIFIER	-0.358526	0.486	0.36
RS4511996	4	9939818	C	SLC2A9	intron_variant	MODIFIER	-0.478505	0.248	0.45
VAR_CHR4_9940175	4	9940175	T	SLC2A9	intron_variant	MODIFIER	-0.349365	0.511	-
RS192930761	4	9940346	T	SLC2A9	intron_variant	MODIFIER	0.139325	4.031	0.31
RS185415458	4	9940428	A	SLC2A9	intron_variant	MODIFIER	0.958397	10.42	0.38
VAR_CHR4_9940567	4	9940567	T	SLC2A9	intron_variant	MODIFIER	-0.494203	0.227	-
RS5028843	4	9940806	T	SLC2A9	intron_variant	MODIFIER	-0.055293	2.086	0.27
VAR_CHR4_9940859	4	9940859	A	SLC2A9	intron_variant	MODIFIER	0.250153	5.199	-
RS118123197	4	9940970	G	SLC2A9	intron_variant	MODIFIER	0.025817	2.838	0.19
RS73096647	4	9940994	T	SLC2A9	intron_variant	MODIFIER	-0.654866	0.092	0.22
VAR_CHR4_9941195	4	9941195	G	SLC2A9	intron_variant	MODIFIER	0.075854	3.352	-
RS4697913	4	9941262	A	SLC2A9	intron_variant	MODIFIER	1.157742	11.52	0.17
RS147123083	4	9941295	C	SLC2A9	intron_variant	MODIFIER	-0.378217	0.436	0.15
VAR_CHR4_9941301	4	9941301	G	SLC2A9	intron_variant	MODIFIER	-0.034918	2.263	-
RS7675964	4	9941434	A	SLC2A9	intron_variant	MODIFIER	-0.440098	0.309	0.26
VAR_CHR4_9941689	4	9941689	C	SLC2A9	intron_variant	MODIFIER	-0.073925	1.932	-
RS13142273	4	9941959	A	SLC2A9	intron_variant	MODIFIER	-	-	0.3
VAR_CHR4_9942352	4	9942352	A	SLC2A9	intron_variant	MODIFIER	-	-	-

RS34658962	4	9942390	G	SLC2A9	intron_variant	MODIFIER	-0.011292	2.479	0.21
VAR_CHR4_9942538	4	9942538	G	SLC2A9	intron_variant	MODIFIER	0.132455	3.957	-
RS149285862	4	9942564	C	SLC2A9	intron_variant	MODIFIER	0.011805	2.7	0.28
RS4697698	4	9942577	A	SLC2A9	intron_variant	MODIFIER	-0.515593	0.201	0.28
VAR_CHR4_9942578	4	9942578	T	SLC2A9	intron_variant	MODIFIER	-0.455528	0.283	-
RS7669296	4	9942642	G	SLC2A9	intron_variant	MODIFIER	-	-	0.3
VAR_CHR4_9942665	4	9942665	G	SLC2A9	intron_variant	MODIFIER	-0.785944	0.046	-
VAR_CHR4_9942691	4	9942691	A	SLC2A9	intron_variant	MODIFIER	-	-	-
RS146242682	4	9942753	C	SLC2A9	intron_variant	MODIFIER	0.03539	2.934	0.19
RS139350408	4	9942774	G	SLC2A9	intron_variant	MODIFIER	-0.017616	2.42	0.17
VAR_CHR4_9943064	4	9943064	A	SLC2A9	intron_variant	MODIFIER	0.082932	3.426	-
RS13139970	4	9943185	T	SLC2A9	intron_variant	MODIFIER	0.118167	3.803	0.36
VAR_CHR4_9943262	4	9943262	G	SLC2A9	intron_variant	MODIFIER	-0.269375	0.778	-
VAR_CHR4_9943306	4	9943306	C	SLC2A9	intron_variant	MODIFIER	-0.135321	1.482	-
RS2276965	4	9943475	C	SLC2A9	intron_variant	MODIFIER	-0.360071	0.482	0.41
RS2276964	4	9943499	A	SLC2A9	intron_variant	MODIFIER	-	-	0.34
RS4292327	4	9943700	C	SLC2A9	intron_variant	MODIFIER	0.114714	3.766	0.12
VAR_CHR4_9943731	4	9943731	A	SLC2A9	intron_variant	MODIFIER	0.262272	5.321	-
RS151156660	4	9943977	A	SLC2A9	intron_variant	MODIFIER	-0.149696	1.389	0.15
RS12498742	4	9944052	C	SLC2A9	intron_variant	MODIFIER	0.25236	5.221	0.16
VAR_CHR4_9944094	4	9944094	A	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9944374	4	9944374	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS141780701	4	9944409	A	SLC2A9	intron_variant	MODIFIER	0.255756	5.255	0.2
VAR_CHR4_9944414	4	9944414	T	SLC2A9	intron_variant	MODIFIER	0.029074	2.871	-
VAR_CHR4_9944535	4	9944535	G	SLC2A9	intron_variant	MODIFIER	1.203073	11.76	-
RS6449144	4	9944650	C	SLC2A9	intron_variant	MODIFIER	0.084526	3.443	0.4

RS182592473	4	9944765	T	SLC2A9	intron_variant	MODIFIER	-0.508159	0.21	0.35
RS138558177	4	9944956	C	SLC2A9	intron_variant	MODIFIER	-0.263845	0.8	0.26
RS181452327	4	9945038	C	SLC2A9	intron_variant	MODIFIER	0.152827	4.176	0.18
RS1007872	4	9945148	T	SLC2A9	intron_variant	MODIFIER	-0.321239	0.594	0.16
VAR_CHR4_9945179	4	9945179	A	SLC2A9	intron_variant	MODIFIER	-0.045209	2.173	-
RS190373872	4	9945222	T	SLC2A9	intron_variant	MODIFIER	-0.501394	0.218	0.2
RS4235346	4	9945296	G	SLC2A9	intron_variant	MODIFIER	-0.23129	0.942	0.18
RS4697699	4	9945722	G	SLC2A9	intron_variant	MODIFIER	0.450655	7.042	0.16
RS4697700	4	9945792	G	SLC2A9	intron_variant	MODIFIER	-	-	0.17
RS4697701	4	9946095	T	SLC2A9	intron_variant	MODIFIER	-0.555247	0.161	0.24
RS10939620	4	9946132	G	SLC2A9	intron_variant	MODIFIER	-0.071031	1.955	0.28
RS16891234	4	9946163	A	SLC2A9	intron_variant	MODIFIER	-0.123335	1.563	0.23
VAR_CHR4_9946259	4	9946259	T	SLC2A9	intron_variant	MODIFIER	-0.020585	2.393	-
RS146017173	4	9946290	A	SLC2A9	intron_variant	MODIFIER	0.21025	4.787	0.23
RS71603976	4	9946337	G	SLC2A9	intron_variant	MODIFIER	0.003745	2.622	0.25
VAR_CHR4_9946407	4	9946407	G	SLC2A9	intron_variant	MODIFIER	-0.438006	0.313	-
RS4475146	4	9946656	T	SLC2A9	intron_variant	MODIFIER	0.315203	5.84	0.31
VAR_CHR4_9946797	4	9946797	G	SLC2A9	intron_variant	MODIFIER	-0.260825	0.813	-
RS74561581	4	9946846	G	SLC2A9	intron_variant	MODIFIER	-0.078798	1.893	0.21
RS111338560	4	9946875	T	SLC2A9	intron_variant	MODIFIER	-0.650879	0.094	0.21
VAR_CHR4_9946890	4	9946890	A	SLC2A9	intron_variant	MODIFIER	-0.01293	2.464	-
RS115770226	4	9946911	C	SLC2A9	intron_variant	MODIFIER	-0.265042	0.795	0.25
VAR_CHR4_9946949	4	9946949	T	SLC2A9	intron_variant	MODIFIER	-0.38177	0.428	-
VAR_CHR4_9946960	4	9946960	G	SLC2A9	intron_variant	MODIFIER	0.065785	3.246	-
RS78801470	4	9947090	T	SLC2A9	intron_variant	MODIFIER	-0.634692	0.103	0.26
RS2018643	4	9947121	A	SLC2A9	intron_variant	MODIFIER	0.067332	3.262	0.28

VAR_CHR4_9947167	4	9947167	T	SLC2A9	intron_variant	MODIFIER	-0.108928	1.665	-
RS77459722	4	9947200	T	SLC2A9	intron_variant	MODIFIER	-0.747305	0.056	0.21
VAR_CHR4_9947201	4	9947201	A	SLC2A9	intron_variant	MODIFIER	0.145379	4.096	-
RS1122141	4	9947278	A	SLC2A9	intron_variant	MODIFIER	-0.217864	1.007	0.24
VAR_CHR4_9947406	4	9947406	T	SLC2A9	intron_variant	MODIFIER	0.052769	3.111	-
RS151104273	4	9947481	T	SLC2A9	intron_variant	MODIFIER	-0.297984	0.671	0.12
RS1122142	4	9947548	C	SLC2A9	intron_variant	MODIFIER	-0.44563	0.299	0.17
RS4621431	4	9947590	C	SLC2A9	intron_variant	MODIFIER	-0.479401	0.247	0.17
VAR_CHR4_9947625	4	9947625	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS4339211	4	9947658	G	SLC2A9	intron_variant	MODIFIER	-0.426538	0.333	0.23
RS13116337	4	9947669	T	SLC2A9	intron_variant	MODIFIER	-0.10756	1.674	0.2
VAR_CHR4_9947693	4	9947693	G	SLC2A9	intron_variant	MODIFIER	0.065029	3.238	-
VAR_CHR4_9947728	4	9947728	A	SLC2A9	intron_variant	MODIFIER	-0.230797	0.945	-
RS7694997	4	9947811	T	SLC2A9	intron_variant	MODIFIER	-0.417654	0.351	0.17
VAR_CHR4_9947838	4	9947838	G	SLC2A9	intron_variant	MODIFIER	0.062355	3.21	-
RS144651801	4	9947865	A	SLC2A9	intron_variant	MODIFIER	0.027731	2.857	0.22
RS7686538	4	9948077	G	SLC2A9	intron_variant	MODIFIER	-0.328965	0.57	0.23
VAR_CHR4_9948140	4	9948140	T	SLC2A9	intron_variant	MODIFIER	-0.057711	2.066	-
VAR_CHR4_9948358	4	9948358	C	SLC2A9	intron_variant	MODIFIER	-1.064278	0.012	-
RS4580649	4	9948461	C	SLC2A9	intron_variant	MODIFIER	-0.234946	0.925	0.26
RS115662655	4	9948527	G	SLC2A9	intron_variant	MODIFIER	1.174659	11.61	0.24
RS998676	4	9948564	A	SLC2A9	intron_variant	MODIFIER	0.494295	7.387	0.23
RS998675	4	9948829	G	SLC2A9	intron_variant	MODIFIER	-0.210081	1.046	0.25
RS4408959	4	9948868	G	SLC2A9	intron_variant	MODIFIER	-0.481991	0.243	0.19
RS4276278	4	9948870	A	SLC2A9	intron_variant	MODIFIER	0.275594	5.454	0.18
VAR_CHR4_9949014	4	9949014	T	SLC2A9	intron_variant	MODIFIER	-0.455184	0.284	-

RS191041567	4	9949040	G	SLC2A9	intron_variant	MODIFIER	0.311668	5.806	0.24
VAR_CHR4_9949140	4	9949140	A	SLC2A9	intron_variant	MODIFIER	-0.236335	0.919	-
RS139007297	4	9949355	A	SLC2A9	intron_variant	MODIFIER	-0.100632	1.725	0.21
RS71603977	4	9949386	G	SLC2A9	intron_variant	MODIFIER	-0.454369	0.285	0.21
VAR_CHR4_9949563	4	9949563	A	SLC2A9	intron_variant	MODIFIER	0.318056	5.867	-
VAR_CHR4_9949633	4	9949633	T	SLC2A9	intron_variant	MODIFIER	0.112024	3.737	-
RS13151331	4	9949839	A	SLC2A9	intron_variant	MODIFIER	-0.111941	1.643	0.22
VAR_CHR4_9950247	4	9950247	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS114525330	4	9950381	G	SLC2A9	intron_variant	MODIFIER	0.230877	5.001	0.2
VAR_CHR4_9950432	4	9950432	A	SLC2A9	intron_variant	MODIFIER	-0.026516	2.339	-
RS116956085	4	9950451	T	SLC2A9	intron_variant	MODIFIER	1.558268	13.62	0.23
RS76698299	4	9950471	G	SLC2A9	intron_variant	MODIFIER	0.40192	6.631	0.24
RS79501171	4	9950477	T	SLC2A9	intron_variant	MODIFIER	0.09969	3.605	0.34
RS77304661	4	9950485	A	SLC2A9	intron_variant	MODIFIER	0.234231	5.036	0.25
VAR_CHR4_9950527	4	9950527	G	SLC2A9	intron_variant	MODIFIER	0.240601	5.101	-
RS12498150	4	9950537	G	SLC2A9	intron_variant	MODIFIER	-0.292541	0.691	0.32
RS12498956	4	9950705	G	SLC2A9	intron_variant	MODIFIER	-0.056061	2.079	0.34
RS115272825	4	9950912	C	SLC2A9	intron_variant	MODIFIER	-0.437112	0.314	0.27
VAR_CHR4_9951069	4	9951069	G	SLC2A9	intron_variant	MODIFIER	0.010155	2.684	-
RS13328050	4	9951120	C	SLC2A9	intron_variant	MODIFIER	-0.343213	0.528	0.27
RS1079128	4	9951221	A	SLC2A9	intron_variant	MODIFIER	0.176015	4.425	0.23
RS9993410	4	9951264	G	SLC2A9	intron_variant	MODIFIER	-0.15966	1.327	0.24
VAR_CHR4_9951547	4	9951547	A	SLC2A9	intron_variant	MODIFIER	0.335986	6.036	-
RS77101951	4	9951590	A	SLC2A9	intron_variant	MODIFIER	-0.006133	2.528	0.22
RS11735831	4	9951591	T	SLC2A9	intron_variant	MODIFIER	-0.556709	0.159	0.23
RS10000983	4	9951606	A	SLC2A9	intron_variant	MODIFIER	0.067267	3.262	0.21

RS11726102	4	9951664	G	SLC2A9	intron_variant	MODIFIER	0.105524	3.667	0.17
VAR_CHR4_9951779	4	9951779	C	SLC2A9	intron_variant	MODIFIER	0.137161	4.007	-
RS11723439	4	9951819	A	SLC2A9	intron_variant	MODIFIER	-0.384161	0.422	0.24
VAR_CHR4_9951821	4	9951821	A	SLC2A9	intron_variant	MODIFIER	-0.110129	1.656	-
RS4235347	4	9951956	G	SLC2A9	intron_variant	MODIFIER	-0.276271	0.751	0.2
RS4235348	4	9951968	A	SLC2A9	intron_variant	MODIFIER	-0.003053	2.557	0.17
VAR_CHR4_9951999	4	9951999	T	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9952001	4	9952001	T	SLC2A9	intron_variant	MODIFIER	-0.289368	0.702	-
RS7376505	4	9952744	G	SLC2A9	intron_variant	MODIFIER	-0.109994	1.657	0.15
RS7377578	4	9952775	A	SLC2A9	intron_variant	MODIFIER	0.342315	6.095	0.17
VAR_CHR4_9952982	4	9952982	A	SLC2A9	intron_variant	MODIFIER	-	-	-
RS13101688	4	9953011	G	SLC2A9	intron_variant	MODIFIER	-	-	0.18
RS35371429	4	9953031	G	SLC2A9	intron_variant	MODIFIER	0.375195	6.395	0.19
RS62294293	4	9953086	T	SLC2A9	intron_variant	MODIFIER	0.119141	3.813	0.16
RS10006833	4	9953097	A	SLC2A9	intron_variant	MODIFIER	0.562973	7.896	0.17
RS7377625	4	9953099	A	SLC2A9	intron_variant	MODIFIER	0.177878	4.445	0.16
RS4455410	4	9953297	A	SLC2A9	intron_variant	MODIFIER	1.259386	12.06	0.22
RS4546242	4	9953314	T	SLC2A9	intron_variant	MODIFIER	-0.227592	0.96	0.19
RS4560411	4	9953361	T	SLC2A9	intron_variant	MODIFIER	0.007245	2.656	0.13
RS4407505	4	9953367	A	SLC2A9	intron_variant	MODIFIER	0.601601	8.167	0.23
RS4467563	4	9953460	T	SLC2A9	intron_variant	MODIFIER	0.158006	4.232	0.18
RS4467564	4	9953472	C	SLC2A9	intron_variant	MODIFIER	-0.342769	0.529	0.19
RS4467565	4	9953487	T	SLC2A9	intron_variant	MODIFIER	-	-	0.27
RS186942366	4	9953786	G	SLC2A9	intron_variant	MODIFIER	-	-	0.19
RS4292332	4	9953830	G	SLC2A9	intron_variant	MODIFIER	-0.211131	1.04	0.23
RS79679425	4	9953853	A	SLC2A9	intron_variant	MODIFIER	0.076579	3.359	0.23

RS4292333	4	9953871	C	SLC2A9	intron_variant	MODIFIER	-1.042072	0.013	0.17
RS4447861	4	9953940	G	SLC2A9	intron_variant	MODIFIER	0.488714	7.344	0.15
RS4459990	4	9954005	A	SLC2A9	intron_variant	MODIFIER	0.216901	4.856	0.16
RS4495037	4	9954050	G	SLC2A9	intron_variant	MODIFIER	0.172831	4.391	0.13
VAR_CHR4_9954426	4	9954426	T	SLC2A9	intron_variant	MODIFIER	0.042059	3.002	-
RS9994266	4	9954450	C	SLC2A9	intron_variant	MODIFIER	0.18242	4.493	0.19
RS116882299	4	9954549	G	SLC2A9	intron_variant	MODIFIER	-0.509245	0.208	0.19
RS16891285	4	9954630	G	SLC2A9	intron_variant	MODIFIER	-	-	0.17
RS11723382	4	9954660	A	SLC2A9	intron_variant	MODIFIER	0.102006	3.629	0.18
RS7376948	4	9954708	C	SLC2A9	intron_variant	MODIFIER	0.171478	4.376	0.18
RS7375587	4	9954758	T	SLC2A9	intron_variant	MODIFIER	-0.164616	1.297	0.15
RS7378305	4	9954893	G	SLC2A9	intron_variant	MODIFIER	-0.317182	0.607	0.23
RS7375599	4	9954918	T	SLC2A9	intron_variant	MODIFIER	-0.326125	0.579	0.17
VAR_CHR4_9954919	4	9954919	T	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9954931	4	9954931	T	SLC2A9	intron_variant	MODIFIER	-0.813916	0.04	-
VAR_CHR4_9954973	4	9954973	A	SLC2A9	intron_variant	MODIFIER	0.302435	5.717	-
VAR_CHR4_9955130	4	9955130	T	SLC2A9	intron_variant	MODIFIER	-0.125902	1.545	-
RS7378340	4	9955198	G	SLC2A9	intron_variant	MODIFIER	-0.368672	0.46	0.22
RS7375642	4	9955236	T	SLC2A9	intron_variant	MODIFIER	-0.806525	0.041	0.17
RS7375643	4	9955239	T	SLC2A9	intron_variant	MODIFIER	-0.222808	0.983	0.16
VAR_CHR4_9955248	4	9955248	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS6837224	4	9955255	C	SLC2A9	intron_variant	MODIFIER	-0.429394	0.328	0.17
RS13435674	4	9955746	C	SLC2A9	intron_variant	MODIFIER	-0.1652	1.294	0.2
RS114557276	4	9955748	A	SLC2A9	intron_variant	MODIFIER	0.215711	4.844	0.2
VAR_CHR4_9955750	4	9955750	G	SLC2A9	intron_variant	MODIFIER	0.351153	6.177	-
RS4306953	4	9955776	C	SLC2A9	intron_variant	MODIFIER	-0.861916	0.031	0.17

VAR_CHR4_9955857	4	9955857	A	SLC2A9	intron_variant	MODIFIER	0.003258	2.617	-
RS4519796	4	9955936	T	SLC2A9	intron_variant	MODIFIER	-0.027674	2.328	0.2
RS4311316	4	9955971	G	SLC2A9	intron_variant	MODIFIER	-0.249698	0.86	0.21
RS4481233	4	9956079	A	SLC2A9	intron_variant	MODIFIER	0.043737	3.019	0.22
VAR_CHR4_9956093	4	9956093	A	SLC2A9	intron_variant	MODIFIER	-0.407957	0.37	-
RS4314284	4	9956096	G	SLC2A9	intron_variant	MODIFIER	-0.369112	0.459	0.23
RS4312756	4	9956107	C	SLC2A9	intron_variant	MODIFIER	-0.388896	0.411	0.19
RS4312757	4	9956145	A	SLC2A9	intron_variant	MODIFIER	0.106383	3.676	0.23
VAR_CHR4_9956210	4	9956210	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS6814664	4	9956228	G	SLC2A9	intron_variant	MODIFIER	-0.236832	0.917	0.23
VAR_CHR4_9956249	4	9956249	T	SLC2A9	intron_variant	MODIFIER	-0.40604	0.374	-
RS6449154	4	9956404	G	SLC2A9	intron_variant	MODIFIER	0.333132	6.01	0.2
RS6414766	4	9956474	C	SLC2A9	intron_variant	MODIFIER	-0.377451	0.438	0.2
VAR_CHR4_9956572	4	9956572	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS71603978	4	9956576	T	SLC2A9	intron_variant	MODIFIER	-0.097006	1.752	0.19
RS6449156	4	9956712	G	SLC2A9	intron_variant	MODIFIER	-	-	0.22
VAR_CHR4_9957248	4	9957248	G	SLC2A9	intron_variant	MODIFIER	0.477793	7.259	-
VAR_CHR4_9957376	4	9957376	C	SLC2A9	intron_variant	MODIFIER	0.012901	2.711	-
RS34297373	4	9958081	C	SLC2A9	intron_variant	MODIFIER	0.019469	2.775	0.12
RS139721393	4	9958093	G	SLC2A9	intron_variant	MODIFIER	-	-	0.16
RS28715627	4	9958140	A	SLC2A9	intron_variant	MODIFIER	0.368542	6.335	0.26
RS17245436	4	9958169	T	SLC2A9	intron_variant	MODIFIER	-0.125964	1.545	0.17
RS17185835	4	9958180	A	SLC2A9	intron_variant	MODIFIER	-0.140944	1.445	0.23
RS17185870	4	9958214	G	SLC2A9	intron_variant	MODIFIER	-0.185242	1.178	0.16
VAR_CHR4_9958239	4	9958239	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS28677023	4	9958326	G	SLC2A9	intron_variant	MODIFIER	-0.11713	1.606	0.26

RS28602527	4	9958327	C	SLC2A9	intron_variant	MODIFIER	-0.394584	0.399	0.26
VAR_CHR4_9958340	4	9958340	G	SLC2A9	intron_variant	MODIFIER	-0.043316	2.189	-
RS59924619	4	9958342	G	SLC2A9	intron_variant	MODIFIER	-0.161882	1.313	0.21
VAR_CHR4_9958357	4	9958357	T	SLC2A9	intron_variant	MODIFIER	-0.06111	2.037	-
VAR_CHR4_9958380	4	9958380	A	SLC2A9	intron_variant	MODIFIER	-0.182089	1.195	-
VAR_CHR4_9958526	4	9958526	G	SLC2A9	intron_variant	MODIFIER	-0.073316	1.937	-
RS11724510	4	9958583	G	SLC2A9	intron_variant	MODIFIER	-0.279415	0.739	0.19
RS79996818	4	9958614	T	SLC2A9	intron_variant	MODIFIER	-0.195763	1.12	0.16
RS182701836	4	9958619	A	SLC2A9	intron_variant	MODIFIER	0.112066	3.737	0.17
RS6815001	4	9958662	C	SLC2A9	intron_variant	MODIFIER	-0.374818	0.445	0.2
RS6849717	4	9958719	A	SLC2A9	intron_variant	MODIFIER	0.219918	4.888	0.27
RS6849729	4	9958732	A	SLC2A9	intron_variant	MODIFIER	0.21963	4.885	0.26
VAR_CHR4_9958761	4	9958761	A	SLC2A9	intron_variant	MODIFIER	-0.008626	2.504	-
RS6843873	4	9958788	T	SLC2A9	intron_variant	MODIFIER	-0.234568	0.927	0.17
RS6850143	4	9958924	A	SLC2A9	intron_variant	MODIFIER	-0.11958	1.589	0.19
RS6844316	4	9958977	T	SLC2A9	intron_variant	MODIFIER	-0.028484	2.321	0.14
VAR_CHR4_9958986	4	9958986	T	SLC2A9	intron_variant	MODIFIER	0.064331	3.231	-
RS13106991	4	9959011	T	SLC2A9	intron_variant	MODIFIER	-0.392742	0.403	0.17
RS6834893	4	9959123	G	SLC2A9	intron_variant	MODIFIER	1.952696	15.91	0.18
RS6816053	4	9959188	C	SLC2A9	intron_variant	MODIFIER	-0.593818	0.129	0.16
RS6844787	4	9959233	T	SLC2A9	intron_variant	MODIFIER	-0.554122	0.162	0.18
RS79323395	4	9959267	T	SLC2A9	intron_variant	MODIFIER	-0.266452	0.79	0.18
RS10001964	4	9959275	G	SLC2A9	intron_variant	MODIFIER	-0.375394	0.443	0.14
VAR_CHR4_9959310	4	9959310	A	SLC2A9	intron_variant	MODIFIER	-	-	-
RS28513781	4	9959334	C	SLC2A9	intron_variant	MODIFIER	-0.587991	0.134	0.15
RS4515163	4	9959603	G	SLC2A9	intron_variant	MODIFIER	-0.324334	0.584	0.22

RS76779802	4	9959798	C	SLC2A9	intron_variant	MODIFIER	-0.473902	0.255	0.17
RS28837683	4	9959808	G	SLC2A9	intron_variant	MODIFIER	-0.231336	0.942	0.13
RS62294331	4	9959889	T	SLC2A9	intron_variant	MODIFIER	-0.16235	1.311	0.14
RS13114090	4	9959899	A	SLC2A9	intron_variant	MODIFIER	-0.083801	1.854	0.14
RS62294332	4	9959989	A	SLC2A9	intron_variant	MODIFIER	0.260436	5.303	0.19
RS73227853	4	9960126	G	SLC2A9	intron_variant	MODIFIER	0.052946	3.113	0.17
RS57574512	4	9960182	A	SLC2A9	intron_variant	MODIFIER	-0.207347	1.06	0.18
RS13145108	4	9960196	C	SLC2A9	intron_variant	MODIFIER	-0.083103	1.859	0.14
VAR_CHR4_9960394	4	9960394	G	SLC2A9	intron_variant	MODIFIER	0.040586	2.987	-
RS6449157	4	9960442	C	SLC2A9	intron_variant	MODIFIER	-0.490204	0.232	0.21
RS6449158	4	9960459	A	SLC2A9	intron_variant	MODIFIER	0.06358	3.223	0.22
RS6449159	4	9960498	C	SLC2A9	intron_variant	MODIFIER	-0.39644	0.395	0.19
RS138949074	4	9960629	G	SLC2A9	intron_variant	MODIFIER	-0.052571	2.109	0.21
VAR_CHR4_9960643	4	9960643	C	SLC2A9	intron_variant	MODIFIER	0.068562	3.275	-
RS80180400	4	9960699	G	SLC2A9	intron_variant	MODIFIER	-	-	0.22
VAR_CHR4_9960707	4	9960707	A	SLC2A9	intron_variant	MODIFIER	-0.124861	1.552	-
VAR_CHR4_9960762	4	9960762	T	SLC2A9	intron_variant	MODIFIER	-0.240795	0.899	-
RS7699609	4	9961059	T	SLC2A9	intron_variant	MODIFIER	-0.61279	0.116	0.22
RS34560968	4	9961119	T	SLC2A9	intron_variant	MODIFIER	-0.13153	1.507	0.28
RS7672947	4	9961368	C	SLC2A9	intron_variant	MODIFIER	-0.622203	0.11	0.33
RS140186219	4	9961404	T	SLC2A9	intron_variant	MODIFIER	-0.471997	0.258	0.34
RS189377152	4	9961537	C	SLC2A9	intron_variant	MODIFIER	-	-	0.35
RS150823559	4	9961605	A	SLC2A9	intron_variant	MODIFIER	0.052131	3.105	0.36
VAR_CHR4_9961958	4	9961958	A	SLC2A9	intron_variant	MODIFIER	0.024719	2.827	-
VAR_CHR4_9961960	4	9961960	A	SLC2A9	intron_variant	MODIFIER	-0.131346	1.508	-
VAR_CHR4_9962079	4	9962079	G	SLC2A9	intron_variant	MODIFIER	-0.416138	0.353	-

RS17245723	4	9962218	T	SLC2A9	intron_variant	MODIFIER	-0.018876	2.409	0.41
RS75389148	4	9962226	G	SLC2A9	intron_variant	MODIFIER	-	-	0.33
RS187215218	4	9962245	T	SLC2A9	intron_variant	MODIFIER	-0.185637	1.176	0.33
RS189073544	4	9962303	T	SLC2A9	intron_variant	MODIFIER	0.094469	3.549	0.29
VAR_CHR4_9962592	4	9962592	A	SLC2A9	intron_variant	MODIFIER	-0.146043	1.412	-
RS11942223	4	9962765	G	SLC2A9	intron_variant	MODIFIER	-0.044734	2.177	0.32
VAR_CHR4_9962807	4	9962807	G	SLC2A9	intron_variant	MODIFIER	-0.49249	0.229	-
VAR_CHR4_9962831	4	9962831	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS13121355	4	9962931	G	SLC2A9	intron_variant	MODIFIER	0.004683	2.631	0.3
RS6836706	4	9964251	A	SLC2A9	intron_variant	MODIFIER	0.136873	4.004	0.16
RS34245354	4	9964312	T	SLC2A9	intron_variant	MODIFIER	-0.229357	0.951	0.22
VAR_CHR4_9964348	4	9964348	G	SLC2A9	intron_variant	MODIFIER	-0.08166	1.87	-
RS6850684	4	9964380	C	SLC2A9	intron_variant	MODIFIER	-0.374369	0.446	0.22
RS77265107	4	9964507	G	SLC2A9	intron_variant	MODIFIER	-0.226233	0.966	0.19
RS10018204	4	9964570	G	SLC2A9	intron_variant	MODIFIER	0.001705	2.602	0.17
RS145364569	4	9964652	T	SLC2A9	intron_variant	MODIFIER	-0.721652	0.064	0.25
RS147258783	4	9964653	C	SLC2A9	intron_variant	MODIFIER	-	-	0.21
RS184843205	4	9964741	T	SLC2A9	intron_variant	MODIFIER	-0.096146	1.759	0.2
RS9994937	4	9964799	C	SLC2A9	intron_variant	MODIFIER	-0.663203	0.088	0.2
RS28613263	4	9964880	G	SLC2A9	intron_variant	MODIFIER	-0.131059	1.51	0.23
RS28558552	4	9964913	C	SLC2A9	intron_variant	MODIFIER	-0.168802	1.272	0.24
RS6839490	4	9965000	G	SLC2A9	intron_variant	MODIFIER	0.180426	4.472	0.36
RS62294334	4	9965079	A	SLC2A9	intron_variant	MODIFIER	-0.001938	2.567	0.41
RS79765234	4	9965112	C	SLC2A9	intron_variant	MODIFIER	-0.074426	1.928	0.49
VAR_CHR4_9965134	4	9965134	T	SLC2A9	intron_variant	MODIFIER	-0.323266	0.588	-
RS6856127	4	9965443	A	SLC2A9	intron_variant	MODIFIER	0.243181	5.128	0.24

RS6840802	4	9965633	G	SLC2A9	intron_variant	MODIFIER	-0.382015	0.427	0.25
VAR_CHR4_9965721	4	9965721	T	SLC2A9	intron_variant	MODIFIER	-0.358969	0.485	-
RS60285303	4	9965730	G	SLC2A9	intron_variant	MODIFIER	-	-	0.27
VAR_CHR4_9965736	4	9965736	A	SLC2A9	intron_variant	MODIFIER	-0.804387	0.042	-
VAR_CHR4_9965826	4	9965826	T	SLC2A9	intron_variant	MODIFIER	-0.394982	0.398	-
VAR_CHR4_9965912	4	9965912	T	SLC2A9	intron_variant	MODIFIER	-0.344189	0.525	-
RS6449171	4	9965998	A	SLC2A9	intron_variant	MODIFIER	0.158355	4.235	0.34
RS6449172	4	9966036	T	SLC2A9	intron_variant	MODIFIER	-0.112753	1.637	0.28
RS6449173	4	9966105	C	SLC2A9	intron_variant	MODIFIER	-0.193066	1.135	0.29
RS6847019	4	9966249	G	SLC2A9	intron_variant	MODIFIER	-0.343146	0.528	0.28
RS138547806	4	9966274	G	SLC2A9	intron_variant	MODIFIER	0.478586	7.265	0.29
VAR_CHR4_9966361	4	9966361	A	SLC2A9	intron_variant	MODIFIER	0.154247	4.191	-
RS7442295	4	9966380	C	SLC2A9	intron_variant	MODIFIER	-0.498684	0.221	0.21
RS6449174	4	9966422	G	SLC2A9	intron_variant	MODIFIER	0.005311	2.637	0.23
VAR_CHR4_9966448	4	9966448	A	SLC2A9	intron_variant	MODIFIER	0.016215	2.743	-
RS9998811	4	9966477	T	SLC2A9	intron_variant	MODIFIER	-0.37776	0.437	0.26
RS145375160	4	9966540	A	SLC2A9	intron_variant	MODIFIER	0.845727	9.743	0.2
RS7658170	4	9966593	A	SLC2A9	intron_variant	MODIFIER	0.263883	5.337	0.2
RS6449175	4	9966610	A	SLC2A9	intron_variant	MODIFIER	0.017178	2.753	0.25
RS7663079	4	9966771	A	SLC2A9	intron_variant	MODIFIER	0.177235	4.438	0.16
RS7657340	4	9966772	T	SLC2A9	intron_variant	MODIFIER	-0.142931	1.432	0.13
RS7663097	4	9966791	A	SLC2A9	intron_variant	MODIFIER	0.029632	2.876	0.18
RS35110076	4	9966793	T	SLC2A9	intron_variant	MODIFIER	-0.202498	1.085	0.14
RS35380388	4	9966870	A	SLC2A9	intron_variant	MODIFIER	0.555274	7.841	0.18
RS138327996	4	9966876	T	SLC2A9	intron_variant	MODIFIER	-0.304039	0.65	0.16
RS114337273	4	9966943	A	SLC2A9	intron_variant	MODIFIER	0.103701	3.647	0.24

RS7676733	4	9966956	C	SLC2A9	intron_variant	MODIFIER	-0.494346	0.227	0.3
RS143790062	4	9967015	T	SLC2A9	intron_variant	MODIFIER	-0.502212	0.217	0.27
RS10017674	4	9967053	A	SLC2A9	intron_variant	MODIFIER	0.242039	5.116	0.24
RS113995040	4	9967255	C	SLC2A9	intron_variant	MODIFIER	-0.086713	1.831	0.14
RS16891489	4	9967314	C	SLC2A9	intron_variant	MODIFIER	-0.146523	1.409	0.26
VAR_CHR4_9967330	4	9967330	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS61691299	4	9967369	A	SLC2A9	intron_variant	MODIFIER	0.502421	7.449	0.13
RS7435196	4	9967556	T	SLC2A9	intron_variant	MODIFIER	-0.366184	0.466	0.12
VAR_CHR4_9967568	4	9967568	A	SLC2A9	intron_variant	MODIFIER	-0.208689	1.053	-
VAR_CHR4_9967589	4	9967589	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS7434391	4	9967682	G	SLC2A9	intron_variant	MODIFIER	-0.005905	2.53	0.25
RS7437120	4	9967683	A	SLC2A9	intron_variant	MODIFIER	0.049433	3.077	0.23
VAR_CHR4_9967695	4	9967695	T	SLC2A9	intron_variant	MODIFIER	-0.224874	0.973	-
RS6449176	4	9967843	C	SLC2A9	intron_variant	MODIFIER	-0.540505	0.175	0.19
RS6449177	4	9968050	A	SLC2A9	intron_variant	MODIFIER	-0.639182	0.1	0.17
RS60125439	4	9968232	G	SLC2A9	intron_variant	MODIFIER	-	-	0.2
RS186704661	4	9968476	G	SLC2A9	intron_variant	MODIFIER	0.403536	6.645	0.25
RS6449178	4	9968684	G	SLC2A9	intron_variant	MODIFIER	-0.010518	2.486	0.36
VAR_CHR4_9968774	4	9968774	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS189114622	4	9968928	A	SLC2A9	intron_variant	MODIFIER	2.082025	16.74	0.24
RS184866950	4	9969035	G	SLC2A9	intron_variant	MODIFIER	0.324348	5.927	0.19
VAR_CHR4_9969043	4	9969043	C	SLC2A9	intron_variant	MODIFIER	0.118696	3.808	-
RS6449179	4	9969117	C	SLC2A9	intron_variant	MODIFIER	-0.468882	0.262	0.24
VAR_CHR4_9969156	4	9969156	A	SLC2A9	intron_variant	MODIFIER	-	-	-
RS189718883	4	9969184	A	SLC2A9	intron_variant	MODIFIER	0.066668	3.255	0.26
RS144742400	4	9969210	A	SLC2A9	intron_variant	MODIFIER	-	-	0.2

VAR_CHR4_9969218	4	9969218	A	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9969230	4	9969230	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS181232702	4	9969374	T	SLC2A9	intron_variant	MODIFIER	-	-	0.15
RS77666919	4	9969479	G	SLC2A9	intron_variant	MODIFIER	-	-	0.26
RS7677710	4	9969517	A	SLC2A9	intron_variant	MODIFIER	0.579764	8.015	0.2
RS7683283	4	9969974	A	SLC2A9	intron_variant	MODIFIER	0.12121	3.835	0.27
RS62295967	4	9970052	T	SLC2A9	intron_variant	MODIFIER	-0.380799	0.43	0.31
VAR_CHR4_9970123	4	9970123	T	SLC2A9	intron_variant	MODIFIER	-0.23354	0.932	-
RS143530991	4	9970161	A	SLC2A9	intron_variant	MODIFIER	0.293419	5.63	0.3
RS74285646	4	9970411	T	SLC2A9	intron_variant	MODIFIER	0.16063	4.26	0.28
VAR_CHR4_9970562	4	9970562	A	SLC2A9	intron_variant	MODIFIER	-0.389727	0.409	-
RS7376960	4	9970570	C	SLC2A9	intron_variant	MODIFIER	-0.637648	0.101	0.24
RS6449183	4	9970691	G	SLC2A9	intron_variant	MODIFIER	-1.10853	0.01	0.22
RS80061611	4	9970733	C	SLC2A9	intron_variant	MODIFIER	-0.263535	0.802	0.21
VAR_CHR4_9970825	4	9970825	C	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9970860	4	9970860	C	SLC2A9	intron_variant	MODIFIER	-0.333285	0.557	-
VAR_CHR4_9970941	4	9970941	A	SLC2A9	intron_variant	MODIFIER	0.26972	5.396	-
RS4292328	4	9970962	G	SLC2A9	intron_variant	MODIFIER	-0.236306	0.919	0.3
RS4473653	4	9971058	T	SLC2A9	intron_variant	MODIFIER	0.96414	10.45	0.2
VAR_CHR4_9971133	4	9971133	T	SLC2A9	intron_variant	MODIFIER	-0.74359	0.057	-
VAR_CHR4_9971141	4	9971141	G	SLC2A9	intron_variant	MODIFIER	-0.221614	0.988	-
RS146658616	4	9971172	G	SLC2A9	intron_variant	MODIFIER	-0.056407	2.077	0.21
VAR_CHR4_9971179	4	9971179	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS28610447	4	9971517	A	SLC2A9	intron_variant	MODIFIER	-0.143356	1.429	0.24
RS116585088	4	9971539	C	SLC2A9	intron_variant	MODIFIER	-	-	0.25
VAR_CHR4_9971567	4	9971567	T	SLC2A9	intron_variant	MODIFIER	-0.487395	0.236	-

RS188311840	4	9971583	T	SLC2A9	intron_variant	MODIFIER	-0.39684	0.394	0.28
RS7439210	4	9971749	C	SLC2A9	intron_variant	MODIFIER	-	-	0.18
VAR_CHR4_9971846	4	9971846	C	SLC2A9	intron_variant	MODIFIER	-0.538826	0.176	-
RS73227873	4	9971903	A	SLC2A9	intron_variant	MODIFIER	0.183994	4.51	0.2
RS191268745	4	9971929	T	SLC2A9	intron_variant	MODIFIER	0.024098	2.821	0.2
VAR_CHR4_9971939	4	9971939	A	SLC2A9	intron_variant	MODIFIER	-0.007585	2.514	-
RS148968285	4	9971943	A	SLC2A9	intron_variant	MODIFIER	0.021984	2.8	0.2
RS60045583	4	9971950	C	SLC2A9	intron_variant	MODIFIER	-0.204979	1.072	0.2
RS58130873	4	9972081	A	SLC2A9	intron_variant	MODIFIER	-0.057703	2.066	0.25
RS117822964	4	9972133	G	SLC2A9	intron_variant	MODIFIER	-	-	0.28
RS13132625	4	9972163	T	SLC2A9	intron_variant	MODIFIER	0.07359	3.328	0.3
VAR_CHR4_9972281	4	9972281	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS13103690	4	9972778	A	SLC2A9	intron_variant	MODIFIER	0.017534	2.756	0.21
RS13103879	4	9972879	A	SLC2A9	intron_variant	MODIFIER	-0.166886	1.283	0.26
RS146914131	4	9972920	G	SLC2A9	intron_variant	MODIFIER	-0.558884	0.157	0.24
RS143024417	4	9973126	T	SLC2A9	intron_variant	MODIFIER	-0.204792	1.073	0.24
RS139311846	4	9973173	T	SLC2A9	intron_variant	MODIFIER	0.148663	4.131	0.25
RS4333184	4	9973576	A	SLC2A9	intron_variant	MODIFIER	-0.034747	2.265	0.23
RS6449196	4	9973660	G	SLC2A9	intron_variant	MODIFIER	-0.207883	1.057	0.24
VAR_CHR4_9973684	4	9973684	G	SLC2A9	intron_variant	MODIFIER	0.124427	3.87	-
VAR_CHR4_9973695	4	9973695	A	SLC2A9	intron_variant	MODIFIER	-0.328268	0.572	-
RS6852441	4	9973744	G	SLC2A9	intron_variant	MODIFIER	-0.594977	0.128	0.19
RS4639073	4	9973781	G	SLC2A9	intron_variant	MODIFIER	-0.02578	2.345	0.24
RS4476596	4	9973789	G	SLC2A9	intron_variant	MODIFIER	-0.349435	0.511	0.16
RS146760627	4	9973884	A	SLC2A9	intron_variant	MODIFIER	0.073244	3.324	0.27
RS6449201	4	9973894	G	SLC2A9	intron_variant	MODIFIER	-0.81974	0.039	0.29

VAR_CHR4_9974002	4	9974002	A	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9974022	4	9974022	C	SLC2A9	intron_variant	MODIFIER	-0.113722	1.63	-
RS6449202	4	9974043	A	SLC2A9	intron_variant	MODIFIER	0.141789	4.057	0.27
VAR_CHR4_9974178	4	9974178	C	SLC2A9	intron_variant	MODIFIER	-0.243925	0.885	-
RS13126729	4	9974186	T	SLC2A9	intron_variant	MODIFIER	-0.594382	0.129	0.2
RS7695113	4	9974258	G	SLC2A9	intron_variant	MODIFIER	-0.008119	2.509	0.19
VAR_CHR4_9974329	4	9974329	C	SLC2A9	intron_variant	MODIFIER	0.143936	4.08	-
RS6853922	4	9974538	C	SLC2A9	intron_variant	MODIFIER	-	-	0.17
VAR_CHR4_9974584	4	9974584	A	SLC2A9	intron_variant	MODIFIER	-	-	-
RS1071988	4	9974638	C	SLC2A9	intron_variant	MODIFIER	-0.289387	0.702	0.19
RS67820465	4	9975873	T	SLC2A9	intron_variant	MODIFIER	0.219484	4.883	0.14
RS10939637	4	9977577	T	SLC2A9	intron_variant	MODIFIER	0.210832	4.793	0.29
VAR_CHR4_9977628	4	9977628	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS10939638	4	9977675	A	SLC2A9	intron_variant	MODIFIER	0.758561	9.205	0.16
VAR_CHR4_9977748	4	9977748	A	SLC2A9	intron_variant	MODIFIER	-0.394369	0.399	-
VAR_CHR4_9977797	4	9977797	G	SLC2A9	intron_variant	MODIFIER	0.050323	3.086	-
RS182996926	4	9977899	T	SLC2A9	intron_variant	MODIFIER	-	-	0.28
RS4505821	4	9978094	C	SLC2A9	intron_variant	MODIFIER	0.922789	10.21	0.22
RS62295971	4	9978142	C	SLC2A9	intron_variant	MODIFIER	-0.39184	0.405	0.29
VAR_CHR4_9978151	4	9978151	G	SLC2A9	intron_variant	MODIFIER	0.181015	4.478	-
VAR_CHR4_9978225	4	9978225	A	SLC2A9	intron_variant	MODIFIER	0.314348	5.832	-
VAR_CHR4_9978283	4	9978283	T	SLC2A9	intron_variant	MODIFIER	-0.104942	1.694	-
VAR_CHR4_9978293	4	9978293	C	SLC2A9	intron_variant	MODIFIER	-0.116225	1.612	-
RS143862618	4	9978295	T	SLC2A9	intron_variant	MODIFIER	0.119156	3.813	0.21
RS16868246	4	9978305	G	SLC2A9	intron_variant	MODIFIER	-0.874439	0.029	0.27
VAR_CHR4_9978395	4	9978395	G	SLC2A9	intron_variant	MODIFIER	-	-	-

VAR_CHR4_9978702	4	9978702	T	SLC2A9	intron_variant	MODIFIER	-0.392458	0.403	-
RS35954357	4	9978758	G	SLC2A9	intron_variant	MODIFIER	-	-	0.25
RS34707376	4	9978901	T	SLC2A9	intron_variant	MODIFIER	-0.398863	0.389	0.17
RS147804285	4	9978922	A	SLC2A9	intron_variant	MODIFIER	-	-	0.15
VAR_CHR4_9979148	4	9979148	T	SLC2A9	intron_variant	MODIFIER	-0.369608	0.457	-
RS75964023	4	9979159	A	SLC2A9	intron_variant	MODIFIER	-0.005286	2.536	0.17
RS142490971	4	9979261	C	SLC2A9	intron_variant	MODIFIER	-0.094717	1.77	0.2
RS13103497	4	9979262	C	SLC2A9	intron_variant	MODIFIER	-0.147603	1.402	0.1
RS185776752	4	9979272	T	SLC2A9	intron_variant	MODIFIER	-1.096793	0.01	0.16
RS73227883	4	9979279	G	SLC2A9	intron_variant	MODIFIER	0.036613	2.946	0.19
RS13144899	4	9979302	A	SLC2A9	intron_variant	MODIFIER	-0.328019	0.573	0.15
RS189331504	4	9979303	A	SLC2A9	intron_variant	MODIFIER	-0.394326	0.399	0.16
VAR_CHR4_9979570	4	9979570	T	SLC2A9	intron_variant	MODIFIER	-0.321033	0.595	-
RS13145554	4	9979589	A	SLC2A9	intron_variant	MODIFIER	-0.195414	1.122	0.33
RS13125476	4	9979614	T	SLC2A9	intron_variant	MODIFIER	-0.189778	1.153	0.34
VAR_CHR4_9979807	4	9979807	T	SLC2A9	intron_variant	MODIFIER	0.048405	3.066	-
VAR_CHR4_9979938	4	9979938	C	SLC2A9	intron_variant	MODIFIER	-0.213853	1.027	-
VAR_CHR4_9979995	4	9979995	C	SLC2A9	intron_variant	MODIFIER	-0.490993	0.231	-
RS11723970	4	9980462	G	SLC2A9	intron_variant	MODIFIER	-0.091015	1.798	0.27
VAR_CHR4_9980539	4	9980539	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS11722229	4	9980697	G	SLC2A9	intron_variant	MODIFIER	-0.03039	2.304	0.42
VAR_CHR4_9980942	4	9980942	T	SLC2A9	intron_variant	MODIFIER	-0.549598	0.166	-
RS186014393	4	9981011	A	SLC2A9	intron_variant	MODIFIER	0.180997	4.478	0.3
VAR_CHR4_9981025	4	9981025	C	SLC2A9	intron_variant	MODIFIER	-0.330499	0.565	-
VAR_CHR4_9981113	4	9981113	T	SLC2A9	intron_variant	MODIFIER	-0.272277	0.767	-
VAR_CHR4_9981135	4	9981135	C	SLC2A9	intron_variant	MODIFIER	-0.241556	0.895	-

VAR_CHR4_9981262	4	9981262	A	SLC2A9	intron_variant	MODIFIER	0.260686	5.305	-
RS882222	4	9981294	T	SLC2A9	intron_variant	MODIFIER	-0.415683	0.354	0.2
VAR_CHR4_9981302	4	9981302	A	SLC2A9	intron_variant	MODIFIER	0.150511	4.151	-
VAR_CHR4_9981322	4	9981322	C	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9981412	4	9981412	T	SLC2A9	intron_variant	MODIFIER	-0.200691	1.094	-
VAR_CHR4_9981457	4	9981457	A	SLC2A9	intron_variant	MODIFIER	-0.102007	1.715	-
VAR_CHR4_9981528	4	9981528	G	SLC2A9	intron_variant	MODIFIER	0.096644	3.572	-
RS138866566	4	9981599	A	SLC2A9	intron_variant	MODIFIER	0.698201	8.815	0.19
RS882223	4	9981625	G	SLC2A9	intron_variant	MODIFIER	0.138626	4.023	0.21
VAR_CHR4_9981647	4	9981647	A	SLC2A9	intron_variant	MODIFIER	-0.011366	2.478	-
RS4364264	4	9981683	A	SLC2A9	intron_variant	MODIFIER	0.029489	2.875	0.18
RS190338030	4	9981687	T	SLC2A9	intron_variant	MODIFIER	0.534711	7.691	0.26
RS138073909	4	9981754	T	SLC2A9	intron_variant	MODIFIER	-0.393553	0.401	0.24
RS13131257	4	9981889	A	SLC2A9	intron_variant	MODIFIER	0.426611	6.842	0.23
RS115360140	4	9981905	C	SLC2A9	intron_variant	MODIFIER	-0.198384	1.106	0.17
RS116839315	4	9981909	A	SLC2A9	intron_variant	MODIFIER	-	-	0.25
VAR_CHR4_9981924	4	9981924	C	SLC2A9	intron_variant	MODIFIER	-0.271586	0.769	-
RS76457286	4	9981950	A	SLC2A9	intron_variant	MODIFIER	-0.022304	2.377	0.23
RS13145758	4	9981997	C	SLC2A9	intron_variant	MODIFIER	-0.605925	0.121	0.23
RS13125029	4	9982029	C	SLC2A9	intron_variant	MODIFIER	-0.131702	1.506	0.26
RS13125209	4	9982044	T	SLC2A9	intron_variant	MODIFIER	-0.012105	2.472	0.18
RS13115193	4	9982191	G	SLC2A9	intron_variant	MODIFIER	-0.138186	1.463	0.24
RS202000076	4	9982203	T	SLC2A9	intron_variant	MODIFIER	0.411119	6.71	0.16
RS13125646	4	9982330	T	SLC2A9	synonymous_variant	LOW	-0.933311	0.022	0.35
VAR_CHR4_9982643	4	9982643	A	SLC2A9	intron_variant	MODIFIER	-0.396249	0.395	-
RS372620891	4	9983094	T	SLC2A9	intron_variant	MODIFIER	0.085902	3.458	-

VAR_CHR4_9983219	4	9983219	C	SLC2A9	intron_variant	MODIFIER	-0.047569	2.152	-
RS142956580	4	9983278	A	SLC2A9	intron_variant	MODIFIER	0.561934	7.888	0.46
VAR_CHR4_9983310	4	9983310	T	SLC2A9	intron_variant	MODIFIER	0.187743	4.549	-
VAR_CHR4_9983694	4	9983694	A	SLC2A9	intron_variant	MODIFIER	-0.525361	0.19	-
VAR_CHR4_9983747	4	9983747	T	SLC2A9	intron_variant	MODIFIER	-0.241037	0.898	-
RS115464061	4	9983834	T	SLC2A9	intron_variant	MODIFIER	-0.383087	0.425	0.49
VAR_CHR4_9983888	4	9983888	A	SLC2A9	intron_variant	MODIFIER	0.164351	4.3	-
VAR_CHR4_9983996	4	9983996	T	SLC2A9	intron_variant	MODIFIER	-0.256809	0.829	-
VAR_CHR4_9984415	4	9984415	G	SLC2A9	intron_variant	MODIFIER	0.036019	2.94	-
RS10003001	4	9984475	G	SLC2A9	intron_variant	MODIFIER	-0.187446	1.166	0.28
VAR_CHR4_9984495	4	9984495	C	SLC2A9	intron_variant	MODIFIER	-0.049919	2.132	-
RS57250714	4	9984529	A	SLC2A9	intron_variant	MODIFIER	-0.197017	1.114	0.15
RS9994216	4	9984541	C	SLC2A9	intron_variant	MODIFIER	-0.758398	0.053	0.17
VAR_CHR4_9984543	4	9984543	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS74510990	4	9984586	T	SLC2A9	intron_variant	MODIFIER	-0.510079	0.207	0.16
RS185248830	4	9984698	T	SLC2A9	intron_variant	MODIFIER	-0.405284	0.376	0.15
RS181900390	4	9984711	T	SLC2A9	intron_variant	MODIFIER	0.064356	3.231	0.16
RS10033424	4	9984786	C	SLC2A9	intron_variant	MODIFIER	-	-	0.13
VAR_CHR4_9984788	4	9984788	G	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9984843	4	9984843	A	SLC2A9	intron_variant	MODIFIER	-0.020598	2.393	-
VAR_CHR4_9984889	4	9984889	C	SLC2A9	intron_variant	MODIFIER	-0.655944	0.091	-
VAR_CHR4_9984971	4	9984971	A	SLC2A9	intron_variant	MODIFIER	-	-	-
RS10033612	4	9985006	G	SLC2A9	intron_variant	MODIFIER	-0.61884	0.112	0.18
RS116602069	4	9985235	A	SLC2A9	intron_variant	MODIFIER	-0.122555	1.568	0.19
RS7679724	4	9985376	C	SLC2A9	intron_variant	MODIFIER	-0.702211	0.071	0.13
RS11723591	4	9985398	T	SLC2A9	intron_variant	MODIFIER	-	-	0.19

RS73805439	4	9985429	C	SLC2A9	intron_variant	MODIFIER	-0.283178	0.725	0.32
RS7660895	4	9985445	T	SLC2A9	intron_variant	MODIFIER	-0.29749	0.673	0.27
RS7680126	4	9985596	C	SLC2A9	intron_variant	MODIFIER	-0.188484	1.16	0.23
VAR_CHR4_9985652	4	9985652	G	SLC2A9	intron_variant	MODIFIER	-0.134959	1.484	-
RS17246501	4	9985710	G	SLC2A9	intron_variant	MODIFIER	-0.744163	0.057	0.24
RS369965226	4	9985736	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS77140241	4	9985774	T	SLC2A9	intron_variant	MODIFIER	-0.339868	0.538	0.29
RS11930388	4	9985884	G	SLC2A9	intron_variant	MODIFIER	-0.194615	1.126	0.21
VAR_CHR4_9986164	4	9986164	A	SLC2A9	intron_variant	MODIFIER	0.617453	8.276	-
RS9992406	4	9986288	G	SLC2A9	intron_variant	MODIFIER	-0.021971	2.38	0.35
RS147170567	4	9986307	A	SLC2A9	intron_variant	MODIFIER	0.299864	5.692	0.29
RS73100621	4	9986339	C	SLC2A9	intron_variant	MODIFIER	-	-	0.16
VAR_CHR4_9986597	4	9986597	A	SLC2A9	intron_variant	MODIFIER	-0.102249	1.713	-
RS77275218	4	9986616	A	SLC2A9	intron_variant	MODIFIER	0.16619	4.32	0.26
RS6849736	4	9986783	T	SLC2A9	intron_variant	MODIFIER	-0.301663	0.659	0.2
RS6849962	4	9986903	T	SLC2A9	intron_variant	MODIFIER	-0.498781	0.221	0.23
RS6836200	4	9986915	G	SLC2A9	intron_variant	MODIFIER	0.132921	3.962	0.32
RS140530586	4	9987011	T	SLC2A9	intron_variant	MODIFIER	-0.153326	1.366	0.31
RS3733590	4	9987226	G	SLC2A9	intron_variant	MODIFIER	0.455229	7.079	0.2
RS368261141	4	9987246	A	SLC2A9	intron_variant	MODIFIER	0.045416	3.036	-
RS3733589	4	9987324	T	SLC2A9	synonymous_variant	LOW	1.085184	11.13	0.29
RS3775949	4	9987667	C	SLC2A9	intron_variant	MODIFIER	0.101358	3.622	0.32
RS16891746	4	9987722	T	SLC2A9	intron_variant	MODIFIER	-0.538452	0.177	0.41
VAR_CHR4_9988213	4	9988213	A	SLC2A9	intron_variant	MODIFIER	0.112222	3.739	-
RS16868271	4	9989047	C	SLC2A9	intron_variant	MODIFIER	-0.257332	0.827	0.29
RS142869655	4	9989220	G	SLC2A9	intron_variant	MODIFIER	0.576497	7.992	0.44

RS4385059	4	9989233	G	SLC2A9	intron_variant	MODIFIER	0.09774	3.584	0.47
RS73100632	4	9989354	G	SLC2A9	intron_variant	MODIFIER	-	-	0.38
RS193015978	4	9989415	T	SLC2A9	intron_variant	MODIFIER	-0.377621	0.438	0.3
VAR_CHR4_9989486	4	9989486	C	SLC2A9	intron_variant	MODIFIER	0.902589	10.09	-
RS113188799	4	9989602	C	SLC2A9	intron_variant	MODIFIER	-0.197385	1.112	0.45
RS113451098	4	9989663	T	SLC2A9	intron_variant	MODIFIER	0.898074	10.06	0.45
RS143440569	4	9989751	T	SLC2A9	intron_variant	MODIFIER	-0.015449	2.44	0.39
VAR_CHR4_9989861	4	9989861	G	SLC2A9	intron_variant	MODIFIER	0.766024	9.252	-
RS4502681	4	9990172	G	SLC2A9	intron_variant	MODIFIER	0.928001	10.24	0.43
RS17187075	4	9990328	G	SLC2A9	intron_variant	MODIFIER	-	-	0.41
RS141224249	4	9990429	C	SLC2A9	intron_variant	MODIFIER	-0.095764	1.762	0.31
RS150665766	4	9990467	A	SLC2A9	intron_variant	MODIFIER	0.201486	4.695	0.3
VAR_CHR4_9990575	4	9990575	G	SLC2A9	intron_variant	MODIFIER	-0.607001	0.12	-
RS77223742	4	9990639	G	SLC2A9	intron_variant	MODIFIER	-0.312775	0.621	0.39
RS66647240	4	9990658	T	SLC2A9	intron_variant	MODIFIER	-0.175042	1.236	0.42
VAR_CHR4_9990810	4	9990810	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS117023033	4	9990851	C	SLC2A9	intron_variant	MODIFIER	-	-	0.43
RS75137127	4	9990917	C	SLC2A9	intron_variant	MODIFIER	0.087229	3.472	0.5
VAR_CHR4_9991236	4	9991236	G	SLC2A9	intron_variant	MODIFIER	0.118507	3.806	-
RS12646380	4	9991502	G	SLC2A9	intron_variant	MODIFIER	-0.032135	2.288	0.37
RS114056737	4	9991519	A	SLC2A9	intron_variant	MODIFIER	0.13686	4.004	0.34
VAR_CHR4_9991626	4	9991626	T	SLC2A9	intron_variant	MODIFIER	-0.089582	1.809	-
RS76800309	4	9991723	A	SLC2A9	intron_variant	MODIFIER	-0.351296	0.506	0.31
RS10011206	4	9991955	G	SLC2A9	intron_variant	MODIFIER	-0.011278	2.479	0.4
VAR_CHR4_9992098	4	9992098	A	SLC2A9	intron_variant	MODIFIER	0.345699	6.127	-
RS115764731	4	9992179	T	SLC2A9	intron_variant	MODIFIER	-0.396574	0.394	0.34

RS144208664	4	9992183	G	SLC2A9	intron_variant	MODIFIER	-	-	0.33
RS77376600	4	9992231	A	SLC2A9	intron_variant	MODIFIER	0.46227	7.136	0.45
VAR_CHR4_9992359	4	9992359	C	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9992478	4	9992478	A	SLC2A9	intron_variant	MODIFIER	0.128157	3.91	-
RS182664578	4	9992626	C	SLC2A9	intron_variant	MODIFIER	-0.34031	0.536	0.33
RS68013308	4	9992672	T	SLC2A9	intron_variant	MODIFIER	-0.352371	0.503	0.31
VAR_CHR4_9992735	4	9992735	T	SLC2A9	intron_variant	MODIFIER	-0.52418	0.191	-
VAR_CHR4_9992808	4	9992808	A	SLC2A9	intron_variant	MODIFIER	-0.027199	2.333	-
RS62296002	4	9992862	A	SLC2A9	intron_variant	MODIFIER	0.222605	4.916	0.4
RS188941768	4	9992967	T	SLC2A9	intron_variant	MODIFIER	-0.408611	0.369	0.52
RS114663735	4	9992998	G	SLC2A9	intron_variant	MODIFIER	0.18411	4.511	0.44
VAR_CHR4_9993138	4	9993138	A	SLC2A9	intron_variant	MODIFIER	-0.702197	0.071	-
RS183004276	4	9993178	T	SLC2A9	intron_variant	MODIFIER	-0.259538	0.818	0.29
VAR_CHR4_9993326	4	9993326	G	SLC2A9	intron_variant	MODIFIER	-0.222289	0.985	-
RS147002367	4	9993348	A	SLC2A9	intron_variant	MODIFIER	-	-	0.33
RS77870747	4	9993636	G	SLC2A9	intron_variant	MODIFIER	0.115186	3.771	0.27
RS55921149	4	9993743	A	SLC2A9	intron_variant	MODIFIER	-0.280534	0.735	0.25
RS76466354	4	9993744	T	SLC2A9	intron_variant	MODIFIER	-0.475882	0.252	0.27
RS7678012	4	9993772	G	SLC2A9	intron_variant	MODIFIER	0.205829	4.74	0.27
RS7663032	4	9993838	G	SLC2A9	intron_variant	MODIFIER	-0.368651	0.46	0.3
RS372494279	4	9993951	C	SLC2A9	intron_variant	MODIFIER	0.115186	3.771	-
RS6449213	4	9994215	G	SLC2A9	intron_variant	MODIFIER	-0.206412	1.064	0.33
RS17246745	4	9994583	G	SLC2A9	intron_variant	MODIFIER	0.357266	6.233	0.33
VAR_CHR4_9995119	4	9995119	C	SLC2A9	intron_variant	MODIFIER	-0.15798	1.337	-
VAR_CHR4_9995139	4	9995139	G	SLC2A9	intron_variant	MODIFIER	-0.078793	1.893	-
RS3775948	4	9995182	C	SLC2A9	intron_variant	MODIFIER	-0.284835	0.719	0.23

RS3775947	4	9995240	G	SLC2A9	intron_variant	MODIFIER	-0.495365	0.226	0.11
RS3775946	4	9995256	T	SLC2A9	intron_variant	MODIFIER	0.089594	3.497	0.24
RS12499857	4	9995376	T	SLC2A9	intron_variant	MODIFIER	-0.218074	1.006	0.23
RS376626145	4	9995417	A	SLC2A9	intron_variant	MODIFIER	0.350244	6.169	-
RS139711307	4	9995461	A	SLC2A9	intron_variant	MODIFIER	0.282729	5.525	0.18
VAR_CHR4_9995520	4	9995520	A	SLC2A9	intron_variant	MODIFIER	-0.077487	1.903	-
RS145772196	4	9995523	G	SLC2A9	intron_variant	MODIFIER	-	-	0.24
RS117348803	4	9995554	A	SLC2A9	intron_variant	MODIFIER	0.185247	4.523	0.2
RS114837129	4	9995626	A	SLC2A9	intron_variant	MODIFIER	0.319814	5.884	0.17
RS7696983	4	9995829	T	SLC2A9	intron_variant	MODIFIER	-0.177915	1.219	0.37
RS3796842	4	9995851	A	SLC2A9	intron_variant	MODIFIER	-	-	0.31
VAR_CHR4_9995999	4	9995999	C	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9996140	4	9996140	G	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_9996377	4	9996377	G	SLC2A9	intron_variant	MODIFIER	0.037876	2.959	-
RS4428284	4	9996392	T	SLC2A9	intron_variant	MODIFIER	0.035216	2.932	0.26
RS9998739	4	9996509	C	SLC2A9	intron_variant	MODIFIER	-0.318203	0.604	0.28
RS113995811	4	9996604	A	SLC2A9	intron_variant	MODIFIER	0.308776	5.778	0.2
RS16891923	4	9996661	T	SLC2A9	intron_variant	MODIFIER	0.110747	3.723	0.27
VAR_CHR4_9996737	4	9996737	G	SLC2A9	intron_variant	MODIFIER	0.11159	3.732	-
RS183021241	4	9996817	T	SLC2A9	intron_variant	MODIFIER	1.945002	15.87	0.27
RS16891926	4	9996852	A	SLC2A9	intron_variant	MODIFIER	-0.050517	2.127	0.25
RS13111638	4	9996890	A	SLC2A9	intron_variant	MODIFIER	0.243148	5.127	0.28
RS34501273	4	9996996	A	SLC2A9	intron_variant	MODIFIER	0.256496	5.263	0.24
RS4547795	4	9997060	G	SLC2A9	intron_variant	MODIFIER	0.005377	2.638	0.33
RS79652759	4	9997071	T	SLC2A9	intron_variant	MODIFIER	-0.300531	0.662	0.25
RS4529048	4	9997112	G	SLC2A9	intron_variant	MODIFIER	-0.36051	0.481	0.23

VAR_CHR4_9997215	4	9997215	A	SLC2A9	intron_variant	MODIFIER	-0.109036	1.664	-
RS13127090	4	9997216	T	SLC2A9	intron_variant	MODIFIER	-0.647131	0.096	0.25
RS3733588	4	9997303	C	SLC2A9	intron_variant	MODIFIER	-0.457989	0.279	0.34
RS3733587	4	9997434	T	SLC2A9	intron_variant	MODIFIER	-0.031564	2.293	0.29
RS3733586	4	9997534	G	SLC2A9	intron_variant	MODIFIER	-0.352878	0.501	0.27
VAR_CHR4_9997579	4	9997579	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS13101772	4	9997724	T	SLC2A9	intron_variant	MODIFIER	0.152064	4.168	0.31
RS146364149	4	9997755	G	SLC2A9	intron_variant	MODIFIER	-	-	0.26
VAR_CHR4_9997757	4	9997757	G	SLC2A9	intron_variant	MODIFIER	-0.030753	2.3	-
RS7669607	4	9997801	A	SLC2A9	intron_variant	MODIFIER	0.213559	4.821	0.23
RS13118801	4	9997816	G	SLC2A9	intron_variant	MODIFIER	0.145913	4.102	0.18
VAR_CHR4_9997820	4	9997820	G	SLC2A9	intron_variant	MODIFIER	-0.0542	2.095	-
RS149636792	4	9997925	A	SLC2A9	intron_variant	MODIFIER	-0.426423	0.334	0.22
RS4575994	4	9997979	T	SLC2A9	intron_variant	MODIFIER	-0.301931	0.658	0.21
VAR_CHR4_9998103	4	9998103	T	SLC2A9	intron_variant	MODIFIER	-0.189216	1.156	-
RS75241535	4	9998144	A	SLC2A9	intron_variant	MODIFIER	0.224837	4.939	0.3
VAR_CHR4_9998194	4	9998194	T	SLC2A9	intron_variant	MODIFIER	-0.222461	0.984	-
RS16891971	4	9998376	T	SLC2A9	intron_variant	MODIFIER	0.319432	5.88	0.34
RS148875253	4	9998420	C	SLC2A9	synonymous_variant	LOW	-	-	0.34
RS10939650	4	9998440	G	SLC2A9	synonymous_variant	LOW	1.474254	13.18	0.34
RS13113918	4	9998493	T	SLC2A9	missense_variant	MODERATE	5.027153	25.2	0.47
RS28592748	4	9998605	A	SLC2A9	intron_variant	MODIFIER	0.135653	3.991	0.46
RS80081453	4	9998878	T	SLC2A9	intron_variant	MODIFIER	0.895226	10.05	0.18
RS147608456	4	9998889	T	SLC2A9	intron_variant	MODIFIER	0.501278	7.441	0.19
RS77152814	4	9999041	A	SLC2A9	intron_variant	MODIFIER	-0.080464	1.88	0.3
RS34788376	4	9999054	T	SLC2A9	intron_variant	MODIFIER	-0.763096	0.052	0.19

RS10008035	4	9999335	C	SLC2A9	intron_variant	MODIFIER	-0.807891	0.041	0.25
RS11943372	4	9999346	A	SLC2A9	intron_variant	MODIFIER	0.200664	4.686	0.22
RS35438220	4	9999398	G	SLC2A9	intron_variant	MODIFIER	-0.026534	2.339	0.17
VAR_CHR4_9999412	4	9999412	G	SLC2A9	intron_variant	MODIFIER	-0.010797	2.484	-
VAR_CHR4_9999449	4	9999449	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS190593177	4	9999464	T	SLC2A9	intron_variant	MODIFIER	-0.462956	0.271	0.22
RS13121211	4	9999539	C	SLC2A9	intron_variant	MODIFIER	-0.073282	1.937	0.19
RS11732054	4	9999877	G	SLC2A9	intron_variant	MODIFIER	-0.068804	1.974	0.28
RS117319367	4	9999878	T	SLC2A9	intron_variant	MODIFIER	-0.319546	0.599	0.25
VAR_CHR4_9999978	4	9999978	A	SLC2A9	intron_variant	MODIFIER	-	-	-
RS7696536	4	10000236	C	SLC2A9	intron_variant	MODIFIER	0.021697	2.797	0.31
RS143442126	4	10000250	C	SLC2A9	intron_variant	MODIFIER	0.296037	5.655	0.31
RS78002041	4	10000356	T	SLC2A9	intron_variant	MODIFIER	-0.305466	0.646	0.27
VAR_CHR4_10000372	4	10000372	T	SLC2A9	intron_variant	MODIFIER	-0.074913	1.924	-
RS79113604	4	10000412	T	SLC2A9	intron_variant	MODIFIER	-	-	0.27
RS7678287	4	10000501	T	SLC2A9	intron_variant	MODIFIER	-0.184337	1.183	0.3
RS35933067	4	10000508	C	SLC2A9	intron_variant	MODIFIER	-0.534993	0.18	0.33
VAR_CHR4_10000672	4	10000672	C	SLC2A9	intron_variant	MODIFIER	-0.139658	1.453	-
RS144708782	4	10000684	T	SLC2A9	intron_variant	MODIFIER	-0.11546	1.618	0.43
VAR_CHR4_10000731	4	10000731	A	SLC2A9	intron_variant	MODIFIER	0.040244	2.983	-
VAR_CHR4_10000886	4	10000886	G	SLC2A9	intron_variant	MODIFIER	-0.309347	0.633	-
RS7683856	4	10000947	T	SLC2A9	intron_variant	MODIFIER	-0.02283	2.372	0.46
VAR_CHR4_10001025	4	10001025	A	SLC2A9	intron_variant	MODIFIER	-0.38163	0.428	-
VAR_CHR4_10001421	4	10001421	A	SLC2A9	intron_variant	MODIFIER	0.027782	2.858	-
RS147456393	4	10001487	T	SLC2A9	intron_variant	MODIFIER	-0.387433	0.415	0.2
RS184993936	4	10001500	C	SLC2A9	intron_variant	MODIFIER	-	-	0.24

RS34407859	4	10001652	A	SLC2A9	intron_variant	MODIFIER	0.420255	6.788	0.3
RS7695555	4	10001656	G	SLC2A9	intron_variant	MODIFIER	-0.159427	1.328	0.3
VAR_CHR4_10001735	4	10001735	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS12650373	4	10001795	G	SLC2A9	intron_variant	MODIFIER	-0.151027	1.38	0.31
RS7662439	4	10001799	C	SLC2A9	intron_variant	MODIFIER	-0.671695	0.084	0.35
RS10516195	4	10001833	A	SLC2A9	intron_variant	MODIFIER	-0.18417	1.184	0.31
RS116274461	4	10001841	A	SLC2A9	intron_variant	MODIFIER	0.248485	5.182	0.33
RS1014290	4	10001861	C	SLC2A9	intron_variant	MODIFIER	-0.368381	0.461	0.31
RS111459781	4	10002108	A	SLC2A9	intron_variant	MODIFIER	-0.551338	0.164	0.22
RS78921276	4	10002138	T	SLC2A9	intron_variant	MODIFIER	-0.138829	1.459	0.22
RS12507330	4	10002195	T	SLC2A9	intron_variant	MODIFIER	-0.436909	0.315	0.27
RS79107516	4	10002226	A	SLC2A9	intron_variant	MODIFIER	0.248303	5.18	0.28
RS116449637	4	10002242	A	SLC2A9	intron_variant	MODIFIER	0.278148	5.479	0.36
VAR_CHR4_10002254	4	10002254	G	SLC2A9	intron_variant	MODIFIER	0.047012	3.052	-
VAR_CHR4_10002318	4	10002318	T	SLC2A9	intron_variant	MODIFIER	-0.370485	0.455	-
RS7696895	4	10002425	A	SLC2A9	intron_variant	MODIFIER	0.307981	5.771	0.28
VAR_CHR4_10002457	4	10002457	T	SLC2A9	intron_variant	MODIFIER	-0.248637	0.864	-
RS78389225	4	10002487	T	SLC2A9	intron_variant	MODIFIER	0.031431	2.894	0.29
VAR_CHR4_10002504	4	10002504	T	SLC2A9	intron_variant	MODIFIER	-0.354352	0.497	-
VAR_CHR4_10002535	4	10002535	C	SLC2A9	intron_variant	MODIFIER	-0.32113	0.594	-
VAR_CHR4_10002537	4	10002537	A	SLC2A9	intron_variant	MODIFIER	-0.229597	0.95	-
VAR_CHR4_10002587	4	10002587	G	SLC2A9	intron_variant	MODIFIER	0.896121	10.05	-
VAR_CHR4_10002611	4	10002611	G	SLC2A9	intron_variant	MODIFIER	-0.113263	1.633	-
RS9991278	4	10002665	A	SLC2A9	intron_variant	MODIFIER	-0.256379	0.831	0.31
VAR_CHR4_10002666	4	10002666	T	SLC2A9	intron_variant	MODIFIER	-0.205799	1.068	-
RS4591605	4	10002719	A	SLC2A9	intron_variant	MODIFIER	0.070589	3.296	0.33

VAR_CHR4_10002893	4	10002893	T	SLC2A9	intron_variant	MODIFIER	0.14866	4.131	-
VAR_CHR4_10002908	4	10002908	A	SLC2A9	intron_variant	MODIFIER	0.53775	7.713	-
RS191409840	4	10003259	A	SLC2A9	intron_variant	MODIFIER	0.673199	8.651	0.34
RS4622999	4	10003395	G	SLC2A9	intron_variant	MODIFIER	0.031733	2.897	0.42
RS59707854	4	10003450	A	SLC2A9	intron_variant	MODIFIER	0.151378	4.16	0.26
RS141562596	4	10003451	A	SLC2A9	intron_variant	MODIFIER	0.306601	5.758	0.31
RS185586853	4	10003466	T	SLC2A9	intron_variant	MODIFIER	-0.643263	0.098	0.31
RS368171065	4	10003531	G	SLC2A9	intron_variant	MODIFIER	-0.127991	1.531	-
VAR_CHR4_10003582	4	10003582	A	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10003729	4	10003729	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS193293531	4	10003735	T	SLC2A9	intron_variant	MODIFIER	-0.320668	0.596	0.24
RS372300250	4	10003739	T	SLC2A9	intron_variant	MODIFIER	0.009094	2.674	-
RS139768772	4	10003765	T	SLC2A9	intron_variant	MODIFIER	-0.339506	0.539	0.31
RS149390450	4	10003912	G	SLC2A9	intron_variant	MODIFIER	-0.179713	1.209	0.28
RS7657096	4	10004000	C	SLC2A9	intron_variant	MODIFIER	-0.247708	0.868	0.26
VAR_CHR4_10004006	4	10004006	T	SLC2A9	intron_variant	MODIFIER	-0.855557	0.032	-
VAR_CHR4_10004039	4	10004039	T	SLC2A9	intron_variant	MODIFIER	-0.018744	2.41	-
VAR_CHR4_10004164	4	10004164	G	SLC2A9	intron_variant	MODIFIER	0.086733	3.467	-
RS76138462	4	10004489	C	SLC2A9	intron_variant	MODIFIER	-0.349473	0.511	0.12
RS139788797	4	10004503	C	SLC2A9	intron_variant	MODIFIER	-	-	0.13
VAR_CHR4_10004517	4	10004517	A	SLC2A9	intron_variant	MODIFIER	0.087352	3.473	-
RS74377900	4	10004548	T	SLC2A9	intron_variant	MODIFIER	-0.339106	0.54	0.1
RS17247314	4	10004743	C	SLC2A9	intron_variant	MODIFIER	-	-	0.27
RS74915949	4	10004778	A	SLC2A9	intron_variant	MODIFIER	0.180146	4.469	0.26
VAR_CHR4_10004785	4	10004785	G	SLC2A9	intron_variant	MODIFIER	0.109545	3.71	-
VAR_CHR4_10004788	4	10004788	T	SLC2A9	intron_variant	MODIFIER	-0.41928	0.347	-

RS10018663	4	10004797	G	SLC2A9	intron_variant	MODIFIER	0.053335	3.117	0.29
RS10018666	4	10004805	G	SLC2A9	intron_variant	MODIFIER	-0.152163	1.373	0.23
RS10023068	4	10004832	T	SLC2A9	intron_variant	MODIFIER	-0.178783	1.214	0.16
RS16892069	4	10004849	G	SLC2A9	intron_variant	MODIFIER	1.343719	12.5	0.3
RS76624494	4	10004892	A	SLC2A9	intron_variant	MODIFIER	0.034526	2.925	0.24
RS78533886	4	10004894	A	SLC2A9	intron_variant	MODIFIER	0.304265	5.735	0.21
RS143175986	4	10004949	G	SLC2A9	intron_variant	MODIFIER	-0.066552	1.992	0.3
RS77203987	4	10005207	T	SLC2A9	intron_variant	MODIFIER	-0.098156	1.744	0.13
RS188428223	4	10005294	G	SLC2A9	intron_variant	MODIFIER	-	-	0.25
RS191580578	4	10005340	G	SLC2A9	intron_variant	MODIFIER	-0.310201	0.63	0.23
RS6853437	4	10005435	C	SLC2A9	intron_variant	MODIFIER	0.289993	5.596	0.31
RS6833878	4	10005555	T	SLC2A9	intron_variant	MODIFIER	-0.223786	0.978	0.3
RS76275868	4	10005708	T	SLC2A9	intron_variant	MODIFIER	-0.090035	1.805	0.26
VAR_CHR4_10005785	4	10005785	T	SLC2A9	intron_variant	MODIFIER	-0.077433	1.904	-
VAR_CHR4_10005875	4	10005875	G	SLC2A9	intron_variant	MODIFIER	1.73297	14.6	-
RS751092	4	10005897	G	SLC2A9	intron_variant	MODIFIER	-0.805748	0.042	0.35
VAR_CHR4_10005965	4	10005965	G	SLC2A9	intron_variant	MODIFIER	0.344609	6.117	-
VAR_CHR4_10006072	4	10006072	T	SLC2A9	intron_variant	MODIFIER	-0.304358	0.649	-
RS148984563	4	10006244	T	SLC2A9	intron_variant	MODIFIER	-0.048515	2.144	0.28
RS10022499	4	10006537	G	SLC2A9	intron_variant	MODIFIER	0.171779	4.379	0.32
VAR_CHR4_10006555	4	10006555	T	SLC2A9	intron_variant	MODIFIER	0.043082	3.012	-
VAR_CHR4_10006592	4	10006592	A	SLC2A9	intron_variant	MODIFIER	0.073896	3.331	-
RS10016075	4	10006663	C	SLC2A9	intron_variant	MODIFIER	1.159021	11.53	0.26
VAR_CHR4_10006761	4	10006761	G	SLC2A9	intron_variant	MODIFIER	1.151845	11.49	-
RS138550267	4	10006778	A	SLC2A9	intron_variant	MODIFIER	-	-	0.2
RS78963587	4	10006827	A	SLC2A9	intron_variant	MODIFIER	0.506803	7.483	0.19

RS76388621	4	10006915	A	SLC2A9	intron_variant	MODIFIER	0.208487	4.768	0.22
RS146357305	4	10006926	T	SLC2A9	intron_variant	MODIFIER	-0.361752	0.478	0.25
RS9291640	4	10007086	G	SLC2A9	intron_variant	MODIFIER	-0.53288	0.182	0.14
RS9291641	4	10007259	G	SLC2A9	intron_variant	MODIFIER	-0.605054	0.121	0.2
RS114727892	4	10007265	T	SLC2A9	intron_variant	MODIFIER	-0.19058	1.148	0.2
RS9291642	4	10007275	G	SLC2A9	intron_variant	MODIFIER	-0.583479	0.137	0.18
RS12507050	4	10007305	A	SLC2A9	intron_variant	MODIFIER	0.379115	6.43	0.22
VAR_CHR4_10007357	4	10007357	G	SLC2A9	intron_variant	MODIFIER	0.073085	3.323	-
RS35201034	4	10007451	G	SLC2A9	intron_variant	MODIFIER	-	-	0.22
VAR_CHR4_10007772	4	10007772	C	SLC2A9	intron_variant	MODIFIER	0.274249	5.441	-
RS3796841	4	10007904	G	SLC2A9	intron_variant	MODIFIER	0.199564	4.675	0.45
RS3796840	4	10008121	A	SLC2A9	intron_variant	MODIFIER	0.45912	7.111	0.62
RS146017478	4	10008122	T	SLC2A9	intron_variant	MODIFIER	-0.064943	2.005	0.63
VAR_CHR4_10008178	4	10008178	T	SLC2A9	intron_variant	MODIFIER	-0.067602	1.983	-
VAR_CHR4_10008194	4	10008194	A	SLC2A9	intron_variant	MODIFIER	-	-	-
RS13117275	4	10008242	G	SLC2A9	intron_variant	MODIFIER	-	-	0.24
RS144431047	4	10008268	A	SLC2A9	intron_variant	MODIFIER	0.416211	6.754	0.2
RS4543113	4	10008305	T	SLC2A9	intron_variant	MODIFIER	0.317389	5.861	0.21
VAR_CHR4_10008328	4	10008328	T	SLC2A9	intron_variant	MODIFIER	0.035024	2.93	-
VAR_CHR4_10008485	4	10008485	T	SLC2A9	intron_variant	MODIFIER	-0.035004	2.262	-
RS36058283	4	10008512	T	SLC2A9	intron_variant	MODIFIER	0.189864	4.572	0.27
VAR_CHR4_10008637	4	10008637	G	SLC2A9	intron_variant	MODIFIER	0.076418	3.358	-
RS74606663	4	10008654	A	SLC2A9	intron_variant	MODIFIER	0.042138	3.002	0.25
RS74838002	4	10008678	G	SLC2A9	intron_variant	MODIFIER	-0.034781	2.264	0.3
VAR_CHR4_10008687	4	10008687	G	SLC2A9	intron_variant	MODIFIER	-0.174821	1.237	-
VAR_CHR4_10008732	4	10008732	G	SLC2A9	intron_variant	MODIFIER	-0.080588	1.879	-

RS67968745	4	10008749	T	SLC2A9	intron_variant	MODIFIER	-0.067895	1.981	0.34
VAR_CHR4_10008938	4	10008938	A	SLC2A9	intron_variant	MODIFIER	-0.018632	2.411	-
RS75896783	4	10008964	A	SLC2A9	intron_variant	MODIFIER	0.186615	4.538	0.32
RS77251997	4	10009064	A	SLC2A9	intron_variant	MODIFIER	0.283603	5.533	0.32
VAR_CHR4_10009112	4	10009112	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS6449217	4	10009151	T	SLC2A9	intron_variant	MODIFIER	-	-	0.28
VAR_CHR4_10009179	4	10009179	T	SLC2A9	intron_variant	MODIFIER	-0.240513	0.9	-
RS150962779	4	10009240	C	SLC2A9	intron_variant	MODIFIER	-0.4032	0.38	0.27
VAR_CHR4_10009267	4	10009267	T	SLC2A9	intron_variant	MODIFIER	0.800183	9.465	-
VAR_CHR4_10009391	4	10009391	G	SLC2A9	intron_variant	MODIFIER	-0.256303	0.832	-
RS6449218	4	10009444	A	SLC2A9	intron_variant	MODIFIER	0.081653	3.413	0.28
RS78441715	4	10009808	C	SLC2A9	intron_variant	MODIFIER	-0.422417	0.341	0.36
RS3796839	4	10009917	T	SLC2A9	intron_variant	MODIFIER	0.152497	4.172	0.41
VAR_CHR4_10010030	4	10010030	C	SLC2A9	intron_variant	MODIFIER	0.281228	5.51	-
RS80331485	4	10010129	A	SLC2A9	intron_variant	MODIFIER	-0.058577	2.058	0.29
RS7700047	4	10010542	G	SLC2A9	intron_variant	MODIFIER	-0.249798	0.859	0.27
VAR_CHR4_10010651	4	10010651	C	SLC2A9	intron_variant	MODIFIER	-0.160401	1.322	-
RS3796838	4	10011030	G	SLC2A9	intron_variant	MODIFIER	-0.050984	2.123	0.18
RS3796837	4	10011321	C	SLC2A9	intron_variant	MODIFIER	-	-	0.16
RS148934813	4	10011336	G	SLC2A9	intron_variant	MODIFIER	-0.123507	1.562	0.17
RS3796836	4	10011345	C	SLC2A9	intron_variant	MODIFIER	-0.607313	0.12	0.14
VAR_CHR4_10011367	4	10011367	G	SLC2A9	intron_variant	MODIFIER	-0.222127	0.986	-
RS3796835	4	10011530	G	SLC2A9	intron_variant	MODIFIER	-0.008361	2.507	0.23
RS57905135	4	10011542	T	SLC2A9	intron_variant	MODIFIER	-0.85047	0.033	0.2
RS185780638	4	10011560	A	SLC2A9	intron_variant	MODIFIER	-0.331613	0.562	0.25
VAR_CHR4_10011580	4	10011580	A	SLC2A9	intron_variant	MODIFIER	0.041044	2.991	-

RS115787217	4	10011959	T	SLC2A9	intron_variant	MODIFIER	-0.120796	1.58	0.23
RS3775945	4	10011996	A	SLC2A9	intron_variant	MODIFIER	-	-	0.18
VAR_CHR4_10012005	4	10012005	A	SLC2A9	intron_variant	MODIFIER	0.664631	8.594	-
VAR_CHR4_10012061	4	10012061	C	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10012078	4	10012078	G	SLC2A9	intron_variant	MODIFIER	-0.005096	2.537	-
VAR_CHR4_10012105	4	10012105	T	SLC2A9	intron_variant	MODIFIER	-0.275382	0.755	-
RS6822988	4	10012210	T	SLC2A9	intron_variant	MODIFIER	0.032179	2.902	0.21
RS12642431	4	10012235	A	SLC2A9	intron_variant	MODIFIER	-	-	0.17
RS7666545	4	10012372	G	SLC2A9	intron_variant	MODIFIER	0.054914	3.133	0.22
RS115301551	4	10012506	T	SLC2A9	intron_variant	MODIFIER	-0.459597	0.277	0.22
VAR_CHR4_10012590	4	10012590	G	SLC2A9	intron_variant	MODIFIER	-0.419289	0.347	-
RS141833488	4	10012661	G	SLC2A9	intron_variant	MODIFIER	-0.209133	1.05	0.17
VAR_CHR4_10012720	4	10012720	T	SLC2A9	intron_variant	MODIFIER	-0.466285	0.266	-
RS3796834	4	10012846	G	SLC2A9	intron_variant	MODIFIER	-0.048201	2.147	0.15
VAR_CHR4_10012872	4	10012872	A	SLC2A9	intron_variant	MODIFIER	-0.12278	1.567	-
RS3796833	4	10012878	G	SLC2A9	intron_variant	MODIFIER	-0.152061	1.374	0.16
VAR_CHR4_10013037	4	10013037	T	SLC2A9	intron_variant	MODIFIER	0.006636	2.65	-
RS6845554	4	10013173	C	SLC2A9	intron_variant	MODIFIER	-0.009992	2.491	0.24
RS3756238	4	10013202	A	SLC2A9	intron_variant	MODIFIER	0.033239	2.912	0.26
RS10939654	4	10013344	T	SLC2A9	intron_variant	MODIFIER	-0.861305	0.031	0.21
RS3756237	4	10013378	T	SLC2A9	intron_variant	MODIFIER	-0.290182	0.699	0.16
VAR_CHR4_10013450	4	10013450	T	SLC2A9	intron_variant	MODIFIER	-0.600824	0.124	-
RS3756236	4	10013463	T	SLC2A9	intron_variant	MODIFIER	-	-	0.22
RS143903193	4	10013481	T	SLC2A9	intron_variant	MODIFIER	-0.328165	0.573	0.25
VAR_CHR4_10013631	4	10013631	A	SLC2A9	intron_variant	MODIFIER	0.099187	3.599	-
RS78698809	4	10013759	T	SLC2A9	intron_variant	MODIFIER	-0.482686	0.242	0.34

RS4280729	4	10013861	A	SLC2A9	intron_variant	MODIFIER	0.551236	7.811	0.27
RS73805487	4	10014098	T	SLC2A9	intron_variant	MODIFIER	0.13166	3.948	0.19
RS115847025	4	10014140	A	SLC2A9	intron_variant	MODIFIER	-	-	0.16
RS55811736	4	10014221	T	SLC2A9	intron_variant	MODIFIER	-0.026078	2.343	0.22
RS144338226	4	10014349	A	SLC2A9	intron_variant	MODIFIER	-0.419256	0.347	0.17
RS59871456	4	10014441	T	SLC2A9	intron_variant	MODIFIER	-0.373207	0.449	0.18
RS73805488	4	10014459	T	SLC2A9	intron_variant	MODIFIER	-0.406303	0.373	0.18
RS1122966	4	10014476	C	SLC2A9	intron_variant	MODIFIER	-0.445249	0.3	0.18
RS10939655	4	10014642	A	SLC2A9	intron_variant	MODIFIER	-	-	0.2
RS10939656	4	10014646	G	SLC2A9	intron_variant	MODIFIER	-0.085349	1.841	0.2
RS56190921	4	10014713	A	SLC2A9	intron_variant	MODIFIER	-0.142551	1.434	0.23
RS147716199	4	10014714	T	SLC2A9	intron_variant	MODIFIER	-0.665199	0.087	0.23
VAR_CHR4_10014719	4	10014719	C	SLC2A9	intron_variant	MODIFIER	-0.209654	1.048	-
RS76421184	4	10014874	G	SLC2A9	intron_variant	MODIFIER	0.063707	3.224	0.24
RS61312541	4	10015159	A	SLC2A9	intron_variant	MODIFIER	-0.043715	2.186	0.37
RS182589584	4	10015162	C	SLC2A9	intron_variant	MODIFIER	-0.476249	0.252	0.32
RS3756235	4	10015511	C	SLC2A9	intron_variant	MODIFIER	-0.252468	0.848	0.37
VAR_CHR4_10015600	4	10015600	A	SLC2A9	intron_variant	MODIFIER	0.187939	4.552	-
RS3796832	4	10015865	A	SLC2A9	intron_variant	MODIFIER	0.297891	5.673	0.25
RS3796831	4	10015952	C	SLC2A9	intron_variant	MODIFIER	-	-	0.2
RS73805489	4	10016010	T	SLC2A9	intron_variant	MODIFIER	0.211094	4.796	0.26
VAR_CHR4_10016055	4	10016055	G	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10016076	4	10016076	A	SLC2A9	intron_variant	MODIFIER	0.174097	4.404	-
RS73805490	4	10016079	A	SLC2A9	intron_variant	MODIFIER	0.412347	6.721	0.21
VAR_CHR4_10016201	4	10016201	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS4144	4	10016322	G	SLC2A9	intron_variant	MODIFIER	0.199893	4.678	0.21

RS78203288	4	10016397	A	SLC2A9	intron_variant	MODIFIER	0.274374	5.442	0.19
RS12641340	4	10016426	A	SLC2A9	intron_variant	MODIFIER	-	-	0.17
RS184493584	4	10016429	T	SLC2A9	intron_variant	MODIFIER	-0.140061	1.451	0.24
VAR_CHR4_10016444	4	10016444	C	SLC2A9	intron_variant	MODIFIER	0.131023	3.941	-
VAR_CHR4_10016652	4	10016652	A	SLC2A9	intron_variant	MODIFIER	0.129957	3.93	-
RS76920131	4	10016666	A	SLC2A9	intron_variant	MODIFIER	-0.711794	0.068	0.26
RS4318649	4	10016815	G	SLC2A9	intron_variant	MODIFIER	0.230667	4.999	0.29
RS4318650	4	10016868	G	SLC2A9	intron_variant	MODIFIER	-0.363273	0.474	0.36
VAR_CHR4_10016870	4	10016870	G	SLC2A9	intron_variant	MODIFIER	-0.193391	1.133	-
RS115848729	4	10016909	T	SLC2A9	intron_variant	MODIFIER	-0.349708	0.51	0.39
VAR_CHR4_10016937	4	10016937	T	SLC2A9	intron_variant	MODIFIER	-0.51	0.208	-
VAR_CHR4_10017153	4	10017153	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS11736410	4	10017241	T	SLC2A9	intron_variant	MODIFIER	0.08222	3.419	0.31
VAR_CHR4_10017318	4	10017318	A	SLC2A9	intron_variant	MODIFIER	0.18902	4.563	-
VAR_CHR4_10017334	4	10017334	A	SLC2A9	intron_variant	MODIFIER	0.01553	2.736	-
RS11736479	4	10017387	G	SLC2A9	intron_variant	MODIFIER	-	-	0.23
VAR_CHR4_10017454	4	10017454	C	SLC2A9	intron_variant	MODIFIER	-0.632619	0.104	-
RS13113730	4	10017628	A	SLC2A9	intron_variant	MODIFIER	-0.080435	1.88	0.22
RS34644460	4	10017639	T	SLC2A9	intron_variant	MODIFIER	-0.077601	1.903	0.2
VAR_CHR4_10017660	4	10017660	A	SLC2A9	intron_variant	MODIFIER	-0.3377	0.544	-
VAR_CHR4_10017698	4	10017698	T	SLC2A9	intron_variant	MODIFIER	-0.290809	0.697	-
RS138640667	4	10017699	T	SLC2A9	intron_variant	MODIFIER	-0.443966	0.302	0.18
RS141767347	4	10017723	G	SLC2A9	intron_variant	MODIFIER	-	-	0.18
VAR_CHR4_10017740	4	10017740	A	SLC2A9	intron_variant	MODIFIER	-0.412286	0.361	-
RS62293387	4	10017801	A	SLC2A9	intron_variant	MODIFIER	-0.315419	0.613	0.16
RS77554178	4	10017836	C	SLC2A9	intron_variant	MODIFIER	-	-	0.23

RS35271694	4	10017838	T	SLC2A9	intron_variant	MODIFIER	-0.319792	0.599	0.17
RS114197051	4	10017907	A	SLC2A9	intron_variant	MODIFIER	-0.243144	0.888	0.2
RS12500805	4	10017979	A	SLC2A9	intron_variant	MODIFIER	-0.246707	0.873	0.2
RS114664540	4	10017980	T	SLC2A9	intron_variant	MODIFIER	-0.377277	0.439	0.21
RS6857001	4	10018080	C	SLC2A9	intron_variant	MODIFIER	-1.02885	0.014	0.18
RS6827754	4	10018153	T	SLC2A9	intron_variant	MODIFIER	-0.395044	0.398	0.17
VAR_CHR4_10018166	4	10018166	T	SLC2A9	intron_variant	MODIFIER	0.042593	3.007	-
RS13151113	4	10018178	T	SLC2A9	intron_variant	MODIFIER	-0.013355	2.46	0.23
RS6827785	4	10018205	A	SLC2A9	intron_variant	MODIFIER	-0.395426	0.397	0.21
VAR_CHR4_10018364	4	10018364	T	SLC2A9	intron_variant	MODIFIER	-0.083722	1.854	-
VAR_CHR4_10018420	4	10018420	A	SLC2A9	intron_variant	MODIFIER	-	-	-
RS6857693	4	10018435	T	SLC2A9	intron_variant	MODIFIER	-0.103274	1.706	0.18
VAR_CHR4_10018514	4	10018514	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS6844329	4	10018544	G	SLC2A9	intron_variant	MODIFIER	-0.199853	1.099	0.16
VAR_CHR4_10018555	4	10018555	G	SLC2A9	intron_variant	MODIFIER	-0.099633	1.733	-
RS35866697	4	10018604	T	SLC2A9	intron_variant	MODIFIER	-0.222052	0.986	0.15
RS150504446	4	10018685	T	SLC2A9	intron_variant	MODIFIER	-0.3376	0.544	0.18
RS140334704	4	10018737	T	SLC2A9	intron_variant	MODIFIER	-0.204651	1.073	0.25
VAR_CHR4_10018806	4	10018806	T	SLC2A9	intron_variant	MODIFIER	-0.151497	1.377	-
RS35099040	4	10018839	G	SLC2A9	intron_variant	MODIFIER	-0.011656	2.476	0.31
RS140873488	4	10018937	C	SLC2A9	intron_variant	MODIFIER	-	-	0.46
RS3796830	4	10019135	C	SLC2A9	intron_variant	MODIFIER	-0.473291	0.256	0.49
RS3796829	4	10019138	C	SLC2A9	intron_variant	MODIFIER	-	-	0.44
RS13107466	4	10019390	T	SLC2A9	intron_variant	MODIFIER	-0.232898	0.935	0.33
RS142989755	4	10019494	T	SLC2A9	intron_variant	MODIFIER	0.076946	3.363	0.24
RS13128214	4	10019536	A	SLC2A9	intron_variant	MODIFIER	-0.031663	2.292	0.27

RS13128385	4	10019563	G	SLC2A9	intron_variant	MODIFIER	-0.14006	1.451	0.23
RS28449404	4	10019678	G	SLC2A9	intron_variant	MODIFIER	-0.076328	1.913	0.2
RS13133766	4	10019732	A	SLC2A9	intron_variant	MODIFIER	0.020637	2.787	0.14
RS28607048	4	10019851	G	SLC2A9	intron_variant	MODIFIER	-	-	0.13
RS73229818	4	10019884	A	SLC2A9	intron_variant	MODIFIER	-0.194814	1.125	0.13
RS3775944	4	10019974	C	SLC2A9	intron_variant	MODIFIER	-0.996897	0.016	0.9
RS3775943	4	10019984	G	SLC2A9	intron_variant	MODIFIER	0.060208	3.188	0.7
RS3775942	4	10020307	T	SLC2A9	intron_variant	MODIFIER	-0.18161	1.198	0.18
VAR_CHR4_10020358	4	10020358	C	SLC2A9	intron_variant	MODIFIER	-0.07787	1.9	-
RS2240720	4	10020480	A	SLC2A9	intron_variant	MODIFIER	0.353209	6.196	0.25
RS2240721	4	10020564	T	SLC2A9	intron_variant	MODIFIER	0.64588	8.469	0.37
RS377565288	4	10020588	T	SLC2A9	intron_variant	MODIFIER	0.525945	7.626	-
VAR_CHR4_10020755	4	10020755	A	SLC2A9	intron_variant	MODIFIER	0.287961	5.576	-
RS2240722	4	10020757	C	SLC2A9	intron_variant	MODIFIER	-0.180207	1.206	0.38
RS145038256	4	10020996	C	SLC2A9	intron_variant	MODIFIER	-	-	0.33
VAR_CHR4_10021017	4	10021017	A	SLC2A9	intron_variant	MODIFIER	0.584547	8.049	-
VAR_CHR4_10021026	4	10021026	T	SLC2A9	intron_variant	MODIFIER	0.331791	5.997	-
VAR_CHR4_10021028	4	10021028	T	SLC2A9	intron_variant	MODIFIER	0.399241	6.607	-
RS2240723	4	10021151	T	SLC2A9	intron_variant	MODIFIER	-0.091884	1.791	0.23
RS2240724	4	10021290	G	SLC2A9	intron_variant	MODIFIER	-	-	0.25
VAR_CHR4_10021323	4	10021323	T	SLC2A9	intron_variant	MODIFIER	0.304815	5.74	-
RS13122112	4	10021404	T	SLC2A9	intron_variant	MODIFIER	-0.488303	0.235	0.34
VAR_CHR4_10021460	4	10021460	A	SLC2A9	intron_variant	MODIFIER	0.814626	9.554	-
RS140253713	4	10021624	A	SLC2A9	intron_variant	MODIFIER	0.059947	3.185	0.33
RS116687792	4	10021629	T	SLC2A9	intron_variant	MODIFIER	-0.31329	0.62	0.43
VAR_CHR4_10021637	4	10021637	C	SLC2A9	intron_variant	MODIFIER	-	-	-

VAR_CHR4_10021709	4	10021709	T	SLC2A9	intron_variant	MODIFIER	0.363181	6.287	-
RS13106922	4	10021759	C	SLC2A9	intron_variant	MODIFIER	0.103739	3.648	0.44
RS79234071	4	10021760	G	SLC2A9	intron_variant	MODIFIER	-0.16083	1.32	0.36
RS150349587	4	10021922	A	SLC2A9	intron_variant	MODIFIER	0.597993	8.142	0.33
RS75871043	4	10021952	T	SLC2A9	intron_variant	MODIFIER	0.400714	6.62	0.34
RS12647117	4	10022059	G	SLC2A9	intron_variant	MODIFIER	0.258974	5.288	0.2
RS75234256	4	10022072	A	SLC2A9	intron_variant	MODIFIER	0.200144	4.681	0.2
RS13114106	4	10022125	G	SLC2A9	intron_variant	MODIFIER	0.238872	5.084	0.21
RS114847096	4	10022161	G	SLC2A9	intron_variant	MODIFIER	0.082959	3.427	0.17
VAR_CHR4_10022272	4	10022272	T	SLC2A9	intron_variant	MODIFIER	0.192582	4.601	-
RS3756234	4	10022474	A	SLC2A9	intron_variant	MODIFIER	0.501869	7.445	0.21
VAR_CHR4_10022598	4	10022598	T	SLC2A9	intron_variant	MODIFIER	0.035314	2.933	-
RS143194815	4	10022632	A	SLC2A9	intron_variant	MODIFIER	0.381063	6.447	0.19
RS112540012	4	10022648	T	SLC2A9	intron_variant	MODIFIER	-0.187681	1.164	0.21
RS2276963	4	10022839	T	SLC2A9	intron_variant	MODIFIER	-0.062702	2.024	0.18
RS2276962	4	10022880	G	SLC2A9	intron_variant	MODIFIER	0.245803	5.154	0.15
RS138627925	4	10022895	A	SLC2A9	intron_variant	MODIFIER	-0.290675	0.697	0.18
RS2276961	4	10022981	A	SLC2A9	intron_variant	MODIFIER	2.508716	19.52	0.6
RS28496610	4	10023228	C	SLC2A9	intron_variant	MODIFIER	-0.369901	0.457	0.48
RS12506364	4	10023448	A	SLC2A9	intron_variant	MODIFIER	-0.023859	2.363	0.34
RS184730016	4	10023507	T	SLC2A9	intron_variant	MODIFIER	-0.643343	0.098	0.25
VAR_CHR4_10023840	4	10023840	C	SLC2A9	intron_variant	MODIFIER	0.031222	2.892	-
RS7663044	4	10023939	G	SLC2A9	intron_variant	MODIFIER	-0.193226	1.134	0.35
RS146158632	4	10023965	A	SLC2A9	intron_variant	MODIFIER	0.216864	4.856	0.35
RS3756233	4	10024157	A	SLC2A9	intron_variant	MODIFIER	-0.045724	2.168	0.35
VAR_CHR4_10024169	4	10024169	C	SLC2A9	intron_variant	MODIFIER	-0.443387	0.303	-

RS115048086	4	10024267	C	SLC2A9	intron_variant	MODIFIER	-0.229722	0.95	0.35
RS12509955	4	10024303	G	SLC2A9	intron_variant	MODIFIER	0.010386	2.686	0.36
RS75101489	4	10024413	T	SLC2A9	intron_variant	MODIFIER	-0.205326	1.07	0.34
VAR_CHR4_10024740	4	10024740	C	SLC2A9	intron_variant	MODIFIER	-0.235553	0.923	-
RS115945847	4	10024745	G	SLC2A9	intron_variant	MODIFIER	-0.227811	0.959	0.32
VAR_CHR4_10024885	4	10024885	G	SLC2A9	intron_variant	MODIFIER	0.041248	2.993	-
VAR_CHR4_10024911	4	10024911	T	SLC2A9	intron_variant	MODIFIER	-0.412613	0.361	-
VAR_CHR4_10024940	4	10024940	A	SLC2A9	intron_variant	MODIFIER	0.374633	6.39	-
RS3775941	4	10025093	T	SLC2A9	intron_variant	MODIFIER	-	-	0.19
RS3775940	4	10025163	T	SLC2A9	intron_variant	MODIFIER	-	-	0.35
RS75468543	4	10025257	A	SLC2A9	intron_variant	MODIFIER	-0.125938	1.545	0.35
RS3775939	4	10025296	C	SLC2A9	intron_variant	MODIFIER	-	-	0.28
RS7696092	4	10025320	T	SLC2A9	intron_variant	MODIFIER	0.028148	2.861	0.27
VAR_CHR4_10025326	4	10025326	A	SLC2A9	intron_variant	MODIFIER	0.08095	3.405	-
RS13148476	4	10025398	A	SLC2A9	intron_variant	MODIFIER	0.342531	6.097	0.21
RS186970316	4	10025425	T	SLC2A9	intron_variant	MODIFIER	-0.566908	0.15	0.28
RS76552410	4	10025485	A	SLC2A9	intron_variant	MODIFIER	0.105464	3.666	0.27
VAR_CHR4_10025537	4	10025537	T	SLC2A9	intron_variant	MODIFIER	-0.480782	0.245	-
RS3756231	4	10025544	C	SLC2A9	intron_variant	MODIFIER	-0.295978	0.678	0.22
VAR_CHR4_10025855	4	10025855	A	SLC2A9	intron_variant	MODIFIER	0.221193	4.901	-
VAR_CHR4_10026104	4	10026104	A	SLC2A9	intron_variant	MODIFIER	-0.062934	2.022	-
VAR_CHR4_10026105	4	10026105	T	SLC2A9	intron_variant	MODIFIER	-0.276041	0.752	-
VAR_CHR4_10026132	4	10026132	C	SLC2A9	intron_variant	MODIFIER	-0.296249	0.677	-
RS146930596	4	10026293	A	SLC2A9	intron_variant	MODIFIER	-	-	0.34
RS186727677	4	10026464	G	SLC2A9	intron_variant	MODIFIER	0.021179	2.792	0.25
RS116108158	4	10026574	G	SLC2A9	intron_variant	MODIFIER	0.235592	5.05	0.39

RS55959894	4	10026580	T	SLC2A9	intron_variant	MODIFIER	-0.781354	0.047	0.35
RS59234705	4	10026745	G	SLC2A9	intron_variant	MODIFIER	0.086634	3.466	0.33
RS73229828	4	10026833	C	SLC2A9	intron_variant	MODIFIER	-0.438344	0.312	0.29
RS4345181	4	10026864	A	SLC2A9	intron_variant	MODIFIER	-	-	0.17
VAR_CHR4_10026910	4	10026910	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS77684901	4	10026937	A	SLC2A9	intron_variant	MODIFIER	-0.103955	1.701	0.17
RS74642414	4	10026993	G	SLC2A9	intron_variant	MODIFIER	-0.299213	0.667	0.14
VAR_CHR4_10027024	4	10027024	C	SLC2A9	intron_variant	MODIFIER	-0.584191	0.136	-
VAR_CHR4_10027126	4	10027126	C	SLC2A9	intron_variant	MODIFIER	-0.359162	0.484	-
RS10030570	4	10027160	C	SLC2A9	intron_variant	MODIFIER	-0.183181	1.189	0.58
RS6819833	4	10027354	G	SLC2A9	intron_variant	MODIFIER	-0.184126	1.184	0.46
RS6820230	4	10027542	G	SLC2A9	missense_variant	MODERATE	0.081146	3.407	0.21
RS144215444	4	10027570	T	SLC2A9	missense_variant	MODERATE	0.65498	8.53	0.2
RS201988226	4	10027616	G	SLC2A9	5_prime_UTR_variant	MODIFIER	0.163643	4.292	0.63
RS6449237	4	10027643	T	SLC2A9	intron_variant	MODIFIER	0.830178	9.649	0.13
RS74794351	4	10027664	C	SLC2A9	intron_variant	MODIFIER	-0.393249	0.402	0.21
VAR_CHR4_10027691	4	10027691	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS6449238	4	10027744	C	SLC2A9	intron_variant	MODIFIER	-0.157536	1.34	0.16
VAR_CHR4_10027769	4	10027769	A	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10027795	4	10027795	T	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10027922	4	10027922	A	SLC2A9	intron_variant	MODIFIER	-0.298717	0.669	-
RS7683792	4	10027969	A	SLC2A9	intron_variant	MODIFIER	-0.092531	1.786	0.11
VAR_CHR4_10028062	4	10028062	T	SLC2A9	intron_variant	MODIFIER	0.116379	3.783	-
RS7697004	4	10028077	C	SLC2A9	intron_variant	MODIFIER	-0.534671	0.18	0.17
VAR_CHR4_10028127	4	10028127	A	SLC2A9	intron_variant	MODIFIER	0.040887	2.99	-
RS7669090	4	10028131	G	SLC2A9	intron_variant	MODIFIER	-0.099901	1.731	0.23

VAR_CHR4_10028159	4	10028159	G	SLC2A9	intron_variant	MODIFIER	-0.122162	1.571	-
RS141946400	4	10028185	T	SLC2A9	intron_variant	MODIFIER	-0.413841	0.358	0.16
RS7697416	4	10028287	C	SLC2A9	intron_variant	MODIFIER	-0.138484	1.461	0.17
RS13149985	4	10028390	T	SLC2A9	intron_variant	MODIFIER	-0.386083	0.418	0.13
RS140176097	4	10028408	C	SLC2A9	intron_variant	MODIFIER	-	-	0.18
VAR_CHR4_10028415	4	10028415	A	SLC2A9	intron_variant	MODIFIER	0.013582	2.717	-
RS191622025	4	10028422	A	SLC2A9	intron_variant	MODIFIER	0.115633	3.775	0.17
RS36084205	4	10028678	G	SLC2A9	intron_variant	MODIFIER	-0.22631	0.966	0.9
RS13141233	4	10028729	G	SLC2A9	intron_variant	MODIFIER	1.705702	14.44	0.6
VAR_CHR4_10028775	4	10028775	C	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10028792	4	10028792	C	SLC2A9	intron_variant	MODIFIER	-0.074183	1.93	-
RS34325511	4	10028867	C	SLC2A9	intron_variant	MODIFIER	-0.984858	0.017	0.7
RS34709913	4	10028955	G	SLC2A9	intron_variant	MODIFIER	-0.028955	2.317	0.13
VAR_CHR4_10029217	4	10029217	G	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10029420	4	10029420	C	SLC2A9	intron_variant	MODIFIER	0.262968	5.328	-
RS144402103	4	10029470	C	SLC2A9	intron_variant	MODIFIER	-0.53785	0.177	0.31
VAR_CHR4_10029546	4	10029546	A	SLC2A9	intron_variant	MODIFIER	-0.514256	0.203	-
VAR_CHR4_10029629	4	10029629	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS59077355	4	10029731	A	SLC2A9	intron_variant	MODIFIER	0.8079	9.513	0.27
RS147018551	4	10029755	G	SLC2A9	intron_variant	MODIFIER	-	-	0.29
VAR_CHR4_10029927	4	10029927	T	SLC2A9	intron_variant	MODIFIER	-0.771156	0.05	-
RS370769581	4	10029946	A	SLC2A9	intron_variant	MODIFIER	-0.208538	1.053	-
VAR_CHR4_10030015	4	10030015	A	SLC2A9	intron_variant	MODIFIER	0.020341	2.784	-
RS6820616	4	10030076	T	SLC2A9	intron_variant	MODIFIER	-0.355063	0.495	0.34
VAR_CHR4_10030108	4	10030108	A	SLC2A9	intron_variant	MODIFIER	-0.296763	0.676	-
VAR_CHR4_10030283	4	10030283	T	SLC2A9	intron_variant	MODIFIER	-0.31323	0.62	-

VAR_CHR4_10030366	4	10030366	T	SLC2A9	intron_variant	MODIFIER	-0.134053	1.49	-
RS115588006	4	10030411	C	SLC2A9	intron_variant	MODIFIER	1.240237	11.96	0.24
VAR_CHR4_10030437	4	10030437	T	SLC2A9	intron_variant	MODIFIER	-0.705546	0.07	-
VAR_CHR4_10030519	4	10030519	T	SLC2A9	intron_variant	MODIFIER	-0.396092	0.395	-
RS74472339	4	10030605	C	SLC2A9	intron_variant	MODIFIER	-0.199951	1.098	0.17
RS6826764	4	10030794	C	SLC2A9	intron_variant	MODIFIER	-0.129014	1.524	0.19
RS115453215	4	10030813	G	SLC2A9	intron_variant	MODIFIER	0.281867	5.516	0.28
RS190373654	4	10030822	A	SLC2A9	intron_variant	MODIFIER	0.232216	5.015	0.25
VAR_CHR4_10030938	4	10030938	G	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10030987	4	10030987	A	SLC2A9	intron_variant	MODIFIER	-0.003728	2.55	-
RS6827401	4	10031066	C	SLC2A9	intron_variant	MODIFIER	-0.527855	0.188	0.36
RS12500810	4	10031068	T	SLC2A9	intron_variant	MODIFIER	-0.19564	1.121	0.39
RS6846692	4	10031133	G	SLC2A9	intron_variant	MODIFIER	-0.194536	1.127	0.2
RS6856396	4	10031163	T	SLC2A9	intron_variant	MODIFIER	-0.308644	0.635	0.19
RS12506455	4	10031569	T	SLC2A9	intron_variant	MODIFIER	-	-	0.38
RS141846487	4	10031965	C	SLC2A9	intron_variant	MODIFIER	-0.329854	0.567	0.48
VAR_CHR4_10032096	4	10032096	T	SLC2A9	intron_variant	MODIFIER	0.404905	6.657	-
VAR_CHR4_10032292	4	10032292	T	SLC2A9	intron_variant	MODIFIER	-0.68168	0.079	-
VAR_CHR4_10032359	4	10032359	G	SLC2A9	intron_variant	MODIFIER	0.525037	7.62	-
VAR_CHR4_10032439	4	10032439	A	SLC2A9	intron_variant	MODIFIER	0.230734	5	-
RS10939663	4	10032516	C	SLC2A9	intron_variant	MODIFIER	0.143434	4.075	0.43
RS13148371	4	10032561	A	SLC2A9	intron_variant	MODIFIER	0.286335	5.56	0.44
VAR_CHR4_10032680	4	10032680	T	SLC2A9	intron_variant	MODIFIER	0.038349	2.964	-
RS112395808	4	10033035	T	SLC2A9	intron_variant	MODIFIER	0.112025	3.737	0.33
VAR_CHR4_10033275	4	10033275	T	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10033416	4	10033416	T	SLC2A9	intron_variant	MODIFIER	0.0818	3.414	-

RS13135351	4	10033525	T	SLC2A9	intron_variant	MODIFIER	-0.259946	0.816	0.35
RS12506122	4	10033538	T	SLC2A9	intron_variant	MODIFIER	0.190851	4.582	0.33
VAR_CHR4_10033630	4	10033630	T	SLC2A9	intron_variant	MODIFIER	0.046446	3.046	-
VAR_CHR4_10033646	4	10033646	T	SLC2A9	intron_variant	MODIFIER	-0.210958	1.041	-
VAR_CHR4_10033794	4	10033794	A	SLC2A9	intron_variant	MODIFIER	-0.256668	0.83	-
RS149022308	4	10033810	G	SLC2A9	intron_variant	MODIFIER	0.007285	2.656	0.32
RS143022050	4	10033811	C	SLC2A9	intron_variant	MODIFIER	-0.452573	0.288	0.32
VAR_CHR4_10033892	4	10033892	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS73229836	4	10033933	A	SLC2A9	intron_variant	MODIFIER	0.202106	4.701	0.24
RS192585916	4	10033979	T	SLC2A9	intron_variant	MODIFIER	-0.34265	0.53	0.24
VAR_CHR4_10034103	4	10034103	T	SLC2A9	intron_variant	MODIFIER	-0.846053	0.034	-
VAR_CHR4_10034318	4	10034318	G	SLC2A9	intron_variant	MODIFIER	0.072441	3.316	-
RS138940331	4	10034683	A	SLC2A9	intron_variant	MODIFIER	0.376108	6.403	0.32
RS115066640	4	10034740	A	SLC2A9	intron_variant	MODIFIER	0.34886	6.156	0.35
VAR_CHR4_10034830	4	10034830	A	SLC2A9	intron_variant	MODIFIER	1.330501	12.43	-
VAR_CHR4_10034867	4	10034867	A	SLC2A9	intron_variant	MODIFIER	0.601657	8.168	-
RS138323944	4	10034929	G	SLC2A9	intron_variant	MODIFIER	-0.003181	2.556	0.45
RS13146686	4	10034933	G	SLC2A9	intron_variant	MODIFIER	-0.05624	2.078	0.43
VAR_CHR4_10034958	4	10034958	T	SLC2A9	intron_variant	MODIFIER	-0.09589	1.761	-
RS111953533	4	10035016	T	SLC2A9	intron_variant	MODIFIER	-0.097003	1.752	0.35
RS75968456	4	10035028	T	SLC2A9	intron_variant	MODIFIER	-0.788257	0.045	0.43
VAR_CHR4_10035233	4	10035233	T	SLC2A9	intron_variant	MODIFIER	0.028947	2.869	-
RS112298408	4	10035244	T	SLC2A9	intron_variant	MODIFIER	-0.188588	1.159	0.27
VAR_CHR4_10035319	4	10035319	A	SLC2A9	intron_variant	MODIFIER	0.233088	5.024	-
VAR_CHR4_10035337	4	10035337	A	SLC2A9	intron_variant	MODIFIER	0.130007	3.93	-
VAR_CHR4_10035353	4	10035353	T	SLC2A9	intron_variant	MODIFIER	-0.299256	0.667	-

VAR_CHR4_10035366	4	10035366	T	SLC2A9	intron_variant	MODIFIER	0.314089	5.829	-
RS11722930	4	10035454	T	SLC2A9	intron_variant	MODIFIER	-0.083169	1.859	0.24
RS190876865	4	10035522	C	SLC2A9	intron_variant	MODIFIER	-0.278097	0.744	0.28
RS78507984	4	10035608	A	SLC2A9	intron_variant	MODIFIER	-0.360243	0.481	0.34
VAR_CHR4_10035630	4	10035630	C	SLC2A9	intron_variant	MODIFIER	-0.250622	0.856	-
VAR_CHR4_10035637	4	10035637	C	SLC2A9	intron_variant	MODIFIER	-	-	-
RS16892419	4	10035702	T	SLC2A9	intron_variant	MODIFIER	-0.089833	1.807	0.22
RS16892420	4	10035715	T	SLC2A9	intron_variant	MODIFIER	-0.14096	1.445	0.26
VAR_CHR4_10035961	4	10035961	C	SLC2A9	intron_variant	MODIFIER	-0.247443	0.869	-
VAR_CHR4_10036061	4	10036061	A	SLC2A9	intron_variant	MODIFIER	-0.034374	2.268	-
RS10006397	4	10036140	G	SLC2A9	intron_variant	MODIFIER	-0.165921	1.289	0.25
RS76099163	4	10036146	G	SLC2A9	intron_variant	MODIFIER	0.080147	3.397	0.26
RS11727199	4	10036190	A	SLC2A9	intron_variant	MODIFIER	0.087323	3.473	0.25
RS139613826	4	10036199	T	SLC2A9	intron_variant	MODIFIER	-0.644589	0.097	0.19
RS3733585	4	10036339	C	SLC2A9	intron_variant	MODIFIER	-0.416086	0.354	0.29
RS116694479	4	10036357	G	SLC2A9	intron_variant	MODIFIER	-0.024326	2.359	0.3
RS41268375	4	10036359	G	SLC2A9	intron_variant	MODIFIER	-	-	0.22
RS3733584	4	10036506	G	SLC2A9	intron_variant	MODIFIER	0.221801	4.907	0.25
RS3822250	4	10036630	A	SLC2A9	intron_variant	MODIFIER	0.222966	4.919	0.18
VAR_CHR4_10036700	4	10036700	C	SLC2A9	intron_variant	MODIFIER	-0.449382	0.293	-
RS149752397	4	10036783	G	SLC2A9	intron_variant	MODIFIER	0.046555	3.047	0.27
VAR_CHR4_10036917	4	10036917	T	SLC2A9	intron_variant	MODIFIER	-	-	-
RS73806483	4	10036932	A	SLC2A9	intron_variant	MODIFIER	0.293076	5.626	0.3
VAR_CHR4_10036949	4	10036949	G	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10036995	4	10036995	T	SLC2A9	intron_variant	MODIFIER	-0.227116	0.962	-
VAR_CHR4_10037052	4	10037052	C	SLC2A9	intron_variant	MODIFIER	-0.823429	0.038	-

VAR_CHR4_10037210	4	10037210	C	SLC2A9	intron_variant	MODIFIER	-0.018251	2.414	-
RS13145442	4	10037261	T	SLC2A9	intron_variant	MODIFIER	-0.433852	0.32	0.18
RS145299659	4	10037264	A	SLC2A9	intron_variant	MODIFIER	-0.176808	1.226	0.18
VAR_CHR4_10037265	4	10037265	T	SLC2A9	intron_variant	MODIFIER	-0.80342	0.042	-
VAR_CHR4_10037288	4	10037288	T	SLC2A9	intron_variant	MODIFIER	-0.339846	0.538	-
VAR_CHR4_10037328	4	10037328	G	SLC2A9	intron_variant	MODIFIER	-	-	-
RS11731110	4	10037346	G	SLC2A9	intron_variant	MODIFIER	-0.061904	2.03	0.24
RS4525975	4	10037390	A	SLC2A9	intron_variant	MODIFIER	-0.777224	0.048	0.24
RS4485819	4	10037393	G	SLC2A9	intron_variant	MODIFIER	-0.123087	1.564	0.23
VAR_CHR4_10037457	4	10037457	C	SLC2A9	intron_variant	MODIFIER	-0.07974	1.886	-
VAR_CHR4_10037563	4	10037563	T	SLC2A9	intron_variant	MODIFIER	-0.726138	0.063	-
RS12642537	4	10037621	T	SLC2A9	intron_variant	MODIFIER	-0.149011	1.393	0.17
RS10939665	4	10037628	G	SLC2A9	intron_variant	MODIFIER	0.117915	3.8	0.21
VAR_CHR4_10037934	4	10037934	A	SLC2A9	intron_variant	MODIFIER	-0.282468	0.728	-
VAR_CHR4_10037956	4	10037956	T	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10038001	4	10038001	A	SLC2A9	intron_variant	MODIFIER	-0.277478	0.747	-
VAR_CHR4_10038018	4	10038018	T	SLC2A9	intron_variant	MODIFIER	-0.208233	1.055	-
VAR_CHR4_10038070	4	10038070	T	SLC2A9	intron_variant	MODIFIER	-0.493073	0.229	-
RS10012779	4	10038112	G	SLC2A9	intron_variant	MODIFIER	-0.778569	0.048	0.32
RS9291645	4	10038254	C	SLC2A9	intron_variant	MODIFIER	-0.496315	0.224	0.23
RS141090791	4	10038434	T	SLC2A9	intron_variant	MODIFIER	-0.765871	0.051	0.25
VAR_CHR4_10038481	4	10038481	C	SLC2A9	intron_variant	MODIFIER	0.139292	4.03	-
RS35249656	4	10038542	T	SLC2A9	intron_variant	MODIFIER	-0.27394	0.76	0.24
VAR_CHR4_10038560	4	10038560	G	SLC2A9	intron_variant	MODIFIER	0.018803	2.769	-
RS16892449	4	10038591	G	SLC2A9	intron_variant	MODIFIER	-	-	0.22
RS13139055	4	10038924	A	SLC2A9	intron_variant	MODIFIER	-0.061891	2.031	0.23

VAR_CHR4_10038956	4	10038956	T	SLC2A9	intron_variant	MODIFIER	-0.752278	0.055	-
RS181519830	4	10038962	A	SLC2A9	intron_variant	MODIFIER	-	-	0.22
RS184460416	4	10039001	G	SLC2A9	intron_variant	MODIFIER	-0.040474	2.214	0.26
RS74544177	4	10039070	C	SLC2A9	intron_variant	MODIFIER	-0.556148	0.16	0.1
RS146808983	4	10039331	T	SLC2A9	intron_variant	MODIFIER	-0.299013	0.668	0.21
RS12506932	4	10039528	T	SLC2A9	intron_variant	MODIFIER	-0.439296	0.31	0.3
RS186278403	4	10039890	C	SLC2A9	intron_variant	MODIFIER	-0.199478	1.101	0.1
VAR_CHR4_10039930	4	10039930	C	SLC2A9	intron_variant	MODIFIER	0.359002	6.249	-
RS71603981	4	10039965	A	SLC2A9	intron_variant	MODIFIER	-0.088246	1.819	0.12
VAR_CHR4_10040062	4	10040062	G	SLC2A9	intron_variant	MODIFIER	-0.187435	1.166	-
RS190603187	4	10040125	G	SLC2A9	intron_variant	MODIFIER	-0.360543	0.481	0.17
RS55668232	4	10040162	C	SLC2A9	intron_variant	MODIFIER	-0.281332	0.732	0.22
RS13115776	4	10040189	C	SLC2A9	intron_variant	MODIFIER	-	-	0.27
RS16892474	4	10040220	T	SLC2A9	intron_variant	MODIFIER	0.074799	3.341	0.21
RS59319978	4	10040221	G	SLC2A9	intron_variant	MODIFIER	-0.0387	2.23	0.28
RS16892475	4	10040273	G	SLC2A9	intron_variant	MODIFIER	0.338278	6.058	0.22
VAR_CHR4_10040390	4	10040390	T	SLC2A9	intron_variant	MODIFIER	-0.5504	0.165	-
VAR_CHR4_10040522	4	10040522	T	SLC2A9	intron_variant	MODIFIER	0.055597	3.14	-
VAR_CHR4_10040586	4	10040586	C	SLC2A9	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10040622	4	10040622	T	SLC2A9	intron_variant	MODIFIER	-0.323383	0.587	-
RS186682810	4	10040752	C	SLC2A9	intron_variant	MODIFIER	-0.172835	1.248	0.18
RS10516196	4	10040965	A	SLC2A9	intron_variant	MODIFIER	-0.071164	1.954	0.21
RS200677384	4	10041001	T	SLC2A9	intron_variant	MODIFIER	-0.380109	0.432	0.25
RS12508991	4	10041104	A	SLC2A9	intron_variant	MODIFIER	-0.010021	2.491	0.25
RS10029311	4	10041134	A	SLC2A9	intron_variant	MODIFIER	0.253831	5.236	0.18
VAR_CHR4_10041212	4	10041212	A	SLC2A9	intron_variant	MODIFIER	0.262247	5.321	-

RS183417303	4	10041406	G	SLC2A9	intron_variant	MODIFIER	-0.248827	0.863	0.13
RS11734786	4	10041499	G	SLC2A9	intron_variant	MODIFIER	0.733661	9.046	0.6
RS16892493	4	10041647	A	SLC2A9	intron_variant	MODIFIER	-0.037467	2.241	0.15
RS143368624	4	10042027	A	SLC2A9	upstream_gene_variant	MODIFIER	0.181142	4.479	0.53
RS10516197	4	10042100	A	SLC2A9	upstream_gene_variant	MODIFIER	0.108535	3.699	0.39
RS7679916	4	10042160	A	SLC2A9	upstream_gene_variant	MODIFIER	0.217267	4.86	0.43
RS61446121	4	10042242	A	SLC2A9	upstream_gene_variant	MODIFIER	-0.089794	1.807	0.33
VAR_CHR4_10042306	4	10042306	A	SLC2A9	upstream_gene_variant	MODIFIER	-	-	-
VAR_CHR4_10042453	4	10042453	G	SLC2A9	upstream_gene_variant	MODIFIER	0.138436	4.021	-
RS141899952	4	10042458	C	SLC2A9	upstream_gene_variant	MODIFIER	-0.400905	0.385	0.19
RS7349721	4	10042562	T	SLC2A9	upstream_gene_variant	MODIFIER	-0.004181	2.546	0.19
RS61476037	4	10042673	A	SLC2A9	upstream_gene_variant	MODIFIER	0.190562	4.579	0.19
RS75245044	4	10042686	T	SLC2A9	upstream_gene_variant	MODIFIER	-0.19484	1.125	0.26
VAR_CHR4_10042692	4	10042692	G	SLC2A9	upstream_gene_variant	MODIFIER	-	-	-
RS13137074	4	10042842	A	SLC2A9	upstream_gene_variant	MODIFIER	-0.319403	0.6	0.27
RS7685958	4	10042850	C	SLC2A9	upstream_gene_variant	MODIFIER	-	-	0.23
RS13101785	4	10042915	T	SLC2A9	upstream_gene_variant	MODIFIER	-	-	0.25
RS13137343	4	10043028	T	SLC2A9	upstream_gene_variant	MODIFIER	-0.00008	2.585	0.23
VAR_CHR4_10043133	4	10043133	G	SLC2A9	upstream_gene_variant	MODIFIER	0.14497	4.091	-
VAR_CHR4_10043549	4	10043549	C	SLC2A9	upstream_gene_variant	MODIFIER	-0.104628	1.696	-
VAR_CHR4_10043631	4	10043631	C	SLC2A9	upstream_gene_variant	MODIFIER	-0.421178	0.344	-
RS36036984	4	10043632	A	SLC2A9	upstream_gene_variant	MODIFIER	0.088579	3.486	0.4
VAR_CHR4_10043645	4	10043645	T	SLC2A9	upstream_gene_variant	MODIFIER	-0.309905	0.631	-
RS181844636	4	10043648	A	SLC2A9	upstream_gene_variant	MODIFIER	0.022847	2.809	0.35
VAR_CHR4_10043649	4	10043649	T	SLC2A9	upstream_gene_variant	MODIFIER	-0.314896	0.614	-
RS6850166	4	10043688	G	SLC2A9	upstream_gene_variant	MODIFIER	0.187405	4.546	0.27

VAR_CHR4_10043689	4	10043689	T	SLC2A9	upstream_gene_variant	MODIFIER	0.12374	3.863	-
RS62293415	4	10043886	G	SLC2A9	upstream_gene_variant	MODIFIER	0.273139	5.43	0.18
RS13124007	4	10043931	G	SLC2A9	upstream_gene_variant	MODIFIER	-	-	0.16
RS13144709	4	10044182	A	SLC2A9	upstream_gene_variant	MODIFIER	-0.276941	0.749	0.31
VAR_CHR4_10044266	4	10044266	A	SLC2A9	upstream_gene_variant	MODIFIER	-	-	-
RS13110307	4	10044364	G	SLC2A9	upstream_gene_variant	MODIFIER	-0.188197	1.161	0.18
RS186762677	4	10044374	T	SLC2A9	upstream_gene_variant	MODIFIER	-0.985709	0.017	0.19
VAR_CHR4_10044515	4	10044515	A	SLC2A9	upstream_gene_variant	MODIFIER	-	-	-
RS73229842	4	10044524	A	SLC2A9	upstream_gene_variant	MODIFIER	0.061233	3.199	0.32
RS13122689	4	10044648	C	SLC2A9	upstream_gene_variant	MODIFIER	0.478585	7.265	0.16
VAR_CHR4_10044689	4	10044689	A	SLC2A9	upstream_gene_variant	MODIFIER	1.056212	10.98	-
RS13129453	4	10044784	G	SLC2A9	upstream_gene_variant	MODIFIER	0.178896	4.455	0.2
RS79063585	4	10044942	C	SLC2A9	upstream_gene_variant	MODIFIER	1.266631	12.1	0.19
RS115037048	4	10044970	T	SLC2A9	upstream_gene_variant	MODIFIER	1.078795	11.1	0.19
RS375676428	4	10045025	G	SLC2A9	upstream_gene_variant	MODIFIER	0.546164	7.775	-
RS12504565	4	10045145	T	SLC2A9	upstream_gene_variant	MODIFIER	-0.2447	0.881	0.22
VAR_CHR4_10045184	4	10045184	T	SLC2A9	upstream_gene_variant	MODIFIER	-0.092195	1.789	-
VAR_CHR4_10045363	4	10045363	T	SLC2A9	upstream_gene_variant	MODIFIER	-0.003872	2.549	-
RS4529049	4	10045389	A	SLC2A9	upstream_gene_variant	MODIFIER	0.256644	5.264	0.24
RS4637402	4	10045430	A	SLC2A9	upstream_gene_variant	MODIFIER	0.008124	2.664	0.3
RS34160786	4	10045586	T	SLC2A9	upstream_gene_variant	MODIFIER	-0.008724	2.503	0.28
RS76156864	4	10045602	C	SLC2A9	upstream_gene_variant	MODIFIER	-0.195095	1.124	0.2
VAR_CHR4_10045619	4	10045619	T	SLC2A9	upstream_gene_variant	MODIFIER	0.546422	7.777	-
RS188139530	4	10045623	C	SLC2A9	upstream_gene_variant	MODIFIER	0.542611	7.749	0.19
RS7442336	4	10045783	T	SLC2A9	upstream_gene_variant	MODIFIER	-0.830863	0.037	0.17
RS115184754	4	10045813	G	SLC2A9	upstream_gene_variant	MODIFIER	-0.320318	0.597	0.17

RS10939669	4	10045827	C	SLC2A9	upstream_gene_variant	MODIFIER	-0.171437	1.257	0.14
VAR_CHR4_10045871	4	10045871	C	SLC2A9	upstream_gene_variant	MODIFIER	-0.197218	1.113	-
VAR_CHR4_10046071	4	10046071	A	SLC2A9	upstream_gene_variant	MODIFIER	-0.048644	2.143	-
RS35782952	4	10046095	T	SLC2A9	upstream_gene_variant	MODIFIER	0.05811	3.166	0.37
RS35334203	4	10046171	A	SLC2A9	upstream_gene_variant	MODIFIER	0.006127	2.645	0.35
RS11734375	4	10046298	C	SLC2A9	upstream_gene_variant	MODIFIER	-0.834588	0.036	0.24
VAR_CHR4_10046551	4	10046551	T	SLC2A9	upstream_gene_variant	MODIFIER	-0.688257	0.077	-
RS56826562	4	10046638	C	SLC2A9	upstream_gene_variant	MODIFIER	0.45091	7.044	0.37
VAR_CHR4_10046649	4	10046649	G	SLC2A9	upstream_gene_variant	MODIFIER	0.573537	7.971	-
VAR_CHR4_10046992	4	10046992	T	-	intergenic_variant	MODIFIER	-0.124598	1.554	-
VAR_CHR4_10047075	4	10047075	C	-	intergenic_variant	MODIFIER	-0.8454	0.034	-
RS189690296	4	10047085	A	-	intergenic_variant	MODIFIER	0.370639	6.354	0.45
RS74812044	4	10047289	G	-	regulatory_region_variant	MODIFIER	0.188551	4.558	0.55
RS79756119	4	10047352	G	-	regulatory_region_variant	MODIFIER	-0.112457	1.639	0.5
VAR_CHR4_10047361	4	10047361	C	-	regulatory_region_variant	MODIFIER	-0.082149	1.867	-
RS141494666	4	10047443	T	-	regulatory_region_variant	MODIFIER	-0.433043	0.321	0.47
VAR_CHR4_10047533	4	10047533	C	-	regulatory_region_variant	MODIFIER	-0.676109	0.082	-
VAR_CHR4_10048187	4	10048187	T	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_10048233	4	10048233	A	-	intergenic_variant	MODIFIER	-0.577543	0.142	-
RS35250962	4	10048271	A	-	intergenic_variant	MODIFIER	0.11761	3.797	0.34
VAR_CHR4_10048635	4	10048635	A	-	intergenic_variant	MODIFIER	-0.068047	1.98	-
RS192186455	4	10048639	C	-	intergenic_variant	MODIFIER	-0.441511	0.306	0.3
RS115793604	4	10048667	G	-	intergenic_variant	MODIFIER	0.106784	3.68	0.37
VAR_CHR4_10048705	4	10048705	A	-	intergenic_variant	MODIFIER	-0.179562	1.21	-
VAR_CHR4_10048770	4	10048770	T	-	intergenic_variant	MODIFIER	-0.114122	1.627	-
RS28730480	4	10048867	G	-	intergenic_variant	MODIFIER	-0.600983	0.124	0.33

RS35750364	4	10049049	G	-	intergenic_variant	MODIFIER	-0.054217	2.095	0.39
RS145160523	4	10049182	T	-	intergenic_variant	MODIFIER	-0.136876	1.471	0.24
RS151119440	4	10049553	A	-	intergenic_variant	MODIFIER	-0.07521	1.922	0.3
VAR_CHR4_10049655	4	10049655	T	-	intergenic_variant	MODIFIER	-0.164958	1.295	-
RS4608811	4	10049675	T	-	intergenic_variant	MODIFIER	0.032227	2.902	0.27
RS4391034	4	10049700	A	-	intergenic_variant	MODIFIER	0.29538	5.649	0.25
RS75488049	4	10049995	T	-	intergenic_variant	MODIFIER	0.100405	3.612	0.19
VAR_CHR4_10050012	4	10050012	T	-	intergenic_variant	MODIFIER	-0.340338	0.536	-
RS733175	4	10050141	G	-	intergenic_variant	MODIFIER	-0.145644	1.415	0.23
VAR_CHR4_10050181	4	10050181	A	-	intergenic_variant	MODIFIER	0.000643	2.592	-
RS4484299	4	10050451	T	-	intergenic_variant	MODIFIER	-0.446807	0.297	0.15
RS148951726	4	10050581	A	-	intergenic_variant	MODIFIER	-0.252196	0.849	0.2
RS10939671	4	10050815	G	-	intergenic_variant	MODIFIER	-0.537507	0.178	0.35
RS137996170	4	10050875	T	-	intergenic_variant	MODIFIER	0.226264	4.954	0.32
RS78594917	4	10051008	A	-	intergenic_variant	MODIFIER	-0.125994	1.545	0.17
VAR_CHR4_10051050	4	10051050	G	-	intergenic_variant	MODIFIER	-0.16159	1.315	-
RS148269664	4	10051246	T	-	intergenic_variant	MODIFIER	-0.551158	0.164	0.27
VAR_CHR4_10051422	4	10051422	C	-	intergenic_variant	MODIFIER	-0.149432	1.39	-
VAR_CHR4_10051439	4	10051439	T	-	intergenic_variant	MODIFIER	-0.344079	0.526	-
VAR_CHR4_10051504	4	10051504	A	-	intergenic_variant	MODIFIER	-0.352103	0.503	-
RS13137795	4	10051506	T	-	intergenic_variant	MODIFIER	-0.383907	0.423	0.23
RS116804408	4	10051544	G	-	intergenic_variant	MODIFIER	-0.21365	1.028	0.25
VAR_CHR4_10051568	4	10051568	T	-	intergenic_variant	MODIFIER	0.047795	3.06	-
RS6820188	4	10051655	A	-	intergenic_variant	MODIFIER	-0.170356	1.263	0.25
RS12511989	4	10051658	T	-	intergenic_variant	MODIFIER	-0.294026	0.685	0.21
RS6829727	4	10051672	G	-	intergenic_variant	MODIFIER	-0.159093	1.33	0.21

RS12499734	4	10051761	A	-	intergenic_variant	MODIFIER	-0.025039	2.352	0.38
RS77165435	4	10051846	A	-	intergenic_variant	MODIFIER	-0.007867	2.511	0.44
RS117443909	4	10051860	A	-	intergenic_variant	MODIFIER	-0.217902	1.007	0.35
RS117657217	4	10051878	A	-	intergenic_variant	MODIFIER	-	-	0.27
RS78319160	4	10051944	A	-	intergenic_variant	MODIFIER	0.27652	5.463	0.34
VAR_CHR4_10052084	4	10052084	C	-	intergenic_variant	MODIFIER	-0.257602	0.826	-
RS10939672	4	10052136	C	-	intergenic_variant	MODIFIER	-0.246135	0.875	0.25
VAR_CHR4_10052153	4	10052153	A	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_10052411	4	10052411	T	-	regulatory_region_variant	MODIFIER	0.711443	8.902	-
RS143484897	4	10052434	T	-	regulatory_region_variant	MODIFIER	-0.632156	0.104	0.22
RS147171965	4	10052455	A	-	regulatory_region_variant	MODIFIER	0.055019	3.134	0.26
VAR_CHR4_10052488	4	10052488	T	-	regulatory_region_variant	MODIFIER	0.103568	3.646	-
RS75604947	4	10052521	C	-	regulatory_region_variant	MODIFIER	-	-	0.16
RS6821843	4	10052528	T	-	regulatory_region_variant	MODIFIER	0.161401	4.268	0.16
VAR_CHR4_10052578	4	10052578	G	-	regulatory_region_variant	MODIFIER	0.004861	2.633	-
RS6822023	4	10052594	A	-	regulatory_region_variant	MODIFIER	0.379666	6.435	0.16
RS6837659	4	10052610	G	-	intergenic_variant	MODIFIER	0.629913	8.361	0.14
RS182571761	4	10052728	T	-	intergenic_variant	MODIFIER	0.179618	4.463	0.19
RS13150928	4	10052961	A	-	intergenic_variant	MODIFIER	-0.10475	1.695	0.28
RS13120348	4	10053155	C	-	intergenic_variant	MODIFIER	-	-	0.17
RS148791554	4	10053243	T	-	intergenic_variant	MODIFIER	0.0892	3.493	0.16
RS57897925	4	10053281	T	-	intergenic_variant	MODIFIER	-0.302888	0.654	0.17
RS35501905	4	10053431	A	-	intergenic_variant	MODIFIER	0.22686	4.96	0.14
VAR_CHR4_10053472	4	10053472	T	-	intergenic_variant	MODIFIER	-0.10989	1.658	-
RS9884416	4	10053735	T	-	regulatory_region_variant	MODIFIER	-0.578337	0.141	0.14
VAR_CHR4_10054033	4	10054033	C	-	intergenic_variant	MODIFIER	-	-	-

RS150138969	4	10054037	C	-	intergenic_variant	MODIFIER	-0.170109	1.264	0.16
RS12108388	4	10054337	T	-	intergenic_variant	MODIFIER	-	-	0.17
RS76958015	4	10054406	C	-	intergenic_variant	MODIFIER	-0.109085	1.663	0.15
RS7677939	4	10054434	C	-	intergenic_variant	MODIFIER	-	-	0.14
RS138605713	4	10054468	A	-	intergenic_variant	MODIFIER	0.162284	4.278	0.16
RS7659924	4	10054616	G	-	intergenic_variant	MODIFIER	-	-	0.14
RS7678346	4	10054624	A	-	intergenic_variant	MODIFIER	0.237194	5.066	0.18
RS7663448	4	10054787	G	-	intergenic_variant	MODIFIER	0.139639	4.034	0.15
VAR_CHR4_10054835	4	10054835	T	-	intergenic_variant	MODIFIER	-0.118144	1.599	-
RS147973376	4	10054851	T	-	intergenic_variant	MODIFIER	-0.280985	0.733	0.16
VAR_CHR4_10055028	4	10055028	A	-	intergenic_variant	MODIFIER	-0.328333	0.572	-
VAR_CHR4_10055116	4	10055116	G	-	intergenic_variant	MODIFIER	-	-	-
RS13112782	4	10055123	G	-	intergenic_variant	MODIFIER	-0.158702	1.333	0.14
RS13127630	4	10055179	A	-	intergenic_variant	MODIFIER	-0.709659	0.068	0.13
RS11723250	4	10055339	G	-	intergenic_variant	MODIFIER	0.17632	4.428	0.13
RS35276762	4	10055354	C	-	intergenic_variant	MODIFIER	-0.31927	0.6	0.19
RS73212808	4	10055439	G	-	intergenic_variant	MODIFIER	-	-	0.8
RS114852474	4	10055680	T	-	intergenic_variant	MODIFIER	-0.156587	1.346	0.13
VAR_CHR4_10055757	4	10055757	T	-	intergenic_variant	MODIFIER	0.130131	3.932	-
VAR_CHR4_10055812	4	10055812	A	-	intergenic_variant	MODIFIER	-0.258542	0.822	-
RS10939679	4	10055855	G	-	intergenic_variant	MODIFIER	0.365742	6.31	0.21
RS10939680	4	10055905	T	-	intergenic_variant	MODIFIER	-	-	0.21
RS10939681	4	10055964	G	-	intergenic_variant	MODIFIER	-0.239303	0.906	0.18
VAR_CHR4_10055978	4	10055978	C	-	intergenic_variant	MODIFIER	-0.410346	0.365	-
RS190578816	4	10056029	C	-	intergenic_variant	MODIFIER	-	-	0.13
VAR_CHR4_10056069	4	10056069	G	-	intergenic_variant	MODIFIER	-0.083616	1.855	-

RS7683832	4	10056082	T	-	intergenic_variant	MODIFIER	-0.352157	0.503	0.12
VAR_CHR4_10056211	4	10056211	T	-	intergenic_variant	MODIFIER	0.13638	3.999	-
VAR_CHR4_10056248	4	10056248	C	-	intergenic_variant	MODIFIER	-	-	-
RS7671266	4	10056376	G	-	intergenic_variant	MODIFIER	0.085866	3.457	0.23
RS114163284	4	10056598	G	-	intergenic_variant	MODIFIER	-	-	0.64
VAR_CHR4_10058246	4	10058246	T	-	intergenic_variant	MODIFIER	-0.221509	0.989	-
VAR_CHR4_10058329	4	10058329	G	-	intergenic_variant	MODIFIER	0.024714	2.827	-
VAR_CHR4_10058411	4	10058411	T	-	intergenic_variant	MODIFIER	0.222008	4.91	-
VAR_CHR4_10058529	4	10058529	A	-	intergenic_variant	MODIFIER	0.255608	5.254	-
RS6812851	4	10058703	C	-	intergenic_variant	MODIFIER	-0.457015	0.281	0.35
VAR_CHR4_10058812	4	10058812	T	-	intergenic_variant	MODIFIER	-	-	-
RS180730877	4	10059028	A	-	intergenic_variant	MODIFIER	-0.068407	1.977	0.49
RS151186539	4	10059113	A	-	intergenic_variant	MODIFIER	-	-	0.38
RS140319372	4	10059212	G	-	intergenic_variant	MODIFIER	-0.311882	0.624	0.4
VAR_CHR4_10059286	4	10059286	G	-	intergenic_variant	MODIFIER	-	-	-
RS112961298	4	10059331	A	-	intergenic_variant	MODIFIER	-0.149803	1.388	0.25
RS181870973	4	10059332	T	-	intergenic_variant	MODIFIER	-0.735218	0.06	0.24
RS714872	4	10059351	G	-	intergenic_variant	MODIFIER	-0.140043	1.451	0.3
RS10516198	4	10059448	G	-	intergenic_variant	MODIFIER	0.192654	4.602	0.29
RS150363708	4	10059465	C	-	intergenic_variant	MODIFIER	-	-	0.27
RS185886938	4	10059506	C	-	intergenic_variant	MODIFIER	-	-	0.23
RS714873	4	10059618	C	-	intergenic_variant	MODIFIER	-0.46943	0.262	0.36
RS714871	4	10059631	C	-	intergenic_variant	MODIFIER	-0.57647	0.143	0.28
RS183077226	4	10059735	A	-	intergenic_variant	MODIFIER	-0.283142	0.725	0.39
RS138440736	4	10063784	C	-	intergenic_variant	MODIFIER	-0.304676	0.648	0.16
RS143025215	4	10063998	T	-	intergenic_variant	MODIFIER	-	-	0.24

RS7676605	4	10064004	A	-	intergenic_variant	MODIFIER	0.180267	4.47	0.25
RS73212817	4	10064011	G	-	intergenic_variant	MODIFIER	-0.207902	1.057	0.24
VAR_CHR4_10064032	4	10064032	T	-	intergenic_variant	MODIFIER	-	-	-
RS183300357	4	10064053	A	-	intergenic_variant	MODIFIER	-0.172291	1.252	0.14
RS7661701	4	10064098	G	-	intergenic_variant	MODIFIER	-0.312659	0.622	0.22
VAR_CHR4_10064151	4	10064151	G	-	intergenic_variant	MODIFIER	-	-	-
RS141419440	4	10064533	C	-	intergenic_variant	MODIFIER	-	-	0.35
RS115281176	4	10064638	G	-	intergenic_variant	MODIFIER	0.086323	3.462	0.36
RS114489981	4	10064751	T	-	intergenic_variant	MODIFIER	-0.973234	0.018	0.32
VAR_CHR4_10064766	4	10064766	T	-	intergenic_variant	MODIFIER	-0.381687	0.428	-
RS61154897	4	10064778	G	-	intergenic_variant	MODIFIER	-	-	0.41
RS6836961	4	10064824	T	-	regulatory_region_variant	MODIFIER	-0.007244	2.517	0.34
RS116003078	4	10064887	A	-	regulatory_region_variant	MODIFIER	-0.044468	2.179	0.4
VAR_CHR4_10065005	4	10065005	T	-	regulatory_region_variant	MODIFIER	2.047591	16.52	-
RS139294906	4	10065049	T	-	regulatory_region_variant	MODIFIER	-	-	0.34
VAR_CHR4_10065121	4	10065121	G	-	intergenic_variant	MODIFIER	1.498014	13.3	-
RS77882555	4	10065218	A	-	regulatory_region_variant	MODIFIER	1.243525	11.97	0.53
VAR_CHR4_10065355	4	10065355	C	-	regulatory_region_variant	MODIFIER	-0.170581	1.262	-
RS114670878	4	10065356	G	-	regulatory_region_variant	MODIFIER	0.184074	4.51	0.45
VAR_CHR4_10065399	4	10065399	A	-	regulatory_region_variant	MODIFIER	0.641328	8.438	-
VAR_CHR4_10065474	4	10065474	C	-	regulatory_region_variant	MODIFIER	-	-	-
RS185568946	4	10065741	C	-	regulatory_region_variant	MODIFIER	-0.301567	0.659	0.3
VAR_CHR4_10065769	4	10065769	T	-	regulatory_region_variant	MODIFIER	-0.349435	0.511	-
RS35150828	4	10065873	T	-	intergenic_variant	MODIFIER	-0.723191	0.064	0.16
RS13102085	4	10065886	G	-	intergenic_variant	MODIFIER	-0.196311	1.117	0.21
VAR_CHR4_10070612	4	10070612	C	-	intergenic_variant	MODIFIER	0.247211	5.169	-

VAR_CHR4_10070694	4	10070694	G	-	intergenic_variant	MODIFIER	-0.043294	2.189	-
RS118085234	4	10070745	T	-	intergenic_variant	MODIFIER	0.257309	5.271	0.38
RS145097623	4	10070809	A	-	intergenic_variant	MODIFIER	0.427519	6.85	0.41
VAR_CHR4_10070873	4	10070873	G	-	intergenic_variant	MODIFIER	-0.054122	2.096	-
RS78310306	4	10070938	T	-	intergenic_variant	MODIFIER	0.079681	3.392	0.42
RS183004032	4	10070939	A	-	intergenic_variant	MODIFIER	0.192888	4.604	0.43
VAR_CHR4_10075174	4	10075174	A	WDR1	downstream_gene_variant	MODIFIER	-0.032904	2.281	-
RS10939691	4	10075184	C	WDR1	downstream_gene_variant	MODIFIER	-0.298919	0.668	0.33
VAR_CHR4_10075310	4	10075310	C	WDR1	downstream_gene_variant	MODIFIER	0.431958	6.887	-
VAR_CHR4_10075365	4	10075365	G	WDR1	downstream_gene_variant	MODIFIER	-0.266092	0.791	-
VAR_CHR4_10075423	4	10075423	T	WDR1	downstream_gene_variant	MODIFIER	0.061036	3.197	-
RS11731597	4	10075485	A	WDR1	downstream_gene_variant	MODIFIER	0.182011	4.489	0.29
VAR_CHR4_10075775	4	10075775	G	WDR1	downstream_gene_variant	MODIFIER	-	-	-
RS143154707	4	10075922	A	WDR1	downstream_gene_variant	MODIFIER	-0.36224	0.476	0.33
VAR_CHR4_10076235	4	10076235	C	WDR1	3_prime_UTR_variant	MODIFIER	-	-	-
VAR_CHR4_10076430	4	10076430	C	WDR1	3_prime_UTR_variant	MODIFIER	0.080774	3.403	-
RS140280208	4	10076495	C	WDR1	3_prime_UTR_variant	MODIFIER	-0.316503	0.609	0.5
RS9732	4	10076658	G	WDR1	3_prime_UTR_variant	MODIFIER	0.355206	6.214	0.42
VAR_CHR4_10076666	4	10076666	G	WDR1	3_prime_UTR_variant	MODIFIER	-	-	-
RS2278119	4	10076674	T	WDR1	3_prime_UTR_variant	MODIFIER	-0.232483	0.937	0.49
VAR_CHR4_10076680	4	10076680	C	WDR1	3_prime_UTR_variant	MODIFIER	-0.240736	0.899	-
RS2278120	4	10076687	C	WDR1	3_prime_UTR_variant	MODIFIER	-	-	0.53
RS9926	4	10076860	T	WDR1	3_prime_UTR_variant	MODIFIER	0.807853	9.512	0.54
VAR_CHR4_10076873	4	10076873	G	WDR1	3_prime_UTR_variant	MODIFIER	-	-	-
VAR_CHR4_10077133	4	10077133	A	WDR1	intron_variant	MODIFIER	-0.039347	2.224	-
VAR_CHR4_10077356	4	10077356	T	WDR1	intron_variant	MODIFIER	0.261695	5.315	-

VAR_CHR4_10077447	4	10077447	A	WDR1	intron_variant	MODIFIER	0.017642	2.757	-
RS3775936	4	10077542	G	WDR1	intron_variant	MODIFIER	-	-	0.29
RS3775935	4	10077638	G	WDR1	intron_variant	MODIFIER	-0.012866	2.464	0.35
VAR_CHR4_10077821	4	10077821	A	WDR1	intron_variant	MODIFIER	0.58413	8.046	-
RS142669794	4	10077833	A	WDR1	intron_variant	MODIFIER	0.290883	5.605	0.32
VAR_CHR4_10077834	4	10077834	T	WDR1	intron_variant	MODIFIER	-0.1285	1.527	-
RS146322815	4	10077891	T	WDR1	intron_variant	MODIFIER	-0.646731	0.096	0.28
RS202170447	4	10078105	A	WDR1	intron_variant	MODIFIER	0.08832	3.483	0.34
VAR_CHR4_10078201	4	10078201	A	WDR1	intron_variant	MODIFIER	0.230957	5.002	-
VAR_CHR4_10078219	4	10078219	A	WDR1	intron_variant	MODIFIER	0.150567	4.152	-
VAR_CHR4_10078308	4	10078308	T	WDR1	intron_variant	MODIFIER	-0.379675	0.433	-
RS3775933	4	10078453	A	WDR1	intron_variant	MODIFIER	0.104909	3.66	0.2
VAR_CHR4_10078458	4	10078458	A	WDR1	intron_variant	MODIFIER	-0.241136	0.897	-
RS190321252	4	10078462	G	WDR1	intron_variant	MODIFIER	-	-	0.2
VAR_CHR4_10078527	4	10078527	G	WDR1	intron_variant	MODIFIER	0.135116	3.985	-
VAR_CHR4_10078631	4	10078631	T	WDR1	intron_variant	MODIFIER	-0.16925	1.269	-
VAR_CHR4_10078649	4	10078649	G	WDR1	intron_variant	MODIFIER	-0.166631	1.285	-
VAR_CHR4_10078746	4	10078746	A	WDR1	intron_variant	MODIFIER	-0.096219	1.758	-
RS73212828	4	10078756	A	WDR1	intron_variant	MODIFIER	0.186369	4.535	0.25
RS73212830	4	10078759	A	WDR1	intron_variant	MODIFIER	-	-	0.21
VAR_CHR4_10078946	4	10078946	G	WDR1	missense_variant	MODERATE	3.225132	22.8	-
RS34193855	4	10079377	A	WDR1	splice_region_variant,synonymous_variant	LOW	2.461525	19.22	0.55
VAR_CHR4_10079442	4	10079442	A	WDR1	missense_variant	MODERATE	3.771434	23.4	-
RS186889066	4	10079513	T	WDR1	missense_variant	MODERATE	1.48092	13.21	0.57
VAR_CHR4_10079670	4	10079670	G	WDR1	intron_variant	MODIFIER	-0.182812	1.191	-
VAR_CHR4_10079775	4	10079775	C	WDR1	intron_variant	MODIFIER	-0.000943	2.577	-

VAR_CHR4_10079891	4	10079891	A	WDR1	intron_variant	MODIFIER	0.141457	4.054	-
RS144081055	4	10079982	G	WDR1	intron_variant	MODIFIER	-	-	0.3
RS2241469	4	10080462	T	WDR1	intron_variant	MODIFIER	0.238604	5.081	0.22
VAR_CHR4_10083014	4	10083014	T	WDR1	synonymous_variant	LOW	0.385426	6.486	-
RS190162322	4	10083020	T	WDR1	synonymous_variant	LOW	0.268491	5.383	0.34
VAR_CHR4_10083028	4	10083028	A	WDR1	missense_variant	MODERATE	0.524331	7.614	-
VAR_CHR4_10083077	4	10083077	G	WDR1	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10084604	4	10084604	C	WDR1	intron_variant	MODIFIER	-	-	-
RS149455738	4	10084616	A	WDR1	intron_variant	MODIFIER	-0.212119	1.035	0.22
RS11930870	4	10084634	C	WDR1	intron_variant	MODIFIER	0.080005	3.395	0.3
VAR_CHR4_10085541	4	10085541	A	WDR1	intron_variant	MODIFIER	0.266804	5.366	-
RS141899745	4	10085615	A	WDR1	intron_variant	MODIFIER	0.167668	4.335	0.12
VAR_CHR4_10085673	4	10085673	C	WDR1	intron_variant	MODIFIER	-0.093355	1.78	-
VAR_CHR4_10085750	4	10085750	T	WDR1	intron_variant	MODIFIER	-0.071598	1.951	-
VAR_CHR4_10085771	4	10085771	A	WDR1	intron_variant	MODIFIER	0.495233	7.395	-
RS112787794	4	10085853	C	WDR1	intron_variant	MODIFIER	-1.098125	0.01	0.21
VAR_CHR4_10085886	4	10085886	G	WDR1	intron_variant	MODIFIER	-	-	-
RS2241472	4	10085902	C	WDR1	intron_variant	MODIFIER	-	-	0.15
RS2241473	4	10085949	T	WDR1	intron_variant	MODIFIER	-0.386277	0.417	0.13
RS79133792	4	10085970	G	WDR1	intron_variant	MODIFIER	-	-	0.16
RS2241474	4	10086015	G	WDR1	intron_variant	MODIFIER	0.550222	7.804	0.32
RS370935468	4	10086053	G	WDR1	intron_variant	MODIFIER	-	-	-
RS2241475	4	10086188	C	WDR1	intron_variant	MODIFIER	0.61246	8.242	0.18
RS368727336	4	10086217	C	WDR1	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10086323	4	10086323	T	WDR1	intron_variant	MODIFIER	-0.164626	1.297	-
VAR_CHR4_10086328	4	10086328	A	WDR1	intron_variant	MODIFIER	-0.162243	1.311	-

VAR_CHR4_10086329	4	10086329	T	WDR1	intron_variant	MODIFIER	-0.838456	0.035	-
RS56402960	4	10086473	T	WDR1	intron_variant	MODIFIER	-	-	0.13
VAR_CHR4_10086525	4	10086525	G	WDR1	intron_variant	MODIFIER	-0.478103	0.249	-
RS187257950	4	10086536	T	WDR1	intron_variant	MODIFIER	-0.871868	0.03	0.2
RS2241476	4	10086547	G	WDR1	intron_variant	MODIFIER	0.213594	4.822	0.19
RS138633352	4	10086552	T	WDR1	intron_variant	MODIFIER	-0.175608	1.232	0.12
VAR_CHR4_10086586	4	10086586	T	WDR1	intron_variant	MODIFIER	-0.077507	1.903	-
VAR_CHR4_10086608	4	10086608	G	WDR1	intron_variant	MODIFIER	0.178055	4.446	-
RS2241477	4	10086670	A	WDR1	intron_variant	MODIFIER	0.444657	6.993	0.13
RS140346523	4	10086671	T	WDR1	intron_variant	MODIFIER	0.109548	3.71	0.15
RS41268387	4	10089539	G	WDR1	missense_variant	MODERATE	3.677091	23.3	0.32
RS202097102	4	10089550	T	WDR1	synonymous_variant	LOW	0.611177	8.233	0.23
VAR_CHR4_10089721	4	10089721	T	WDR1	intron_variant	MODIFIER	0.096505	3.571	-
RS2241480	4	10089763	A	WDR1	intron_variant	MODIFIER	0.031409	2.894	0.22
VAR_CHR4_10089801	4	10089801	A	WDR1	intron_variant	MODIFIER	-0.10388	1.701	-
RS734122	4	10089865	T	WDR1	intron_variant	MODIFIER	-0.038549	2.231	0.21
VAR_CHR4_10089949	4	10089949	A	WDR1	stop_gained	HIGH	12.558807	39	-
VAR_CHR4_10090075	4	10090075	T	WDR1	intron_variant	MODIFIER	0.189361	4.567	-
VAR_CHR4_10090359	4	10090359	T	WDR1	synonymous_variant	LOW	-	-	-
VAR_CHR4_10090385	4	10090385	G	WDR1	intron_variant	MODIFIER	0.020627	2.787	-
VAR_CHR4_10090574	4	10090574	A	WDR1	intron_variant	MODIFIER	0.30751	5.766	-
RS147506185	4	10090638	T	WDR1	intron_variant	MODIFIER	0.225043	4.941	0.18
RS113063781	4	10090639	A	WDR1	intron_variant	MODIFIER	-0.201305	1.091	0.25
RS12500653	4	10090763	G	WDR1	intron_variant	MODIFIER	-	-	0.17
VAR_CHR4_10090840	4	10090840	T	WDR1	intron_variant	MODIFIER	0.214504	4.831	-
RS3775932	4	10090930	T	WDR1	intron_variant	MODIFIER	0.075954	3.353	0.22

RS3775931	4	10090931	A	WDR1	intron_variant	MODIFIER	0.078572	3.38	0.22
RS191058500	4	10091090	A	WDR1	intron_variant	MODIFIER	0.26392	5.338	0.2
RS3775930	4	10091098	C	WDR1	intron_variant	MODIFIER	-0.653635	0.093	0.22
VAR_CHR4_10091163	4	10091163	T	WDR1	intron_variant	MODIFIER	-0.038239	2.234	-
VAR_CHR4_10091205	4	10091205	T	WDR1	intron_variant	MODIFIER	-0.234144	0.929	-
VAR_CHR4_10091270	4	10091270	T	WDR1	intron_variant	MODIFIER	-0.235568	0.923	-
VAR_CHR4_10091339	4	10091339	C	WDR1	intron_variant	MODIFIER	-0.423033	0.34	-
VAR_CHR4_10091387	4	10091387	A	WDR1	intron_variant	MODIFIER	0.552252	7.819	-
VAR_CHR4_10091424	4	10091424	G	WDR1	intron_variant	MODIFIER	-0.373072	0.449	-
RS12646099	4	10091454	C	WDR1	intron_variant	MODIFIER	-0.304137	0.65	0.17
VAR_CHR4_10091515	4	10091515	A	WDR1	intron_variant	MODIFIER	0.503601	7.458	-
VAR_CHR4_10091789	4	10091789	T	WDR1	intron_variant	MODIFIER	0.093046	3.534	-
RS183254695	4	10091858	T	WDR1	intron_variant	MODIFIER	-0.345973	0.52	0.28
VAR_CHR4_10091897	4	10091897	C	WDR1	intron_variant	MODIFIER	-	-	-
RS144314662	4	10091911	T	WDR1	intron_variant	MODIFIER	-0.065075	2.004	0.31
VAR_CHR4_10092098	4	10092098	A	WDR1	intron_variant	MODIFIER	0.022716	2.807	-
RS113133542	4	10092310	A	WDR1	intron_variant	MODIFIER	0.032194	2.902	0.23
RS185076494	4	10092363	T	WDR1	intron_variant	MODIFIER	-0.044331	2.18	0.38
RS4289442	4	10092522	A	WDR1	intron_variant	MODIFIER	-0.541812	0.173	0.34
RS145613518	4	10092565	A	WDR1	intron_variant	MODIFIER	0.059227	3.178	0.35
RS3796826	4	10092728	T	WDR1	intron_variant	MODIFIER	-0.743734	0.057	0.27
VAR_CHR4_10092795	4	10092795	T	WDR1	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10092796	4	10092796	T	WDR1	intron_variant	MODIFIER	-0.043152	2.19	-
VAR_CHR4_10092829	4	10092829	G	WDR1	intron_variant	MODIFIER	-	-	-
RS3796825	4	10092879	T	WDR1	intron_variant	MODIFIER	-	-	0.28
RS137942938	4	10092976	A	WDR1	intron_variant	MODIFIER	0.576355	7.991	0.27

VAR_CHR4_10093084	4	10093084	C	WDR1	intron_variant	MODIFIER	-	-	-
RS73212848	4	10093299	G	WDR1	intron_variant	MODIFIER	-0.655586	0.092	0.33
VAR_CHR4_10093333	4	10093333	A	WDR1	intron_variant	MODIFIER	0.438073	6.938	-
VAR_CHR4_10093370	4	10093370	A	WDR1	intron_variant	MODIFIER	0.502633	7.451	-
VAR_CHR4_10093384	4	10093384	G	WDR1	intron_variant	MODIFIER	-0.329448	0.569	-
VAR_CHR4_10093469	4	10093469	T	WDR1	intron_variant	MODIFIER	-0.116485	1.611	-
RS7683948	4	10093478	C	WDR1	intron_variant	MODIFIER	-0.723822	0.063	0.23
VAR_CHR4_10093550	4	10093550	A	WDR1	intron_variant	MODIFIER	0.37019	6.35	-
RS3796823	4	10093609	A	WDR1	intron_variant	MODIFIER	-0.266054	0.791	0.23
VAR_CHR4_10093617	4	10093617	A	WDR1	intron_variant	MODIFIER	0.217847	4.866	-
RS3796822	4	10093651	G	WDR1	intron_variant	MODIFIER	-	-	0.2
RS139966035	4	10093670	G	WDR1	intron_variant	MODIFIER	-	-	0.25
RS3796821	4	10093714	G	WDR1	intron_variant	MODIFIER	0.281782	5.515	0.23
VAR_CHR4_10093867	4	10093867	A	WDR1	intron_variant	MODIFIER	-0.073058	1.939	-
VAR_CHR4_10093908	4	10093908	A	WDR1	intron_variant	MODIFIER	0.143366	4.074	-
VAR_CHR4_10093943	4	10093943	A	WDR1	intron_variant	MODIFIER	0.040925	2.99	-
RS34517659	4	10094042	C	WDR1	intron_variant	MODIFIER	-0.528051	0.187	0.2
RS146292965	4	10094058	T	WDR1	intron_variant	MODIFIER	-0.326631	0.577	0.27
RS139535718	4	10094060	T	WDR1	intron_variant	MODIFIER	-0.377572	0.438	0.23
RS3756226	4	10094105	C	WDR1	intron_variant	MODIFIER	-0.463435	0.271	0.28
VAR_CHR4_10094106	4	10094106	C	WDR1	intron_variant	MODIFIER	-0.043546	2.187	-
RS3756225	4	10094133	G	WDR1	intron_variant	MODIFIER	-	-	0.24
VAR_CHR4_10094155	4	10094155	A	WDR1	intron_variant	MODIFIER	0.225876	4.95	-
VAR_CHR4_10094251	4	10094251	T	WDR1	intron_variant	MODIFIER	1.372404	12.64	-
VAR_CHR4_10094319	4	10094319	T	WDR1	intron_variant	MODIFIER	-0.04525	2.172	-
VAR_CHR4_10094363	4	10094363	G	WDR1	intron_variant	MODIFIER	1.077365	11.09	-

RS117670209	4	10094380	T	WDR1	intron_variant	MODIFIER	0.428439	6.857	0.21
RS142164246	4	10094496	T	WDR1	intron_variant	MODIFIER	0.414357	6.738	0.26
RS117154942	4	10094590	G	WDR1	intron_variant	MODIFIER	0.466211	7.167	0.31
RS3822247	4	10094671	T	WDR1	intron_variant	MODIFIER	-0.034704	2.265	0.31
RS3822246	4	10094698	T	WDR1	intron_variant	MODIFIER	-0.046598	2.161	0.33
RS3822245	4	10094783	G	WDR1	intron_variant	MODIFIER	-0.478895	0.248	0.33
VAR_CHR4_10094790	4	10094790	C	WDR1	intron_variant	MODIFIER	-0.01183	2.474	-
RS28380210	4	10094865	C	WDR1	intron_variant	MODIFIER	-0.164158	1.3	0.22
RS3822243	4	10094882	C	WDR1	intron_variant	MODIFIER	-	-	0.28
RS3822242	4	10094904	G	WDR1	intron_variant	MODIFIER	-0.048409	2.145	0.31
RS3822241	4	10094931	T	WDR1	intron_variant	MODIFIER	-0.09444	1.772	0.21
VAR_CHR4_10094981	4	10094981	G	WDR1	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10095292	4	10095292	A	WDR1	intron_variant	MODIFIER	0.807883	9.513	-
VAR_CHR4_10095439	4	10095439	C	WDR1	intron_variant	MODIFIER	-	-	-
RS188356704	4	10095461	T	WDR1	intron_variant	MODIFIER	-0.136189	1.476	0.36
RS3822239	4	10095539	T	WDR1	intron_variant	MODIFIER	-	-	0.41
RS79380329	4	10095642	G	WDR1	intron_variant	MODIFIER	-0.121404	1.576	0.38
RS62288519	4	10095725	A	WDR1	intron_variant	MODIFIER	0.125857	3.885	0.31
VAR_CHR4_10095790	4	10095790	A	WDR1	intron_variant	MODIFIER	0.254918	5.247	-
VAR_CHR4_10095806	4	10095806	A	WDR1	intron_variant	MODIFIER	0.12285	3.853	-
RS149279261	4	10095998	A	WDR1	intron_variant	MODIFIER	0.477036	7.253	0.24
VAR_CHR4_10096014	4	10096014	A	WDR1	intron_variant	MODIFIER	0.01417	2.723	-
RS11727087	4	10096020	A	WDR1	intron_variant	MODIFIER	-0.06632	1.994	0.23
RS2278121	4	10096134	T	WDR1	intron_variant	MODIFIER	0.120153	3.824	0.22
VAR_CHR4_10096146	4	10096146	A	WDR1	intron_variant	MODIFIER	-0.32016	0.597	-
RS143334639	4	10096196	A	WDR1	intron_variant	MODIFIER	-0.121227	1.577	0.16

RS73212853	4	10096230	A	WDR1	intron_variant	MODIFIER	-0.16978	1.266	0.21
RS2278122	4	10096241	A	WDR1	intron_variant	MODIFIER	0.276059	5.459	0.17
VAR_CHR4_10096318	4	10096318	G	WDR1	intron_variant	MODIFIER	0.239304	5.088	-
VAR_CHR4_10096346	4	10096346	C	WDR1	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10096349	4	10096349	T	WDR1	intron_variant	MODIFIER	-0.092179	1.789	-
RS79422384	4	10096428	A	WDR1	intron_variant	MODIFIER	-0.175706	1.232	0.24
RS376929668	4	10096685	T	WDR1	intron_variant	MODIFIER	0.261372	5.312	-
VAR_CHR4_10096691	4	10096691	G	WDR1	intron_variant	MODIFIER	-	-	-
RS10939702	4	10096692	A	WDR1	intron_variant	MODIFIER	0.026233	2.842	0.29
RS2278123	4	10096772	G	WDR1	intron_variant	MODIFIER	-0.346597	0.519	0.33
VAR_CHR4_10096785	4	10096785	G	WDR1	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10096869	4	10096869	T	WDR1	intron_variant	MODIFIER	0.054548	3.129	-
RS149807407	4	10097202	A	WDR1	intron_variant	MODIFIER	-0.171339	1.257	0.26
RS189839379	4	10097319	A	WDR1	intron_variant	MODIFIER	0.307784	5.769	0.31
RS112724359	4	10097321	T	WDR1	intron_variant	MODIFIER	-0.102988	1.708	0.23
RS145275096	4	10097322	A	WDR1	intron_variant	MODIFIER	0.20156	4.696	0.29
VAR_CHR4_10097380	4	10097380	T	WDR1	intron_variant	MODIFIER	-0.180844	1.203	-
RS147639097	4	10097445	A	WDR1	intron_variant	MODIFIER	0.493154	7.379	0.23
RS3796820	4	10097446	T	WDR1	intron_variant	MODIFIER	-0.047591	2.152	0.26
VAR_CHR4_10097586	4	10097586	G	WDR1	intron_variant	MODIFIER	-0.649235	0.095	-
RS142048822	4	10097655	C	WDR1	intron_variant	MODIFIER	-0.44736	0.296	0.31
RS735527	4	10097745	C	WDR1	intron_variant	MODIFIER	0.127816	3.907	0.31
RS3796818	4	10097976	A	WDR1	intron_variant	MODIFIER	0.172211	4.384	0.39
RS180989473	4	10098078	A	WDR1	intron_variant	MODIFIER	0.273383	5.432	0.31
RS11726271	4	10098192	T	WDR1	intron_variant	MODIFIER	-0.924155	0.023	0.36
RS76098280	4	10098369	G	WDR1	intron_variant	MODIFIER	1.063969	11.02	0.38

RS58981012	4	10098404	C	WDR1	intron_variant	MODIFIER	-0.254684	0.838	0.42
VAR_CHR4_10098507	4	10098507	C	WDR1	intron_variant	MODIFIER	-0.427747	0.331	-
RS183640684	4	10098540	A	WDR1	intron_variant	MODIFIER	0.266924	5.368	0.34
VAR_CHR4_10098618	4	10098618	T	WDR1	intron_variant	MODIFIER	-0.349742	0.51	-
VAR_CHR4_10098840	4	10098840	G	WDR1	intron_variant	MODIFIER	-0.093309	1.78	-
RS41268389	4	10099277	T	WDR1	intron_variant	MODIFIER	-0.167746	1.278	0.38
RS13441	4	10099340	G	WDR1	intron_variant	MODIFIER	0.475919	7.244	0.38
RS182603736	4	10099381	T	WDR1	intron_variant	MODIFIER	4.259146	23.9	0.42
RS374891992	4	10100729	A	WDR1	intron_variant	MODIFIER	2.685795	20.7	-
RS2241484	4	10100801	G	WDR1	intron_variant	MODIFIER	-0.009741	2.494	0.25
VAR_CHR4_10100814	4	10100814	A	WDR1	intron_variant	MODIFIER	-0.045569	2.169	-
VAR_CHR4_10100820	4	10100820	G	WDR1	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10105476	4	10105476	A	WDR1	intron_variant	MODIFIER	0.553014	7.824	-
RS200525851	4	10105567	C	WDR1	intron_variant	MODIFIER	6.132663	28.4	0.34
RS3756224	4	10105739	G	WDR1	intron_variant	MODIFIER	0.009691	2.679	0.16
RS3756223	4	10105797	G	WDR1	intron_variant	MODIFIER	0.369611	6.345	0.18
VAR_CHR4_10105980	4	10105980	T	WDR1	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10106072	4	10106072	T	WDR1	intron_variant	MODIFIER	-0.313825	0.618	-
VAR_CHR4_10106147	4	10106147	T	WDR1	intron_variant	MODIFIER	-0.137302	1.469	-
RS115861646	4	10106292	T	WDR1	intron_variant	MODIFIER	0.064385	3.231	0.38
RS114614628	4	10106366	A	WDR1	intron_variant	MODIFIER	0.604829	8.19	0.44
RS149878055	4	10106769	G	WDR1	intron_variant	MODIFIER	0.325748	5.94	0.27
RS12509609	4	10106798	A	WDR1	intron_variant	MODIFIER	-0.246215	0.875	0.3
RS12506562	4	10106954	C	WDR1	intron_variant	MODIFIER	-0.205575	1.069	0.22
RS12509713	4	10107069	A	WDR1	intron_variant	MODIFIER	0.074026	3.332	0.23
RS12509714	4	10107091	C	WDR1	intron_variant	MODIFIER	-	-	0.18

VAR_CHR4_10107101	4	10107101	C	WDR1	intron_variant	MODIFIER	-0.209882	1.047	-
VAR_CHR4_10107289	4	10107289	T	WDR1	intron_variant	MODIFIER	0.134075	3.974	-
RS4697703	4	10107431	C	WDR1	intron_variant	MODIFIER	-0.300393	0.663	0.26
RS35411989	4	10107439	A	WDR1	intron_variant	MODIFIER	-0.14282	1.433	0.25
VAR_CHR4_10107475	4	10107475	T	WDR1	intron_variant	MODIFIER	0.255534	5.253	-
RS149192460	4	10107656	A	WDR1	intron_variant	MODIFIER	0.170507	4.366	0.2
VAR_CHR4_10107760	4	10107760	A	WDR1	intron_variant	MODIFIER	-0.112339	1.64	-
RS4697704	4	10107789	A	WDR1	intron_variant	MODIFIER	-0.026132	2.342	0.25
VAR_CHR4_10108096	4	10108096	A	WDR1	intron_variant	MODIFIER	0.259407	5.292	-
RS4697705	4	10108127	T	WDR1	intron_variant	MODIFIER	0.470091	7.198	0.27
RS187708863	4	10108147	C	WDR1	intron_variant	MODIFIER	-	-	0.3
VAR_CHR4_10108159	4	10108159	A	WDR1	intron_variant	MODIFIER	0.207981	4.763	-
VAR_CHR4_10108163	4	10108163	A	WDR1	intron_variant	MODIFIER	0.384632	6.479	-
VAR_CHR4_10108210	4	10108210	T	WDR1	intron_variant	MODIFIER	0.17132	4.374	-
RS151325127	4	10108295	A	WDR1	intron_variant	MODIFIER	1.821484	15.11	0.52
VAR_CHR4_10108315	4	10108315	G	WDR1	intron_variant	MODIFIER	1.004378	10.69	-
VAR_CHR4_10108385	4	10108385	T	WDR1	intron_variant	MODIFIER	1.834821	15.19	-
RS192893054	4	10108402	T	WDR1	intron_variant	MODIFIER	-	-	0.55
VAR_CHR4_10108441	4	10108441	G	WDR1	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10108449	4	10108449	A	WDR1	intron_variant	MODIFIER	0.374793	6.392	-
VAR_CHR4_10108569	4	10108569	T	WDR1	intron_variant	MODIFIER	-0.044374	2.18	-
VAR_CHR4_10108688	4	10108688	T	WDR1	intron_variant	MODIFIER	-0.026806	2.336	-
VAR_CHR4_10108728	4	10108728	G	WDR1	intron_variant	MODIFIER	-	-	-
RS147031819	4	10108734	T	WDR1	intron_variant	MODIFIER	-0.443549	0.303	0.48
VAR_CHR4_10108951	4	10108951	A	WDR1	intron_variant	MODIFIER	0.545461	7.77	-
VAR_CHR4_10109053	4	10109053	T	WDR1	intron_variant	MODIFIER	-0.286832	0.711	-

VAR_CHR4_10109070	4	10109070	T	WDR1	intron_variant	MODIFIER	-0.358142	0.487	-
RS11732818	4	10109123	T	WDR1	intron_variant	MODIFIER	-0.143448	1.429	0.42
VAR_CHR4_10109185	4	10109185	G	WDR1	intron_variant	MODIFIER	-0.144369	1.423	-
RS143897850	4	10109234	C	WDR1	intron_variant	MODIFIER	-	-	0.32
VAR_CHR4_10109590	4	10109590	A	WDR1	intron_variant	MODIFIER	-0.098027	1.745	-
VAR_CHR4_10109685	4	10109685	C	WDR1	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10109687	4	10109687	A	WDR1	intron_variant	MODIFIER	-0.222191	0.986	-
VAR_CHR4_10109801	4	10109801	G	WDR1	intron_variant	MODIFIER	-0.306376	0.643	-
RS114435427	4	10109853	T	WDR1	intron_variant	MODIFIER	0.226458	4.956	0.37
RS148476605	4	10109875	T	WDR1	intron_variant	MODIFIER	-0.385504	0.419	0.38
RS142699433	4	10109920	T	WDR1	intron_variant	MODIFIER	-0.215312	1.019	0.35
VAR_CHR4_10110270	4	10110270	T	WDR1	intron_variant	MODIFIER	0.366081	6.313	-
VAR_CHR4_10110342	4	10110342	G	WDR1	intron_variant	MODIFIER	0.779166	9.335	-
VAR_CHR4_10110362	4	10110362	G	WDR1	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10110374	4	10110374	A	WDR1	intron_variant	MODIFIER	0.370535	6.353	-
RS12509674	4	10115290	A	WDR1	intron_variant	MODIFIER	0.15783	4.23	0.32
RS4348091	4	10115363	G	WDR1	intron_variant	MODIFIER	-0.326499	0.578	0.24
RS148022027	4	10115379	T	WDR1	intron_variant	MODIFIER	-	-	0.24
RS141019279	4	10115418	T	WDR1	intron_variant	MODIFIER	-0.637343	0.101	0.21
VAR_CHR4_10115424	4	10115424	T	WDR1	intron_variant	MODIFIER	0.189051	4.563	-
VAR_CHR4_10115473	4	10115473	T	WDR1	intron_variant	MODIFIER	-0.047571	2.152	-
RS12498927	4	10115523	C	WDR1	intron_variant	MODIFIER	-0.446907	0.297	0.23
RS150709642	4	10115645	A	WDR1	intron_variant	MODIFIER	0.404879	6.656	0.32
RS137926524	4	10115657	G	WDR1	intron_variant	MODIFIER	0.019096	2.771	0.35
RS57757169	4	10115703	T	WDR1	intron_variant	MODIFIER	-0.343038	0.529	0.29
VAR_CHR4_10115710	4	10115710	A	WDR1	intron_variant	MODIFIER	0.45267	7.058	-

VAR_CHR4_10115771	4	10115771	T	WDR1	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10116167	4	10116167	T	WDR1	intron_variant	MODIFIER	-0.220397	0.994	-
VAR_CHR4_10116511	4	10116511	T	WDR1	intron_variant	MODIFIER	0.158586	4.238	-
VAR_CHR4_10116516	4	10116516	A	WDR1	intron_variant	MODIFIER	-0.407001	0.372	-
VAR_CHR4_10116567	4	10116567	T	WDR1	intron_variant	MODIFIER	0.332122	6	-
VAR_CHR4_10116764	4	10116764	A	WDR1	intron_variant	MODIFIER	0.317145	5.859	-
RS10939710	4	10116801	G	WDR1	intron_variant	MODIFIER	-0.157669	1.339	0.2
RS12501855	4	10116852	G	WDR1	intron_variant	MODIFIER	0.110561	3.721	0.2
VAR_CHR4_10116853	4	10116853	G	WDR1	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10116864	4	10116864	A	WDR1	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10116931	4	10116931	C	WDR1	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10116942	4	10116942	A	WDR1	intron_variant	MODIFIER	0.513399	7.533	-
VAR_CHR4_10116999	4	10116999	C	WDR1	intron_variant	MODIFIER	-0.21054	1.043	-
VAR_CHR4_10117136	4	10117136	T	WDR1	intron_variant	MODIFIER	-0.032723	2.283	-
RS191837179	4	10117189	T	WDR1	intron_variant	MODIFIER	0.273257	5.431	0.32
RS78892247	4	10117216	C	WDR1	intron_variant	MODIFIER	-	-	0.31
RS145242845	4	10117256	T	WDR1	intron_variant	MODIFIER	0.183612	4.506	0.32
RS73212886	4	10117430	A	WDR1	intron_variant	MODIFIER	0.994643	10.63	0.31
VAR_CHR4_10117634	4	10117634	A	WDR1	intron_variant	MODIFIER	0.847808	9.756	-
RS2303401	4	10117638	G	WDR1	intron_variant	MODIFIER	-	-	0.42
VAR_CHR4_10117655	4	10117655	T	WDR1	intron_variant	MODIFIER	0.127047	3.898	-
RS73104537	4	10117716	A	WDR1	intron_variant	MODIFIER	0.698421	8.817	0.29
RS35782983	4	10117728	T	WDR1	intron_variant	MODIFIER	0.53149	7.667	0.32
VAR_CHR4_10117737	4	10117737	T	WDR1	missense_variant,splice_region_variant	MODERATE	0.485897	7.322	-
RS79673783	4	10117866	G	WDR1	splice_region_variant,intron_variant	LOW	-	-	0.21
VAR_CHR4_10117939	4	10117939	A	WDR1	intron_variant	MODIFIER	1.213266	11.82	-

RS377426881	4	10117974	T	WDR1	intron_variant	MODIFIER	0.719104	8.952	-
RS34768406	4	10118350	T	WDR1	5_prime_UTR_variant	MODIFIER	0.379416	6.433	0.52
RS11557743	4	10118377	C	WDR1	5_prime_UTR_variant	MODIFIER	-	-	0.52
VAR_CHR4_10118628	4	10118628	T	WDR1	upstream_gene_variant	MODIFIER	0.530183	7.658	-
RS12503122	4	10118631	G	WDR1	upstream_gene_variant	MODIFIER	0.459825	7.116	0.46
VAR_CHR4_10118676	4	10118676	T	WDR1	upstream_gene_variant	MODIFIER	0.323425	5.918	-
RS12502958	4	10118703	C	WDR1	upstream_gene_variant	MODIFIER	-1.020454	0.014	0.41
RS142771591	4	10118716	C	WDR1	upstream_gene_variant	MODIFIER	0.101693	3.626	0.36
RS56158923	4	10118725	A	WDR1	upstream_gene_variant	MODIFIER	0.349743	6.164	0.4
VAR_CHR4_10118731	4	10118731	T	WDR1	upstream_gene_variant	MODIFIER	-0.059714	2.049	-
RS79835095	4	10118733	A	WDR1	upstream_gene_variant	MODIFIER	0.258774	5.286	0.34
RS12498474	4	10118738	A	WDR1	upstream_gene_variant	MODIFIER	0.271639	5.415	0.34
VAR_CHR4_10118742	4	10118742	A	WDR1	upstream_gene_variant	MODIFIER	0.192881	4.604	-
RS3822259	4	10118745	A	WDR1	upstream_gene_variant	MODIFIER	0.284217	5.539	0.37
VAR_CHR4_10118748	4	10118748	G	WDR1	upstream_gene_variant	MODIFIER	-0.410655	0.365	-
RS190351940	4	10118855	A	WDR1	upstream_gene_variant	MODIFIER	0.781724	9.351	0.41
RS3806817	4	10118914	A	WDR1	upstream_gene_variant	MODIFIER	0.456023	7.086	0.23
RS370833528	4	10118918	A	WDR1	upstream_gene_variant	MODIFIER	0.105285	3.664	-
VAR_CHR4_10118942	4	10118942	A	WDR1	upstream_gene_variant	MODIFIER	0.637276	8.411	-
VAR_CHR4_10119009	4	10119009	A	WDR1	upstream_gene_variant	MODIFIER	0.389128	6.519	-
RS73104539	4	10119015	G	WDR1	upstream_gene_variant	MODIFIER	0.360849	6.266	0.23
RS35289776	4	10119034	C	WDR1	upstream_gene_variant	MODIFIER	-0.115965	1.614	0.26
VAR_CHR4_10119117	4	10119117	A	WDR1	upstream_gene_variant	MODIFIER	0.195715	4.634	-
RS3806816	4	10119170	C	WDR1	upstream_gene_variant	MODIFIER	0.068613	3.276	0.22
VAR_CHR4_10119171	4	10119171	C	WDR1	upstream_gene_variant	MODIFIER	-	-	-
RS140057997	4	10119181	A	WDR1	upstream_gene_variant	MODIFIER	-0.27924	0.74	0.18

VAR_CHR4_10119183	4	10119183	A	WDR1	upstream_gene_variant	MODIFIER	0.204551	4.727	-
RS76813200	4	10119244	A	WDR1	upstream_gene_variant	MODIFIER	-	-	0.19
RS371440376	4	10119264	A	WDR1	upstream_gene_variant	MODIFIER	0.297322	5.668	-
VAR_CHR4_10119290	4	10119290	G	WDR1	upstream_gene_variant	MODIFIER	0.071332	3.304	-
RS187998726	4	10119299	C	WDR1	upstream_gene_variant	MODIFIER	-0.052243	2.112	0.24
VAR_CHR4_10119309	4	10119309	T	WDR1	upstream_gene_variant	MODIFIER	0.038475	2.965	-
RS112172557	4	10119316	T	WDR1	upstream_gene_variant	MODIFIER	0.004273	2.627	0.22
RS114110578	4	10119328	T	WDR1	upstream_gene_variant	MODIFIER	0.001909	2.604	0.26
VAR_CHR4_10119332	4	10119332	T	WDR1	upstream_gene_variant	MODIFIER	-0.299214	0.667	-
VAR_CHR4_10119356	4	10119356	A	WDR1	upstream_gene_variant	MODIFIER	0.075519	3.348	-
RS189232743	4	10119398	G	WDR1	upstream_gene_variant	MODIFIER	-	-	0.31
RS35758343	4	10119404	G	WDR1	upstream_gene_variant	MODIFIER	-0.115809	1.615	0.28
RS4697923	4	10119444	C	WDR1	upstream_gene_variant	MODIFIER	-0.125203	1.55	0.25
RS150359939	4	10119449	A	WDR1	upstream_gene_variant	MODIFIER	0.353496	6.199	0.25
RS73212889	4	10119454	C	WDR1	upstream_gene_variant	MODIFIER	-0.153857	1.363	0.24
VAR_CHR4_10119521	4	10119521	T	WDR1	upstream_gene_variant	MODIFIER	-0.303165	0.653	-
VAR_CHR4_10119556	4	10119556	T	WDR1	upstream_gene_variant	MODIFIER	-0.324837	0.583	-
VAR_CHR4_10119577	4	10119577	A	WDR1	upstream_gene_variant	MODIFIER	-	-	-
RS4697706	4	10119601	A	WDR1	upstream_gene_variant	MODIFIER	-0.294579	0.683	0.29
VAR_CHR4_10119620	4	10119620	C	WDR1	upstream_gene_variant	MODIFIER	-0.191449	1.144	-
RS117309606	4	10119652	C	WDR1	upstream_gene_variant	MODIFIER	-0.26441	0.798	0.25
VAR_CHR4_10119665	4	10119665	G	WDR1	upstream_gene_variant	MODIFIER	-0.471772	0.258	-
VAR_CHR4_10119672	4	10119672	C	WDR1	upstream_gene_variant	MODIFIER	-0.901103	0.026	-
VAR_CHR4_10119680	4	10119680	T	WDR1	upstream_gene_variant	MODIFIER	-0.729042	0.062	-
VAR_CHR4_10119717	4	10119717	T	WDR1	upstream_gene_variant	MODIFIER	0.012121	2.703	-
RS138678760	4	10119745	A	WDR1	upstream_gene_variant	MODIFIER	0.298346	5.678	0.33

VAR_CHR4_10119781	4	10119781	T	WDR1	upstream_gene_variant	MODIFIER	-0.14023	1.449	-
RS4697707	4	10119787	A	WDR1	upstream_gene_variant	MODIFIER	0.108345	3.697	0.26
RS12505056	4	10119794	G	WDR1	upstream_gene_variant	MODIFIER	0.067271	3.262	0.27
RS368778860	4	10119798	A	WDR1	upstream_gene_variant	MODIFIER	0.248262	5.179	-
VAR_CHR4_10119808	4	10119808	A	WDR1	upstream_gene_variant	MODIFIER	0.245501	5.151	-
RS13141629	4	10119816	C	WDR1	upstream_gene_variant	MODIFIER	-0.114984	1.621	0.28
RS183854319	4	10119877	A	WDR1	upstream_gene_variant	MODIFIER	0.132648	3.959	0.29
RS192936490	4	10119886	A	WDR1	upstream_gene_variant	MODIFIER	-0.23467	0.927	0.31
RS76411769	4	10119897	G	WDR1	upstream_gene_variant	MODIFIER	-	-	0.31
RS55817941	4	10119903	G	WDR1	upstream_gene_variant	MODIFIER	-	-	0.27
RS73212890	4	10119911	C	WDR1	upstream_gene_variant	MODIFIER	-0.294904	0.682	0.3
RS141516970	4	10119919	T	WDR1	upstream_gene_variant	MODIFIER	-0.540213	0.175	0.24
RS191385164	4	10119920	T	WDR1	upstream_gene_variant	MODIFIER	-0.177322	1.223	0.25
RS73212891	4	10119942	T	WDR1	upstream_gene_variant	MODIFIER	-0.141277	1.443	0.26
VAR_CHR4_10119960	4	10119960	G	WDR1	upstream_gene_variant	MODIFIER	-	-	-
RS3822236	4	10119961	C	WDR1	upstream_gene_variant	MODIFIER	-0.548306	0.167	0.28
VAR_CHR4_10119974	4	10119974	C	WDR1	upstream_gene_variant	MODIFIER	-	-	-
RS13148445	4	10119995	T	WDR1	upstream_gene_variant	MODIFIER	-	-	0.24
RS11727818	4	10120018	C	WDR1	upstream_gene_variant	MODIFIER	-0.462182	0.273	0.23
RS3756222	4	10120091	G	WDR1	upstream_gene_variant	MODIFIER	-0.41567	0.354	0.25
VAR_CHR4_10120142	4	10120142	C	WDR1	upstream_gene_variant	MODIFIER	-0.205239	1.07	-
VAR_CHR4_10120144	4	10120144	C	WDR1	upstream_gene_variant	MODIFIER	-0.46097	0.274	-
RS80059751	4	10120152	A	WDR1	upstream_gene_variant	MODIFIER	-0.969198	0.018	0.27
VAR_CHR4_10120177	4	10120177	G	WDR1	upstream_gene_variant	MODIFIER	-0.005059	2.538	-
VAR_CHR4_10120197	4	10120197	G	WDR1	upstream_gene_variant	MODIFIER	-0.181117	1.201	-
VAR_CHR4_10120218	4	10120218	A	WDR1	upstream_gene_variant	MODIFIER	0.291809	5.614	-

RS191054451	4	10120242	G	WDR1	upstream_gene_variant	MODIFIER	-0.191733	1.142	0.23
RS79876692	4	10120257	T	WDR1	upstream_gene_variant	MODIFIER	0.083606	3.433	0.21
RS3756220	4	10120258	G	WDR1	upstream_gene_variant	MODIFIER	-0.103311	1.705	0.24
VAR_CHR4_10120264	4	10120264	T	WDR1	upstream_gene_variant	MODIFIER	-0.345829	0.521	-
RS3756219	4	10120364	C	WDR1	upstream_gene_variant	MODIFIER	0.074415	3.336	0.19
RS148545499	4	10120374	A	WDR1	upstream_gene_variant	MODIFIER	0.253738	5.235	0.24
RS3756218	4	10120376	C	WDR1	upstream_gene_variant	MODIFIER	-	-	0.22
VAR_CHR4_10120395	4	10120395	A	WDR1	upstream_gene_variant	MODIFIER	0.361917	6.276	-
VAR_CHR4_10120439	4	10120439	T	WDR1	upstream_gene_variant	MODIFIER	-0.860133	0.032	-
VAR_CHR4_10120485	4	10120485	A	WDR1	upstream_gene_variant	MODIFIER	0.300855	5.702	-
RS181095964	4	10120538	A	WDR1	upstream_gene_variant	MODIFIER	0.263457	5.333	0.22
VAR_CHR4_10120559	4	10120559	C	WDR1	upstream_gene_variant	MODIFIER	-	-	-
RS12374229	4	10120565	T	WDR1	upstream_gene_variant	MODIFIER	-0.647645	0.096	0.23
RS12374320	4	10120609	G	WDR1	upstream_gene_variant	MODIFIER	0.15839	4.236	0.25
RS12374294	4	10120654	A	WDR1	upstream_gene_variant	MODIFIER	0.191988	4.594	0.24
RS76056379	4	10120680	A	WDR1	upstream_gene_variant	MODIFIER	-0.014996	2.445	0.24
VAR_CHR4_10120688	4	10120688	A	WDR1	upstream_gene_variant	MODIFIER	-0.587407	0.134	-
RS142603647	4	10120692	C	WDR1	upstream_gene_variant	MODIFIER	-	-	0.27
RS140866200	4	10120768	G	WDR1	upstream_gene_variant	MODIFIER	-0.073078	1.939	0.25
VAR_CHR4_10120782	4	10120782	G	WDR1	upstream_gene_variant	MODIFIER	-	-	-
VAR_CHR4_10120852	4	10120852	A	WDR1	upstream_gene_variant	MODIFIER	-0.345867	0.521	-
RS3756217	4	10120898	T	WDR1	upstream_gene_variant	MODIFIER	-0.332439	0.56	0.25
RS182392177	4	10120953	C	WDR1	upstream_gene_variant	MODIFIER	-0.425444	0.336	0.2
VAR_CHR4_10120962	4	10120962	A	WDR1	upstream_gene_variant	MODIFIER	-0.833634	0.036	-
VAR_CHR4_10121018	4	10121018	A	WDR1	upstream_gene_variant	MODIFIER	0.123711	3.862	-
RS73212895	4	10121025	A	WDR1	upstream_gene_variant	MODIFIER	-0.06364	2.016	0.26

RS7656624	4	10121097	G	WDR1	upstream_gene_variant	MODIFIER	0.292783	5.623	0.3
VAR_CHR4_10121130	4	10121130	C	WDR1	upstream_gene_variant	MODIFIER	-	-	-
VAR_CHR4_10121186	4	10121186	T	WDR1	upstream_gene_variant	MODIFIER	-	-	-
RS4697708	4	10121189	G	WDR1	upstream_gene_variant	MODIFIER	0.066012	3.248	0.25
RS4697709	4	10121237	C	WDR1	upstream_gene_variant	MODIFIER	-0.257639	0.826	0.23
RS3756215	4	10121260	C	WDR1	upstream_gene_variant	MODIFIER	-0.236423	0.919	0.32
RS143745354	4	10121365	G	WDR1	upstream_gene_variant	MODIFIER	-0.016599	2.43	0.21
RS78153443	4	10121446	G	WDR1	upstream_gene_variant	MODIFIER	-0.480673	0.245	0.22
VAR_CHR4_10121450	4	10121450	A	WDR1	upstream_gene_variant	MODIFIER	-0.007281	2.517	-
VAR_CHR4_10121474	4	10121474	A	WDR1	upstream_gene_variant	MODIFIER	-0.384015	0.423	-
VAR_CHR4_10121493	4	10121493	A	WDR1	upstream_gene_variant	MODIFIER	-	-	-
VAR_CHR4_10121515	4	10121515	T	WDR1	upstream_gene_variant	MODIFIER	-0.295824	0.679	-
RS184065097	4	10121526	A	WDR1	upstream_gene_variant	MODIFIER	0.096576	3.571	0.22
RS189746790	4	10121576	T	WDR1	upstream_gene_variant	MODIFIER	-0.333181	0.557	0.22
VAR_CHR4_10121607	4	10121607	A	WDR1	upstream_gene_variant	MODIFIER	-0.361808	0.477	-
VAR_CHR4_10121625	4	10121625	G	WDR1	upstream_gene_variant	MODIFIER	-	-	-
RS35865690	4	10121629	C	WDR1	upstream_gene_variant	MODIFIER	-0.26733	0.786	0.23
RS55973727	4	10121632	T	WDR1	upstream_gene_variant	MODIFIER	-0.162595	1.309	0.23
RS146310357	4	10121691	T	WDR1	upstream_gene_variant	MODIFIER	0.022271	2.803	0.24
RS139299672	4	10121717	T	WDR1	upstream_gene_variant	MODIFIER	-0.293744	0.686	0.25
VAR_CHR4_10121719	4	10121719	G	WDR1	upstream_gene_variant	MODIFIER	-0.438834	0.311	-
RS56393964	4	10121747	C	WDR1	upstream_gene_variant	MODIFIER	-0.116515	1.61	0.25
VAR_CHR4_10121801	4	10121801	A	WDR1	upstream_gene_variant	MODIFIER	-0.113432	1.632	-
VAR_CHR4_10121803	4	10121803	A	WDR1	upstream_gene_variant	MODIFIER	0.085014	3.448	-
VAR_CHR4_10121811	4	10121811	A	WDR1	upstream_gene_variant	MODIFIER	-0.025477	2.348	-
VAR_CHR4_10121906	4	10121906	C	WDR1	upstream_gene_variant	MODIFIER	0.152587	4.173	-

VAR_CHR4_10121962	4	10121962	C	WDR1	upstream_gene_variant	MODIFIER	-0.171677	1.255	-
RS73212898	4	10121994	A	WDR1	upstream_gene_variant	MODIFIER	-0.063177	2.02	0.24
VAR_CHR4_10122007	4	10122007	A	WDR1	upstream_gene_variant	MODIFIER	-0.304253	0.65	-
VAR_CHR4_10122031	4	10122031	A	WDR1	upstream_gene_variant	MODIFIER	0.320348	5.889	-
VAR_CHR4_10122052	4	10122052	A	WDR1	upstream_gene_variant	MODIFIER	0.33272	6.006	-
VAR_CHR4_10122145	4	10122145	T	WDR1	upstream_gene_variant	MODIFIER	-0.038521	2.231	-
VAR_CHR4_10122195	4	10122195	C	WDR1	upstream_gene_variant	MODIFIER	-	-	-
RS73212899	4	10122237	C	WDR1	upstream_gene_variant	MODIFIER	-	-	0.28
VAR_CHR4_10122248	4	10122248	A	WDR1	upstream_gene_variant	MODIFIER	0.148948	4.134	-
VAR_CHR4_10122450	4	10122450	T	WDR1	upstream_gene_variant	MODIFIER	-0.290894	0.697	-
VAR_CHR4_10122489	4	10122489	T	WDR1	upstream_gene_variant	MODIFIER	-0.646028	0.097	-
VAR_CHR4_10122496	4	10122496	A	WDR1	upstream_gene_variant	MODIFIER	0.104048	3.651	-
VAR_CHR4_10122523	4	10122523	G	WDR1	upstream_gene_variant	MODIFIER	-0.485668	0.238	-
VAR_CHR4_10122595	4	10122595	T	WDR1	upstream_gene_variant	MODIFIER	-0.767974	0.05	-
RS55959038	4	10122612	C	WDR1	upstream_gene_variant	MODIFIER	-0.456194	0.282	0.18
VAR_CHR4_10122613	4	10122613	A	WDR1	upstream_gene_variant	MODIFIER	0.265209	5.35	-
RS62286562	4	10122636	A	WDR1	upstream_gene_variant	MODIFIER	0.018677	2.767	0.28
RS140762331	4	10122639	G	WDR1	upstream_gene_variant	MODIFIER	-0.292567	0.691	0.26
VAR_CHR4_10122642	4	10122642	A	WDR1	upstream_gene_variant	MODIFIER	0.016226	2.743	-
RS4697710	4	10122649	G	WDR1	upstream_gene_variant	MODIFIER	-0.106649	1.681	0.32
RS62286563	4	10122665	C	WDR1	upstream_gene_variant	MODIFIER	-0.054192	2.095	0.38
VAR_CHR4_10122715	4	10122715	C	WDR1	upstream_gene_variant	MODIFIER	-0.307378	0.639	-
RS13118272	4	10122722	G	WDR1	upstream_gene_variant	MODIFIER	-0.059287	2.052	0.41
RS6825888	4	10122734	G	WDR1	upstream_gene_variant	MODIFIER	-0.210476	1.044	0.4
VAR_CHR4_10122751	4	10122751	T	WDR1	upstream_gene_variant	MODIFIER	-0.584369	0.136	-
RS191999259	4	10122923	A	WDR1	upstream_gene_variant	MODIFIER	0.049651	3.079	0.25

RS4235353	4	10122934	A	WDR1	upstream_gene_variant	MODIFIER	0.020976	2.79	0.26
VAR_CHR4_10122936	4	10122936	A	WDR1	upstream_gene_variant	MODIFIER	-0.09957	1.733	-
VAR_CHR4_10122938	4	10122938	A	WDR1	upstream_gene_variant	MODIFIER	0.093094	3.534	-
RS4235354	4	10122942	T	WDR1	upstream_gene_variant	MODIFIER	-0.404982	0.376	0.25
VAR_CHR4_10122946	4	10122946	A	WDR1	upstream_gene_variant	MODIFIER	0.257571	5.274	-
VAR_CHR4_10122992	4	10122992	A	WDR1	upstream_gene_variant	MODIFIER	-0.037822	2.237	-
VAR_CHR4_10123047	4	10123047	T	WDR1	upstream_gene_variant	MODIFIER	-0.117471	1.604	-
RS192261037	4	10123052	A	WDR1	upstream_gene_variant	MODIFIER	-0.155919	1.35	0.19
RS4235355	4	10123078	T	WDR1	upstream_gene_variant	MODIFIER	-0.155572	1.352	0.16
RS4235356	4	10123106	G	WDR1	upstream_gene_variant	MODIFIER	-	-	0.15
VAR_CHR4_10123129	4	10123129	A	WDR1	upstream_gene_variant	MODIFIER	0.192105	4.596	-
RS73212900	4	10123182	A	WDR1	upstream_gene_variant	MODIFIER	0.190203	4.576	0.2
RS4311315	4	10123191	G	WDR1	upstream_gene_variant	MODIFIER	-0.028054	2.325	0.21
RS79824251	4	10123215	A	WDR1	upstream_gene_variant	MODIFIER	0.320842	5.894	0.28
RS78403883	4	10123282	A	WDR1	upstream_gene_variant	MODIFIER	0.417928	6.768	0.31
RS35523212	4	10123377	C	WDR1	upstream_gene_variant	MODIFIER	-0.570828	0.147	0.37
RS13119731	4	10123381	T	WDR1	upstream_gene_variant	MODIFIER	-	-	0.33
RS34651105	4	10123382	A	WDR1	upstream_gene_variant	MODIFIER	0.267444	5.373	0.34
RS34426660	4	10123392	A	WDR1	upstream_gene_variant	MODIFIER	0.036578	2.946	0.35
RS112574087	4	10123401	A	WDR1	upstream_gene_variant	MODIFIER	0.067262	3.262	0.35
RS75245155	4	10123443	A	WDR1	upstream_gene_variant	MODIFIER	0.106587	3.678	0.43
RS189291952	4	10123542	A	WDR1	upstream_gene_variant	MODIFIER	-0.074179	1.93	0.45
VAR_CHR4_10123549	4	10123549	A	WDR1	upstream_gene_variant	MODIFIER	0.051387	3.097	-
RS56178126	4	10123581	A	WDR1	upstream_gene_variant	MODIFIER	0.207711	4.76	0.4
RS144151269	4	10123654	C	-	regulatory_region_variant	MODIFIER	-0.358051	0.487	0.28
RS12506893	4	10123665	A	-	intergenic_variant	MODIFIER	0.367357	6.325	0.32

RS184598209	4	10123700	A	-	intergenic_variant	MODIFIER	0.055409	3.138	0.23
RS113216760	4	10123751	G	-	intergenic_variant	MODIFIER	0.046017	3.042	0.17
VAR_CHR4_10123874	4	10123874	G	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_10123931	4	10123931	T	-	intergenic_variant	MODIFIER	-0.628968	0.106	-
RS10516201	4	10123941	G	-	intergenic_variant	MODIFIER	-1.455304	0.003	0.29
VAR_CHR4_10123983	4	10123983	A	-	intergenic_variant	MODIFIER	0.006574	2.649	-
VAR_CHR4_10124003	4	10124003	A	-	intergenic_variant	MODIFIER	-0.137814	1.465	-
VAR_CHR4_10124107	4	10124107	A	-	intergenic_variant	MODIFIER	-0.231403	0.942	-
VAR_CHR4_10124120	4	10124120	A	-	intergenic_variant	MODIFIER	-0.138874	1.458	-
RS113888816	4	10124168	A	-	intergenic_variant	MODIFIER	-0.239803	0.903	0.36
RS4697924	4	10124239	G	-	intergenic_variant	MODIFIER	0.097236	3.578	0.32
RS111297105	4	10124266	A	-	intergenic_variant	MODIFIER	-0.212215	1.035	0.34
RS144868267	4	10124267	T	-	intergenic_variant	MODIFIER	-0.727529	0.062	0.34
VAR_CHR4_10124275	4	10124275	C	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_10124293	4	10124293	T	-	intergenic_variant	MODIFIER	-	-	-
RS4697925	4	10124330	G	-	intergenic_variant	MODIFIER	-	-	0.3
RS77564396	4	10124346	T	-	intergenic_variant	MODIFIER	-0.201595	1.089	0.29
VAR_CHR4_10124390	4	10124390	C	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_10124403	4	10124403	C	-	intergenic_variant	MODIFIER	0.20394	4.721	-
RS181130991	4	10124446	T	-	intergenic_variant	MODIFIER	-0.210161	1.045	0.27
RS115099116	4	10124481	T	-	intergenic_variant	MODIFIER	-0.695675	0.074	0.28
RS189745455	4	10124529	A	-	intergenic_variant	MODIFIER	0.039792	2.979	0.24
RS4697926	4	10124567	G	-	intergenic_variant	MODIFIER	0.09709	3.577	0.21
RS78126175	4	10124724	T	-	regulatory_region_variant	MODIFIER	-0.199019	1.103	0.21
RS4444830	4	10124819	G	-	regulatory_region_variant	MODIFIER	0.1197	3.819	0.23
RS4456954	4	10124838	G	-	regulatory_region_variant	MODIFIER	-	-	0.24

RS62286568	4	10124889	A	-	regulatory_region_variant	MODIFIER	-0.156462	1.347	0.27
VAR_CHR4_10124890	4	10124890	T	-	regulatory_region_variant	MODIFIER	-0.426991	0.333	-
RS112061366	4	10124944	A	-	regulatory_region_variant	MODIFIER	0.12302	3.855	0.33
RS115217731	4	10125002	A	-	regulatory_region_variant	MODIFIER	0.315362	5.842	0.3
VAR_CHR4_10125011	4	10125011	G	-	regulatory_region_variant	MODIFIER	-	-	-
VAR_CHR4_10125110	4	10125110	A	-	regulatory_region_variant	MODIFIER	0.263948	5.338	-
VAR_CHR4_10125127	4	10125127	C	-	regulatory_region_variant	MODIFIER	-0.648291	0.095	-
RS4383618	4	10125151	G	-	regulatory_region_variant	MODIFIER	-0.021793	2.382	0.22
RS62286569	4	10125157	C	-	regulatory_region_variant	MODIFIER	-	-	0.27
RS4572881	4	10125200	C	-	regulatory_region_variant	MODIFIER	-	-	0.24
RS715979	4	10125242	C	-	regulatory_region_variant	MODIFIER	-	-	0.35
RS3886038	4	10125255	A	-	regulatory_region_variant	MODIFIER	0.364788	6.302	0.35
VAR_CHR4_10125290	4	10125290	T	-	regulatory_region_variant	MODIFIER	-	-	-
RS138121361	4	10125318	A	-	regulatory_region_variant	MODIFIER	0.090813	3.51	0.38
RS4337733	4	10125335	A	-	regulatory_region_variant	MODIFIER	0.294238	5.638	0.42
VAR_CHR4_10125357	4	10125357	G	-	regulatory_region_variant	MODIFIER	-	-	-
RS4393996	4	10125359	G	-	regulatory_region_variant	MODIFIER	-	-	0.48
RS7668175	4	10125782	G	-	regulatory_region_variant	MODIFIER	-0.204781	1.073	0.28
RS7699512	4	10125808	A	-	regulatory_region_variant	MODIFIER	-0.176146	1.229	0.27
RS7699671	4	10125874	A	-	regulatory_region_variant	MODIFIER	-0.015474	2.44	0.26
RS10516202	4	10125945	C	-	regulatory_region_variant	MODIFIER	-	-	0.33
RS11722946	4	10125990	C	-	regulatory_region_variant	MODIFIER	-0.199126	1.102	0.24
VAR_CHR4_10126049	4	10126049	T	-	regulatory_region_variant	MODIFIER	-0.48412	0.241	-
RS11722989	4	10126139	C	-	regulatory_region_variant	MODIFIER	0.058909	3.175	0.27
VAR_CHR4_10126148	4	10126148	A	-	regulatory_region_variant	MODIFIER	0.156882	4.22	-
RS11723016	4	10126189	C	-	regulatory_region_variant	MODIFIER	-0.36945	0.458	0.27

RS6820009	4	10126235	G	-	regulatory_region_variant	MODIFIER	-0.025881	2.344	0.3
RS73215003	4	10126317	C	-	regulatory_region_variant	MODIFIER	-	-	0.27
VAR_CHR4_10126324	4	10126324	T	-	regulatory_region_variant	MODIFIER	-0.252621	0.847	-
VAR_CHR4_10126355	4	10126355	T	-	regulatory_region_variant	MODIFIER	-0.437823	0.313	-
RS149660051	4	10126420	T	-	intergenic_variant	MODIFIER	-0.761714	0.052	0.32
RS145477423	4	10126467	C	-	intergenic_variant	MODIFIER	-0.188048	1.162	0.28
VAR_CHR4_10126506	4	10126506	T	-	intergenic_variant	MODIFIER	-0.337733	0.544	-
VAR_CHR4_10126520	4	10126520	A	-	intergenic_variant	MODIFIER	-0.196969	1.114	-
RS10155429	4	10126527	T	-	intergenic_variant	MODIFIER	-0.114429	1.625	0.31
RS111445952	4	10126541	C	-	intergenic_variant	MODIFIER	-0.266053	0.791	0.31
RS6449286	4	10126699	T	-	intergenic_variant	MODIFIER	-	-	0.31
RS73215005	4	10126701	T	-	intergenic_variant	MODIFIER	-0.686759	0.077	0.4
VAR_CHR4_10126714	4	10126714	C	-	intergenic_variant	MODIFIER	-0.327291	0.575	-
RS115404519	4	10126733	G	-	intergenic_variant	MODIFIER	-	-	0.39
VAR_CHR4_10126738	4	10126738	A	-	intergenic_variant	MODIFIER	-0.239234	0.906	-
VAR_CHR4_10126826	4	10126826	A	-	intergenic_variant	MODIFIER	0.053986	3.124	-
RS144582637	4	10146434	C	-	intergenic_variant	MODIFIER	-0.592166	0.13	0.35
RS4697932	4	10146454	G	-	intergenic_variant	MODIFIER	-0.131461	1.507	0.37
RS141596931	4	10146470	T	-	intergenic_variant	MODIFIER	-	-	0.3
RS189596279	4	10146488	T	-	intergenic_variant	MODIFIER	0.085921	3.458	0.27
RS4697933	4	10146493	T	-	intergenic_variant	MODIFIER	0.056918	3.154	0.27
RS4697715	4	10146654	T	-	intergenic_variant	MODIFIER	-0.390823	0.407	0.29
VAR_CHR4_10146741	4	10146741	G	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_10146815	4	10146815	G	-	intergenic_variant	MODIFIER	0.483135	7.301	-
VAR_CHR4_10146845	4	10146845	A	-	intergenic_variant	MODIFIER	1.961139	15.97	-
RS56169830	4	10146964	C	-	intergenic_variant	MODIFIER	-0.688112	0.077	0.21

RS71603992	4	10147046	C	-	intergenic_variant	MODIFIER	0.077552	3.369	0.28
RS114772240	4	10147073	C	-	intergenic_variant	MODIFIER	0.36088	6.266	0.21
VAR_CHR4_10147087	4	10147087	C	-	intergenic_variant	MODIFIER	0.044083	3.022	-
VAR_CHR4_10147093	4	10147093	C	-	intergenic_variant	MODIFIER	-0.023832	2.363	-
VAR_CHR4_10147094	4	10147094	A	-	intergenic_variant	MODIFIER	0.385858	6.49	-
RS62287542	4	10147096	T	-	intergenic_variant	MODIFIER	-0.026113	2.342	0.24
RS62287543	4	10147119	T	-	intergenic_variant	MODIFIER	-0.141456	1.442	0.25
VAR_CHR4_10151894	4	10151894	A	-	intergenic_variant	MODIFIER	0.032311	2.903	-
VAR_CHR4_10151964	4	10151964	A	-	intergenic_variant	MODIFIER	0.190402	4.578	-
VAR_CHR4_10152036	4	10152036	A	-	intergenic_variant	MODIFIER	-0.143514	1.428	-
RS111935504	4	10152112	T	-	intergenic_variant	MODIFIER	-0.679707	0.08	0.33
RS192344071	4	10152114	C	-	intergenic_variant	MODIFIER	-	-	0.27
VAR_CHR4_10152133	4	10152133	A	-	intergenic_variant	MODIFIER	-0.197814	1.109	-
VAR_CHR4_10152139	4	10152139	A	-	intergenic_variant	MODIFIER	-0.411868	0.362	-
VAR_CHR4_10152277	4	10152277	C	-	intergenic_variant	MODIFIER	-0.063697	2.016	-
RS4697939	4	10152302	T	-	intergenic_variant	MODIFIER	-0.219038	1.001	0.34
RS4697940	4	10152329	G	-	intergenic_variant	MODIFIER	-	-	0.29
RS731069	4	10152431	G	-	intergenic_variant	MODIFIER	-0.008045	2.51	0.33
RS78882332	4	10152491	A	-	intergenic_variant	MODIFIER	0.049803	3.081	0.27
RS200061806	4	10152581	G	-	intergenic_variant	MODIFIER	0.043763	3.019	0.38
RS731070	4	10152582	A	-	intergenic_variant	MODIFIER	0.121808	3.842	0.3
VAR_CHR4_10152680	4	10152680	G	-	intergenic_variant	MODIFIER	-	-	-
RS185146232	4	10152702	G	-	intergenic_variant	MODIFIER	-	-	0.3
RS2241464	4	10158961	T	-	intergenic_variant	MODIFIER	-0.231451	0.942	0.26
RS185686223	4	10159007	A	-	regulatory_region_variant	MODIFIER	-0.174334	1.24	0.33
RS2241465	4	10159020	G	-	regulatory_region_variant	MODIFIER	-0.66534	0.087	0.36

RS78491056	4	10159056	C	-	regulatory_region_variant	MODIFIER	-0.175034	1.236	0.32
RS188587273	4	10159074	T	-	regulatory_region_variant	MODIFIER	-0.589966	0.132	0.28
RS2241466	4	10159103	A	-	regulatory_region_variant	MODIFIER	-0.248418	0.865	0.32
VAR_CHR4_10159232	4	10159232	T	-	regulatory_region_variant	MODIFIER	0.012094	2.703	-
VAR_CHR4_10159286	4	10159286	C	-	regulatory_region_variant	MODIFIER	-0.426666	0.333	-
VAR_CHR4_10159328	4	10159328	A	-	regulatory_region_variant	MODIFIER	-0.485589	0.239	-
VAR_CHR4_10159347	4	10159347	T	-	regulatory_region_variant	MODIFIER	-0.431057	0.325	-
VAR_CHR4_10159448	4	10159448	C	-	regulatory_region_variant	MODIFIER	-0.293424	0.687	-
RS10007416	4	10159457	G	-	regulatory_region_variant	MODIFIER	-0.400507	0.386	0.35
RS112359089	4	10159462	C	-	regulatory_region_variant	MODIFIER	-0.430933	0.325	0.32
VAR_CHR4_10159481	4	10159481	T	-	regulatory_region_variant	MODIFIER	-0.201247	1.091	-
RS75044083	4	10159491	T	-	regulatory_region_variant	MODIFIER	-	-	0.37
VAR_CHR4_10159537	4	10159537	A	-	regulatory_region_variant	MODIFIER	-0.559114	0.157	-
RS2241467	4	10159554	T	-	regulatory_region_variant	MODIFIER	-0.176754	1.226	0.36
VAR_CHR4_10159643	4	10159643	A	-	regulatory_region_variant	MODIFIER	0.013961	2.721	-
RS138437679	4	10159647	G	-	regulatory_region_variant	MODIFIER	0.063786	3.225	0.38
VAR_CHR4_10159687	4	10159687	G	-	regulatory_region_variant	MODIFIER	0.047901	3.061	-
RS10002562	4	10159736	C	-	regulatory_region_variant	MODIFIER	-	-	0.41
VAR_CHR4_10159766	4	10159766	T	-	regulatory_region_variant	MODIFIER	-	-	-
VAR_CHR4_10159801	4	10159801	G	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_10159858	4	10159858	A	-	intergenic_variant	MODIFIER	0.352842	6.193	-
VAR_CHR4_10159975	4	10159975	A	-	intergenic_variant	MODIFIER	0.62237	8.31	-
RS372641102	4	10160070	A	-	intergenic_variant	MODIFIER	0.130321	3.934	-
RS187409592	4	10160110	G	-	intergenic_variant	MODIFIER	-0.223052	0.981	0.42
VAR_CHR4_10160135	4	10160135	C	-	intergenic_variant	MODIFIER	-0.593359	0.13	-
VAR_CHR4_10160221	4	10160221	T	-	intergenic_variant	MODIFIER	0.119703	3.819	-

RS76985474	4	10160421	G	-	intergenic_variant	MODIFIER	-	-	0.23
VAR_CHR4_10160449	4	10160449	A	-	intergenic_variant	MODIFIER	-0.136064	1.477	-
RS4579113	4	10160450	T	-	intergenic_variant	MODIFIER	-0.259973	0.816	0.28
RS150707370	4	10160471	A	-	intergenic_variant	MODIFIER	-0.677426	0.081	0.28
RS13147600	4	10160489	A	-	intergenic_variant	MODIFIER	0.185404	4.525	0.28
VAR_CHR4_10160529	4	10160529	G	-	intergenic_variant	MODIFIER	0.097063	3.576	-
VAR_CHR4_10160679	4	10160679	C	-	intergenic_variant	MODIFIER	-0.237532	0.914	-
RS114506235	4	10160734	C	-	intergenic_variant	MODIFIER	-0.197927	1.109	0.27
VAR_CHR4_10161969	4	10161969	T	-	regulatory_region_variant	MODIFIER	-0.130212	1.516	-
RS6851365	4	10162149	A	-	regulatory_region_variant	MODIFIER	-0.582139	0.138	0.36
RS116021881	4	10162150	T	-	regulatory_region_variant	MODIFIER	-0.741078	0.058	0.35
VAR_CHR4_10162180	4	10162180	T	-	regulatory_region_variant	MODIFIER	-0.470132	0.26	-
VAR_CHR4_10162183	4	10162183	G	-	regulatory_region_variant	MODIFIER	-	-	-
RS2215693	4	10166349	C	-	intergenic_variant	MODIFIER	-0.384609	0.421	0.24
RS76617398	4	10166350	A	-	intergenic_variant	MODIFIER	-0.408247	0.369	0.18
RS150984370	4	10166374	C	-	intergenic_variant	MODIFIER	-0.524104	0.192	0.2
VAR_CHR4_10166475	4	10166475	G	-	regulatory_region_variant	MODIFIER	-0.339634	0.538	-
VAR_CHR4_10166533	4	10166533	T	-	regulatory_region_variant	MODIFIER	0.238689	5.082	-
RS17385001	4	10166591	A	-	regulatory_region_variant	MODIFIER	-	-	0.34
VAR_CHR4_10166734	4	10166734	T	-	regulatory_region_variant	MODIFIER	-	-	-
RS200270677	4	10166759	A	-	regulatory_region_variant	MODIFIER	0.382238	6.458	0.32
VAR_CHR4_10166794	4	10166794	T	-	regulatory_region_variant	MODIFIER	-0.111175	1.648	-
VAR_CHR4_10166804	4	10166804	C	-	regulatory_region_variant	MODIFIER	-0.593197	0.13	-
VAR_CHR4_10166817	4	10166817	C	-	regulatory_region_variant	MODIFIER	-0.248647	0.864	-
VAR_CHR4_10166829	4	10166829	C	-	regulatory_region_variant	MODIFIER	-0.449613	0.293	-
VAR_CHR4_10166830	4	10166830	T	-	regulatory_region_variant	MODIFIER	0.198428	4.663	-

RS11724641	4	10166994	C	-	regulatory_region_variant	MODIFIER	-0.385752	0.419	0.28
RS115190002	4	10167042	T	-	intergenic_variant	MODIFIER	0.299266	5.687	0.25
VAR_CHR4_10167052	4	10167052	A	-	intergenic_variant	MODIFIER	0.394527	6.566	-
RS192862502	4	10167079	A	-	intergenic_variant	MODIFIER	-	-	0.21
RS184297548	4	10167081	A	-	intergenic_variant	MODIFIER	-0.367359	0.463	0.24
RS7659717	4	10167217	G	-	intergenic_variant	MODIFIER	0.060281	3.189	0.26
VAR_CHR4_10167245	4	10167245	G	-	intergenic_variant	MODIFIER	-0.328483	0.572	-
VAR_CHR4_10173433	4	10173433	T	-	intergenic_variant	MODIFIER	-0.348074	0.514	-
VAR_CHR4_10173461	4	10173461	G	-	intergenic_variant	MODIFIER	-0.106759	1.68	-
VAR_CHR4_10173502	4	10173502	T	-	intergenic_variant	MODIFIER	-0.367267	0.463	-
VAR_CHR4_10173503	4	10173503	T	-	intergenic_variant	MODIFIER	0.055925	3.144	-
RS371897323	4	10173597	G	-	intergenic_variant	MODIFIER	-0.045195	2.173	-
VAR_CHR4_10173619	4	10173619	A	-	intergenic_variant	MODIFIER	-0.011155	2.48	-
RS10034405	4	10173696	C	-	intergenic_variant	MODIFIER	-0.284596	0.72	0.25
VAR_CHR4_10173746	4	10173746	C	-	intergenic_variant	MODIFIER	-0.247001	0.871	-
RS4697953	4	10173753	G	-	intergenic_variant	MODIFIER	-	-	0.22
RS114748506	4	10173798	A	-	intergenic_variant	MODIFIER	0.303274	5.725	0.13
VAR_CHR4_10173802	4	10173802	A	-	intergenic_variant	MODIFIER	0.107523	3.688	-
RS55760253	4	10173889	A	-	intergenic_variant	MODIFIER	0.187626	4.548	0.16
VAR_CHR4_10173934	4	10173934	A	-	intergenic_variant	MODIFIER	0.261164	5.31	-
RS76903922	4	10173951	T	-	intergenic_variant	MODIFIER	-0.025506	2.348	0.18
VAR_CHR4_10173984	4	10173984	A	-	intergenic_variant	MODIFIER	-0.029678	2.31	-
VAR_CHR4_10173991	4	10173991	A	-	intergenic_variant	MODIFIER	0.026902	2.849	-
RS114656953	4	10173995	A	-	intergenic_variant	MODIFIER	0.351898	6.184	0.16
RS77093467	4	10173996	T	-	intergenic_variant	MODIFIER	-0.070424	1.96	0.19
RS112967961	4	10174114	T	-	intergenic_variant	MODIFIER	-0.029052	2.316	0.26

RS4697718	4	10174139	A	-	intergenic_variant	MODIFIER	0.324622	5.93	0.28
RS4697719	4	10174158	C	-	intergenic_variant	MODIFIER	-0.257176	0.828	0.27
RS4697720	4	10174190	G	-	intergenic_variant	MODIFIER	-0.074265	1.929	0.26
RS188401313	4	10174211	G	-	intergenic_variant	MODIFIER	-0.076689	1.91	0.27
RS4697721	4	10174217	C	-	intergenic_variant	MODIFIER	-0.420197	0.346	0.27
VAR_CHR4_10174239	4	10174239	C	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_10174272	4	10174272	G	-	intergenic_variant	MODIFIER	-0.270619	0.773	-
VAR_CHR4_10174433	4	10174433	A	-	intergenic_variant	MODIFIER	-0.123948	1.559	-
RS4697954	4	10174529	T	-	intergenic_variant	MODIFIER	0.202803	4.709	0.33
RS75987279	4	10174544	A	-	intergenic_variant	MODIFIER	0.280756	5.505	0.27
RS190841282	4	10174588	A	-	intergenic_variant	MODIFIER	-	-	0.31
VAR_CHR4_10174604	4	10174604	G	-	regulatory_region_variant	MODIFIER	0.304137	5.734	-
VAR_CHR4_10174717	4	10174717	C	-	regulatory_region_variant	MODIFIER	-0.183316	1.189	-
VAR_CHR4_10174816	4	10174816	T	-	regulatory_region_variant	MODIFIER	0.25416	5.239	-
VAR_CHR4_10174883	4	10174883	G	-	regulatory_region_variant	MODIFIER	-	-	-
RS6848100	4	10174884	G	-	regulatory_region_variant	MODIFIER	-	-	0.31
RS76367047	4	10174890	A	-	regulatory_region_variant	MODIFIER	0.266745	5.366	0.33
RS62288891	4	10174917	T	-	regulatory_region_variant	MODIFIER	-0.205599	1.069	0.24
VAR_CHR4_10174945	4	10174945	C	-	regulatory_region_variant	MODIFIER	-0.242624	0.891	-
RS6834540	4	10175018	C	-	regulatory_region_variant	MODIFIER	-0.25976	0.817	0.36
RS117405573	4	10175112	T	-	regulatory_region_variant	MODIFIER	-0.560909	0.156	0.42
RS142796555	4	10175198	C	-	regulatory_region_variant	MODIFIER	0.090311	3.505	0.39
VAR_CHR4_10175237	4	10175237	C	-	regulatory_region_variant	MODIFIER	-0.48613	0.238	-
VAR_CHR4_10175358	4	10175358	T	-	regulatory_region_variant	MODIFIER	-	-	-
VAR_CHR4_10175434	4	10175434	A	-	regulatory_region_variant	MODIFIER	0.171877	4.38	-
RS12508854	4	10175508	G	-	regulatory_region_variant	MODIFIER	0.402495	6.636	0.27

RS10017447	4	10175536	G	-	regulatory_region_variant	MODIFIER	0.04969	3.079	0.26
RS75708958	4	10175662	A	-	regulatory_region_variant	MODIFIER	-0.760448	0.052	0.15
RS10024152	4	10175689	T	-	regulatory_region_variant	MODIFIER	-0.433197	0.321	0.2
VAR_CHR4_10175698	4	10175698	T	-	regulatory_region_variant	MODIFIER	-0.635647	0.102	-
VAR_CHR4_10175708	4	10175708	C	-	regulatory_region_variant	MODIFIER	-0.263364	0.802	-
RS139458641	4	10175716	A	-	regulatory_region_variant	MODIFIER	-0.416399	0.353	0.14
VAR_CHR4_10175736	4	10175736	C	-	regulatory_region_variant	MODIFIER	-	-	-
RS76038859	4	10175777	T	-	regulatory_region_variant	MODIFIER	-0.210348	1.044	0.19
RS2903827	4	10175872	G	-	regulatory_region_variant	MODIFIER	-0.038954	2.227	0.22
VAR_CHR4_10175982	4	10175982	A	-	regulatory_region_variant	MODIFIER	0.304292	5.735	-
VAR_CHR4_10176136	4	10176136	A	-	regulatory_region_variant	MODIFIER	0.32817	5.963	-
VAR_CHR4_10176355	4	10176355	T	-	regulatory_region_variant	MODIFIER	0.077114	3.365	-
RS146855072	4	10176388	C	-	regulatory_region_variant	MODIFIER	-	-	0.39
VAR_CHR4_10176508	4	10176508	C	-	intergenic_variant	MODIFIER	0.0503	3.086	-
RS140694008	4	10176576	A	-	intergenic_variant	MODIFIER	0.234021	5.034	0.32
RS6449339	4	10176593	C	-	intergenic_variant	MODIFIER	-0.44071	0.308	0.29
RS115145962	4	10176594	G	-	intergenic_variant	MODIFIER	0.109202	3.706	0.3
VAR_CHR4_10176595	4	10176595	T	-	intergenic_variant	MODIFIER	0.046687	3.049	-
RS73218792	4	10176686	G	-	intergenic_variant	MODIFIER	0.140138	4.039	0.27
RS4697955	4	10176710	A	-	intergenic_variant	MODIFIER	-0.008424	2.506	0.3
RS28660321	4	10207964	C	-	intergenic_variant	MODIFIER	-0.524507	0.191	0.4
VAR_CHR4_10207992	4	10207992	C	-	intergenic_variant	MODIFIER	0.019385	2.774	-
RS181990502	4	10208035	T	-	intergenic_variant	MODIFIER	-0.607077	0.12	0.34
RS78917351	4	10208063	G	-	intergenic_variant	MODIFIER	0.01186	2.7	0.33
VAR_CHR4_10208077	4	10208077	T	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_10208114	4	10208114	T	-	intergenic_variant	MODIFIER	-0.246926	0.872	-

RS10026434	4	10208128	G	-	intergenic_variant	MODIFIER	-0.155436	1.353	0.39
RS11734554	4	10208139	G	-	intergenic_variant	MODIFIER	-0.130327	1.515	0.37
RS190278491	4	10208166	T	-	intergenic_variant	MODIFIER	-0.290485	0.698	0.33
RS11734623	4	10208303	G	-	intergenic_variant	MODIFIER	-0.447916	0.296	0.16
RS115537618	4	10208341	A	-	intergenic_variant	MODIFIER	-0.29747	0.673	0.19
VAR_CHR4_10208399	4	10208399	G	-	intergenic_variant	MODIFIER	0.069419	3.284	-
VAR_CHR4_10208427	4	10208427	A	-	intergenic_variant	MODIFIER	-0.136473	1.474	-
RS59035374	4	10208487	A	-	intergenic_variant	MODIFIER	0.028267	2.862	0.2
RS116796391	4	10208635	T	-	intergenic_variant	MODIFIER	-0.355596	0.494	0.26
RS6826185	4	10208656	C	-	intergenic_variant	MODIFIER	-0.352007	0.504	0.33
RS6812759	4	10208686	A	-	intergenic_variant	MODIFIER	0.213706	4.823	0.26
RS6812780	4	10208725	A	-	intergenic_variant	MODIFIER	0.177569	4.441	0.25
RS6826450	4	10208778	C	-	intergenic_variant	MODIFIER	-0.41135	0.363	0.2
RS6845818	4	10208794	A	-	intergenic_variant	MODIFIER	-0.683006	0.079	0.24
VAR_CHR4_10208797	4	10208797	A	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_10208805	4	10208805	G	-	intergenic_variant	MODIFIER	0.024032	2.82	-
VAR_CHR4_10241757	4	10241757	A	-	intergenic_variant	MODIFIER	0.122835	3.853	-
RS28649726	4	10241845	A	-	intergenic_variant	MODIFIER	0.345615	6.126	0.25
VAR_CHR4_10241938	4	10241938	T	-	intergenic_variant	MODIFIER	-	-	-
RS62286326	4	10242013	T	-	regulatory_region_variant	MODIFIER	-0.06393	2.014	0.26
RS114026351	4	10242020	G	-	regulatory_region_variant	MODIFIER	-	-	0.26
VAR_CHR4_10242058	4	10242058	C	-	regulatory_region_variant	MODIFIER	-0.15281	1.369	-
RS62286327	4	10242099	C	-	regulatory_region_variant	MODIFIER	-0.287384	0.709	0.28
RS28373109	4	10242134	C	-	regulatory_region_variant	MODIFIER	-0.315698	0.612	0.32
RS17391280	4	10242173	A	-	regulatory_region_variant	MODIFIER	0.468811	7.188	0.3
VAR_CHR4_10242309	4	10242309	T	-	intergenic_variant	MODIFIER	0.182624	4.495	-

RS2013714	4	10242366	G	-	intergenic_variant	MODIFIER	-0.883073	0.028	0.24
RS28688686	4	10242381	T	-	intergenic_variant	MODIFIER	-0.334679	0.553	0.24
RS185167073	4	10242383	A	-	intergenic_variant	MODIFIER	-0.105076	1.693	0.22
RS28490259	4	10242415	C	-	intergenic_variant	MODIFIER	-0.302838	0.655	0.24
RS189576127	4	10242429	A	-	intergenic_variant	MODIFIER	0.210993	4.795	0.25
RS28714541	4	10242438	C	-	intergenic_variant	MODIFIER	-0.315688	0.612	0.22
VAR_CHR4_10242476	4	10242476	G	-	intergenic_variant	MODIFIER	-0.29604	0.678	-
RS62286328	4	10242531	G	-	intergenic_variant	MODIFIER	-0.009431	2.497	0.21
RS741075	4	10242582	A	-	intergenic_variant	MODIFIER	0.152716	4.175	0.21
RS148714209	4	10242651	A	-	intergenic_variant	MODIFIER	0.40922	6.694	0.22
RS13126279	4	10245533	A	-	intergenic_variant	MODIFIER	0.641832	8.442	0.16
VAR_CHR4_10245633	4	10245633	A	-	intergenic_variant	MODIFIER	0.435091	6.913	-
VAR_CHR4_10245641	4	10245641	A	-	intergenic_variant	MODIFIER	0.032876	2.909	-
VAR_CHR4_10245759	4	10245759	C	-	intergenic_variant	MODIFIER	-0.527604	0.188	-
RS80116299	4	10245849	A	-	intergenic_variant	MODIFIER	0.034528	2.925	0.23
RS372420151	4	10245875	T	-	intergenic_variant	MODIFIER	-0.157909	1.338	-
RS6853056	4	10245898	T	-	intergenic_variant	MODIFIER	-0.275261	0.755	0.27
RS28636428	4	10246095	T	-	intergenic_variant	MODIFIER	-0.027316	2.331	0.15
VAR_CHR4_10246107	4	10246107	A	-	intergenic_variant	MODIFIER	0.058913	3.175	-
RS28713317	4	10246121	A	-	intergenic_variant	MODIFIER	0.054183	3.126	0.18
RS193123110	4	10246125	A	-	intergenic_variant	MODIFIER	-0.45795	0.279	0.17
VAR_CHR4_10246152	4	10246152	C	-	intergenic_variant	MODIFIER	-0.201773	1.088	-
VAR_CHR4_10246155	4	10246155	T	-	intergenic_variant	MODIFIER	-0.22554	0.969	-
RS10010635	4	10246272	C	-	intergenic_variant	MODIFIER	-0.541206	0.174	0.28
VAR_CHR4_10246279	4	10246279	G	-	intergenic_variant	MODIFIER	-0.339519	0.539	-
RS10010656	4	10246327	G	-	intergenic_variant	MODIFIER	-	-	0.27

VAR_CHR4_10246344	4	10246344	C	-	intergenic_variant	MODIFIER	-0.169452	1.268	-
RS147548493	4	10246430	C	-	intergenic_variant	MODIFIER	-	-	0.26
RS11732042	4	10246448	A	-	intergenic_variant	MODIFIER	0.036616	2.946	0.25
RS10010907	4	10246609	C	-	intergenic_variant	MODIFIER	-1.348369	0.004	0.23
VAR_CHR4_10246667	4	10246667	G	-	intergenic_variant	MODIFIER	0.107444	3.688	-
RS185855785	4	10246689	C	-	intergenic_variant	MODIFIER	-0.578551	0.141	0.19
RS56278885	4	10246723	C	-	intergenic_variant	MODIFIER	-0.502079	0.217	0.26
RS28507715	4	10246847	C	-	intergenic_variant	MODIFIER	-0.891475	0.027	0.2
RS56170676	4	10246857	C	-	intergenic_variant	MODIFIER	-0.348791	0.512	0.22
VAR_CHR4_10246861	4	10246861	T	-	intergenic_variant	MODIFIER	-0.839599	0.035	-
RS28502637	4	10246961	C	-	intergenic_variant	MODIFIER	-0.474374	0.254	0.23
VAR_CHR4_10247089	4	10247089	T	-	intergenic_variant	MODIFIER	-0.069693	1.966	-
VAR_CHR4_10247171	4	10247171	T	-	intergenic_variant	MODIFIER	-0.038866	2.228	-
RS4697983	4	10247248	C	-	intergenic_variant	MODIFIER	-0.228988	0.953	0.17
RS4698017	4	10298094	C	-	intergenic_variant	MODIFIER	-0.345374	0.522	0.29
RS142819777	4	10298095	T	-	intergenic_variant	MODIFIER	-0.259902	0.817	0.28
VAR_CHR4_10298118	4	10298118	G	-	intergenic_variant	MODIFIER	-0.006129	2.528	-
RS4697744	4	10298147	T	-	intergenic_variant	MODIFIER	0.15316	4.18	0.24
VAR_CHR4_10298197	4	10298197	A	-	intergenic_variant	MODIFIER	-0.830619	0.037	-
VAR_CHR4_10298307	4	10298307	G	-	regulatory_region_variant	MODIFIER	-0.314688	0.615	-
RS151054437	4	10298337	A	-	regulatory_region_variant	MODIFIER	0.030033	2.88	0.3
VAR_CHR4_10298357	4	10298357	T	-	regulatory_region_variant	MODIFIER	-0.273779	0.761	-
VAR_CHR4_10298394	4	10298394	A	-	regulatory_region_variant	MODIFIER	-0.290871	0.697	-
VAR_CHR4_10298473	4	10298473	A	-	regulatory_region_variant	MODIFIER	0.284282	5.54	-
VAR_CHR4_10298492	4	10298492	T	-	regulatory_region_variant	MODIFIER	0.033223	2.912	-
RS74778870	4	10298583	C	-	regulatory_region_variant	MODIFIER	-0.304221	0.65	0.36

VAR_CHR4_10298641	4	10298641	T	-	regulatory_region_variant	MODIFIER	-0.212879	1.031	-
RS11940728	4	10298683	T	-	regulatory_region_variant	MODIFIER	-0.985872	0.017	0.42
RS28798076	4	10298704	G	-	regulatory_region_variant	MODIFIER	-0.015877	2.436	0.38
VAR_CHR4_10298712	4	10298712	G	-	regulatory_region_variant	MODIFIER	0.112808	3.745	-
RS192076740	4	10298859	A	-	intergenic_variant	MODIFIER	0.257619	5.274	0.27
RS116147875	4	10299159	T	-	intergenic_variant	MODIFIER	0.055179	3.136	0.25
VAR_CHR4_10299180	4	10299180	C	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_10299216	4	10299216	C	-	intergenic_variant	MODIFIER	-0.97886	0.018	-
RS193101331	4	10299237	A	-	intergenic_variant	MODIFIER	-0.066686	1.991	0.35
RS1860905	4	10318836	C	-	intergenic_variant	MODIFIER	0.162562	4.281	0.32
RS978466	4	10318938	G	-	intergenic_variant	MODIFIER	-	-	0.44
VAR_CHR4_10318970	4	10318970	C	-	intergenic_variant	MODIFIER	-	-	-
RS11737588	4	10319007	T	-	intergenic_variant	MODIFIER	-0.586161	0.135	0.37
RS143608834	4	10319018	A	-	intergenic_variant	MODIFIER	0.035882	2.939	0.26
VAR_CHR4_10319025	4	10319025	A	-	intergenic_variant	MODIFIER	0.323759	5.921	-
RS150833841	4	10319118	A	-	intergenic_variant	MODIFIER	-0.100138	1.729	0.33
RS978465	4	10319124	T	-	intergenic_variant	MODIFIER	-0.412688	0.36	0.3
VAR_CHR4_10319449	4	10319449	T	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_10319467	4	10319467	A	-	intergenic_variant	MODIFIER	-0.009892	2.492	-
VAR_CHR4_10319500	4	10319500	T	-	intergenic_variant	MODIFIER	-0.591948	0.131	-
RS140307922	4	10323316	A	-	intergenic_variant	MODIFIER	-0.356679	0.491	0.32
RS145097501	4	10323498	A	-	intergenic_variant	MODIFIER	-0.036116	2.253	0.33
VAR_CHR4_10323546	4	10323546	A	-	intergenic_variant	MODIFIER	0.071915	3.31	-
VAR_CHR4_10323559	4	10323559	G	-	intergenic_variant	MODIFIER	0.049305	3.076	-
VAR_CHR4_10323592	4	10323592	T	-	intergenic_variant	MODIFIER	0.097629	3.583	-
VAR_CHR4_10323798	4	10323798	A	-	intergenic_variant	MODIFIER	-0.004524	2.543	-

VAR_CHR4_10323834	4	10323834	G	-	intergenic_variant	MODIFIER	-0.018166	2.415	-
RS993173	4	10323935	G	-	intergenic_variant	MODIFIER	0.062847	3.215	0.31
VAR_CHR4_10336853	4	10336853	C	-	intergenic_variant	MODIFIER	-0.362991	0.474	-
VAR_CHR4_10336890	4	10336890	T	-	intergenic_variant	MODIFIER	-0.294459	0.684	-
RS11729318	4	10336919	G	-	intergenic_variant	MODIFIER	-	-	0.31
VAR_CHR4_10336998	4	10336998	T	-	intergenic_variant	MODIFIER	-0.596734	0.127	-
VAR_CHR4_10337019	4	10337019	A	-	intergenic_variant	MODIFIER	-0.424881	0.337	-
VAR_CHR4_10337084	4	10337084	G	-	intergenic_variant	MODIFIER	-0.258166	0.824	-
VAR_CHR4_10337090	4	10337090	G	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_10337212	4	10337212	A	-	intergenic_variant	MODIFIER	-1.449165	0.003	-
RS17419612	4	10337263	C	-	intergenic_variant	MODIFIER	-0.165529	1.292	0.26
RS10012795	4	10337395	C	-	intergenic_variant	MODIFIER	-0.664291	0.087	0.29
VAR_CHR4_10405136	4	10405136	A	-	intergenic_variant	MODIFIER	-0.050963	2.123	-
VAR_CHR4_10405173	4	10405173	A	-	intergenic_variant	MODIFIER	0.128546	3.914	-
RS79226847	4	10405188	C	-	intergenic_variant	MODIFIER	-0.157076	1.343	0.4
VAR_CHR4_10405517	4	10405517	C	-	regulatory_region_variant	MODIFIER	-0.54351	0.172	-
RS76065252	4	10405534	A	-	regulatory_region_variant	MODIFIER	-0.04221	2.199	0.3
RS111928356	4	10405953	C	-	regulatory_region_variant	MODIFIER	-0.222892	0.982	0.31
RS73224474	4	10405976	G	-	regulatory_region_variant	MODIFIER	-0.068996	1.972	0.28
RS149271942	4	10406112	C	-	intergenic_variant	MODIFIER	-	-	0.35
VAR_CHR4_10406139	4	10406139	A	-	intergenic_variant	MODIFIER	1.879346	15.46	-
RS143364659	4	10416715	A	-	intergenic_variant	MODIFIER	-0.568618	0.149	0.27
RS28733364	4	10416739	A	-	intergenic_variant	MODIFIER	-0.045315	2.172	0.33
RS141578715	4	10416789	A	-	intergenic_variant	MODIFIER	0.110285	3.718	0.18
RS62288489	4	10417142	T	-	intergenic_variant	MODIFIER	-	-	0.32
VAR_CHR4_10417237	4	10417237	A	-	intergenic_variant	MODIFIER	0.250943	5.207	-

RS192985502	4	10417322	A	-	intergenic_variant	MODIFIER	-0.224593	0.974	0.33
VAR_CHR4_10417345	4	10417345	C	-	intergenic_variant	MODIFIER	-	-	-
VAR_CHR4_10417361	4	10417361	A	-	intergenic_variant	MODIFIER	0.214084	4.827	-
RS373311989	4	10417458	C	-	downstream_variant	MODIFIER	0.047815	3.06	-
RS12696844	4	10417629	A	-	intergenic_variant	MODIFIER	-0.671468	0.084	0.23
RS190798554	4	10417844	T	-	intergenic_variant	MODIFIER	-0.350317	0.508	0.22
VAR_CHR4_10417909	4	10417909	G	-	intergenic_variant	MODIFIER	-0.350859	0.507	-
VAR_CHR4_10418059	4	10418059	T	-	intergenic_variant	MODIFIER	-0.310187	0.63	-
RS13125855	4	10418078	C	-	intergenic_variant	MODIFIER	-	-	0.24
RS183535279	4	10418222	G	-	intergenic_variant	MODIFIER	0.145286	4.095	0.34
VAR_CHR4_10418250	4	10418250	C	-	intergenic_variant	MODIFIER	-0.260408	0.814	-
RS148471487	4	10418292	T	-	intergenic_variant	MODIFIER	-0.391561	0.405	0.21
RS60599851	4	10418301	T	-	intergenic_variant	MODIFIER	-0.112407	1.64	0.19
RS7683253	4	10419465	G	-	intergenic_variant	MODIFIER	0.025001	2.83	0.35
RS4128494	4	10419504	G	-	intergenic_variant	MODIFIER	0.1152	3.771	0.33
RS114536276	4	10419593	T	-	intergenic_variant	MODIFIER	0.463502	7.146	0.32
VAR_CHR4_10419685	4	10419685	T	-	intergenic_variant	MODIFIER	-0.060103	2.045	-
VAR_CHR4_10419694	4	10419694	T	-	intergenic_variant	MODIFIER	-0.106778	1.68	-
VAR_CHR4_10419831	4	10419831	G	-	intergenic_variant	MODIFIER	0.243727	5.133	-
RS150233577	4	10419946	C	-	intergenic_variant	MODIFIER	-0.708932	0.069	0.28
VAR_CHR4_10423845	4	10423845	T	-	intergenic_variant	MODIFIER	-0.667824	0.086	-
RS77414593	4	10423854	G	-	intergenic_variant	MODIFIER	-0.043814	2.185	0.19
RS116227902	4	10423924	C	-	intergenic_variant	MODIFIER	-	-	0.27
VAR_CHR4_10424123	4	10424123	A	-	intergenic_variant	MODIFIER	0.753639	9.174	-
VAR_CHR4_10424177	4	10424177	G	-	intergenic_variant	MODIFIER	0.164747	4.304	-
RS35565862	4	10440704	T	ZNF518B	downstream_gene_variant	MODIFIER	-0.035621	2.257	0.32

RS114584694	4	10440811	A	ZNF518B	downstream_gene_variant	MODIFIER	0.258189	5.28	0.34
RS73224492	4	10440925	T	ZNF518B	downstream_gene_variant	MODIFIER	-0.259736	0.817	0.4
RS140477370	4	10440936	A	ZNF518B	downstream_gene_variant	MODIFIER	-	-	0.48
VAR_CHR4_10441131	4	10441131	T	ZNF518B	downstream_gene_variant	MODIFIER	0.062521	3.212	-
RS138757270	4	10441551	A	ZNF518B	3_prime_UTR_variant	MODIFIER	1.430423	12.95	0.54
RS111599809	4	10441716	G	ZNF518B	3_prime_UTR_variant	MODIFIER	0.459628	7.115	0.29
VAR_CHR4_10441853	4	10441853	T	ZNF518B	3_prime_UTR_variant	MODIFIER	0.213992	4.826	-
RS28427256	4	10441896	C	ZNF518B	3_prime_UTR_variant	MODIFIER	-0.060982	2.038	0.47
RS76978600	4	10442048	G	ZNF518B	3_prime_UTR_variant	MODIFIER	1.287653	12.2	0.46
RS78946091	4	10442323	T	ZNF518B	3_prime_UTR_variant	MODIFIER	-	-	0.35
VAR_CHR4_10442363	4	10442363	A	ZNF518B	3_prime_UTR_variant	MODIFIER	0.260841	5.307	-
RS116284607	4	10442399	G	ZNF518B	3_prime_UTR_variant	MODIFIER	1.48229	13.22	0.33
RS115417172	4	10442429	T	ZNF518B	3_prime_UTR_variant	MODIFIER	1.254988	12.03	0.32
RS28519672	4	10442535	T	ZNF518B	3_prime_UTR_variant	MODIFIER	-0.540955	0.174	0.34
RS28553891	4	10442676	T	ZNF518B	3_prime_UTR_variant	MODIFIER	0.097871	3.585	0.33
RS57723486	4	10442700	A	ZNF518B	3_prime_UTR_variant	MODIFIER	0.030064	2.88	0.38
VAR_CHR4_10443042	4	10443042	A	ZNF518B	3_prime_UTR_variant	MODIFIER	0.188508	4.558	-
VAR_CHR4_10443264	4	10443264	A	ZNF518B	3_prime_UTR_variant	MODIFIER	0.286839	5.565	-
RS140972700	4	10443315	C	ZNF518B	3_prime_UTR_variant	MODIFIER	-	-	0.41
VAR_CHR4_10443318	4	10443318	A	ZNF518B	3_prime_UTR_variant	MODIFIER	0.185734	4.528	-
RS4422413	4	10443384	C	ZNF518B	3_prime_UTR_variant	MODIFIER	0.535951	7.7	0.45
RS10938799	4	10443425	T	ZNF518B	3_prime_UTR_variant	MODIFIER	0.017432	2.755	0.44
VAR_CHR4_10443491	4	10443491	T	ZNF518B	3_prime_UTR_variant	MODIFIER	-0.072795	1.941	-
VAR_CHR4_10443534	4	10443534	T	ZNF518B	3_prime_UTR_variant	MODIFIER	0.053784	3.122	-
RS148513455	4	10443673	T	ZNF518B	3_prime_UTR_variant	MODIFIER	-0.098677	1.74	0.41
VAR_CHR4_10443677	4	10443677	G	ZNF518B	3_prime_UTR_variant	MODIFIER	0.17439	4.407	-

VAR_CHR4_10443775	4	10443775	G	ZNF518B	3_prime_UTR_variant	MODIFIER	-0.712485	0.067	-
VAR_CHR4_10443808	4	10443808	T	ZNF518B	3_prime_UTR_variant	MODIFIER	-0.064728	2.007	-
VAR_CHR4_10443922	4	10443922	T	ZNF518B	3_prime_UTR_variant	MODIFIER	0.099906	3.607	-
VAR_CHR4_10444032	4	10444032	G	ZNF518B	3_prime_UTR_variant	MODIFIER	0.768167	9.266	-
VAR_CHR4_10444058	4	10444058	T	ZNF518B	3_prime_UTR_variant	MODIFIER	-	-	-
RS34208161	4	10444106	C	ZNF518B	3_prime_UTR_variant	MODIFIER	0.113973	3.758	0.51
VAR_CHR4_10444176	4	10444176	A	ZNF518B	3_prime_UTR_variant	MODIFIER	-0.266358	0.79	-
VAR_CHR4_10444469	4	10444469	G	ZNF518B	3_prime_UTR_variant	MODIFIER	0.753948	9.176	-
RS3217	4	10444650	A	ZNF518B	3_prime_UTR_variant	MODIFIER	0.371078	6.358	0.48
VAR_CHR4_10444870	4	10444870	T	ZNF518B	missense_variant	MODERATE	5.363609	25.9	-
RS75487798	4	10445207	G	ZNF518B	missense_variant	MODERATE	1.476139	13.19	0.4
RS7694496	4	10445427	T	ZNF518B	synonymous_variant	LOW	-1.161716	0.008	0.41
RS138229174	4	10445436	T	ZNF518B	synonymous_variant	LOW	0.522197	7.598	0.32
VAR_CHR4_10445509	4	10445509	A	ZNF518B	missense_variant	MODERATE	1.635015	14.04	-
VAR_CHR4_10445650	4	10445650	T	ZNF518B	missense_variant	MODERATE	5.818232	27.2	-
RS144356708	4	10445794	A	ZNF518B	missense_variant	MODERATE	3.848004	23.4	0.39
RS145878854	4	10446051	G	ZNF518B	synonymous_variant	LOW	1.381909	12.69	0.53
VAR_CHR4_10446358	4	10446358	T	ZNF518B	missense_variant	MODERATE	0.632301	8.377	-
VAR_CHR4_10446436	4	10446436	T	ZNF518B	missense_variant	MODERATE	3.41941	23	-
RS146679712	4	10446444	G	ZNF518B	synonymous_variant	LOW	-	-	0.34
RS370387533	4	10446598	G	ZNF518B	missense_variant	MODERATE	0.394971	6.57	-
RS144393783	4	10446725	A	ZNF518B	missense_variant	MODERATE	4.290007	24	0.29
RS10016022	4	10446906	T	ZNF518B	missense_variant	MODERATE	1.413856	12.86	0.29
RS200699063	4	10446925	A	ZNF518B	missense_variant	MODERATE	7.276201	34	0.36
RS149561889	4	10447155	A	ZNF518B	synonymous_variant	LOW	-	-	0.29
RS66538112	4	10447168	C	ZNF518B	synonymous_variant	LOW	-	-	0.17

RS73224493	4	10447194	C	ZNF518B	synonymous_variant	LOW	-0.296057	0.678	0.25
RS10016702	4	10447640	T	ZNF518B	missense_variant	MODERATE	0.054376	3.128	0.25
VAR_CHR4_10447663	4	10447663	T	ZNF518B	synonymous_variant	LOW	-	-	-
RS10007352	4	10447679	G	ZNF518B	missense_variant	MODERATE	0.583971	8.044	0.23
RS141392062	4	10447680	T	ZNF518B	synonymous_variant	LOW	-0.213285	1.029	0.21
RS10021506	4	10447848	A	ZNF518B	synonymous_variant	LOW	0.080208	3.397	0.21
RS72648876	4	10447907	A	ZNF518B	stop_gained	HIGH	7.057278	33	0.27
RS76743293	4	10447976	A	ZNF518B	5_prime_UTR_variant	MODIFIER	0.962432	10.44	0.52
VAR_CHR4_10448038	4	10448038	C	ZNF518B	5_prime_UTR_variant	MODIFIER	0.161284	4.267	-
RS28526383	4	10448559	A	ZNF518B	intron_variant	MODIFIER	0.607066	8.205	0.47
RS145464632	4	10448749	G	ZNF518B	intron_variant	MODIFIER	-0.420422	0.345	0.31
VAR_CHR4_10448890	4	10448890	A	ZNF518B	intron_variant	MODIFIER	0.382088	6.457	-
RS115037002	4	10449012	T	ZNF518B	intron_variant	MODIFIER	-0.275096	0.756	0.22
RS28682539	4	10449087	T	ZNF518B	intron_variant	MODIFIER	-0.687894	0.077	0.26
VAR_CHR4_10449194	4	10449194	T	ZNF518B	intron_variant	MODIFIER	-0.796551	0.044	-
RS28460143	4	10450164	G	ZNF518B	intron_variant	MODIFIER	0.142404	4.064	0.39
RS188908273	4	10450390	G	ZNF518B	intron_variant	MODIFIER	-0.016199	2.433	0.36
VAR_CHR4_10450401	4	10450401	C	ZNF518B	intron_variant	MODIFIER	-0.16896	1.271	-
RS115940493	4	10451741	C	ZNF518B	intron_variant	MODIFIER	-0.135109	1.483	0.28
RS73090004	4	10451910	A	ZNF518B	intron_variant	MODIFIER	0.599252	8.151	0.43
RS148679448	4	10452035	G	ZNF518B	intron_variant	MODIFIER	-0.04986	2.132	0.43
RS73090005	4	10452142	C	ZNF518B	intron_variant	MODIFIER	0.083622	3.434	0.44
VAR_CHR4_10452338	4	10452338	C	ZNF518B	intron_variant	MODIFIER	-0.109389	1.661	-
VAR_CHR4_10452407	4	10452407	T	ZNF518B	intron_variant	MODIFIER	-0.40169	0.383	-
RS7674156	4	10452763	G	ZNF518B	intron_variant	MODIFIER	-	-	0.27
RS5028371	4	10452986	C	ZNF518B	intron_variant	MODIFIER	-0.361876	0.477	0.27

VAR_CHR4_10453269	4	10453269	T	ZNF518B	intron_variant	MODIFIER	0.21152	4.8	-
RS151135364	4	10453277	G	ZNF518B	intron_variant	MODIFIER	-	-	0.35
RS115952815	4	10453289	C	ZNF518B	intron_variant	MODIFIER	-0.153149	1.367	0.4
VAR_CHR4_10453388	4	10453388	G	ZNF518B	intron_variant	MODIFIER	0.271445	5.413	-
VAR_CHR4_10453670	4	10453670	T	ZNF518B	intron_variant	MODIFIER	-0.435273	0.317	-
VAR_CHR4_10453772	4	10453772	T	ZNF518B	intron_variant	MODIFIER	-	-	-
RS116288685	4	10453809	G	ZNF518B	intron_variant	MODIFIER	-	-	0.45
RS142068085	4	10453886	A	ZNF518B	intron_variant	MODIFIER	-	-	0.45
VAR_CHR4_10453952	4	10453952	G	ZNF518B	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10454160	4	10454160	T	ZNF518B	intron_variant	MODIFIER	0.304781	5.74	-
VAR_CHR4_10454161	4	10454161	T	ZNF518B	intron_variant	MODIFIER	0.035913	2.939	-
RS150445552	4	10454255	T	ZNF518B	intron_variant	MODIFIER	-0.172758	1.249	0.51
VAR_CHR4_10454329	4	10454329	G	ZNF518B	intron_variant	MODIFIER	0.125205	3.878	-
RS60445736	4	10454511	G	ZNF518B	intron_variant	MODIFIER	-	-	0.37
RS79437705	4	10454593	C	ZNF518B	intron_variant	MODIFIER	-	-	0.32
VAR_CHR4_10456357	4	10456357	T	ZNF518B	intron_variant	MODIFIER	0.732294	9.037	-
RS78432726	4	10456414	T	ZNF518B	intron_variant	MODIFIER	-0.487172	0.236	0.29
RS112389844	4	10456458	T	ZNF518B	5_prime_UTR_variant	MODIFIER	-0.063223	2.019	0.37
VAR_CHR4_10456489	4	10456489	G	ZNF518B	5_prime_UTR_variant	MODIFIER	1.069221	11.05	-
VAR_CHR4_10456614	4	10456614	G	ZNF518B	splice_acceptor_variant	HIGH	3.967492	23.6	-
RS192057509	4	10456639	C	ZNF518B	intron_variant	MODIFIER	1.266116	12.09	0.25
VAR_CHR4_10456669	4	10456669	A	ZNF518B	intron_variant	MODIFIER	0.091919	3.522	-
RS11947336	4	10457384	A	ZNF518B	intron_variant	MODIFIER	0.571687	7.958	0.27
VAR_CHR4_10457389	4	10457389	C	ZNF518B	intron_variant	MODIFIER	-0.074226	1.93	-
VAR_CHR4_10457448	4	10457448	G	ZNF518B	intron_variant	MODIFIER	-0.317357	0.606	-
VAR_CHR4_10457866	4	10457866	A	ZNF518B	intron_variant	MODIFIER	-	-	-

VAR_CHR4_10458085	4	10458085	T	ZNF518B	intron_variant	MODIFIER	0.007645	2.66	-
VAR_CHR4_10458194	4	10458194	T	ZNF518B	intron_variant	MODIFIER	1.713837	14.49	-
RS141037145	4	10458259	T	ZNF518B	intron_variant	MODIFIER	0.599339	8.152	0.32
RS76917885	4	10458486	G	ZNF518B	intron_variant	MODIFIER	0.841877	9.72	0.45
VAR_CHR4_10458530	4	10458530	T	ZNF518B	intron_variant	MODIFIER	0.061618	3.203	-
VAR_CHR4_10458942	4	10458942	C	ZNF518B	splice_region_variant,5_prime_UTR_variant	LOW	-	-	-
VAR_CHR4_10458959	4	10458959	G	ZNF518B	5_prime_UTR_variant	MODIFIER	-	-	-
RS4077362	4	10458969	A	ZNF518B	5_prime_UTR_variant	MODIFIER	1.043999	10.91	0.61
RS113254846	4	10458998	A	ZNF518B	5_prime_UTR_variant	MODIFIER	1.016043	10.75	0.67
RS146876703	4	10459014	T	ZNF518B	5_prime_UTR_variant	MODIFIER	1.063306	11.02	0.65
VAR_CHR4_10459137	4	10459137	G	ZNF518B	upstream_gene_variant	MODIFIER	0.565833	7.916	-
RS189206645	4	10459335	G	ZNF518B	upstream_gene_variant	MODIFIER	-	-	0.35
VAR_CHR4_10459434	4	10459434	G	ZNF518B	upstream_gene_variant	MODIFIER	0.575425	7.984	-
VAR_CHR4_10459500	4	10459500	A	ZNF518B	upstream_gene_variant	MODIFIER	0.762027	9.227	-
VAR_CHR4_10459538	4	10459538	C	ZNF518B	upstream_gene_variant	MODIFIER	0.118159	3.803	-
VAR_CHR4_10459633	4	10459633	T	ZNF518B	upstream_gene_variant	MODIFIER	0.38286	6.463	-
RS367964588	4	10459794	C	ZNF518B	upstream_gene_variant	MODIFIER	-0.206323	1.065	-
VAR_CHR4_10459831	4	10459831	G	ZNF518B	upstream_gene_variant	MODIFIER	-	-	-
RS4075869	4	10459978	C	ZNF518B	upstream_gene_variant	MODIFIER	0.062828	3.215	0.49
RS148442170	4	10462025	A	ZNF518B	upstream_gene_variant	MODIFIER	0.019346	2.774	0.41
VAR_CHR4_10462045	4	10462045	A	ZNF518B	upstream_gene_variant	MODIFIER	0.344036	6.111	-
RS4339203	4	10462106	T	ZNF518B	upstream_gene_variant	MODIFIER	-0.1826	1.193	0.4
RS73224496	4	10462123	T	ZNF518B	upstream_gene_variant	MODIFIER	0.099443	3.602	0.35
RS183203239	4	10462231	A	ZNF518B	upstream_gene_variant	MODIFIER	0.167727	4.336	0.43
RS79526919	4	10462505	C	ZNF518B	upstream_gene_variant	MODIFIER	-0.181832	1.197	0.5
VAR_CHR4_10462649	4	10462649	C	ZNF518B	upstream_gene_variant	MODIFIER	0.051207	3.095	-

VAR_CHR4_10462684	4	10462684	A	ZNF518B	upstream_gene_variant	MODIFIER	0.57635	7.991	-
VAR_CHR4_10462934	4	10462934	A	ZNF518B	upstream_gene_variant	MODIFIER	0.988784	10.6	-
VAR_CHR4_10463022	4	10463022	C	ZNF518B	upstream_gene_variant	MODIFIER	-	-	-
RS11722522	4	10463111	T	ZNF518B	upstream_gene_variant	MODIFIER	0.869906	9.888	0.5
VAR_CHR4_10463131	4	10463131	C	ZNF518B	upstream_gene_variant	MODIFIER	-	-	-
RS73224498	4	10463198	C	ZNF518B	upstream_gene_variant	MODIFIER	0.325455	5.937	0.48
VAR_CHR4_10463353	4	10463353	T	ZNF518B	upstream_gene_variant	MODIFIER	0.538496	7.719	-
VAR_CHR4_10463494	4	10463494	A	ZNF518B	upstream_gene_variant	MODIFIER	0.962622	10.45	-
RS34422255	4	10463704	A	ZNF518B	upstream_gene_variant	MODIFIER	0.373572	6.381	0.36
VAR_CHR4_10464141	4	10464141	G	-	intergenic_variant	MODIFIER	0.06686	3.257	-
RS185278846	4	10464149	G	-	intergenic_variant	MODIFIER	0.159887	4.252	0.36
RS13115661	4	10493961	A	CLNK	intron_variant	MODIFIER	0.258265	5.281	0.33
RS3749558	4	10494003	A	CLNK	intron_variant	MODIFIER	0.187933	4.551	0.42
VAR_CHR4_10494005	4	10494005	G	CLNK	intron_variant	MODIFIER	-	-	-
VAR_CHR4_10494255	4	10494255	A	CLNK	intron_variant	MODIFIER	-0.835846	0.036	-
VAR_CHR4_10494411	4	10494411	A	CLNK	intron_variant	MODIFIER	0.092479	3.528	-
RS67523049	4	10494666	A	CLNK	intron_variant	MODIFIER	-0.085379	1.841	0.29
RS7661796	4	10494721	G	CLNK	intron_variant	MODIFIER	-0.455781	0.283	0.18

APPENDIX 3

Significant Signals in Europeans

VARIANT	P-VALUE	VARIANT	P-VALUE	VARIANT	P-VALUE	VARIANT	P-VALUE	VARIANT	P-VALUE
RS10000983	0.005055797	RS1122141	0.008131323	RS12374229	0.040044102	RS13115193	0.005848098	RS146546936	0.03184307
RS10001964	0.002914223	RS1122142	0.004576044	RS12374294	0.029737456	RS13115469	2.19E-07	RS148951726	0.034754984
RS10002562	0.002726587	RS113888816	0.037829515	RS12498150	0.005055797	RS13115776	0.000106946	RS151054437	0.026953107
RS10006397	0.000566522	RS114506235	0.050957398	RS12498742	1.94E-05	RS13120348	0.000201994	RS16868246	7.43E-06
RS10007416	0.001941053	RS114584694	0.037501928	RS12498956	0.005055797	RS13121211	0.001353139	RS16890979	2.91E-07
RS10010582	9.52E-05	RS115502819	0.04094363	RS12499857	0.002901001	RS13122290	0.010980291	RS16892474	0.02918395
RS10010656	0.000367943	RS11557743	0.001896271	RS12500653	0.010558492	RS13122689	0.000177758	RS17185835	0.00336514
RS10016022	0.004885809	RS11722229	4.49E-06	RS12500805	0.000409247	RS13124007	0.000158013	RS17185870	0.00336514
RS10016075	7.43E-05	RS11722522	0.005352472	RS12500810	0.001452742	RS13124563	0.003369554	RS17187075	0.001860628
RS10017447	0.0132079	RS11722930	0.001515781	RS12501855	0.032655389	RS13125029	0.001738759	RS17245436	0.00336514
RS10017674	0.004512784	RS11722946	0.002369723	RS12504565	0.000177758	RS13125209	4.69E-06	RS17245723	0.004086692
RS10017945	0.000189062	RS11722989	0.002369723	RS12506122	0.000163265	RS13125646	4.69E-06	RS17246501	0.002831431
RS10018204	0.004086692	RS11723016	0.002369723	RS12506364	0.000841326	RS13125855	0.037674677	RS17246745	0.003049617
RS10018663	3.57E-05	RS11723382	0.005848098	RS12506455	0.001452742	RS13126279	0.020207246	RS17247314	0.0009319
RS10018666	7.43E-05	RS11723439	4.54E-06	RS12506562	0.004384471	RS13126729	0.041594147	RS17419612	0.00845591
RS10022499	7.43E-05	RS11723591	0.001845053	RS12506893	0.040432993	RS13128214	0.001341791	RS1860905	0.000101863
RS10023068	7.43E-05	RS11723970	0.007736226	RS12506932	0.001355245	RS13129453	0.000177758	RS2013714	0.007958655
RS10024152	0.005770405	RS11724510	0.002914223	RS12507050	0.000764766	RS13129697	9.35E-06	RS2018643	0.004576044
RS10026434	0.000800673	RS11724641	0.0132079	RS12507330	0.001353139	RS13131257	4.69E-06	RS2240720	0.001341791
RS10027276	0.020002115	RS11726102	3.65E-05	RS12507606	0.000155783	RS13133766	0.001341791	RS2240721	0.001341791
RS1014290	1.17E-05	RS11726271	0.002273027	RS12508854	0.036115733	RS13137069	7.85E-06	RS2240722	0.00080379
RS10516201	0.040432993	RS11727087	0.000582517	RS12508991	0.001515781	RS13137074	0.001515781	RS2240724	0.001331155
RS1071988	1.32E-05	RS11727199	0.001515781	RS12509714	0.003963969	RS13137343	0.001515781	RS2241465	0.013552326

RS1079128	0.005055797	RS11729318	0.000114264	RS12509955	1.81E-06	RS13137795	0.001515781	RS2241472	0.011367107
RS10805343	0.01268127	RS11731110	0.001515781	RS12644592	0.00672353	RS13139055	0.000177758	RS2241473	0.006641465
RS10805346	0.000646726	RS11731597	0.017123731	RS12646099	0.02031343	RS13141233	0.0017764	RS2241474	0.001064861
RS10938799	0.021367772	RS11732054	0.001568946	RS12647117	0.001200286	RS13144709	0.000156227	RS2241475	0.023620758
RS10939605	0.001736432	RS11734375	0.001987587	RS13101785	0.001515781	RS13145442	0.001515781	RS2241476	0.012446806
RS10939614	0.015500168	RS11734554	0.002123501	RS13102085	0.022056251	RS13145554	0.002248305	RS2241477	0.012446806
RS10939620	0.005277204	RS11734623	0.002123501	RS13103497	0.002367312	RS13145758	4.69E-06	RS2241480	0.012446806
RS10939637	1.27E-05	RS11734786	0.001515781	RS13103690	0.008255906	RS13146686	0.000177758	RS2276961	0.000841326
RS10939638	7.43E-06	RS11735831	3.65E-05	RS13103879	0.007053103	RS13148371	0.001452742	RS2278121	0.001055239
RS10939650	7.05E-06	RS11736410	0.001341791	RS13106991	1.88E-05	RS13149985	0.001254263	RS2278122	0.005864212
RS10939655	0.001341791	RS11736479	0.001341791	RS13107466	0.001341791	RS13150928	0.001227972	RS2278123	0.023471432
RS10939656	0.000728132	RS11737685	0.007767677	RS13110307	0.000177758	RS13328050	0.005055797	RS28507715	0.002496661
RS10939665	0.001515781	RS11934363	0.012128234	RS13111638	1.02E-06	RS138416405	0.006663167	RS28513781	0.002505704
RS10939669	0.001309585	RS11935405	0.020002115	RS13112015	0.014705011	RS141037145	0.037501928	RS28558552	0.022904322
RS10939671	0.000137591	RS11942223	1.88E-05	RS13113730	0.001341791	RS143250861	0.00947731	RS28592748	1.36E-06
RS10939672	0.000137591	RS11943372	4.43E-05	RS13113918	1.36E-06	RS144651801	0.008131323	RS28602527	0.002914223
RS28610447	0.002760641	RS3775932	0.009125671	RS4128494	0.008738668	RS4580649	0.004576044	RS62287543	0.008622117
RS28613263	0.004512784	RS3775940	0.000126461	RS4144	9.97E-07	RS4591605	1.36E-06	RS62288489	0.006914101
RS28677023	0.002914223	RS3775944	0.000160759	RS4235345	3.70E-05	RS4608811	0.000566522	RS62288519	0.038228702
RS28715627	0.00336514	RS3775946	1.29E-05	RS4235346	0.005277204	RS4621431	0.004576044	RS62288891	0.029345688
RS28730480	0.000254339	RS3775947	9.10E-06	RS4235347	0.002898648	RS4622999	0.001390063	RS62293330	0.0339596
RS28837683	0.002914223	RS3775948	1.64E-05	RS4235348	0.002898648	RS4637402	3.11E-06	RS62293415	0.003389913
RS2903827	0.000310433	RS3796818	0.013454185	RS4235353	0.000849807	RS4639073	2.00E-05	RS62294290	0.020665341
RS34297373	0.004485642	RS3796825	0.011367107	RS4235354	0.000849807	RS4697693	0.002056833	RS62294331	0.002914223
RS34325511	0.024704382	RS3796826	0.011367107	RS4235355	0.000312253	RS4697694	0.002056833	RS62294332	0.002914223
RS34501273	0.001353139	RS3796829	0.001341791	RS4235356	0.000312253	RS4697698	0.007209815	RS62295971	0.007736226

RS34517659	0.049048506	RS3796832	0.001200286	RS4276278	0.004576044	RS4697699	3.00E-05	RS62296002	0.020665341
RS34709913	0.0017764	RS3796835	6.46E-05	RS4280729	0.000728132	RS4697700	2.95E-05	RS6414766	0.002898648
RS34768406	5.06E-05	RS3796836	0.002229928	RS4292328	0.005848098	RS4697701	0.000110904	RS6449137	0.000241854
RS35099040	0.001341791	RS3796837	0.000175991	RS4292332	0.002898648	RS4697703	0.000137488	RS6449139	0.000122278
RS35150828	0.022056251	RS3796838	4.96E-05	RS4292333	0.002898648	RS4697705	0.002254931	RS6449144	0.049434841
RS35250962	0.001515781	RS3796839	0.000813755	RS4306953	0.002631598	RS4697707	0.000262102	RS6449154	0.002898648
RS35411989	0.043007613	RS3796841	1.05E-06	RS4311316	0.002898648	RS4697708	0.000262102	RS6449156	0.004567023
RS35438220	0.001105304	RS3796842	0.001353139	RS4312757	0.002898648	RS4697710	0.000849807	RS6449157	0.002914223
RS35501905	0.002615129	RS3822236	0.000262102	RS4314284	0.002898648	RS4697718	0.005142546	RS6449158	0.002914223
RS35565862	0.025605997	RS3822241	0.000376303	RS4318649	0.000208584	RS4697719	0.005493192	RS6449159	0.002914223
RS35750364	0.001058387	RS3822242	0.000509234	RS4318650	0.000175991	RS4697720	0.005493192	RS6449171	0.004512784
RS35758343	0.049688513	RS3822246	0.011367107	RS4339211	0.004576044	RS4697721	0.005493192	RS6449172	0.004512784
RS35782983	7.36E-05	RS3822247	0.001107873	RS4376135	0.020002115	RS4697744	0.003343232	RS6449173	1.54E-05
RS35866697	0.001341791	RS3886038	0.028977627	RS4382035	0.020002115	RS4697910	0.001340359	RS6449174	0.004512784
RS35954357	0.002023779	RS41268389	0.013454185	RS4383618	0.003291869	RS4697913	0.000130503	RS6449176	0.003906428
RS35955619	0.007985749	RS4473653	0.003192491	RS4385059	2.49E-06	RS4697924	0.005188922	RS6449177	0.001072223
RS36084205	0.001947712	RS4475146	3.00E-05	RS4389579	0.020002115	RS4697925	0.004497175	RS6449178	0.003371809
RS3733584	0.001515781	RS4481233	4.18E-06	RS4407505	0.002898648	RS4697926	0.004497175	RS6449179	0.003371809
RS3733585	0.001515781	RS4484299	4.58E-06	RS4408959	0.004576044	RS4697933	0.001221311	RS6449183	0.00587844
RS3733586	0.001568946	RS4485819	0.000669663	RS4422413	0.045431741	RS4697954	0.003932581	RS6449196	0.006475073
RS3733588	1.17E-05	RS4495037	0.006669807	RS4428284	1.02E-06	RS4698017	0.003343232	RS6449201	0.003209893
RS3749558	0.010728271	RS4515163	0.002914223	RS4444830	0.002369723	RS5028843	8.72E-05	RS6449202	0.002760641
RS3756215	0.040044102	RS4519796	0.002898648	RS4447861	0.002898648	RS55801162	0.020002115	RS6449213	9.42E-07
RS3756223	0.012007509	RS4525975	5.68E-06	RS4447862	0.000241854	RS55959894	0.001254263	RS6449217	0.000219844
RS3756225	0.000509234	RS4529048	9.95E-06	RS4447863	0.02240052	RS55962381	0.0339596	RS6449286	0.044532105
RS3756236	0.001341791	RS4529049	0.000177758	RS4455410	0.002898648	RS55973727	0.040044102	RS66538112	0.004191708

RS3756237	0.001341791	RS4543113	0.000635963	RS4459990	0.00336514	RS56003345	0.013951052	RS67820465	0.001262566
RS3756238	0.001341791	RS4560411	0.002898648	RS4467563	0.002898648	RS56038393	0.001736432	RS6812759	0.002123501
RS3775930	0.010558492	RS4575994	0.001223013	RS4467564	0.002898648	RS56113653	0.001736432	RS6812780	0.000800673
RS56123633	0.00613405	RS6844316	0.002914223	RS7375642	0.002898648	RS7679724	1.92E-05	RS7678287	1.36E-06
RS56170676	0.002496661	RS6844329	0.001341791	RS7375643	0.005848098	RS7679916	0.001515781	RS9993410	0.005055797
RS56178126	0.000850347	RS6844787	0.002914223	RS7376505	0.002746395	RS7680126	1.04E-05	RS9994216	5.22E-05
RS56239136	0.000721867	RS6845554	0.000175991	RS7376948	0.002898648	RS7683283	0.00449694	RS9994266	0.002898648
RS56278885	0.010464025	RS6846692	0.000525525	RS7376960	2.00E-05	RS7683792	2.61E-06	RS9994937	0.004299582
RS56393964	0.040044102	RS6849717	0.005115878	RS7377578	0.004281628	RS7683856	1.36E-06	RS9998811	1.88E-05
RS57250714	0.001588554	RS6849729	0.002914223	RS7377625	0.002898648	RS7684306	0.014263647		
RS57574512	0.004777374	RS6850143	0.002914223	RS7378305	0.002898648	RS7685958	0.034229262		
RS58130873	0.003209893	RS6850684	0.004086692	RS7378340	0.002898648	RS7686538	0.004576044		
RS58380370	0.001126032	RS6852441	0.003209893	RS741075	0.046553852	RS76903922	0.014416673		
RS58693849	0.03184307	RS6853056	0.000314839	RS7434391	0.003906428	RS7694997	0.004576044		
RS60045583	0.003209893	RS6853437	0.000148871	RS7435196	0.004512784	RS7695555	0.009261838		
RS62286328	0.045193529	RS6855911	0.000152255	RS7437120	0.003906428	RS7696092	2.40E-06		
RS62286568	0.005034463	RS6856127	0.005185606	RS7439210	9.74E-06	RS7696983	1.36E-06		
RS62286569	0.003945068	RS6856396	4.35E-06	RS7442295	1.88E-05	RS7699512	0.002369723		
RS6812851	9.19E-05	RS6857693	0.001341791	RS7442336	0.000177758	RS7699609	0.002162856		
RS6814664	0.002898648	RS714871	9.19E-05	RS74778870	7.21E-05	RS7699671	0.002333749		
RS6815001	0.002914223	RS714873	9.19E-05	RS751092	4.65E-05	RS78917351	6.34E-05		
RS6820188	0.000177758	RS715979	0.040432993	RS76411769	0.040044102	RS79835095	0.031682278		
RS6823324	6.94E-05	RS73212808	0.02798958	RS7656624	0.000262102	RS874432	2.77E-06		
RS6825888	0.040044102	RS73212817	0.008247023	RS7657340	0.004512784	RS882222	0.006998334		
RS6826185	0.002123501	RS73212828	0.009819524	RS7658170	0.004512784	RS882223	0.004864504		
RS6826450	0.002123501	RS73212830	0.009819524	RS7660895	1.92E-05	RS9291640	7.43E-05		

RS6826764	0.000566522	RS73212848	0.000376303	RS7661701	3.68E-06	RS9291641	0.000104457
RS6827401	4.58E-06	RS73212853	0.008809032	RS7663032	1.43E-05	RS9291642	7.43E-07
RS6827754	0.000208584	RS73212886	0.032655389	RS7663044	2.32E-06	RS938552	2.91E-07
RS6827785	0.000208584	RS73212889	0.040044102	RS7663079	0.004512784	RS938554	2.91E-07
RS6829727	0.000177758	RS73212890	0.040044102	RS7663097	0.004512784	RS938555	2.91E-07
RS6829755	0.0339596	RS73212891	0.040044102	RS7666545	4.96E-05	RS938558	0.000360884
RS6832439	2.91E-07	RS73215003	0.001887166	RS7668175	0.002369723	RS938564	6.70E-07
RS6832456	5.61E-07	RS73227883	0.006475073	RS7669090	0.000447902	RS9732	0.007921065
RS6834893	0.002914223	RS733175	0.000566522	RS7669607	1.81E-06	RS978465	0.007958655
RS6836706	0.009641292	RS734122	0.012446806	RS7670751	0.000109224	RS978466	0.006374916
RS6837224	0.001964132	RS734553	1.04E-06	RS7671266	9.11E-06	RS9884416	0.004424817
RS6837336	5.97E-05	RS7349721	0.000669663	RS7672947	0.002898648	RS9926	0.008457474
RS6838021	7.85E-06	RS735527	0.013454185	RS7675964	0.000241854	RS993173	1.85E-05
RS6839490	0.004699344	RS737267	0.000122278	RS7676733	0.004512784	RS998675	0.005277204
RS6840802	0.005234975	RS7375587	0.002898648	RS7677710	0.003371809	RS998676	0.005277204
RS6843873	0.002914223	RS7375599	0.005848098	RS7678012	0.001860628	RS9991278	1.36E-06

APPENDIX 4- CODES--

title: "SingleVariantAnalysis_SLC2A9"
author: "Padmini"
date: "27 October 2017"
output: html_document

Set working directory.
```{r}
setwd("/Users/Padmini/Desktop/SLC2A9/Regression")
getwd()
```
 # --

Import datasets.
PCA information for all subjects was extracted from CoreExomePCAdata.txt and saved as CoreExomeDataPCAextracted.txt.
From the phenotype genotype merged file, subject information was extraced and saved as SubjectsOnly.txt.

Merge files to extract PCA1-10 info for subjects of interest and write merged file onto the folder.
```{r}
data1<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/SubjectsOnly.txt",header = T)
data2<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/CoreExomeDataPCAextracted.txt",header = T)
MERGED<-merge(data1, data2, by="SUBJECT", all.x=T)
write.table(MERGED, "/Users/Padmini/Desktop/SLC2A9/Regression/PCAinfoforSubjects.txt", sep = "\t")
```
Merge files to extract age info info for subjects of interest and write merged file onto the folder.
```{r}
data3<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/SubjectsOnly.txt",header = T)
data4<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/Age.txt",header = T)
MERGED2<-merge(data3, data4, by="SUBJECT", all.x=T)
write.table(MERGED2, "/Users/Padmini/Desktop/SLC2A9/Regression/AGEinfoforSubjects.txt", sep = "\t")
```
Phenotype genotype information extracted from BCISNPmax was merged and saved as Phengenmerged.txt.

PCA data and age data from the above merged files were manually appended into this file and named as SelectPhenGenPCA.txt.
All blanks in this file are replaced with 'NA' (keeping blanks ended up in wrong numbers occasionally in the output file).
This file is imported.

```{r}
SelectPhenGenPCA<-
read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/SelectPhenGenPCA.txt",header = T )
```

 # --

 # Logistic Regression: Loop Models (Binomial)

 # (1) Unadjusted

A. Population: East Polynesian

```{r}
result = data.frame(matrix(nrow=3963,ncol=13))
names(result) = c("SNP", "AA", "AB", "BB", "CaseAA", "CaseAB", "CaseBB", "ControlAA",
"ControlAB", "ControlBB", "TE", "SE", "P")
result$SNP = names(SelectPhenGenPCA) [33:3995]
for(i in 33:3995){
  result[i-32,2] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[1]
  result[i-32,3] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[2]
  result[i-32,4] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[3]
  l = levels(as.factor(unlist(SelectPhenGenPCA[,i])))
  result[i-32,5] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]), levels = l))[1]
  result[i-32,6] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]),levels = l))[2]
  result[i-32,7] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]),levels = l))[3]
  result[i-32,8] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[1]
```

```
  result[i-32,9] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[2]
  result[i-32,10] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[3]
  tryCatch(model <- glm(AFFSTAT~as.numeric(as.factor(unlist(SelectPhenGenPCA[,i]))),
data=SelectPhenGenPCA, subset=ETHCLASS=="EastPolynesian", family=binomial), error=function(e)
NULL)
  tryCatch(result[i-32,11:13] <- coef(summary(model))[2,c(1,2,4)], error = function(e) NULL)
}
```

Write file to my folder.

```{r}
Unadjusted_EastPolynesian = result
write.table(Unadjusted_EastPolynesian,
"/Users/Padmini/Desktop/SLC2A9/Regression/Unadjusted_EastPolynesian.txt", sep = "\t")
rm(result)
```

Import the output file into R workspace and view sample of the output file.

```{r}
Unadjusted_EastPolynesian<-
read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/Unadjusted_EastPolynesian.txt",header = T )
head(Unadjusted_EastPolynesian)
```

B. Population: West Polynesian

```{r}
result = data.frame(matrix(nrow=3963,ncol=13))
names(result) = c("SNP", "AA", "AB", "BB", "CaseAA", "CaseAB", "CaseBB", "ControlAA",
"ControlAB", "ControlBB", "TE", "SE", "P")
result$SNP = names(SelectPhenGenPCA) [33:3995]
for(i in 33:3995){
  result[i-32,2] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[1]
  result[i-32,3] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[2]
  result[i-32,4] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[3]
  l = levels(as.factor(unlist(SelectPhenGenPCA[,i])))
```

```
  result[i-32,5] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]), levels = l))[1]
  result[i-32,6] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]),levels = l))[2]
  result[i-32,7] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]),levels = l))[3]
  result[i-32,8] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[1]
  result[i-32,9] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[2]
  result[i-32,10] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[3]
  tryCatch(model <-
glm(AFFSTAT~as.numeric(as.factor(unlist(SelectPhenGenPCA[,i]))),data=SelectPhenGenPCA,
subset=ETHCLASS=="WestPolynesian", family=binomial), error=function(e) NULL)
  tryCatch(result[i-32,11:13] <- coef(summary(model))[2,c(1,2,4)], error = function(e) NULL)
}
```

Write file to my folder.

```{r}
Unadjusted_WestPolynesian = result
write.table(Unadjusted_WestPolynesian,
"/Users/Padmini/Desktop/SLC2A9/Regression/Unadjusted_WestPolynesian.txt", sep = "\t")
rm(result)
```

Import the output file into R workspace and view sample of the output file.

```{r}
Unadjusted_WestPolynesian<-
read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/Unadjusted_WestPolynesian.txt",header = T )
head(Unadjusted_WestPolynesian)
```

--

C. Population: Caucasian

```{r}
result = data.frame(matrix(nrow=3963,ncol=13))
names(result) = c("SNP", "AA", "AB", "BB", "CaseAA", "CaseAB", "CaseBB", "ControlAA",
"ControlAB", "ControlBB", "TE", "SE", "P")
result$SNP = names(SelectPhenGenPCA) [33:3995]
for(i in 33:3995){
  result[i-32,2] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[1]
  result[i-32,3] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[2]
  result[i-32,4] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[3]
  l = levels(as.factor(unlist(SelectPhenGenPCA[,i])))
  result[i-32,5] = table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="Caucasian"
& SelectPhenGenPCA$AFFECTION=="HyperU"),i]), levels = l))[1]
  result[i-32,6] = table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="Caucasian"
& SelectPhenGenPCA$AFFECTION=="HyperU"),i]),levels = l))[2]
  result[i-32,7] = table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="Caucasian"
& SelectPhenGenPCA$AFFECTION=="HyperU"),i]),levels = l))[3]
  result[i-32,8] = table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="Caucasian"
& SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[1]
  result[i-32,9] = table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="Caucasian"
& SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[2]
  result[i-32,10] = table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="Caucasian"
& SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[3]
  tryCatch(model <- glm(AFFSTAT~as.numeric(as.factor(unlist(SelectPhenGenPCA[,i]))),
data=SelectPhenGenPCA, subset=ETHCLASS=="Caucasian", family=binomial), error=function(e) NULL)
  tryCatch(result[i-32,11:13] <- coef(summary(model))[2,c(1,2,4)], error = function(e) NULL)
}
```

Write file to my folder.

```{r}
Unadjusted_Caucasian = result
write.table(Unadjusted_Caucasian,
"/Users/Padmini/Desktop/SLC2A9/Regression/Unadjusted_Caucasian.txt", sep = "\t")
rm(result)
```

Import the output file into R workspace and view sample of the output file.

```{r}
Unadjusted_Caucasian<-
read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/Unadjusted_Caucasian.txt",header = T )
```

```
head(Unadjusted_Caucasian)
```
```
## ------------------------------------------------------------------------

# (B) Adjusted for AGE (for EP and WP only) and SEX (for all).

## A. Population: East Polynesian
```{r}
result = data.frame(matrix(nrow=3963,ncol=13))
names(result) = c("SNP", "AA", "AB", "BB", "CaseAA", "CaseAB", "CaseBB", "ControlAA",
"ControlAB", "ControlBB", "TE", "SE", "P")
result$SNP = names(SelectPhenGenPCA) [33:3995]
for(i in 33:3995){
  result[i-32,2] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[1]
  result[i-32,3] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[2]
  result[i-32,4] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[3]
  l = levels(as.factor(unlist(SelectPhenGenPCA[,i])))
  result[i-32,5] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]), levels = l))[1]
  result[i-32,6] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]),levels = l))[2]
  result[i-32,7] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]),levels = l))[3]
  result[i-32,8] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[1]
  result[i-32,9] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[2]
  result[i-32,10] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[3]
  tryCatch(model <- glm(AFFSTAT~as.numeric(as.factor(unlist(SelectPhenGenPCA[,i])))+SEX+AGE,
data=SelectPhenGenPCA, subset=ETHCLASS=="EastPolynesian", family=binomial), error=function(e)
NULL)
  tryCatch(result[i-32,11:13] <- coef(summary(model))[2,c(1,2,4)], error = function(e) NULL)
```
```

```
}
```
```
#### Write file to my folder.
```{r}
AGESEXadjusted_EastPolynesian = result
write.table(AGESEXadjusted_EastPolynesian,
"/Users/Padmini/Desktop/SLC2A9/Regression/AGESEXadjusted_EastPolynesian.txt", sep = "\t")
rm(result)
```
Import the output file into R workspace and view sample of the output file.
```{r}
AGESEXadjusted_EastPolynesian<-
read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/AGESEXadjusted_EastPolynesian.txt",header = T
)
head(AGESEXadjusted_EastPolynesian)
```
--

B. Population: West Polynesian
```{r}
result = data.frame(matrix(nrow=3963,ncol=13))
names(result) = c("SNP", "AA", "AB", "BB", "CaseAA", "CaseAB", "CaseBB", "ControlAA",
"ControlAB", "ControlBB", "TE", "SE", "P")
result$SNP = names(SelectPhenGenPCA) [33:3995]
for(i in 33:3995){
  result[i-32,2] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[1]
  result[i-32,3] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[2]
  result[i-32,4] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[3]
  l = levels(as.factor(unlist(SelectPhenGenPCA[,i])))
  result[i-32,5] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]), levels = l))[1]
  result[i-32,6] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]),levels = l))[2]
  result[i-32,7] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]),levels = l))[3]
```
```

```
  result[i-32,8] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[1]
  result[i-32,9] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[2]
  result[i-32,10] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[3]
  tryCatch(model <- glm(AFFSTAT~as.numeric(as.factor(unlist(SelectPhenGenPCA[,i])))+SEX+AGE,
data=SelectPhenGenPCA, subset=ETHCLASS=="WestPolynesian", family=binomial), error=function(e)
NULL)
  tryCatch(result[i-32,11:13] <- coef(summary(model))[2,c(1,2,4)], error = function(e) NULL)
}
```

Write file to my folder.

```{r}
AGESEXadjusted_WestPolynesian = result
write.table(AGESEXadjusted_WestPolynesian,
"/Users/Padmini/Desktop/SLC2A9/Regression/AGESEXadjusted_WestPolynesian.txt", sep = "\t")
rm(result)
```

Import the output file into R workspace and view sample of the output file.

```{r}
AGESEXadjusted_WestPolynesian<-
read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/AGESEXadjusted_WestPolynesian.txt",header =
T )
head(AGESEXadjusted_WestPolynesian)
```

C. Population: Caucasian

```{r}
result = data.frame(matrix(nrow=3963,ncol=13))
names(result) = c("SNP", "AA", "AB", "BB", "CaseAA", "CaseAB", "CaseBB", "ControlAA",
"ControlAB", "ControlBB", "TE", "SE", "P")
result$SNP = names(SelectPhenGenPCA) [33:3995]
for(i in 33:3995){
  result[i-32,2] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[1]
```

```
  result[i-32,3] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[2]
  result[i-32,4] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[3]
  l = levels(as.factor(unlist(SelectPhenGenPCA[,i])))
  result[i-32,5] = table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="Caucasian"
& SelectPhenGenPCA$AFFECTION=="HyperU"),i]), levels = l))[1]
  result[i-32,6] = table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="Caucasian"
& SelectPhenGenPCA$AFFECTION=="HyperU"),i]),levels = l))[2]
  result[i-32,7] = table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="Caucasian"
& SelectPhenGenPCA$AFFECTION=="HyperU"),i]),levels = l))[3]
  result[i-32,8] = table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="Caucasian"
& SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[1]
  result[i-32,9] = table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="Caucasian"
& SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[2]
  result[i-32,10] = table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="Caucasian"
& SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[3]
  tryCatch(model <- glm(AFFSTAT~as.numeric(as.factor(unlist(SelectPhenGenPCA[,i])))+SEX,
data=SelectPhenGenPCA, subset=ETHCLASS=="Caucasian", family=binomial), error=function(e) NULL)
  tryCatch(result[i-32,11:13] <- coef(summary(model))[2,c(1,2,4)], error = function(e) NULL)
}
```

Write file to my folder.

```{r}
SEXadjusted_Caucasian = result
write.table(SEXadjusted_Caucasian,
"/Users/Padmini/Desktop/SLC2A9/Regression/SEXadjusted_Caucasian.txt", sep = "\t")
rm(result)
```

Import the output file into R workspace and view sample of the output file.

```{r}
SEXadjusted_Caucasian<-
read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/SEXadjusted_Caucasian.txt",header = T )
head(SEXadjusted_Caucasian)
```

(C) Adjusted for AGE , SEX and PCA 1-10 (EP and WP only). Age and PCA data not available for most Europeans, so cannot adjust for these for Europeans.

A. Population: East Polynesian

```{r warning=FALSE}
result = data.frame(matrix(nrow=3963,ncol=13))
names(result) = c("SNP", "AA", "AB", "BB", "CaseAA", "CaseAB", "CaseBB", "ControlAA",
"ControlAB", "ControlBB", "TE", "SE", "P")
result$SNP = names(SelectPhenGenPCA) [33:3995]
for(i in 33:3995){
  result[i-32,2] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[1]
  result[i-32,3] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[2]
  result[i-32,4] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[3]
  l = levels(as.factor(unlist(SelectPhenGenPCA[,i])))
  result[i-32,5] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]), levels = l))[1]
  result[i-32,6] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]),levels = l))[2]
  result[i-32,7] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]),levels = l))[3]
  result[i-32,8] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[1]
  result[i-32,9] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[2]
  result[i-32,10] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="EastPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[3]
  tryCatch(model <-
glm(AFFSTAT~as.numeric(as.factor(unlist(SelectPhenGenPCA[,i])))+SEX+AGE+PCA1+PCA2+PCA3+PC
A4+PCA5+PCA6+PCA7+PCA8+PCA9+PCA10, data=SelectPhenGenPCA,
subset=ETHCLASS=="EastPolynesian", family=binomial), error=function(e) NULL)
  tryCatch(result[i-32,11:13] <- coef(summary(model))[2,c(1,2,4)], error = function(e) NULL)
}
```

Write file to my folder.

```{r}
AGESEXPCAadjusted_EastPolynesian = result
```

```
write.table(AGESEXPCAadjusted_EastPolynesian,
"/Users/Padmini/Desktop/SLC2A9/Regression/AGESEXPCAadjusted_EastPolynesian.txt", sep = "\t")
rm(result)
```
```
#### Import the output file into R workspace and view sample of the output file.
```{r}
AGESEXPCAadjusted_EastPolynesian<-
read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/AGESEXPCAadjusted_EastPolynesian.txt",heade
r = T )
head(AGESEXPCAadjusted_EastPolynesian)
```
--

B. Population: West Polynesian
```{r warning=FALSE}
result = data.frame(matrix(nrow=3963,ncol=13))
names(result) = c("SNP", "AA", "AB", "BB", "CaseAA", "CaseAB", "CaseBB", "ControlAA",
"ControlAB", "ControlBB", "TE", "SE", "P")
result$SNP = names(SelectPhenGenPCA) [33:3995]
for(i in 33:3995){
  result[i-32,2] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[1]
  result[i-32,3] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[2]
  result[i-32,4] = levels(as.factor(unlist(SelectPhenGenPCA[,i])))[3]
  l = levels(as.factor(unlist(SelectPhenGenPCA[,i])))
  result[i-32,5] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]), levels = l))[1]
  result[i-32,6] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]),levels = l))[2]
  result[i-32,7] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="HyperU"),i]),levels = l))[3]
  result[i-32,8] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[1]
  result[i-32,9] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[2]
```
```

```
  result[i-32,10] =
table(factor(unlist(SelectPhenGenPCA[(SelectPhenGenPCA$ETHCLASS=="WestPolynesian" &
SelectPhenGenPCA$AFFECTION=="NormoU"),i]),levels = l))[3]
  tryCatch(model <-
glm(AFFSTAT~as.numeric(as.factor(unlist(SelectPhenGenPCA[,i])))+SEX+AGE+PCA1+PCA2+PCA3+PC
A4+PCA5+PCA6+PCA7+PCA8+PCA9+PCA10, data=SelectPhenGenPCA,
subset=ETHCLASS=="WestPolynesian", family=binomial), error=function(e) NULL)
  tryCatch(result[i-32,11:13] <- coef(summary(model))[2,c(1,2,4)], error = function(e) NULL)
}
```

Write file to my folder.

```{r}
AGESEXPCAadjusted_WestPolynesian = result
write.table(AGESEXPCAadjusted_WestPolynesian,
"/Users/Padmini/Desktop/SLC2A9/Regression/AGESEXPCAadjusted_WestPolynesian.txt", sep = "\t")
rm(result)
```

Import the output file into R workspace and view sample of the output file.

```{r}
AGESEXPCAadjusted_WestPolynesian<-
read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/AGESEXPCAadjusted_WestPolynesian.txt",heade
r = T )
head(AGESEXPCAadjusted_WestPolynesian)
```

#----------

To know the percentage of missing values in the dataset.

```{r}
library(naniar)
library(dplyr)
library(visdat)
```

In the SelectPhenGenPCA file, there were blanks in the rsid columns which was not recognized by the naniar and visdat programs which probably consider only NA as missing value. So I made a temporary file in which I replaced all balnks with NA and called it na.txt and used this file to provide details about percentage of missing values.

The agrument warn_large_data is to indicate that the file is big but still work with the whole file without skipping columns.

```{r}
```

```
missing_values <- miss_var_summary(SelectPhenGenPCA, warn_large_data = FALSE)
write.table(missing_values, "/Users/Padmini/Desktop/SLC2A9/Regression/missing_values.txt", sep = "\t")
vis_dat(SelectPhenGenPCA, warn_large_data = FALSE)
vis_miss(SelectPhenGenPCA, warn_large_data = FALSE)
n_miss(SelectPhenGenPCA)
n_complete(SelectPhenGenPCA)
prop_miss(SelectPhenGenPCA)
prop_complete(SelectPhenGenPCA)
```

Merging files to get missing values for significant SNPs.

EP:

```{r}
data1<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/EP-SIGNI-LIST-AGESEXPCAadjusted.txt", header = T )
data2<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/missing_values.txt", header = T )
View(data2)

MERGED<-merge(data1, data2, by = "variable", all.x = T)
View(MERGED)
write.table(MERGED, "/Users/Padmini/Desktop/SLC2A9/Regression/EP_SIGNI_missing_values.txt", sep = "\t")
```

WP:

```{r}
data1<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/WP-SIGNI-LIST-AGESEXPCAadjusted.txt", header = T )
data2<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/missing_values.txt", header = T )
MERGED<-merge(data1, data2, by = "variable", all.x = T)
View(MERGED)
write.table(MERGED, "/Users/Padmini/Desktop/SLC2A9/Regression/WP_SIGNI_missing_values.txt", sep = "\t")
```

Caucasian:

```{r}
data1<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/CAUCASIAN-SIGNI-LIST-SEXPCAadjusted.txt", header = T )
data2<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/missing_values.txt", header = T )
MERGED<-merge(data1, data2, by = "variable", all.x = T)
```

View(MERGED)

write.table(MERGED,

"/Users/Padmini/Desktop/SLC2A9/Regression/CAUCASIAN_SIGNI_missing_values.txt", sep = "\t")

```

*#------------------------------------------------------------------------------*

*# Merging age, sex, PCA adjusted significant SNPs across populations to know how many variants are overlapping.*

```{r}

*data1<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/AGESEXPCAadjusted-EP-SIGNI.txt",header = T )*

*data2<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/AGESEXPCAadjusted-WP-SIGNI.txt",header = T )*

*data3<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/SEXadjusted-CAUCASIAN-SIGNI.txt",header = T )*

*MERGED1<-merge(data1, data2, by = "SNP")*

*View(MERGED1)*

*MERGED2<-merge(data2, data3, by = "SNP")*

*View(MERGED2)*

*MERGED3<-merge(data1, data3, by = "SNP")*

*View(MERGED3)*

*MERGED<-merge(MERGED1, MERGED3, by = "SNP")*

*View(MERGED)*

*write.table(MERGED1, "/Users/Padmini/Desktop/SLC2A9/Regression/EP-WP-SIGNI.txt", sep = "\t")*

*write.table(MERGED2, "/Users/Padmini/Desktop/SLC2A9/Regression/WP-CAUCASIAN-SIGNI.txt", sep = "\t")*

*write.table(MERGED3, "/Users/Padmini/Desktop/SLC2A9/Regression/EP-CAUCASIAN-SIGNI.txt", sep = "\t")*

*write.table(MERGED, "/Users/Padmini/Desktop/SLC2A9/Regression/EP-WP-CAUCASIAN-SIGNI.txt", sep = "\t")*

```

#--

 # Merging unadjusted, age, sex adjusted and age, sex, PCA adjusted significant SNPs files to know how many variants are overlapping.

(screened for sigficant variants and saved relevant details in different files before merging)

EP:
```

```{r}
data1<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/UNADJUSTED-EP-SIGNI.txt",header = T )
data2<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/AGESEXadjusted-EP-SIGNI.txt",header = T )
data3<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/AGESEXPCAadjusted-EP-SIGNI.txt",header = T )
MERGED1<-merge(data1, data2, by = "SNP")
View(MERGED1)
MERGED2<-merge(data2, data3, by = "SNP")
View(MERGED2)
MERGED3<-merge(data1, data3, by = "SNP")
View(MERGED3)
EP<-merge(MERGED1, data3, by = "SNP")
View(EP)
```

WP:

```{r}
data1<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/UNADJUSTED-WP-SIGNI.txt",header = T )
data2<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/AGESEXadjusted-WP-SIGNI.txt",header = T )
data3<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/AGESEXPCAadjusted-WP-SIGNI.txt",header = T )
MERGED1<-merge(data1, data2, by = "SNP")
View(MERGED1)
MERGED2<-merge(data2, data3, by = "SNP")
View(MERGED2)
MERGED3<-merge(data1, data3, by = "SNP")
View(MERGED3)
WP<-merge(MERGED1, data3, by = "SNP")
View(WP)
```

CAUCASIAN:

```{r}
data1<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/UNADJUSTED-CAUCASIAN-SIGNI.txt",header = T )
data2<-read.delim("/Users/Padmini/Desktop/SLC2A9/Regression/SEXadjusted-CAUCASIAN-SIGNI.txt",header = T )
```

MERGED<-merge(data1, data2, by = "SNP")

View(MERGED)

```

*#------------------------------------------------------------------------------*

*# Merging files to get info file for haploview analysis.*

*## EP:*

*```{r}*

*data1<-read.delim("/Users/Padmini/Desktop/SLC2A9/HaploviewAnalysis/EP/EP-SIGNI-LIST-AGESEXPCAadjusted.txt", header = T )*

*data2<-read.delim("/Users/Padmini/Desktop/SLC2A9/HaploviewAnalysis/EP/SLC2A9-marker-location.txt", header = T )*

*MERGED<-merge(data1, data2, by = "SNP", all.x = T)*

*View(MERGED)*

*write.table(MERGED, "/Users/Padmini/Desktop/SLC2A9/HaploviewAnalysis/EP/EP-SIGNI-marker-location.txt", sep = "\t")*

```

WP:

```{r}

data1<-read.delim("/Users/Padmini/Desktop/SLC2A9/HaploviewAnalysis/WP/WP-SIGNI-LIST-AGESEXPCAadjusted.txt", header = T)

data2<-read.delim("/Users/Padmini/Desktop/SLC2A9/HaploviewAnalysis/WP/SLC2A9-marker-location.txt", header = T)

MERGED<-merge(data1, data2, by = "SNP", all.x = T)

View(MERGED)

write.table(MERGED, "/Users/Padmini/Desktop/SLC2A9/HaploviewAnalysis/WP/WP-SIGNI-marker-location.txt", sep = "\t")

```

*#------------------------------------------------------------------------------*
```

The
New Zealand
Medical Journal
Journal of the New Zealand Medical Association
Vol 131 | No 1470 | 23 February 2018

How comprehensive is suicide risk assessment in the emergency department?

E-cigarettes—peering into the mist of uncertainty

Limiting complication rates in implant-based breast reconstruction

E-cigarette use in New Zealand—a systematic review and narrative synthesis

Genetic variants in the *SLC2A9* locus confer risk for hyperuricemia in Māori and Pacific Island individuals

P Parthasarathy, TR Merriman

Department of Biochemistry, School of Biomedical Sciences, University of Otago, Dunedin.

Hyperuricemia, elevated levels of serum urate, is a prerequisite for gouty arthritis. The solute carrier family 2 member 9 (*SLC2A9*) gene that encodes a urate transporter tops the list of hyperuricemic genes. It is a key genetic determinant of serum urate levels and explains about 3% of urate variance. Gout is highly prevalent in the New Zealand Māori and other Polynesian populations. As an attempt to understand the reason for this increased prevalence, this study focused on the identification and characterisation of Polynesian-specific genetic variants within the *SLC2A9* locus conferring susceptibility to hyperuricemia, using the rare variant analysis approach.

The *SLC2A9* locus was resequenced in 809 individuals comprising hyperuricemic cases and normouricemic controls. Based on self-reported ancestry, the cohort was split into two subsets (Polynesian, n=440 and European, n=369). All Polynesians were from New Zealand while Europeans were from New Zealand and the US. Association analysis was carried out to identify risk variants within the *SLC2A9* locus that confer risk for hyperuricemia. Multiple adjusted logistic regression analysis was carried out using R version 3.4.1.

A total of 3,964 variants were identified within the locus, with 100 variants found to be significant in the Polynesian population (OR [95% CI] = 0.10 [0.01;0.88] to 5.43 [1.93;15.33], P_{adj} = 0.00028 to 0.049, $MAF_{controls}$ = 0.014 to 0.535, MAF_{cases} = 0.002 to 0.546). Twenty-five of these variants were found to be Polynesian-specific, among which 14 were found to be novel. These variants will be further analysed, replicated and functionally annotated in a larger cohort as a continuation of this study.

This research would provide a greater insight into the genetic causes of gout. More importantly, the identification of penetrant variants could be applied in precision medicine and public health genomics to improve health outcomes for the target population.

Modulating the immune response to colorectal cancer in mice using a cancer vaccine

GR Niemi,[1] AJ Highton,[1] SM Hook,[2] RA Kemp[1]

[1]Department of Microbiology and Immunology, School of Biomedical Sciences; [2]School of Pharmacy, University of Otago, Dunedin.

Vaccines modulate the host's anti-tumour immune response and represent an area of emerging immunotherapy research for the treatment of cancer, including colorectal cancer (CRC). Murine subcutaneous injections of tumour cell lines are often used to test cancer vaccines for the treatment of CRC. However, we have shown that CRC can also be modelled by a micro-surgical intracaecal injection of the tumour cell CT26, a murine colon adenoma carcinoma.

To determine if the immune response to CRC could be modulated with a cancer vaccine, mice were vaccinated with chitosan hydrogel gel alone, gel and the endogenous tumour peptide AH1, or PBS for the control. Mice were then challenged either subcutaneously or intracaecally with CT26 colon adenoma carcinoma. The immune cells: dendritic cells, macrophages (F480+ and CD11b+), T cells, (CD4+ and CD8+) and B cells were identified via flow cytometry at the tumour site (local immune response) and in the spleen (systemic immune response). Splenic T cell phenotype (antigen experience, memory/regulatory phenotype, cytokine production) was also analysed via flow cytometry.

The chitosan gel vaccine provided protection against tumour growth in both subcutaneous (not significant) and intracaecal models (n=8–9, One-way ANOVA with Tukey post-hoc, P<0.01). In the subcutaneous model, there was no difference in the frequency of infiltrating macrophages, dendritic cells or CD4+ and CD8+ T cells; nor any differences in T cell phenotype; although these experiments need to be repeated. However, in the intracaecal model, protection was correlated with an increase in splenic tumour-antigen specific and IFNγ-producing T cells (n=4–5, One-way ANOVA with Tukey post-hoc, P<0.0001). These cells have also been shown to be important in human CRC.

This work will help link animal models and human data, and potentially translate cancer therapeutics into treatments for human patients.

Secreted amyloid precursor protein-alpha and active peptide fragments regulate neuronal morphology

MJ Wilde, BG Mockett, WC Abraham

Department of Psychology, Brain Health Research Centre, University of Otago.

Neurodegeneration in Alzheimer's Disease is thought to arise both from an excess of pathogenic amyloid-beta and a deficiency of neuroprotective secreted amyloid precursor protein-alpha (sAPPα). To understand more about the biology of sAPPα and two putative active peptide fragments, RER (Arg-Glu-Arg) and 16mer, on normal tissue, we characterised their effects on dendritic complexity and dendritic spine density (two measures of neuronal connectivity).

Primary cultures of rat hippocampal neurons were transduced with green fluorescent protein via lentivirus to enable visualisation, and treated with 1nM sAPPα, RER, 16mer or control peptides for 24 hours, or sAPPα for two hours. Phosphate-buffered saline (PBS) was used as a control. Cultures were treated, then fixed with paraformaldehyde after 21 days *in vitro*. Confocal imaging analysed dendritic complexity

NZMJ 23 February 2018, Vol 131 No 1476
ISSN 1175-8716
www.nzma.org.nz/journal

JOSEPHINE WARING

The Answers Lie Within our Hands

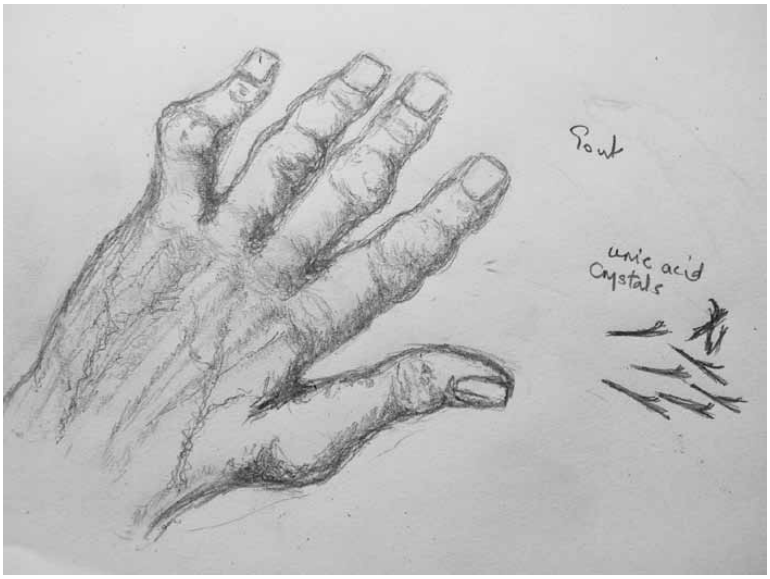


Figure 1. Josephine Waring, *The Answers Lie Within Our Hands* (concept drawing), 2017, graphite on paper.

The work in this exhibition was made in conjunction with Padmini Parthasarathy, from the Department of Biochemistry. She is currently researching the SLC2A9 gene.

> The SLC2A9 gene provides instructions for making a protein called glucose transporter 9 (GLUT9). The GLUT9 protein helps transport a substance called uric acid. Uric acid is a by-product of certain normal chemical reactions in the body. In the bloodstream it acts as an antioxidant, protecting cells from the damaging effects of unstable molecules called free radicals. However, having too much uric acid in the body is toxic, so excess uric acid is removed from the body in urine.[1]

SLC2A9 gene variants have been associated with urinary uric acid concentration, but more research is needed into the how this gene is expressed and environmental factors such as diet in disorders associated with excess uric acid in the bloodstream.[2] Padmini's research focuses on the damage and deformity caused by the deposition of uric acid crystals in the joints at the extremities of our body - the feet and hands.

> ...[while] the role of the SLC2A9 gene in gout may be unclear, it is known that a combination of lifestyle, genetic, and environmental factors play a part in determining the risk of this complex disorder.[3]

Uric crystals look like shards of glass. They deposit in the joints and damage the joint. On an X-ray, they look like a cloud-like density where the joint should be.[4] This is different to what arthritis looks like on X-rays, where you can see where the distorted growth is in the bone at the joint.
Hands are probably our most important tool, and we describe them in many different ways: large, strong, capable, warm, cold, limp, small, slender, elegant, lady-like, delicate, work-worn, arthritic. But there is another word - GOUTY: the hot, swollen, extremely painful and deformed joints, unable to be used as a result of uric acid crystal deposition.

Figure 2. Josephine Waring, *The Answers Lie Within Our Hands*, 2017, stoneware clay with an iron stain and fired to cone 10. One hand cradles cut-out shapes, representing the sharp uric acid crystals, whilst the other lies on a map of the Pacific Ocean.

Josephine Waring is a Ceramic Diploma student at the Dunedin School of Art, Otago Polytechnic.

1. "SLC2A9 Gene: Solute Carrier Family 2 Member 9." *US National Library of Medicine*, https://ghr.nlm.nih.gov/gene/SLC2A9#conditions (accessed 20 August 2018).
2. Erin Ware, et al., "SLC2A9 Genotype is Associated with SLC2A9 Gene Expression and Urinary Uric Acid Concentration." *PLoS*, Vol. 10 (2015), http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0128593.
3. "SLC2A9 Gene: Solute Carrier Family 2 Member 9." *US National Library of Medicine*, https://ghr.nlm.nih.gov/gene/SLC2A9#conditions (accessed 20 August 2018).
4. "Gout- Hand." *Learning Radiology*, http://learningradiology.com/archives2010/C0W%20423-Gout%20hand/goutcorrect.htm. See image of deposition of sodium urate monohydrate crystals in synovial membranes, articular cartilage, ligaments, bursae leading to destruction of cartilage.