DEVELOPING AN ONLINE PORTAL FOR UNRAVELING GENOMIC SIGNATURE OF ARCHAIC DNA THAT ARE RELATED TO MODERN HUMAN GENETIC DISEASES

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Niyazi SENTURK: DEVELOPING AN ONLINE PORTAL FOR UNRAVELING GENOMIC SIGNATURE OF ARCHAIC DNA THAT ARE RELATED TO MODERN HUMAN GENETIC DISEASES

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To my family…

ABSTRACT

Mutations or introgression can cause and rise adaptive allele up which some can be beneficial alleles. Archaic humans lived more than 200,000 years in Europe and Western Asia. They were adapted to these environments and local pathogens of these environments. It is therefore thinkable that modern humans obtained a significant immune advantage from the archaic alleles. First aim of the study is to determine the genetic disease caused alleles that are intogressed from Archaics. Secondly, we designed the *in silico* modelling (http://www.archaics2phenotype.neu.edu.tr) for clinicians and researchers to trace the history of the Neanderthal allele and correlate with the persons' phenotype. To conclude, our developed model will provide the better understanding for the origin of the genetic diseases or traits that are association with Neanderthal genome. Moreover, this precise medicine model will help the individuals and their belonged populations to receive the best treatment. Finally, it will be the strong answer of the question of why there are differences in disease phenotypes in modern humans.

Keywords: Archaic genome; Single-nucleotide polymorphism; Toll-Like Receptor; Allergy; Introgression; Adaptive immunity

ÖZET

Tarih boyunca insan evriminde patojenler ve bu patojenlerin sebep olduğu hastalıklar en önemli seçici güçlerdir. Arkaik insanlar 200.000 yılan fazla bir süredir Avrupa'da ve Batı Asya'da yaşamışlardı. Muhtemelen bu çevreye ve yerel patojenlerine iyi adapte olmuşlardı. Bu nedenle, Avrupa'ya ve Batı Asya'ya gelen modern insanlar ile aralarında gerçekleşen melezleşme ile bağışıklık kazandıkları düşünülmektedir. Çalışmamızın ilk amacı, Arkaik insanlardan modern insanlara aktarılan alellerin neden olduğu hastalıkların belirlenmesidir. İkincisi, klinisyenler ve araştırmacılar için Neanderthal alelinin geçmişini izlemek ve bireylerin fenotipi ile ilişkilendirmek için *in silico* modelleme (http://www.archaics2phenotype.neu.edu.tr) tasarladık. Sonuç olarak, geliştirdiğimiz bu modelimiz, Neandertal genomuyla ilişkili genetik hastalıkların veya özelliklerin kökeni için daha iyi bir anlayış sağlayacaktır. Üstelik, bu oluşturulan *in silico* modeli, bireylerin ve onların ait oldukları popülasyonların en iyi tedaviyi almalarına yardımcı olacaktır. Son olarak, modern insanlarda hastalık fenotiplerinde neden farklılıklar bulunduğu sorusunun güçlü cevabı olacaktır.

Anahtar Kelimeler: Arkaik genom; Tek nükleotid polimorfizmi; Toll benzeri reseptör; Alerji; Introgresyon; Adaptif bağışıklık

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LIST OF ABBREVIATIONS

ACB:	African Caribbean in Barbados
ALS:	Amylotrophic Lateral Sclerosis
ASW:	African Ancestry in Southwest US
BEB:	Bengali in Bangladesh
CD14:	Cluster of differentation 14
CDX:	Chinese Dai in Xishuangbanna, China
CEU:	Utah residents with Northern and Western European ancestry
CHB:	Han Chinese in Bejing, China
CHS:	Southern Han Chinese, China
CLM:	Colombian in Medellin, Colombia
CPU:	Central Processing Unit
DNA:	Deoxyribonucleic acid
DGVa:	Database of Genomic Variants archive
dbSNP:	The Single Nucleotide Polymorphism database
ESN:	Esan in Nigeria
FIN:	Finnish in Finland
FOXP2:	Forkhead box protein P2
GB:	Gigabyte
GBR:	British in England and Scotland
GIH:	Gujarati Indian in Houston, TX
GWAS:	Genome-wide association study
GWD:	Gambian in Western Division, The Gambia
HapMap:	Haplotype Map
IBS:	Iberian populations in Spain
IDE:	Integrated Development Environment
ITU:	Indian Telugu in the UK
JPT:	Japanese in Tokyo, Japan
kb:	Kilobyte
KHV:	Kinh in Ho Chi Minh City, Vietnam

kya:	Thousand years ago
LRR	Leucine-rich repeats
LWK:	Luhya in Webuye, Kenya
MAF:	Minor Allele Frequency
MB:	Megabyte
MNP:	Multinucleotide polymorphisms
MRC1:	Mannose Receptor C-type 1
MSL:	Mende in Sierra Leone
MXL:	Mexican Ancestry in Los Angeles, California
NCBI:	National Center for Biotechnology Information
NHGRI:	National Human Genome Research Institute
PC:	Personal Computer
PEL:	Peruvian in Lima, Peru
PJL:	Punjabi in Lahore, Pakistan
PRR:	Pattern Recognition Receptor
PUR:	Puerto Rican in Puerto Rico
RAM:	Random Access Memory
RPTN:	Repetin
SNP:	Single-nucleotide Polymorphism
SPAG17:	Sperm associated antigen 17
STR:	Short tandem repeats
STU:	Sri Lankan Tamil in the UK
TLR:	Toll-Like Receptor
TSI:	Toscani in Italy
TTF1:	Transcription Termination Factor 1,
YRI:	Yoruba in Ibadan, Nigeria

CHAPTER 1
INTRODUCTION

1.1 General Introduction

Archaic humans lived in more than 200,000 years in Europe and Western Asia (Dannemann *et al.*, 2016). They were well adapted to the surrounding environment and pathogens (Green *et al.*, 2010). Archaic humans are the subspecies of *Homo sapiens*, and include *Homo heidelbergensis*, *Homo rhodesiensis*, *Homo neanderthalensis* and *Homo antecessor*. Anatomically, there is a difference between Archaics and modern humans. Modern humans have evolved from archaics and *Homo erectus*. While modern human were migrating from Africa, they were faced with some difficulties such as different climate, environmental challenges and pathogens in the new region (Dannemann *et al.*, 2016). In the regions where they migrated from Africa, they hybridized with neanderthals and denisovans. Thus, some alleles passed from neanderthals to modern human.

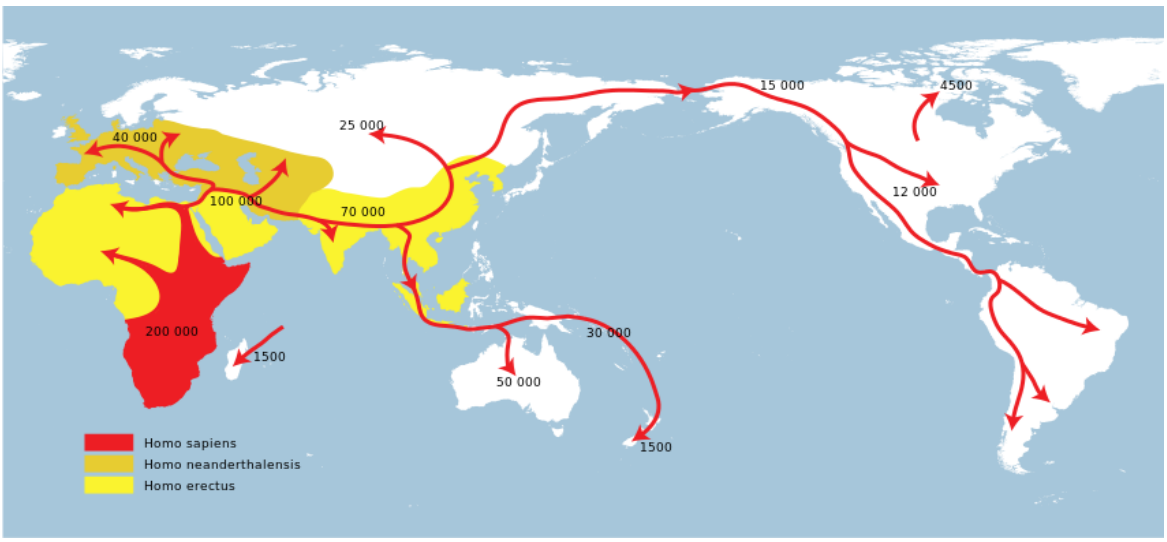


Figure 1.1: *Homo sapiens'* migration routes (adapted from Burenhult, 2000)

This study focused on the genomes which passed from neanderthals to modern humans. Neanderthals have evolved 250,000 years ago and known as *Homo neanderthalensis* (Villa and Roebroeks, 2014). Neanderthals were included geographical spread ranging from England to Siberia. They were squat and powerful hunters. 30,000 years ago *Homo sapiens*

began to spread in the world from Africa (Groucutt *et al.,* 2015). Therefore, Neanderthals and early humans encountered and they mated. Modern genetic data shows, Neanderthals mated with modern humans in Europe when they encountered. As a result, almost 1%- 4% of the modern humans genome consists from Neanderthals spesific genes. Those genes that passed from Neanderthals, provide us to fight against deadly viruses such as Epstein-Barr. However, modern human have received some origin of disease genes from Neanderthals such as Crohn's disease, type 2 diabetes, lupus, heart diseases, depression.

Pattern Recognition Receptors (*PPRs*) are proteins produced by the immune system to recognize microbial pathogens (Janeway and Medzhitov, 2002). In the last decade, Toll-like receptors are one of the most studied families of *PRRs* (Akira *et al.,* 2001). Toll-Like Receptors provide natural immunity against to many pathogens and these receptors recognize the structure of pathogens. Therefore, they are an important defense against pathogens. Toll-like receptors are known to respond to stimuli associated with various pathogens and to provide signal responses necessary for the activation of innate immune effector mechanisms and subsequent development of adaptive immunity (Dannemann *et al.,* 2016). In humans, the *TLR* gene family has 10 functional members (*TLR1 – TLR10*) (Akira *et al.,* 2006). *TLR3*, *TLR7*, *TLR8* and *TLR9*, find in intracellular compartments (Barreiro *et al.,* 2009). But, *TLR1*, *TLR2*, *TLR4*, *TLR5* and *TLR6* are expressed on the cell surface (Quintana-Murci and Clarck, 2013). Especially, Europeans and Asians carry an average of 1 to 4 percent Neanderthal DNA (Green *et al.,* 2010). As a significant proportion of these archaic-spesific DNA are found within *TLR1-TLR6-TLR10* gene cluster, this study focused on single nucleotide polymorphisms within this region.

Previous study indicated that modern humans carry three archaic-like haplotypes and three toll-like receptors passing from archaic humans were identified. Two of these haplotypes resemble to Neanderthal genome and other haplotype resemble to Denisovan genome. SNPs frequency commonly shared in neanderthal-like haplotypes vary in continents and populations. In Europe, allelic frequencies of Neanderthal-like core haplotypes is higher in Southern European populations (Dannemann *et al.,* 2016). For example, Toscani in Italy and Iberian populations in Spain (TSI and IBS with frequencies of 39.3% and 38.3%). And other Europe populations are Finnish in Finland (FIN), British in England and Scotland (GBR) and CEU (frequencies between 14.8% and 26.4%). In Asia, Neanderthal-like allele

frequency core haplotypes is higher in East Asian populations. Such as, Japanese in Tokio (JPT frequency is 53.4%) and Han Chinese (CHB frequency is 53.6%). Others Asians populations frequencies between 21.7% and 41.9% (Figure 1.2) (Dannemann *et al.*, 2016).

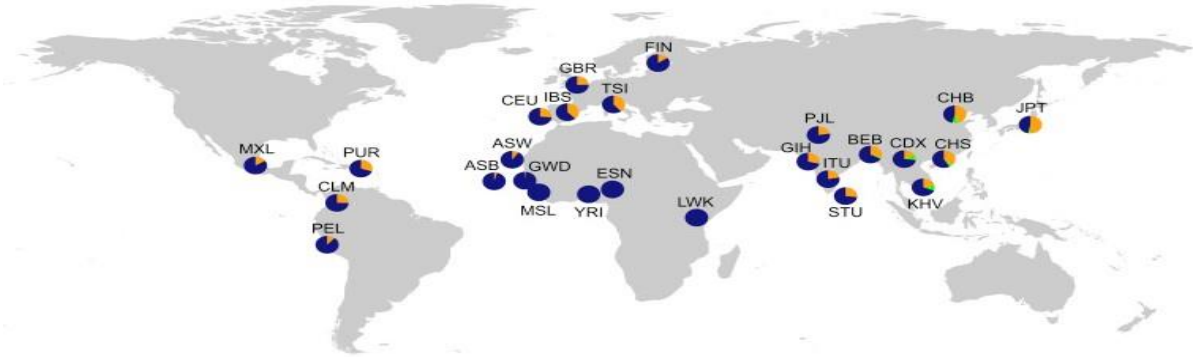


Figure 1.2: Geographic Distribution of the Neanderthal-like *TLR* Haplotypes. World Map in figure 1.2 shows, frequencies of Neanderthal core haplotypes. Archaic-like core haplotype is shown in orange and green; Non-archaic core haplotypes is shown in blue (adapted from Dannemann *et al.*, 2016)

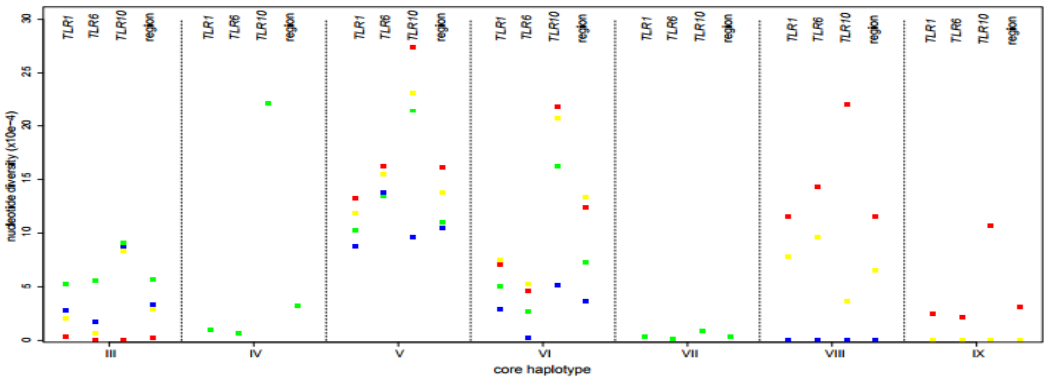


Figure 1.3: Nucleotide diversity within populations for core haplotype. Each color represents a different population (blue represent Europe, red Africa, yellow America and green Asia). III, IV and VII are archaic core haplotypes; V, VI, VIII and IX are non-archaic core haplotypes (adapted from Dannemann *et al.*, 2016)

Human populations that are outside Africa carry an average of 1 to 4 percent Neanderthal DNA (Dannemann *et al.*, 2016). Because, Humans had migrated to Asia and Europe from Africa. And additionally, those humans encountered and hybridized with Neanderthals in

these continents while migrating. These migration routes crossed over Middle-East and Levant region (Groucutt *et al.,* 2015). Georaphically, these regions cover the area surrounding the island Cyprus. With this knowledge, the populations such as Cypriots, Arabs, Turkish, Greek etc. that have been living in the Eastern Mediterranean coasts and surroundings ought to be hybridized with Neanderthals. Therefore, Cypriots (Turkish or Greek) might carry those archaic-like SNPs that have pathogenic effects on modern humans according to previous studies (Dannemann *et al.,* 2016).

1.2 Neanderthal Genome

After the discovery of the first fossils in 1829, new Neanderthal fossils began to surface in an area that covered almost all of Europe (Edgar and Johanson, 2006). Every new fossil which is found, gives us a better explain of what this species looks like. After the human's own genome was fully read in 2003 by the Human Genome Project, the eyes were surrounded by the species closest to us. One of the living candidates was a chimpanzee. The Chimpanzee Genome Project, which started in December 2003, gave its first results in September 2005. Genomic similarities between chimpanzee and human have shed lighted on many evolutionary studies (Culotta and Pennisi, 2005). However, in evolutionarily, there was a species much closer to us than chimpanzees. These species are Neanderthals. But, this species closest to *Homo sapiens* on earth was not alive anymore. And, the only examples that could be obtained were 30-40 thousand years old bone fossils. In Neanderthal genome project, the genome was obtained from the bones found in the Vindija cave. The extracted Neanderthal DNAs were compared to the DNA of five different modern humans (French, Chinese, Papua New Guinea, and Africans from San and Yaruba groups) (Green *et al.,* 2010). The results from the initial analyzes showed that Neanderthal DNA was much more similar to the non-African population's DNA than the African ones. The simplest explanation of this similarity was that there was a gene flow between Neanderthals and humans. There were significant differences between the modern human and the Neanderthal in four different genes. These were *SPAG17* is responsible from sperm motility (Zhang *et al.,* 2005), *PCD16* is responsible from wound healing (Matsuyoshi and Imamura, 1997), *TTF1* is responsible from gene reading, and *RPTN* genes with high expression in hair follicles, skin, and sweat gland (Richard and Manley, 2009). Apart from these, the *MRC1* gene, also found in Neanderthals and modern humans played a role in cell

communication. However, the Neanderthals carried a special mutation in the *MRC1* gene. This mutation was not appear in humans. This mutation had lead to the formation of a pale skin color and red hair for Neanderthals (Kundu *et al.,* 2014). Another gene from the results is the *FOXP2* gene. In modern humans, when the *FOXP2* gene does not work. This gene is called speech gene because speech disorders occur. Also, this gene found in Neanderthals and chimpanzees (Enard *et al.,* 2002). Like these, there are differences in DNA levels among many genes. However, the results show that 99.7% of the human and Neanderthal genome are exactly the same, besides that, human and chimpanzee genome shows 98.8% similarity (Than, 2010).

1.3 Human Genome

In the late 20th century, advances and developments in technology have enabled research on genomic datas. Nowadays, The gene flow between species and when this gene flow occurs can be determined (Altinisik, 2016). In 1987, Rebecca Cann *et al.,* examined mitochondrial genomes of 147 different individuals. It has been shown that the mitochondrial origins in all humans are based on Africa (Cann *et al.,* 1987). Meaning that, all humans have been common ancestor in their roots of mother. In as much as, the mitochondrial DNA is transferred to each humans from their mother (Altinisik, 2016).

Humans had been evolved from *australopithecus* at southern and eastern Africa in 2.5 million years ago. These archaic women and men emigrated to Europe, Asia and North Africa (Harari, 2015). As the spreading area expands, they were encounter with other hominid groups (Neanderthals, Denisovans and other Archaic humans) (Wall *et al.,* 2016). Environmental factors have been shaped the process of human evolution. Surviving in the snowy forests of northern Europe requirement different factors than the moist forests of the indonesian. As a result, many different species came up (Table 1-1). *Homo sapiens* anatomically appeared in africa 200,000 years ago. 50,000 years ago, they achieved modern behavior. They have the abilities of upright posture, abstract thinking, speaking. These capabilities have made they possible to build a wide range of tools, unlike other species in the world. 100,000 years ago, at least six different species of human were lived in the world simultaneously (Harari, 2015). However, in the last 10,000 years, *Homo sapiens* are the only human species living on the earth (Figure 1.4) (Harari, 2015).

SPECIES	HABITAT	AGE RANGE kya
Homo Habilis	Africa	2100-1500
Homo Erectus	Africa, Eurasia(Java,China,India,Caucasus)	1900-70
Homo Rudolfensis	Kenya	1900
Homo Gautengensis	South Africa	1900-600
Homo Ergaster	Eastern and Southern Africa	1800-1300
Homo Antecessor	Spain	1200-800
Homo Cepranensis	Italy	900-350
Homo Heidelbergensis	Europe, Africa, China	600-350
Homo Neanderthalensis	Europe,Western Asia	350-40
Homo Naledi	South Africa	335-236
Homo Tsaichangensis	Taiwan	190-10
Homo Rhodesiensis	Zambia	300-120
Homo Sapiens (Modern Human)	Worldwide	300-present
Homo Floresiensis	Indonesia	190-50
Denisova Hominin	Around Russia	40

Table 1.1: The time intervals and regions inhabited by *homo* species (DiMaggio, 2015; Ferring *et al.*, 2011; Bischoff, *et al.*, 2003; Chang *et al.*, 2015; Zimmer, 2017; Callaway, 2017)

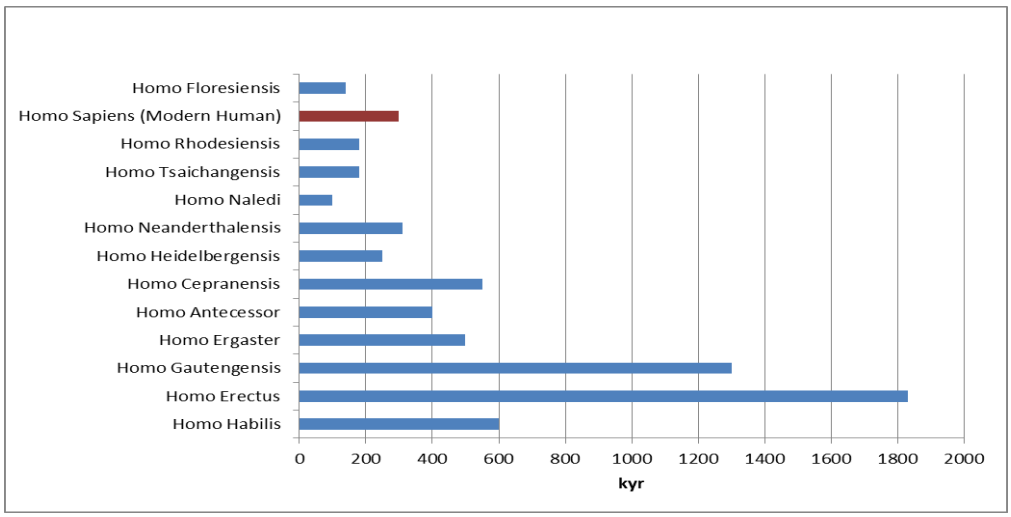


Figure 1.4: The age duration of hominid species in the world. Figure 1.2. shows, *Homo erectus* is the most lived species with 1.8 million years in world. But, *Homo sapiens* is the only live *homo* species in our present day. that is shown in red color in figure

The human genome consists of about $3.2x10^9$ nucleotides. Besides the number of the nucleotides, the genome has approximately 21.000 genes. The human genome is packaged in 24 (22 autosomal, X and Y) different chromosomes (Asan and Dagdeviren, 2012). In human cells, one copy of each chromosome is taken from mother (maternal) and an other one from father (paternal). These are called homologous chromosomes. Non-homologous chromosome pair is the sex chromosomes of males (X and Y chromosomes). While Y

always comes from father and X comes from mother. Thus, the autosomal chromosomes are the same in male and female. But, sex chromosomes are XY for male gender, XX for female gender. Basically, in total there are 46 chromosomes. 44+XY in male, 44+XX in female (Figure 1.5) (Asan and Dagdeviren, 2012).

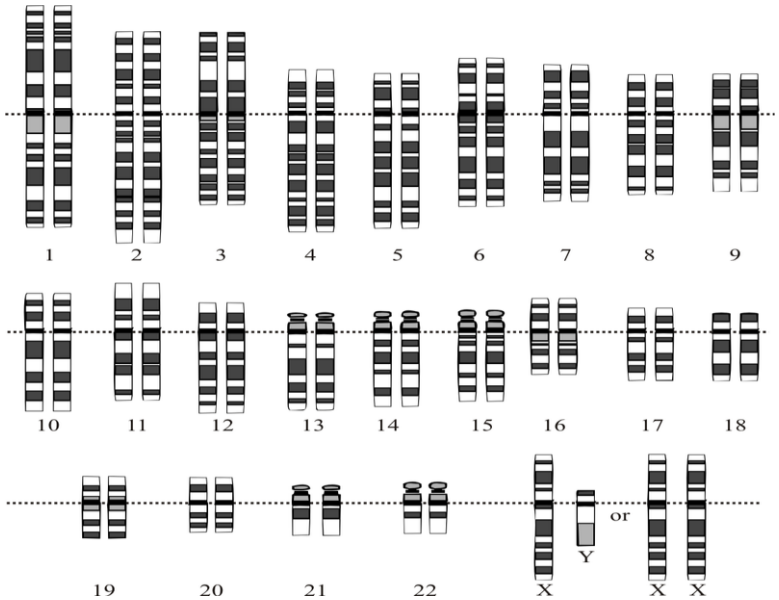


Figure 1.5: Karyotype of Modern Human (personal communication with Dr. Egoren)

1.4 International HapMap Project

The DNA sequence of any two human is approximately 99.5% common. Some human contain a A nucleotide in a certain area of their chromosome, while others contain G. An area containing such a difference is called SNP. And each of these two possibilities is expressed as an allele. One of the most important consequences of SNP is that it causes different genetic traits to be transmitted to the next generation. In brief, SNPs provides genetic diversity. In first stage of Meiosis division, parts of chromosomes break off with crossing-over. That parts can be replace and reconnect to chromosomes. Crossing-over is the parts exchange between the homologous chromatids. But, it causes recombination of genes, but does not cause structural changes in the chromosome. DNA polymorphisms may occur in regions of the protein coding or non-coding regions of the genes (Aksoy and Soydemir, 2017). A single nucleotide change is observed on DNA every 2,000-2,500 bases. This change occurs through transmission or transversion (Özden and Emir, 2006). Transmission is the conversion of a purine base to the other purine base (A → G or G →

A) or a pyrimidine base to another pyrimidine base (T → C or C → T). Furthermore, transversion is the conversion of a purine base (A, G) from pyrimidine bases (C, T) to one (Collins and Juke, 1994). Deletion is the nucleotide deletion from the DNA sequence. As a result, the length of gene is shortened. Inserion is the opposite of deletion. The nucleotide is inserted into the DNA sequence, and the length of the gene increases after insertion. If the gene is that encodes a protein, it will lose its protein function because the amino acid sequence of the protein will change. The HapMap project focuses on SNPs. Every human has two copies of all chromosomes, except for sex chromosomes in the male gender. Besides, allele combinations form the human genotype. The HapMap project had been examines 269 individuals and a few million identified SNPs. And, it published the genotype of these individuals (International HapMap consortium *et al.,* 2003). This project selected four different populations for phase I. 90 individuals from Ibandan, Nigeria (YRI), 90 from Utah residents of northern and western European ancestry (CEU), 44 from Tokyo, Japan (JPT) and 45 from Beijing, China (CHB) (International HapMap consortium *et al.,* 2003). In phase III, 11 global groups have been assembled, ASW, CEU, CHB, CHD, GIH, JPT, LWK, MEX, MKK, TSI and YRI. As a result, 1.6 million common SNPs were genotyped in 1,184 reference individuals in 11 global populations (International HapMap consortium *et al.,* 2010). Furthermore, 10 million common DNA variants have been identified by The Human Genome Project the SNP Consortium and the International HapMap Project (The International HapMap Consortium, 2007). This information along with linkage disequilibrium patterns allows an understanding of genome-wide association studies.

1.5 The Comparison of Neanderthal and Human Genomes

The first encounter between the *Homo sapiens* and the *Homo neanderthalensis* was won by the neanderthals. 100,000 years ago sapiens groups migrated to the north, to the east mediterranean. Those regions were the territory of the neanderthals and therefore, the sapiens could not settle. This may be due to unfavorable climate, local parasites or diseases. Whatever the cause, the *Homo sapiens* were pulled from that area and the middle east remained in control of the neanderthals. About 70 thousand years ago sapiens tribes came out of africa for the second time. This time the *homo sapiens* won and dominated the whole earth, not just the Middle East. They reached Europe and Eastern Asia in a short

period of time. They passed through the open sea about 45,000 years ago and reached in Australia, which was not reached by other humans-like species until that time (Harari, 2015). At the basis of these developments lies the cognitive revolution that emerged 70 to 30 thousand years ago. The cognitive revolution has added new thinking and new communication skills to sapiens. According to the most accepted theory for the cognitive revolution, genetic mutations have altered the internal structure of the brain of *Homo sapiens*. This change has allowed them to think in ways that have never been possible before, and to communicate in new languages (Harari, 2015). Why this mutation took place within DNA of *Homo sapiens* instead of neanderthals? The reason for this mutation to occur in human DNA is just a coincidence. According to this theory, the reason for our species domination of the world is caused only by a mutation that happened in our genes by chance. Since cognitive revolution, the *Homo sapiens* have been had the ability to renew their behavior according to changing needs. This is the basis for the *Homo sapiens* to develop more than other *Homo* species and to dominate the world nowadays.

Paabo *et al.* have been made studies on mitochondrial DNA of Neanderthals. As a result of which Neanderthals did not make any contribution to the modern human mitochondrial DNA (Wong, 2010). Green *et al.*, they examined the cell nucleus using three Neanderthal bones of 38-44 thousand years old, found in the Vindija cave of Croatia. In this study they scanned 60 percent of the Neanderthal genome and studied more than 4 billion nucleotides (Green *et al.*, 2010). After a sufficiently reliable sequence emerged, Neanderthal's genome was compared to five different modern human from different populations. These populations are France, China, Papua New Guinea, South Africa (San) and West Africa (Yoruba). As a result of this comparison, the genomes of European, Asian and Oceanian subjects showed a 1-4 percent association with Neanderthals (Green *et al.*, 2010). In contrast, did not show any similarity with the two African genomes. Although the interesting Neanderthal remains are not found in the East (China and Papua New Guinea), the modern humans living there are as similar to Neanderthals as same rate with the Europeans. Researchers think that modern people, after abandoning Africa about 100,000 years ago, probably made gene flow with the Neanderthals about 45-80,000 years ago in the Middle East or the Eastern Mediterranean (Green *et al.*, 2010). There are also genes that distinguish modern humans from Neanderthals. Researchers have detected 78

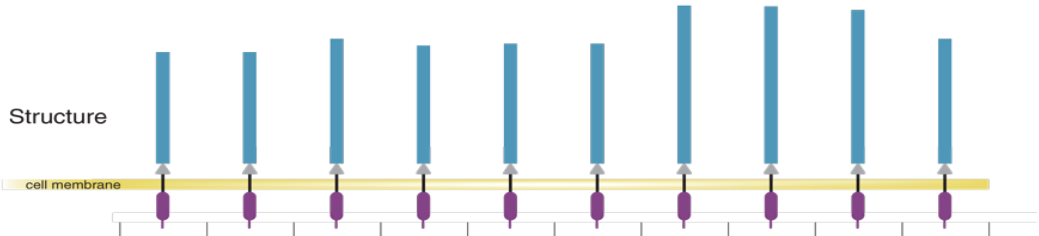
nucleotide differences in the encoded protein. Some of these are known to be related to energy metabolism, wound healing, cognitive development, skeletal development, sperm motility and skin physiology. Such as, mutations of genes related to cognitive development have links to Down syndrome, schizophrenia and autism (Green *et al.*, 2010). It is not yet known what the other differences are about and gives any advantage to modern human.

In 1910 many neanderthal skeletons were found in western and central Europe. According to the data obtained from these skeletons, Neanderthals could not stand upright and less intelligent than modern human. The biggest difference between neanderthal and modern humans is their strength and endurance (Papagianni and Morse, 2013). Neanderthals were stronger and endurance than modern human beings like other prehistoric species of *homo*. The arms and thighs of modern human were thinner than neanderthal. It was important to act quickly because they were hunter-gatherers (Helmuth, 1998). Modern human's hand are thought to have evolved for the delicate grip. Neanderthal males averaged 164 to 168 cm and females 152 to 156 cm tall (Helmuth, 1998).

1.6 Toll-like Receptors (TLRs)

Toll-like receptors are Type 1 transmembrane protein that allows natural immunity against pathogens (Janeway and Medzhitov, 2002). The immune system is divided into two parts, innate immune system and adaptive immune system. The innate immune system uses a tool-like receptor family to recognize natural immune pathogens that evolve during evolution and exist in all animal, plant classes. Toll genes, codes TLRs which is in protein structure. It has also been shown that TLR can mobilize the adaptive immune system in humans (Medzhitov *et al.*, 1997). In humans, the *TLR* family has 10 functional members (TLR1 – TLR10) (Akira et al., 2006). TLR3, TLR7, TLR8 and TLR9, find in intracellular compartments (Barreiro et al., 2009). But, TLR1, TLR2, TLR4, TLR5 and TLR6 are expressed on the cell surface (Quintana-Murci and Clarck, 2013). TLRs are located in membranes as homodimeric or heterodimeric proteins. The TLRs on the membrane outer surface contain LRR and the cytosolic portion contains TIR responsible for signal transduction (Turvey et al., 2010). TLR2 (associated with TLR1 or TLR6) recognizes lipoprotein and peptidoglycans. TLR4 performs recognition of lipopolysaccharides. TLR5 recognizes flajeline (a component of bacterial flasels) and TLR9 recognizes the bacterial CpG DNA sequence (Modlin, 2012). In this defense mechanism, the first and most basic event

that occurs in the host body is the recognition of the pathogen entering the body and the establishment of an inflammatory and immune host response to this pathogen as soon as possible (Utahaisangsook *et al.*, 2002). The human *TLR* genes are located on chromosome 4p14 (*TLR1*), 4q32 (*TLR2*), 4q35 (*TLR3*), 9q32-33 (*TLR4*), 1q33.3 (*TLR5*), 4p16.1 (*TLR6*), Xp22.3 (*TLR7*), Xp22 (*TLR8*) ve 3p21.3 (*TLR9*) (Utahaisangsook *et al.*, 2002). The cytoplasmic portion of IL-1R and the cytoplasmic portion of the Drosophila Toll resemble each other and this area is called the TIR domain (Anderson, 2000). All members of the Toll family are membrane proteins and have extracellular LRR receptors (Anderson, 2000). The extracellular part of the Toll family proteins is extended (550-980 amino acids) and has multiple binding sites (Anderson, 2000). LRRs are short protein modules of 20-29 amino acids and are found in several protein groups (CD14) in addition to *TLR* proteins (Takeuchi and Akira, 2002). *TLRs* have about 200 amino acids in cytoplasmic regions and have a TIR domain (Anderson, 2000).



	TLR1	TLR2	TLR3	TLR4	TLR5	TLR6	TLR7	TLR8	TLR9	TLR10
GenBank Accession #	U88540	U88878 AF051152	U88879	H48602 U88880 U93091	U88881 AF051151	AB020807	AF240467 AF245702	AF245703 AF246971	AF245704 AF259262 AF259263	AF296673
Chromosomal Location	4p14	4q32	4q35	9q32-33	1q33	4p14	Xp22	Xp22	3p21	unknown
# of Amino Acids	786	784	904	839	858	796	1049	1041	1032	811
Molecular Weight (kDa)	84	84	97	90	91	91	121	120	116	95

Figure 1.6: Structure of *TLR* family (adapted from https://resources.rndsystems.com)

This study focus on *TLR1*, *TLR6* and *TLR10*. These are a member of the Toll-like receptor family that plays a key role in the activation of innate immunity. *TLR1* is a protein coding gene. *TLR1*-related diseases are Leprosy 5 and Lyme Disease. It participates in the natural immune response against microbial agents. Especially diacylated and triacylated lipopeptides. Also, It works with *TLR2* to mediate natural immune response against bacterial lipoproteins or lipopeptides.*TLR6* is a protein coding gene. *TLR6*-related diseases are Neurosyphilis and Penicilliosis. It participates in the natural immune response against Gram positive bacteria and fungi. Especially diacylated and less precisely triacylated

lipopeptides. Like the others, *TLR10* is a protein coding gene. *TLR10*-related diseases are Theileriasis and Tonsillitis. It participates in the natural immune response against microbial agents like a *TLR1*(Gene Cards, 2017).

1.7 Software Systems

Software is the name given to all of the programs that enable electronic devices to do a particular functions. In other words, the programming language is used to solve existing problems. Some programming languages are C language, C++, Java, Pascal and etc.

The database is the domain in which information related to each other is stored. Nowadays, databases are using on banking, automotive industry, health information systems, such as in a wide range of computer systems are used to create the infrastructure. Databases, keeping information physically. Also, databases have a logical system.

The database software in this study was built using the C programming language. It is a programming language derived from B programming language in AT&T Bell Laboratories by Ken Thompson and Dennis Ritchie to develop the UNIX operating system (Lawlis, 1997). Despite its developed in 1972, it has been used almost 95% in almost all operating systems (Microsoft Windows, GNU/Linux, BSD, Minix) nowadays.

1.8 History of Cyprus: Cypriots

Cyprus is the third largest island of the Mediterranean. Cyprus is 75 km south of Turkey, 112 km west of Syria, 380 km north of Egypt and 800 km South east of Greece. The first human settlement on the island dates back 12,000 years. It is estimated that the first settlers came from Anatolia and Mesopotamia. Many civilizations dominated Cyprus throughout history (Terali *et al.*, 2014). These civilizations are Egyptians, Phoenicians, Assyrians, Persians, Ancient greeks, Lusignans, Venetians. In 1571 it was conquered by the ottoman empire. Then, island was leased to the kingdom of Britain until 1960. Today, two major ethnic groups live in Cyprus. These are Turkish cypriots and Greek cypriots. Other minor ethnic groups living in the island are Maronites, Armenians and Latins. Turkish Cypriots lived together with other ethnic groups in villages and towns throughout the island until 1963/1974. But in 1974 the Turkish Cypriots moved to Northern Cyprus as group and they started living here (Gurkan and Demirdov, 2014). As a result of the census carried out by the Turkish Cypriot authorities in 2006, the *de jure* population of North Cyprus is

256,644. In these population148,542 were born in Cyprus and 120,007 had both parents born in Cyprus (T.R.N.C. State Planning Organization, 2006).

1.9 Aim of the Study

Aim of this study is to collect previously identified archaic-like SNPs that have clinical significance via meta-analysis. Then, to determine diseases that related genetically to modern humans that received from Neanderthals. Secondly, to develope software program to merge previously identified achaic-like SNPs and their clinical pathogenity. Thus, this study and developed software will give us clues about the origin of the disease for modern humans. Finally, to desing an *in silico* model for clinicians and researchers to trace the history of the archaic alleles and determine the possible correlation with the persons' phenotype will provide better understanding to interpret the underlying mechanisms of the diseases.

CHAPTER 2

MATERIALS AND METHODS

2.1 Materials

2.1.1 Computer

Main material of this thesis was computer and puplished literature from several international genetic databases. The computer was used to create the necessary database for this study. The computer operating system that use in this study was windows 10 Pro. The system processor was Intel (R) Core (TM) i5 CPU and 2.53 GHz. Random Access Memory (RAM) was 3.00GB and memory of computer was 444GB. System type was 32-bit operating system and X64-based processor. The software that created the database was created using the c language via the computer. The software was written on visual studio C++ 2008 edition. Firstly, Visual Studio was loaded on a PC and it required 84 MB of free memory for load visual studio.

2.1.2 Genetic databases

Several well known international genetic databases are used for meta-analysis. These genetic databases are Ensembl (Ensembl, 2016), 1000genome (International Genome, 2016) and dbSNP (National Center for Biotechnology Information, 2014).

The Ensembl genome database project has been started in 1999 between the European Bioinformatics Institute and The Wellcome Trust Sanger Institute with a cooperation. The aim of this genetic database was to create a central resource for researchers who study our species, other vertebrates and model organisms. At Ensembl, sequence data was stored in the MySQL database. Ensembl made these data freely available to researchers around the world. All the data and codes generated within this browser are accessible online. In this browser, there was a database server providing remote access. Moreover, Ensembl has genome browser for different species; such as Ensembl Bacteria contains 44,039 genomes

(43,552 bacteria and 494 archaea) from 8244 species, Ensembl Fungi contains 735 genomes from 444 species, and Ensembl Protists contains 186 genomes from 116 species (Ensembl, 2016).

The 1000 genome project was the research initiated in January 2008 to create the most detailed catalog of human variations. The completion of the human genome project made it possible to obtain the genetics of the human populations and the nature of the genetic diversity. 1000 genome has been generated the largest common catalog of genotype data and human variants. According to populations, genetic data has been stored in 1000 genome databases. There are two genetic variants related to diseases; rare genetic variants with a severe effect, for example, Huntington Disease. And, the second one was the common variants that are mildly effective. The first goal of this database was to create a complete and detailed catalog of human genetic diversity. This catalog can be used in research and aims to estimate population frequencies. The second aim was genotyping of the human genome and the development of the human reference sequences. This database helped to understand the processes underlying the population variation, mutation and recombination (International Genome, 2016).

The Single Nucleotide Polymorphism Database (dbSNP) was created in September 1998. It has been developed by National Center for Biotechnology Information (NCBI) in cooperation with National Human Genome Research Institute (NHGRI). The dbSNP is a free public archive containing genetic diversity of different species. This database does not contain only polymorphisms (SNPs); however, it includes short deletion and insertion polymorphisms (Indels/DIPs), short tandem repeats (STRs), multinucleotide polymorphisms (MNPs), heterozygous sequence and named variants. In the dbSNP, more than 184 million submissions representing, representing over 64 million different variants for 55 organisms (National Center for Biotechnology Information, 2014).

2.2 Methods

At figure 2.1, the workflow of study was given. Firstly, clinical effects and allele frequencies data were collected via various international genetic databases (Ensembl, 1000 genome, dbSNP) by meta-analysis. Then, the database was created with using C programming language via Microsoft Visual studio C ++ 2008 edition. All data obtained by meta-analysis were added to the database. Finally, this completed database has been made available to the users via http://archaics2phenotype.neu.edu.tr.

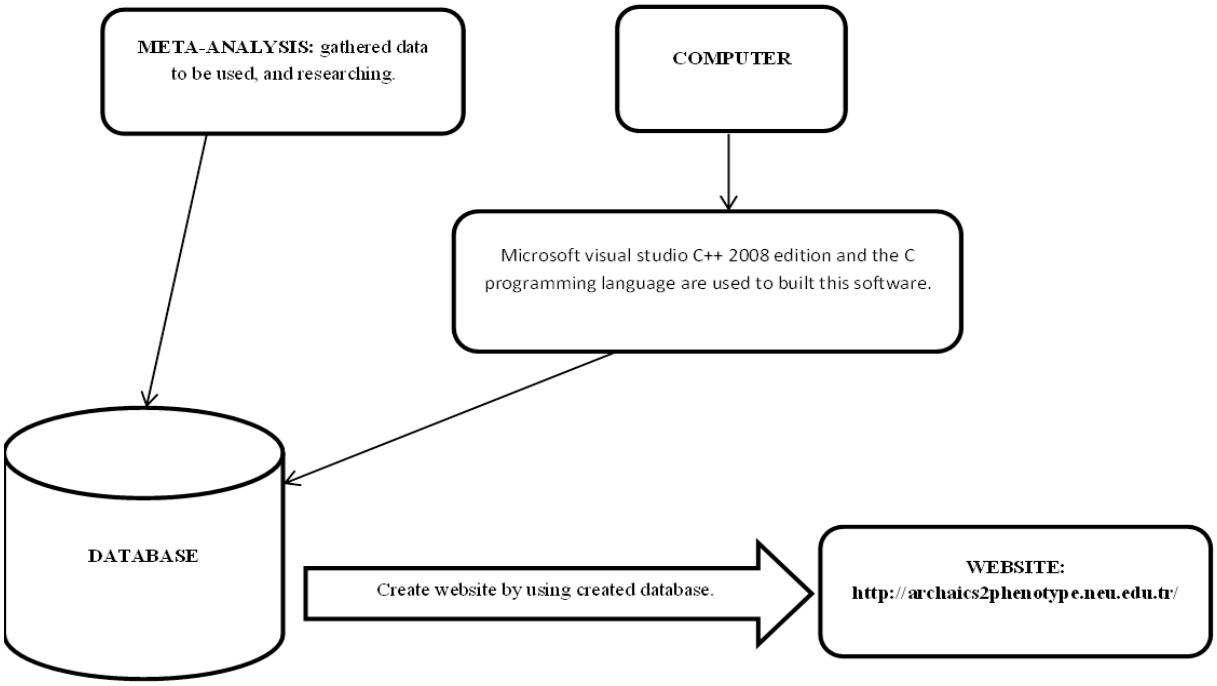


Figure 2.1: Demonstrates the workflow of this study

2.2.1 Determining SNPs within tool-like receptor *(TLR)* genes in human genome

Recent data by Danneman *et al.*, (2016) was used to determine the archaic-like SNPs within the human genome. Datas similar haplotypes of Neanderthal and Human genomes have been obtained fom 1000genome project, Ensembl genome browser 89 and Danneman *et al.*, (2016). Danneman *et al.*, (2016) previously identified 79 archaic-like alleles within *TLR6-TLR1-TLR10* locus that indicating repeated introgression from archaic Humans. Meta-analysis was conducted to find out the clinical significance of those genetic

markers in 1000genome populations. 79 archaic-like SNPs determined by meta-analysis are shown in Table 2.1.

Dannemann *et al.,* (2016) have been used Neanderthal introgression maps of Sankararaman *et al.,* (2014) and Vernot *et al,* (2014) for identify archaic-like haplotypes potentially observed in modern human genomes. The introgression map presented by Sankararaman *et al.,* (2014) provides the possibility of emerging of SNPs on polymorphic positions of Neanderthals in modern humans. Vernot *et al.,* (2014), detected introgress regions of modern people. And, they have been compared these candidate regions with reference from Neanderthal genome. It uses introgression possibilities per SNP for all Asian and all European individuals. It has been calculated the difference between Neandertal probabilities according to distance between neighboring SNP pairs, including three *TLR* genes and an additional region of 50kb (Chromosome 4:38,723,860-38,908,438) (Deamann *et al.,* 2016). Potentially archaic-like SNPs in this region have identified different SNPs in 109 Yoruba individuals in the genome dataset of Neanderthal or Denisovan genomes. Consequently, Deamann *et al.,* (2016) have been agreed that this introgressed region covers chromosome 4 of 143 kb (Chromosome 4:38,760,338–38,905,731) and contains 61 archaic-like SNPs. This region overlaps with two haplotypes identified by Vernot *et al.,* (2014) (Dannemann *et al.,* 2016).

SNP ID	
rs6841698	rs11722813
rs10024216	rs2101521
rs10008492	rs17616434
rs10470854	rs4833103
rs4331786	rs6815814
rs4513579	rs7696175
rs10776482	rs5743810
rs4129009	rs1039559
rs10776483	rs5743794
rs11466657	rs5743788
rs11096955	rs7665774
rs11096956	rs7673348
rs11096957	rs7687447
rs4274855	rs6531672
rs11466645	rs6531673
rs11466640	rs7681628
rs7694115	rs2174284
rs11466617	rs3860069
rs7653908	rs17582830
rs7658893	rs2130296
rs11725309	rs721653
rs10034903	rs902136
rs10004195	rs11943027
rs12233670	rs17582893
rs6834581	rs2381345
rs4833093	rs1873195
rs6531663	rs17582921
rs4543123	rs6851685
rs4624663	rs6835514
rs4833095	rs1604834
rs5743604	rs974734
rs5743596	rs7688418
rs5743595	rs7665932
rs5743594	rs6531677
rs5743592	rs12642243
rs5743571	rs12641669
rs5743565	rs1115259
rs5743563	rs6824769
rs5743562	rs7664107
rs5743557	

Table 2.1: Determining 79 Archaic-like SNPs for study

2.2.2 Performing meta-analysis using international genetic databases

2.2.2.1 Ensembl genetic database

The Ensembl database has the ability to automatically generate graphical representations of the alignment of genes and other genomic data against a reference gene. These are called data fragments. Depending on the research of users, these parts can be opened individually for screen customization. The interface also allows the user to approach a region or move the genome in both directions. This database also shows data at various resolution levels that of DNA and amino acid sequences on from all karyotype to text. Graphics are completed with table images and the data was transferred directly to external with various standard file formats such as FASTA (Ensembl, 2016).

In this thesis, several well-known international genetic databases were examined for meta-analysis. Ensembl genome browser identifed SNPs related with clinical significance. Therefore, Ensembl was one of the picked genetic database for this study. However, information about the population frequencies and pathogenity effects of some archaic-like SNPs also were given by the browser. Besides clinical pathogenity information, chromosome locations, allelic information and other population genetic data such as minor allele frequency (MAF) values have been obtained from the Ensembl database. Given population genetic data are used for Archaic-like SNPs. For example, allele frequencies and genetic frequencies values of five main populations and twenty-six sub-populations were obtained for 79 Archaic-like SNPs. These findings has been obtained using different genetic databases. Nevertheless, the most accurate data has been used after examining the results obtained from different sources.

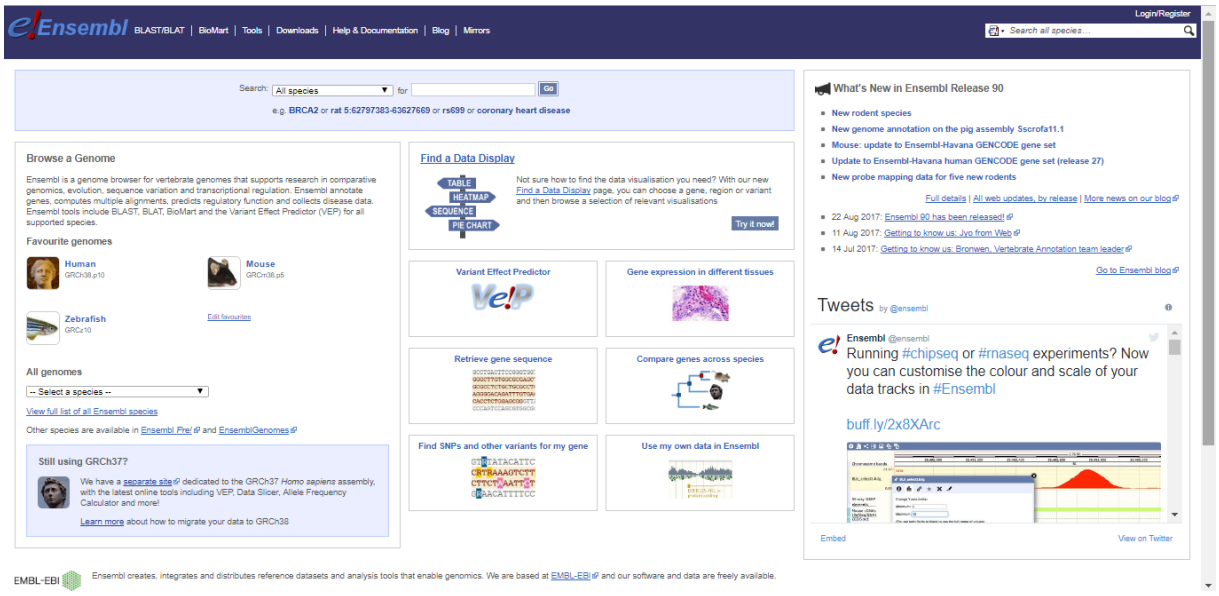


Figure 2.2: Homepage of Ensembl genome database was used as source in the study (adapted from http://www.ensembl.org/index.html)

2.2.2.2 1000genome

Voluntary donor samples were used in phase 3 of the 1000 genome project. The following populations were included in the 1000 genome database. These populations were Yoruba in Ibadan, Nigeria (YRI), Japanese in Tokyo (JPT), Chinese in Beijing (CHB), Utah residents with ancestry from northern and western Europe (CEU), Luhya in Webuye, Kenya (LWK), Maasai in Kinyawa, Kenya (MKK), Toscani in Italy (TSI), Peruvians in Lima, Peru (PEL), Gujarati Indians in Houston (GIH), Chinese in metropolitan Denver (CHD), people of Mexican ancestry in Los Angeles (MXL), and people of African ancestry in the southwestern United States (ASW). The genomic variants of phase 3 were stored in dbSNP and DGVA. Autosomal variants of phase 3 were added in the Ensembl database (International Genome, 2016).

Allele frequencies and genotype frequencies for Archaic-like SNPs has been taken from 1000 genome databases for this study. The data collected separately for eleven different populations. The comparision analysis was done between the results from the 1000 genome and the Ensembl databases. So the results obtained according to populations were examined from different sources. Thus, comparing the accuracy of the findings are important between different reference databases. As well as, diseases caused by these

SNPs were investigated in this database. Thus, diseases detected in the 1000 genome database but not in the Ensembl database have been added on thesis.

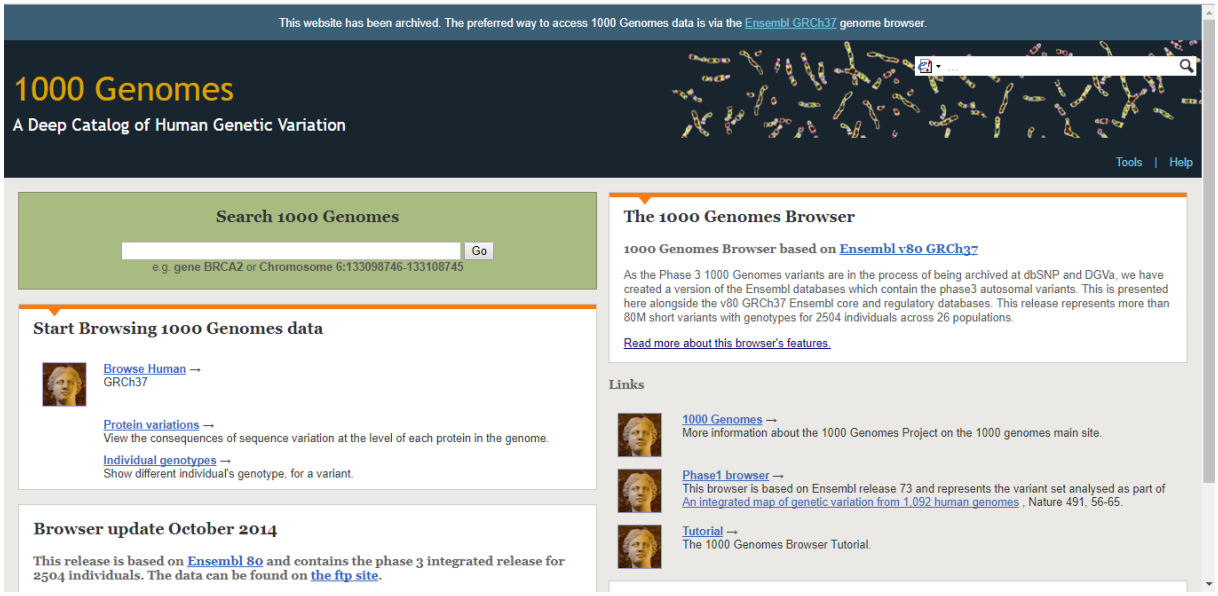


Figure 2.3: Homepage of 1000 genome database was used as source in the study (adapted from http://phase3browser.1000genomes.org/index.html)

2.2.2.3 dbSNP

dbSNP is an online resource applied to assist researchers. Purpose of these database, to create an extensive database for the investigation of genetic variations. The dbSNP was aiming to aid to in basic research, such as access to the molecular variation stored in this database, physical mapping, population genetics, and evolutionary research. In addition, it helps to correlate pharmacogenomic studies and phenotypic characteristics of genetic variation. In dbSNP, every variant sent receives a SNP ID number. These SNP IDs were the identifier for the variants. Also, for each clinical variations, more than one record can be present on dbSNP (National Center for Biotechnology Information, 2014).

In the dbSNP database we looked at allelic and genotypic frequencies relative to eleven different populations and compare them with 1000genome and Ensembl browsers to use the most accurate results. In addition, the provided data examined from all of the above mentioned international genetic databases in this thesis.

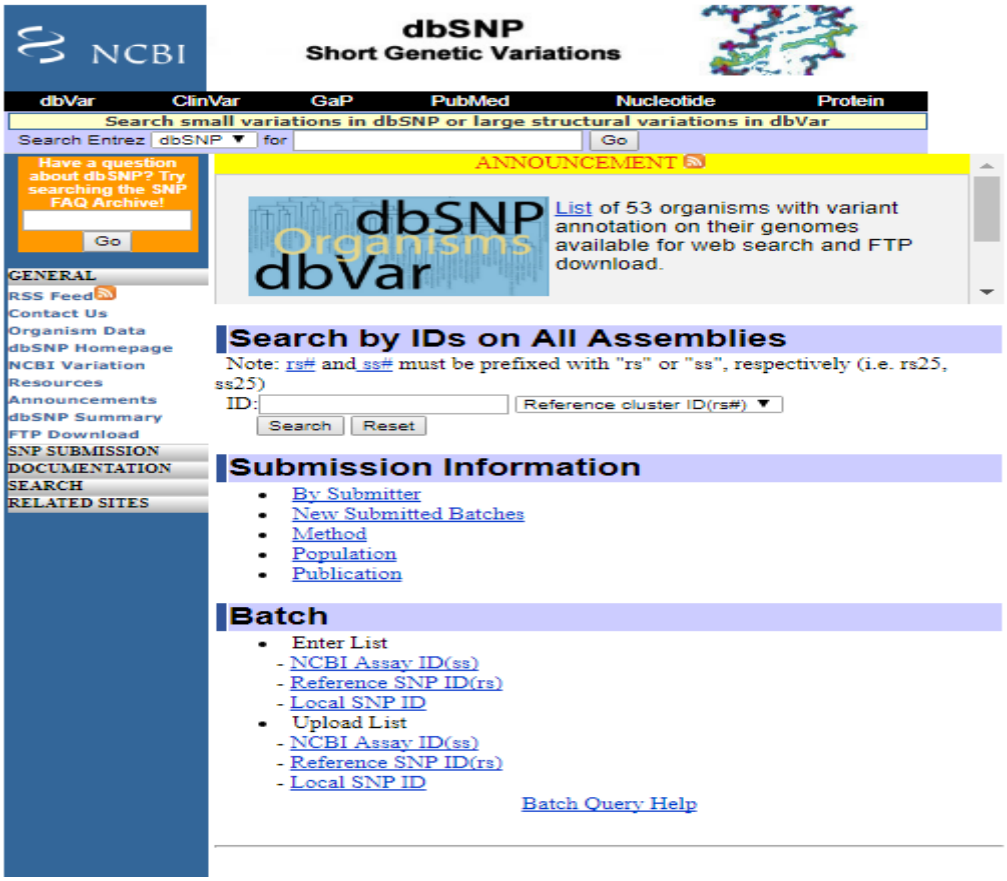


Figure 2.4: Homepage of dbSNP database was used as source in the study (adapted from https://www.ncbi.nlm.nih.gov/projects/SNP/l)

2.3 Creating Software with C Programming Language on Microsoft Visual Studio C++ 2008 Edition.

Computer and Microsoft visual studio C++ 2008 edition and the C programming language were used to built this software. Integrated development environment (IDE) of software is Microsoft visual studio C++ 2008 edition. This visual studio is software development platform. This platform was developed by Microsoft in 2008. This platform was developed in 2008 by Microsoft to create computer programs. In this visual studio can be written with the c or c ++ program language. In this study, the software was created with the c programming language. Visual studio only works on computers with windows operating system. For this reason, the computer operating system must be windows.

After installing visual studio on the computer, started to build the software. Steps taken to start writing computer program in a visual studio. As shown at below with figures.

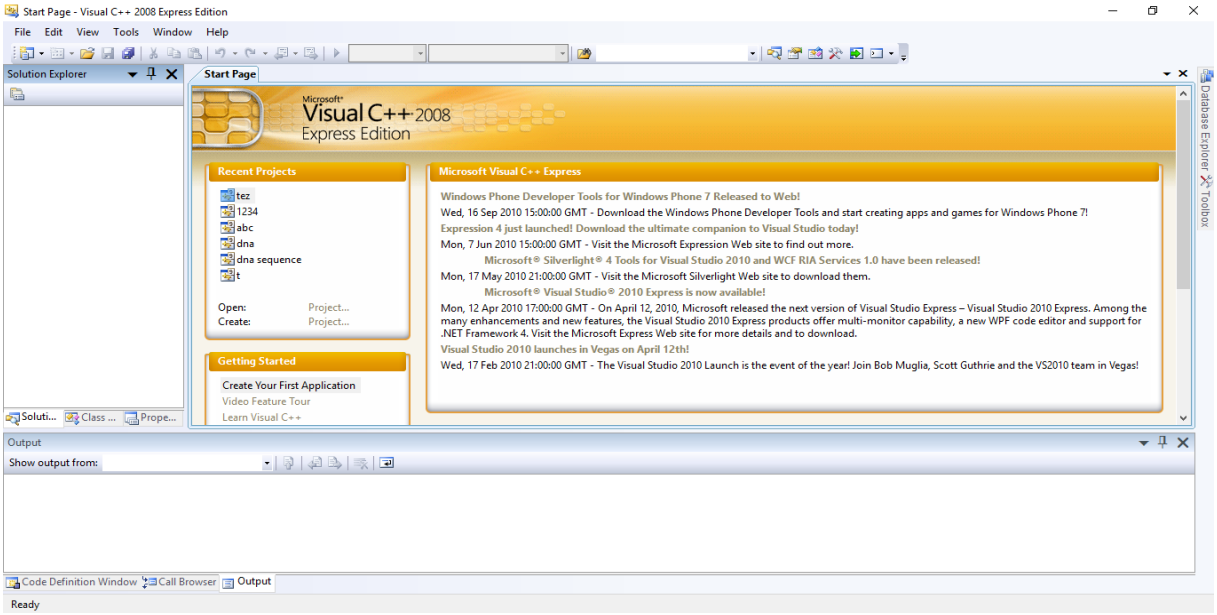


Figure 2.5: Home page of Microsoft visual studio C++ 2008 edition

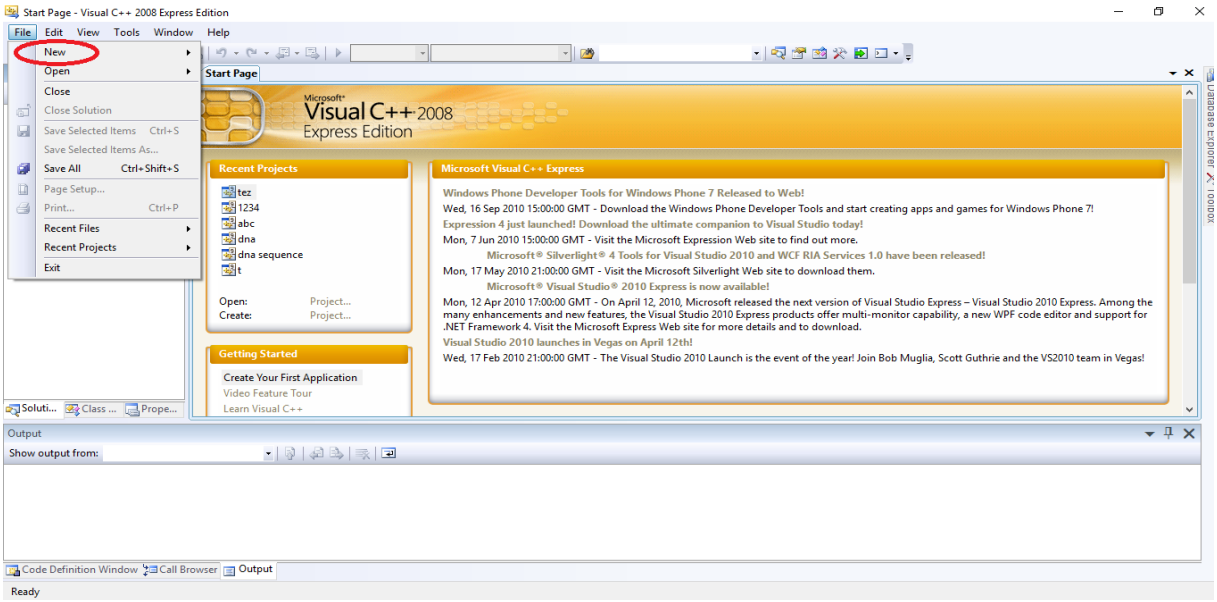


Figure 2.6: Step 1

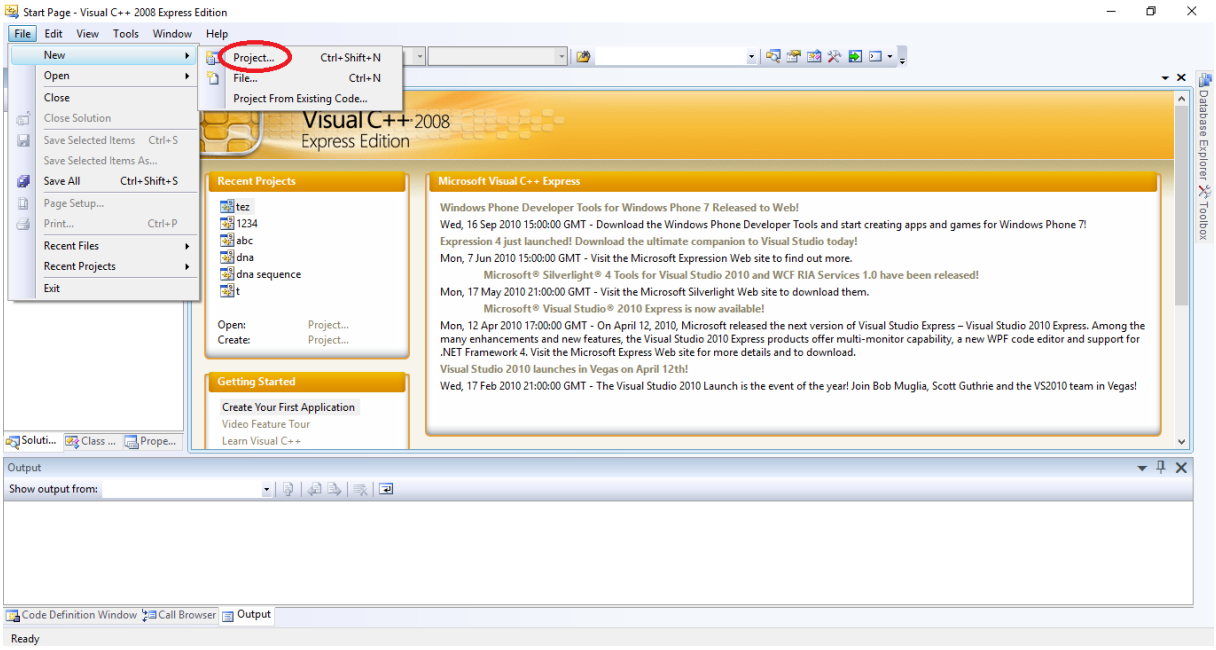


Figure 2.7: Step 2

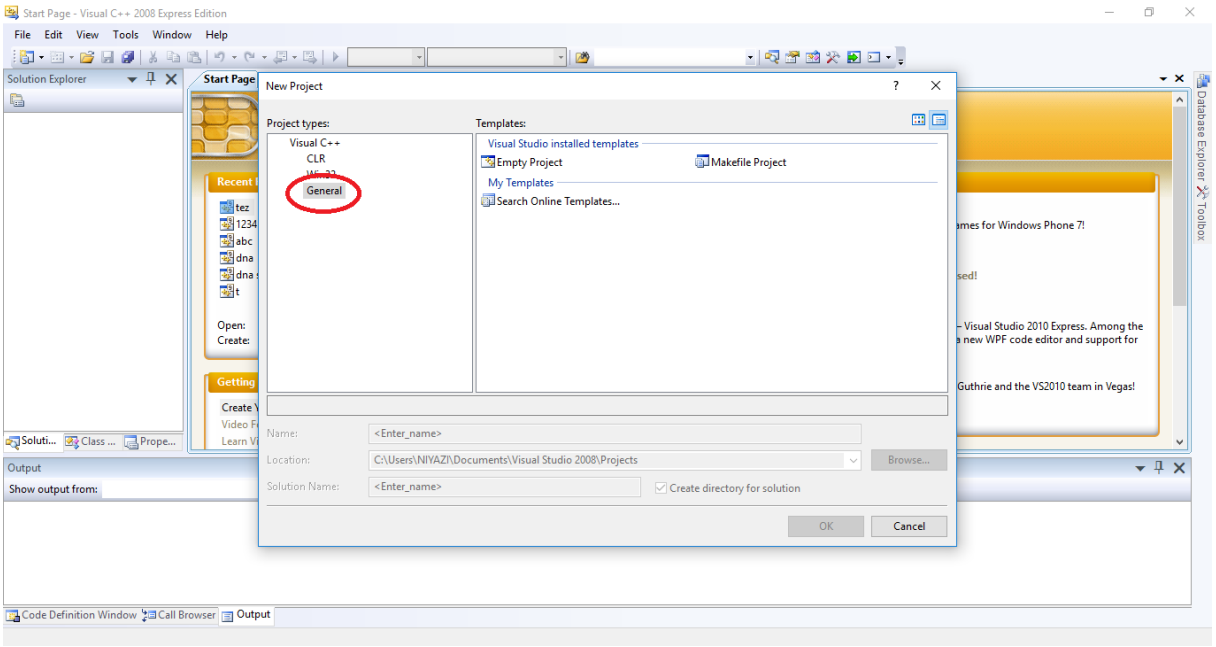


Figure 2.8: Step 3

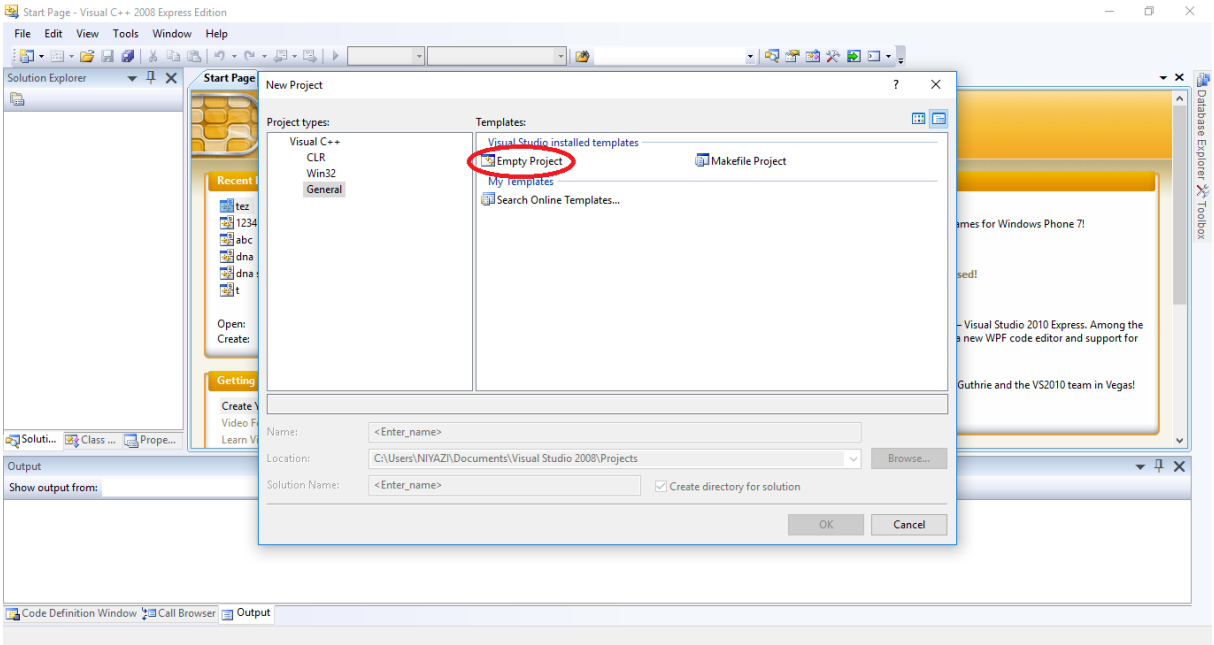


Figure 2.9: Step 4

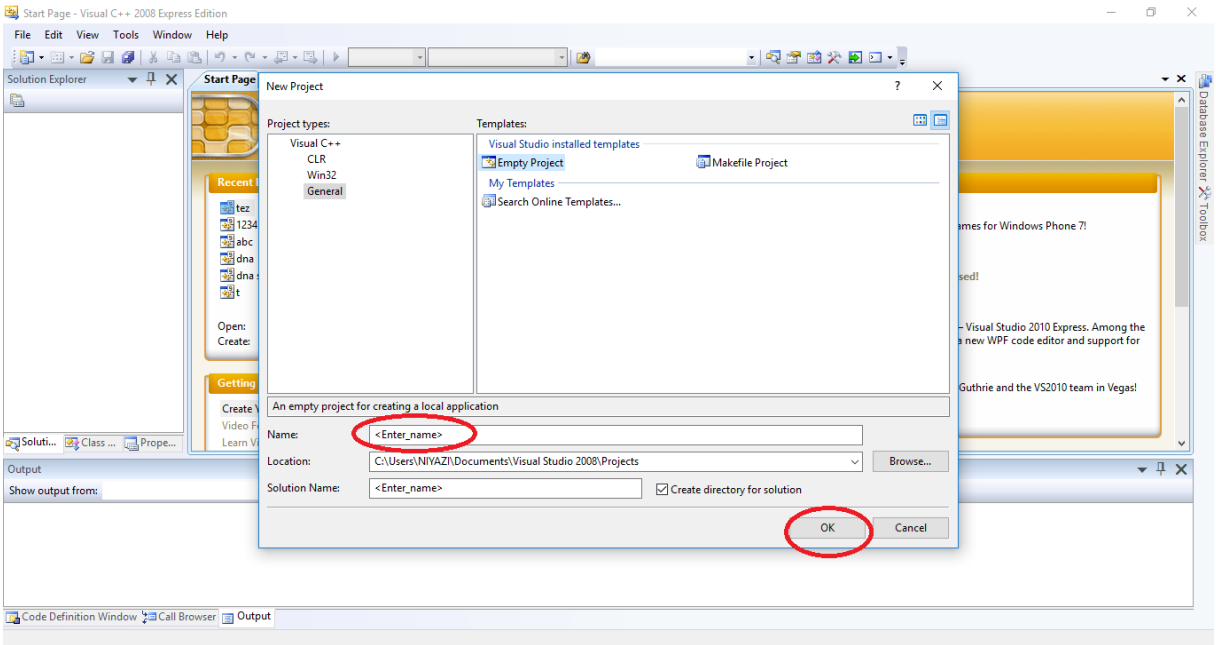


Figure 2.10: Step 5

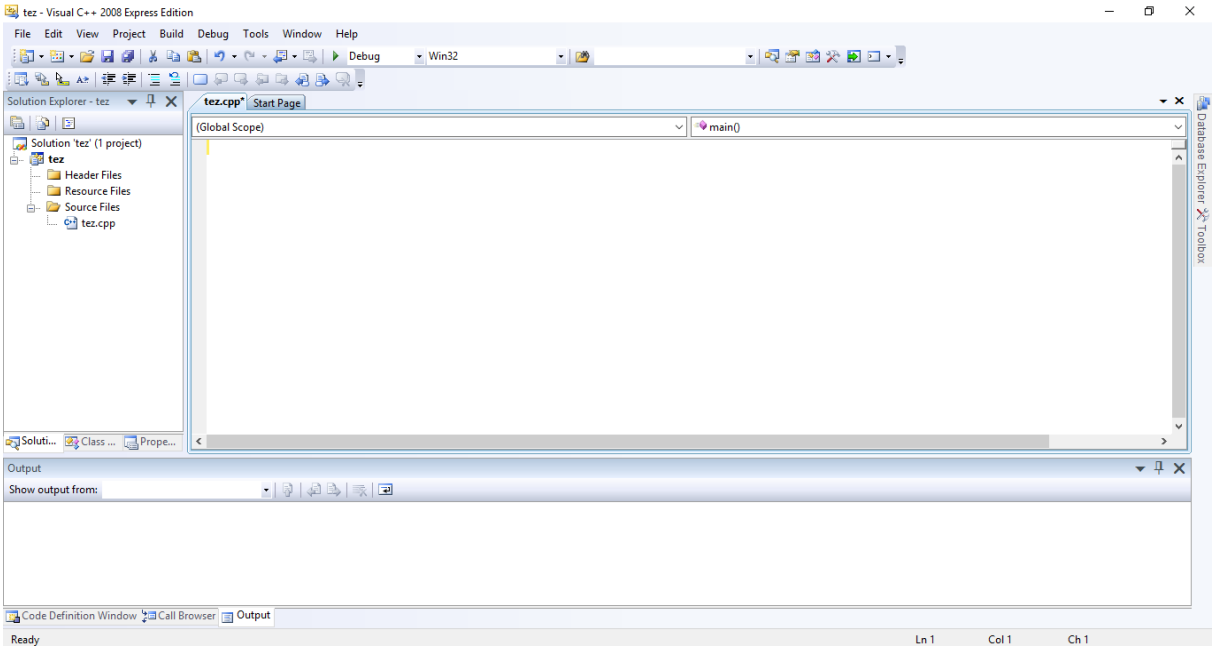


Figure 2.11: Step 6

First click file and then click new (Figure 2.6). After clicking new, click the Project (Figure 2.7). After clicking, New project part will be opened. Then, enter into the general part and selected new Project (Figure 2.9 and 2.10). After you selected the new project, the title of the new project file to be created was typed and clicked to OK button (Figure 2.10). The new project opens and Visual Studio platform was ready to write computer program to develop software (Figure 2.11).

The program started to write with standard input output header and Standard library header. These commands are shown in the following Figure 2.12. The #include <stdio.h> code is the code that adds the standard input and output files to the program. This code allows functions like functions printf () and scanf() to be used in the C programming language. These functions can not be defined by the programmer. These functions were defined in the program language library in visual studio. Thus, it is necessary to add header codes such as stdio.h to use the functions defined. The #include <stdlib.h> code is used to perform macro and general functions (Figure 2.12).

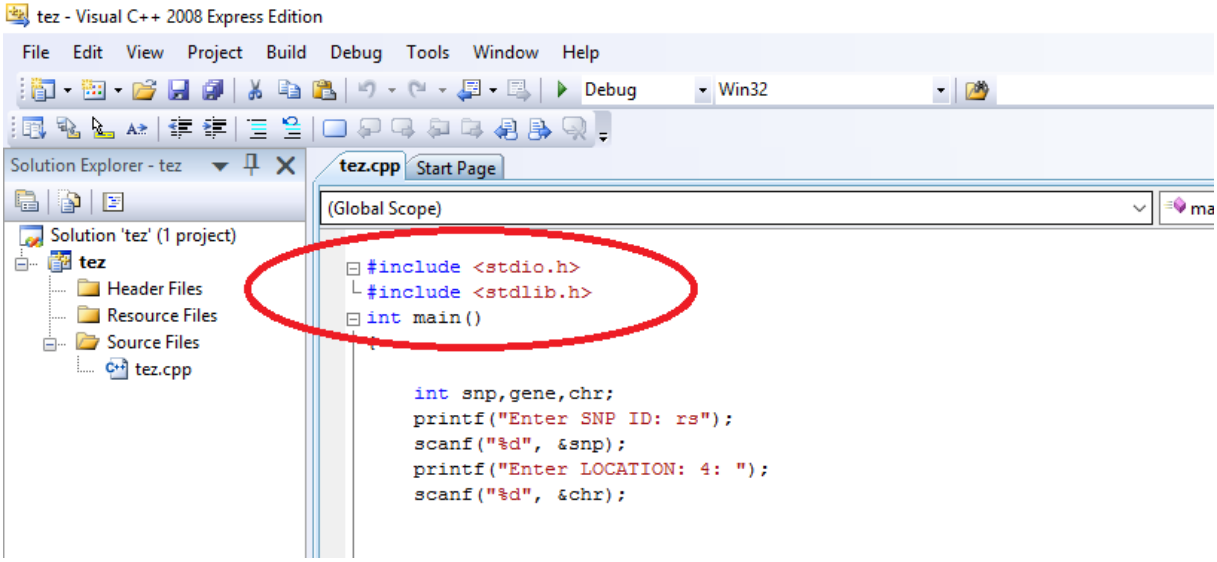


Figure 2.12: Standard input output header

Generated software can be divided into 2 separate sections. The first section is allowing the user to search on the created database. The second section is the part where the database was created. In the first part, software was created to allow the user to search at the created database in two different ways. User can search with SNP ID and chromosome location in created software. As shown in the Figure 2.13 below, in this part of the software firstly defined three characters with the int code. Snp character represents the SNP ID, chr character represents the chromosome location. Then, scanf and printf commands have been used. Printf() is a standard output function. Scanf() is a standard input function. Printf() command was printed "Enter SNP ID" and "Enter Chromosome Location" questions to screen. The scanf command allows the user to write SNP ID and chromosomal location to be searched for two questions displayed on the screen in this section. And, user can search on database with this command.

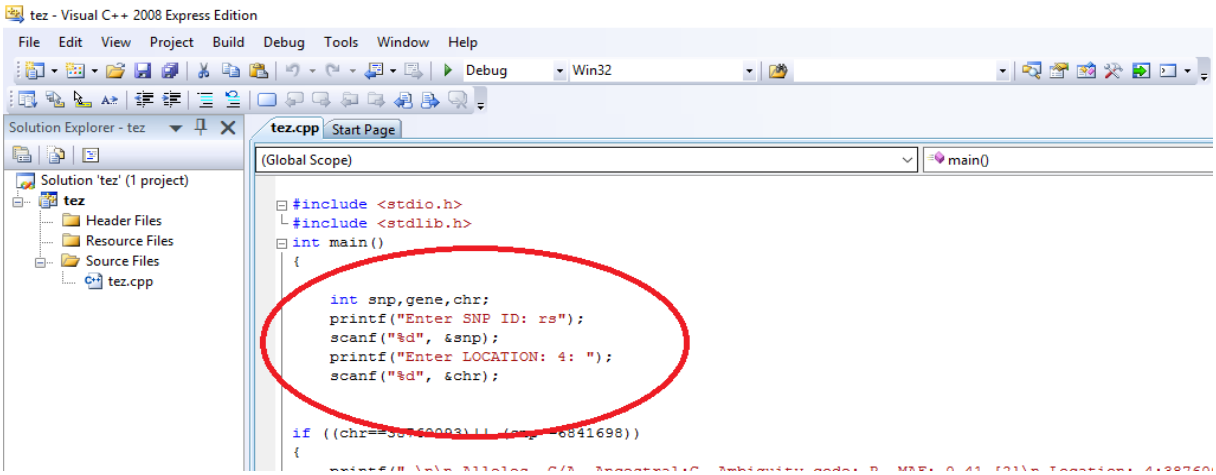


Figure 2.13: First section of program codes on Microsoft visual studio C++ 2008 edition

2.4 Desingning the *in silico* Genome Browser

The second part of the project was desinging the *in silico* genome browser for a first time to show the collection data of all identified Archaic-like SNPs and their clinical significance. Therefore a program algorithm was created to generate the database. The database section has been created using all the data collected for 79 archaic-like SNPs. The SNP variation of ancestral nucleotides, the diseases caused by the SNPs, as well as allele frequencies and genotype frequencies according to 1000genome populations were added to the program algorithm which was created separately for each SNP ID.

Algorithm structure of the database part on the software:

İf (Condition)

{

(functions)

}

Condition provides SNP ID and chromosome locations. If the user enters the SNP ID or chromosome location that provides the correct condition, the printf command is executed in the functions section. The printf() command prints all the data to screen have added to the database about the SNP IDs searched by the user. However, if the condition is not met,

ie if a SNP ID or chromosome location that is not in the database is searched for by the user, "No result" is printed on the screen.

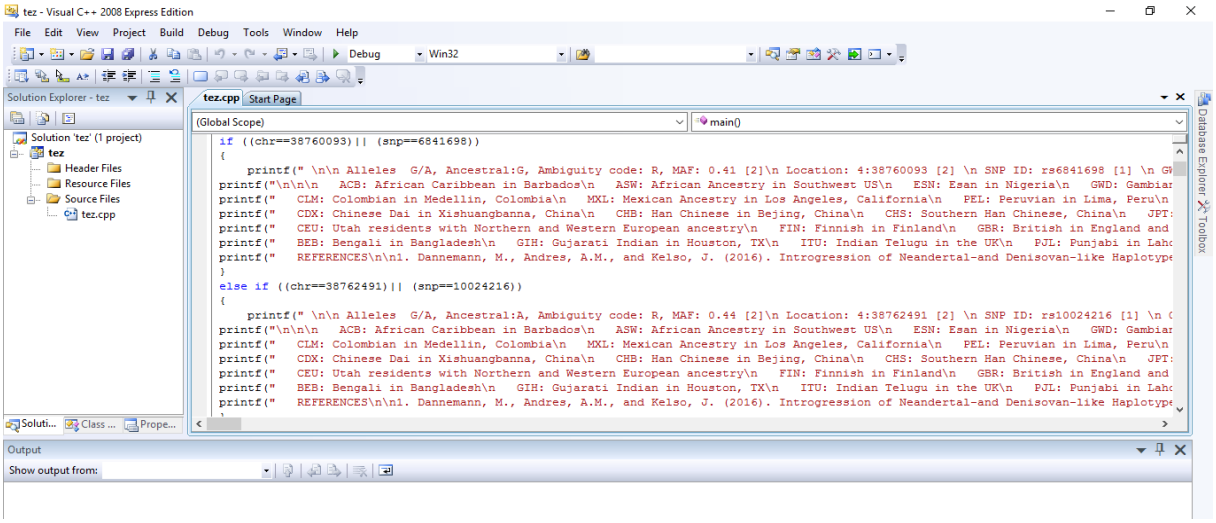


Figure 2.14: A database section of Software on Microsoft visual studio C++ 2008 edition

2.5 Desinging the archaics2phenotype.neu.edu.tr.

Figure 2.15 gives the interface design of the archaics2phenotype.neu.edu.tr. The website was designed as four main sections. These sections are homepage, about us, user guide and contact. The users first accesses the homepage of website. Homepage is search browser. User can make search with SNP IDs and chromosome locations. The user can access the other sections by clicking once. The description of these four sections is given below.

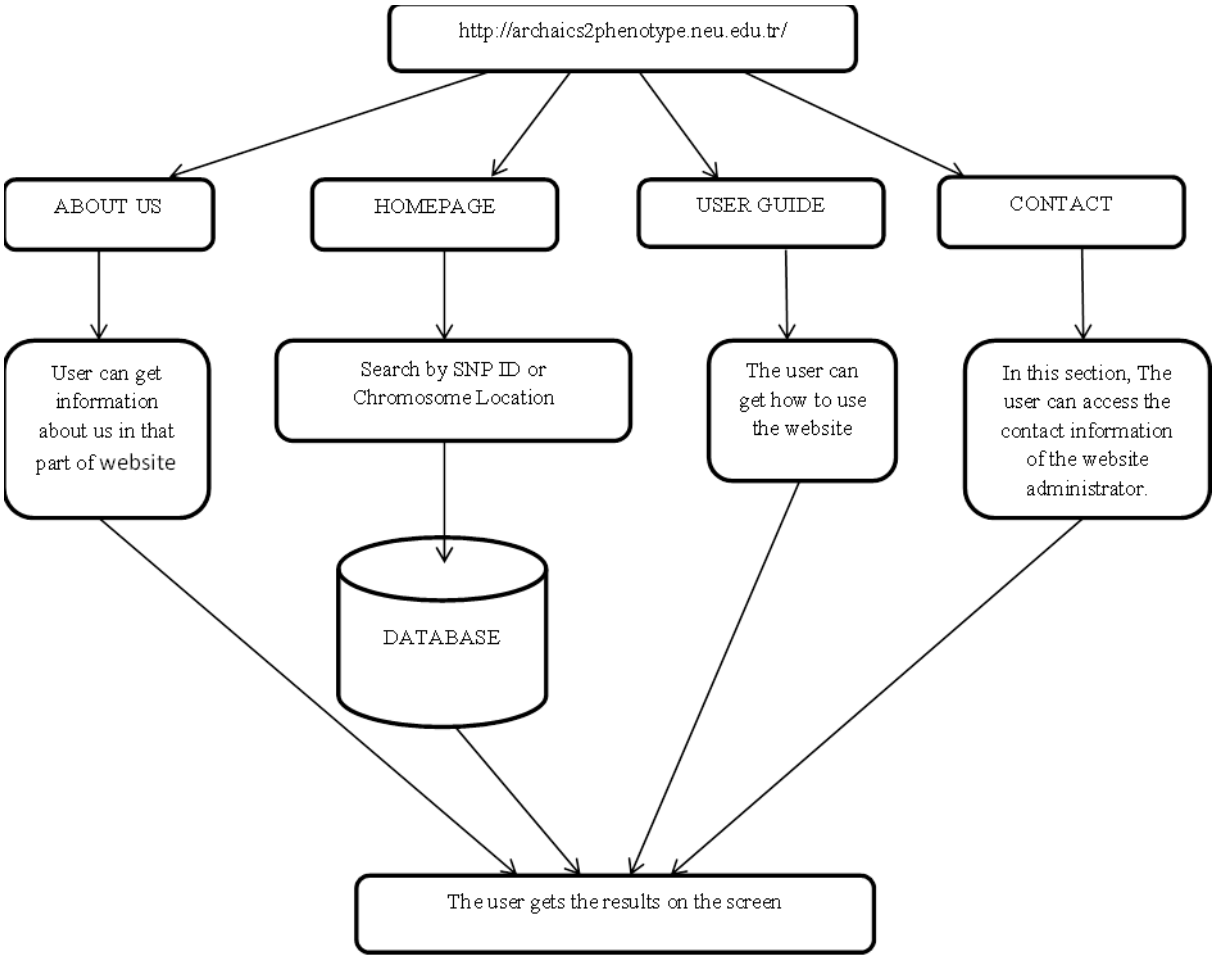


Figure 2.15: Workflow of designed archaics2phenotype.neu.edu.tr

The most important section is the homepage. Because the user can search by SNP IDs or chromosome locations with search browser in this section as mentioned before. if there is a matching result in the database about the SNP ID or chromosome location searched by the user, Website is designed so user can see this matching result on the screen. In the About Us section, the user can get general information about the website. The user guide section was designed for guide to users on the website. In short, it shows the user how to use the website. Contact section was designed to allow the user to communicate with the website administrator. If the user wants to ask anything about the website, or if user wants to learn anything about the website, They can contact from this section (Figure 2.15).

CHAPTER 3

GENERATING THE POPULATION GENETIC DATA BY IDENTIFIED ARCHAIC-LIKE SINGLE NUCLEOTIDE POLYMORPHISMS USING 1000GENOME POPULATIONS: META-ANALYSIS

3.1 Introduction

Archaic humans were adapted to environment and pathogens in Europe and West Asia because, they lived in these regions for more than 200,000 years. Studies determine that, the ancestors of modern humans migrated from Africa, and were hybridized with archaic humans. Therefore, some alleles were transferred to the modern humans from archaic humans. Resulting, almost 1-4% of modern humans' genome consists from Neanderthal-specific genetic materials. Additionally, scientists suggest that these passing alleles help the humans for fighting against viral pathogens (Dannemann *et al.*, 2016).

On the other hand, Wall *et al.* (2016) asserted present day humans carried Neanderthal genome between 1.5–2.1% in non-African populations. However, that percentage can change by populations. For instance, East Asian populations have more Neanderthal DNA than Europeans (Wall *et al.*, 2013). In 2016, researchers studied Oceanian populations and they have revealed that, Oceanian populations carried more Neanderthal DNA than others non-African populations (Sankararaman *et al.*, 2016). Controversy, Vernot *et al.* (2016) defended opposite and suggested Oceanian groups carried less archaic DNA than other non-African populations. The reason of different results in two studies is relied on two different Oceanian population structures have been studies. While, Sankraraman *et al.* (2016) analyzed samples of Papuans, Indigenous Australians and Bougainville islanders, Vernot *et al.* (2016) analyzed Bismarck Archipelago. These reveals, the amount of archaic DNA varies even in sub-groups within the population, and was influenced by historical differences between various Oceanian populations.

Toll-like receptors are a family of proteins. This protein family is very important for immune system. That protein family has 12 different members (*TLR1-TLR13)* (Mahla, 2013). Between 2-5% of Archaic-like genome located in *TLR1-TLR6-TLR10* genes cluster (Dannemann *et al.,* 2016). Dannemann *et al.,* (2016) have picked nine (I-IX) core haplotype sequences that are within the *TLR1-TLR6-TLR10* genes cluster. These haplotypes are Neanderthal (I), Denisovan (II), haplotypes of non-archaic (V, VI, VIII, IX) in present day humans and core haplotypes of archaic-like (III, IV, VII). Two haplotypes resemble to Neanderthal (III and IV) genome and other haplotype resemble to Denisovan (VII) genome. Neanderthal allele contributing through archaic-like SNPs within those seven core haplotypes that are compared with Neanderthal and Denisovan genome sequences. As result of this comparison, core haplotype III, IV and VII are most similar to archaic genome sequences than represents in the present-day humans. All non-African populations contain Neanderthal-like core haplotype III (11%-51%) and haplotype IV is exist in Asian populations (2%-10%). The core haplotype VII of Denisovan-like detected in two individuals of South Asian (Dannemann *et al.,* 2016).

The SNP frequencies that found in archaic-like haplotypes vary by continents and populations (Dannemann *et al.,* 2016). In European population, allele frequencies of archaic-like core haplotypes have been found to be higher in Southern European population (Dannemann *et al.,* 2016). Especially, allele frequencies are %39.3 in Tuscany population (Italy), %38.3 in Iberian population (Spain) (Dannemann, *et al.,* 2016). Other European population frequencies are between %14.8 - %26.4. In Asia, the allele frequency is higher in Eastern Asian population. For instance, allele frequencies of Japanese in Tokyo population is %53.4 (JPT), and frequencies of Han Chinese population is %53.6 (CHB), respectively (Dannemann, *et al.,* 2016). Other Asian population's frequencies are between %21.7 - %41.9 (Dannemann *et al.,* 2016).

3.2 Collecting the Data from Previously Identified Archaic-like Single Nucleotide Polymorphisms (SNPs)

At the beginning, meta-analysis was conducted to collect all the identified archaic-like SNPs. Meta-analysis combines the results of multiple independent studies in a given subject. We used three international genome browsers and scientific articles for meta-analysis. We determined 79 archaic-like SNPs from study of Dannemann *et al.* (2016). Then, 1000genome was used to check for SNPs registration and identification in the 1000genome populations.

Finally, clinical significance of those identified SNPs was determined using those genetic browsers. In this study, three different international databases were used to collect data; Ensembl genome (Ensembl, 2016), 1000genome (International Genome, 2016) and dbSNP (National Center for Biotechnology Information, 2014). Additionally, population genetic information was collected from 1000genome data by Ensemble. Thus, for each population, allele frequencies and genotype frequencies were obtained for each determined SNP (International Genome, 2016).

Table 3.1 shows selected 79 SNPs within the three determined archaic haplotype sequences. For each SNP, registered SNP IDs, polymorphic alleles, ancestral allele, and its ambiguity code and minor allele frequency (MAF) of each SNP is given.

Allele frequency is frequency of occurrence of a specific allele in a population. The number of individuals in a genotype to the ratio of individuals in the population is called the genotype frequency. For example, if A is dominant allele and T is recessive allele, we have three different possibilities for allele combination. These would be AA, AT or TT. Genotype frequency will be how often we see each allele combination in the population. But, allele frequency is how often we see each allele (A or T) in the population. So, numbers of A divided to total numbers of allele (total of A + total of T) or T divided to total numbers of allele in population.

Minor Allele Frequency (MAF) is less common allele frequencies in the populations for each identified SNPs. MAF amount was selected 0,005 or more at the HapMap project. But, that amount was selected less than 0.005 at 1000genome Project (The 1000 Genomes

Project Consortium, 2015). Thus, researchers were aimed to investigate low and rare variants for different populations.

SNP ID	ALLELES	ANCESTRAL	AMBIGUTY CODE	MAF
rs6841698	G/A	G	R	0.41
rs10024216	G/A	A	R	0.44
rs10008492	C/T	T	Y	0.17
rs10470854	G/A	G	R	0.49
rs4331786	C/T	T	Y	0.49
rs4513579	T/C	C	Y	0.30
rs10776482	A/G	G	R	0.30
rs4129009	T/A/C/G	T	N	0.15
rs10776483	A/G	A	R	0.30
rs11466657	A/G	A	R	0.02
rs11096955	T/C/G	T	B	0.50
rs11096956	C/A/T	A	H	0.30
rs11096957	T/G	T	K	0.50
rs4274855	C/T	C	Y	0.16
rs11466645	A/T	A	W	0.16
rs11466640	G/A	G	R	0.16
rs7694115	A/G	G	R	0.49
rs11466617	T/C	T	Y	0.16
rs7653908	G/C	G	S	0.26
rs7658893	G/A	A	R	0.43
rs11725309	T/C	T	Y	0.17
rs10034903	C/G	G	S	0.44
rs10004195	T/A	A	W	0.37
rs12233670	C/T	T	Y	0.41
rs6834581	T/C	T	Y	0.44
rs4833093	G/T	T	K	0.40
rs6531663	T/C	C	Y	0.45
rs4543123	A/G	G	R	0.37
rs4624663	T/C	T	Y	0.03
rs4833095	T/C	C	Y	0.43
rs5743604	A/G	G	R	0.47
rs5743596	G/A	G	R	0.14
rs5743595	A/G	A	R	0.18
rs5743594	G/A	G	R	0.05
rs5743592	A/G	G	R	0.18
rs5743571	C/T	C	Y	0.18
rs5743565	T/C	T	Y	0.18
rs5743563	A/G	G	R	0.18
rs5743562	T/C	T	Y	0.18
rs5743557	G/A	G	R	0.18
rs11722813	C/T	T	Y	0.18
rs2101521	G/A	A	R	0.48
rs17616434	T/C	C	Y	0.43
rs4833103	A/C	C	M	0.14
rs6815814	A/C	C	M	0.44
rs7696175	T/C	C	Y	0.22
rs5743810	A/G	G	R	0.12
rs1039559	G/A	A	R	0.33
rs5743794	C/T	C	Y	0.18
rs5743788	C/G	G	S	0.39
rs7665774	G/C	C	S	0.34
rs7673348	G/A	A	R	0.46
rs7687447	C/G	G	S	0.49
rs6531672	T/C	C	Y	0.33

rs6531673	T/C	C	Y	0.36
rs7681628	G/A	A	R	0.36
rs2174284	C/T	G	Y	0.16
rs3860069	A/C	A	M	0.46
rs17582830	A/G	A	R	0.21
rs2130296	A/G	G	R	0.20
rs721653	T/C	C	Y	0.45
rs902136	C/A/G	A	V	0.45
rs11943027	G/C	C	S	0.12
rs17582893	G/A	G	R	0.17
rs2381345	C/T	T	Y	0.43
rs1873195	C/T	C	Y	0.20
rs17582921	T/C	C	Y	0.17
rs6851685	G/T	T	K	0.24
rs6835514	A/G	G	R	0.37
rs1604834	G/A	A	R	0.44
rs974734	G/C	G	S	0.45
rs7688418	C/G	C	S	0.32
rs7665932	A/C	A	M	0.35
rs6531677	A/G	G	R	0.11
rs12642243	T/A	A	W	0.47
rs12641669	A/C	C	M	0.48
rs1115259	C/A/T	C	H	0.48
rs6824769	T/C	C	Y	0.49
rs7664107	A/T	T	W	0.47

Table 3.1: Determined 79 archaic-like SNPs and their variations of ancestral nucleotides. Alleles show the polymorphic nucleotides for each SNP. Ancestral allele is the trait/allele carried by the common ancestor of the investigated taxon. Ambiguity code shows the ambiguity bases in DNA sequences. MAF give information about the frequency of less seen allele for its SNP in the 1000genome data. In HapMaP phase III, The population genetic data of the twenty-six sub-population of five main populations (Table 3.2) has been used. So, on the database the average amount of all 26 sub-populations MAF values were given

3.3 The Selection of the International Genome Browsers

Three different international genetic data were selected as fundamental confirmation source for this study: Ensembl genome, 1000genome and dbSNP, respectively. The reason for using more than one browser was to compare their results between them and reach the most accurate result. Moreover, another advantage of using different browsers was combining every genome browser different sections. Thus, rich data was collected and varieties of sections were created as a meta-analysis for this study. Allele and genotype frequencies were obtained from 1000genome (International Genome, 2016) and Ensembl (Ensembl, 2016) population genetics' data. Allele and genotype frequencies of each SNP

differ from each population. As mentioned before, Allele frequency is the frequency of having a specific allele in an interested population. As determining the population specific archaic-like SNP data was very important in this study; five different major populations and twenty-six sub-populations were analyzed. Moreover, Ensembl was used to determine SNPs that might develop pathology; the findings also were compared with dbSNP (National Center for Biotechnology Information, 2014) data.

3.4 Merging the Population Genetics Data with Registered Archaic–like Single Nucleotide Polymorphisms (SNPs)

As mentioned in previous section, total number of thirty-one populations' genetic information was used. Table 3.2 illustrates all five-major population, African, American, East Asian, European and South Asian, respectively and their sub-populations.

POPULATION	Africa	America	East Asia	Europe	South Asia
SUB POPULATION	African Caribbean in Barbados	Colombian in Medellin, Colombia	Chinese Dai in Xishuangbanna, China	Utah residents with Northern and Western European ancestry	Bengali in Bangladesh
	African Ancestry in Southwest US	Mexican Ancestry in Los Angeles, California	Han Chinese in Bejing, China	Finnish in Finland	Gujarati Indian in Houston, TX
	Esan in Nigeria	Peruvian in Lima, Peru	Southern Han Chinese, China	British in England and Scotland	Indian Telugu in the UK
	Gambian in Western Division, The Gambia	Puerto Rican in Puerto Rico	Japanese in Tokyo, Japan	Iberian Populations in Spain	Punjabi in Lahore, Pakistan
	Luhya in Webuye, Kenya		Kinh in Ho Chi Minh City, Vietnam	Toscani in Italy	Sri Lankan Tamil in the UK
	Mende in Sierra Leone				
	Yoruba in Ibadan, Nigeria				

Table 3.2: Five main populations and twenty-six sub-populations were used for allele and genotype frequencies.That populations were shown on this table

The main and last list created from 79 carefully selected and previously identified archaic like SNPs (Dannemann *et al.*, 2016). Those SNPs are registered three mentioned genome browsers. For each SNP, allele and genotype frequencies, MAF, ancestral SNP

information, chromosomal location, and importantly, clinical significance were created. For example, Table 3.3 shows information of first selected SNP rs5743557.

Alleles G/A [2]	Ancestral:G [2]	Ambiguity code: R[2]	MAF: 0.18 [2]		
Location: 4:38804475 [2]					
SNP ID: rs5743557 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: The GWAS-identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.821	A: 0.179	G|G: 0.698	A|A: 0.056	A|G: 0.246
AFRICAN	G: 0.988	A: 0.012	G|G: 0.976	A|A: 0.000	A|G: 0.024
ACB	G: 0.974	A: 0.026	G|G: 0.948	A|A: 0.000	A|G: 0.052
ASW	G: 0.926	A: 0.074	G|G: 0.852	A|A: 0.000	A|G: 0.148
ESN	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
GWD	G: 0.991	A: 0.009	G|G: 0.982	A|A: 0.000	A|G: 0.018
LWK	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
MSL	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
YRI	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
AMERICAN	G: 0.852	A: 0.148	G|G: 0.741	A|A: 0.037	A|G: 0.222
CLM	G: 0.840	A: 0.160	G|G: 0.713	A|A: 0.032	A|G: 0.255
MXL	G: 0.891	A: 0.109	G|G: 0.797	A|A: 0.016	A|G: 0.188
PEL	G: 0.941	A: 0.059	G|G: 0.882	A|A: 0.000	A|G: 0.118
PUR	G: 0.764	A: 0.236	G|G: 0.615	A|A: 0.087	A|G: 0.298
EAST ASIAN	G: 0.607	A: 0.393	G|G: 0.385	A|A: 0.171	A|G: 0.444
CDX	G: 0.796	A: 0.204	G|G: 0.634	A|A: 0.043	A|G: 0.323
CHB	G: 0.466	A: 0.534	G|G: 0.223	A|A: 0.291	A|G: 0.485
CHS	G: 0.600	A: 0.400	G|G: 0.352	A|A: 0.152	A|G: 0.495
JPT	G: 0.442	A: 0.558	G|G: 0.183	A|A: 0.298	A|G: 0.519
KHV	G: 0.758	A: 0.242	G|G: 0.566	A|A: 0.051	A|G: 0.384
EUROPEAN	G: 0.779	A: 0.221	G|G: 0.622	A|A: 0.064	A|G: 0.314
CEU	G: 0.813	A: 0.187	G|G: 0.667	A|A: 0.040	A|G: 0.293
FIN	G: 0.904	A: 0.096	G|G: 0.818	A|A: 0.010	A|G: 0.172
GBR	G: 0.830	A: 0.170	G|G: 0.681	A|A: 0.022	A|G: 0.297
IBS	G: 0.692	A: 0.308	G|G: 0.495	A|A: 0.112	A|G: 0.393

TSI	G: 0.678	A: 0.322	G|G: 0.477	A|A: 0.121	A|G: 0.402
SOUTH ASIAN	G: 0.837	A: 0.163	G|G: 0.693	A|A: 0.018	A|G: 0.288
BEB	G: 0.779	A: 0.221	G|G: 0.581	A|A: 0.023	A|G: 0.395
GIH	G: 0.811	A: 0.189	G|G: 0.660	A|A: 0.039	A|G: 0.301
ITU	G: 0.882	A: 0.118	G|G: 0.775	A|A: 0.010	A|G: 0.216
PJL	G: 0.865	A: 0.135	G|G: 0.740	A|A: 0.010	A|G: 0.250
STU	G: 0.843	A: 0.157	G|G: 0.696	A|A: 0.010	A|G: 0.294
REFERENCES					
1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33					
2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html					

Table 3.3: Shows a detailed information for the SNP rs5743557. Detailed report was created for each SNP (see appendix). MAF, chromosomal location, clinical significance, allele frequencies for each population including sub-populations were reported

Alleles G/A [2]	Ancestral:G [2]	Ambiguity code: R [2]	MAF: 0.41 [2]		
Location: 4:387600093 [2]					
SNP ID: rs6841698 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.585	A: 0.415	G|G: 0.348	A|A: 0.178	A|G: 0.474
AFRICAN	G: 0.539	A: 0.461	G|G: 0.289	A|A: 0.210	A|G: 0.501
ACB	G: 0.474	A: 0.526	G|G: 0.219	A|A: 0.271	A|G: 0.510
ASW	G: 0.615	A: 0.385	G|G: 0.393	A|A: 0.164	A|G: 0.443
ESN	G: 0.566	A: 0.434	G|G: 0.313	A|A: 0.182	A|G: 0.505
GWD	G: 0.487	A: 0.513	G|G: 0.204	A|A: 0.230	A|G: 0.566
LWK	G: 0.606	A: 0.394	G|G: 0.394	A|A: 0.182	A|G: 0.424
MSL	G: 0.535	A: 0.465	G|G: 0.271	A|A: 0.200	A|G: 0.529
YRI	G: 0.528	A: 0.472	G|G: 0.278	A|A: 0.222	A|G: 0.500
AMERICAN	G: 0.576	A: 0.424	G|G: 0.343	A|A: 0.190	A|G: 0.467
CLM	G: 0.612	A: 0.388	G|G: 0.383	A|A: 0.160	A|G: 0.457
MXL	G: 0.523	A: 0.477	G|G: 0.250	A|A: 0.203	A|G: 0.547
PEL	G: 0.535	A: 0.465	G|G: 0.306	A|A: 0.235	A|G: 0.459
PUR	G: 0.611	A: 0.389	G|G: 0.394	A|A: 0.173	A|G: 0.433
EAST ASIAN	G: 0.599	A: 0.401	G|G: 0.367	A|A: 0.169	A|G: 0.464
CDX	G: 0.758	A: 0.242	G|G: 0.581	A|A: 0.065	A|G: 0.355

CHB	G: 0.534	A: 0.466	G|G: 0.272	A|A: 0.204	A|G: 0.524
CHS	G: 0.605	A: 0.395	G|G: 0.343	A|A: 0.133	A|G: 0.524
JPT	G: 0.375	A: 0.625	G|G: 0.115	A|A: 0.365	A|G: 0.519
KHV	G: 0.747	A: 0.253	G|G: 0.556	A|A: 0.061	A|G: 0.384
EUROPEAN	G: 0.645	A: 0.355	G|G: 0.427	A|A: 0.137	A|G: 0.435
CEU	G: 0.687	A: 0.313	G|G: 0.444	A|A: 0.071	A|G: 0.485
FIN	G: 0.667	A: 0.333	G|G: 0.485	A|A: 0.152	A|G: 0.364
GBR	G: 0.681	A: 0.319	G|G: 0.451	A|A: 0.088	A|G: 0.462
IBS	G: 0.612	A: 0.388	G|G: 0.364	A|A: 0.140	A|G: 0.495
TSI	G: 0.589	A: 0.411	G|G: 0.402	A|A: 0.224	A|G: 0.374
SOUTH ASIAN	G: 0.578	A: 0.422	G|G: 0.331	A|A: 0.176	A|G: 0.493
BEB	G: 0.610	A: 0.390	G|G: 0.337	A|A: 0.116	A|G: 0.547
GIH	G: 0.617	A: 0.383	G|G: 0.388	A|A: 0.155	A|G: 0.456
ITU	G: 0.564	A: 0.436	G|G: 0.294	A|A: 0.167	A|G: 0.539
PJL	G: 0.594	A: 0.406	G|G: 0.385	A|A: 0.198	A|G: 0.417
STU	G: 0.510	A: 0.490	G|G: 0.255	A|A: 0.235	A|G: 0.510

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1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Table 3.4: Gives an example of second studied SNP rs6841698

Alleles T/C [2]	Ancestral:C [2]	Ambiguity code: Y [2]	MAF: 0.43 [2]

Location: 4:38798089 [2]

SNP ID: rs4833095 [1]

GWAS Trait: Amyotrophic lateral sclerosis, Paget's disease, Helicobacter pylori serologic status, Alcohol consumption, Self-reported allergy, Leprosy, Asthma and Seasonal allergic rhinitis, Hay fever [1,2]

Archaic-like haplotype cluster: Not Known

Clinical Assertion Description: Schuring *et al.* (2009) studied association of an asn248-to-ser (N248S) SNP in the *TLR1* gene and leprosy (LPRS5; 613223) in a Bangladeshi population consisting of 842 patients and 543 controls. They found that the S allele was slightly more frequent among patients than controls (54% vs 51%; OR = 1.12). Homozygosity for S248 was significantly associated with leprosy per se (OR = 1.34), whereas heterozygosity was found to be protective against leprosy (OR = 0.78). In contrast, the homozygous N248 genotype was equally distributed among patients and controls. No difference in allele frequency or genotype was associated with leprosy classification or serologic status. However, patients who experienced erythema nodosum leprosum reactions were more likely to have the N248 allele (68%) than were patients who had no reactions (46%). Schuring *et al.* (2009) noted that amino acid 248 of *TLR*1 is located in the external ligand-binding site of the receptor, and that Omueti *et al.* (2007) had shown that the S248 variant enabled normal function, whereas the N248 variant diminished the response of *TLR1* to bacterial agonists. [3]

Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.425	C: 0.575	T|T: 0.232	C|C: 0.382	C|T: 0.386
AFRICAN	T: 0.120	C: 0.880	T|T: 0.015	C|C: 0.775	C|T: 0.210
ACB	T: 0.161	C: 0.839	T|T: 0.021	C|C: 0.698	C|T: 0.281

ASW	T: 0.230	C: 0.770	T|T: 0.049	C|C: 0.590	C|T: 0.361
ESN	T: 0.106	C: 0.894	T|T: 0.010	C|C: 0.798	C|T: 0.192
GWD	T: 0.142	C: 0.858	T|T: 0.018	C|C: 0.735	C|T: 0.248
LWK	T: 0.076	C: 0.924	T|T: 0.000	C|C: 0.848	C|T: 0.152
MSL	T: 0.071	C: 0.929	T|T: 0.000	C|C: 0.859	C|T: 0.141
YRI	T: 0.093	C: 0.907	T|T: 0.019	C|C: 0.833	C|T: 0.148
AMERICAN	T: 0.527	C: 0.473	T|T: 0.291	C|C: 0.236	C|T: 0.473
CLM	T: 0.553	C: 0.447	T|T: 0.309	C|C: 0.202	C|T: 0.489
MXL	T: 0.508	C: 0.492	T|T: 0.250	C|C: 0.234	C|T: 0.516
PEL	T: 0.494	C: 0.506	T|T: 0.271	C|C: 0.282	C|T: 0.447
PUR	T: 0.543	C: 0.457	T|T: 0.317	C|C: 0.231	C|T: 0.452
EAST ASIAN	T: 0.401	C: 0.599	T|T: 0.165	C|C: 0.363	C|T: 0.472
CDX	T: 0.484	C: 0.516	T|T: 0.247	C|C: 0.280	C|T: 0.473
CHB	T: 0.320	C: 0.680	T|T: 0.087	C|C: 0.447	C|T: 0.466
CHS	T: 0.395	C: 0.605	T|T: 0.152	C|C: 0.362	C|T: 0.486
JPT	T: 0.303	C: 0.697	T|T: 0.087	C|C: 0.481	C|T: 0.433
KHV	T: 0.515	C: 0.485	T|T: 0.263	C|C: 0.232	C|T: 0.505
EUROPEAN	T: 0.720	C: 0.280	T|T: 0.537	C|C: 0.097	C|T: 0.366
CEU	T: 0.793	C: 0.207	T|T: 0.636	C|C: 0.051	C|T: 0.313
FIN	T: 0.848	C: 0.152	T|T: 0.737	C|C: 0.040	C|T: 0.222
GBR	T: 0.802	C: 0.198	T|T: 0.626	C|C: 0.022	C|T: 0.352
IBS	T: 0.575	C: 0.425	T|T: 0.336	C|C: 0.187	C|T: 0.477
TSI	T: 0.607	C: 0.393	T|T: 0.383	C|C: 0.168	C|T: 0.449
SOUTH ASIAN	T: 0.488	C: 0.512	T|T: 0.241	C|C: 0.266	C|T: 0.493
BEB	T: 0.477	C: 0.523	T|T: 0.209	C|C: 0.256	C|T: 0.535
GIH	T: 0.529	C: 0.471	T|T: 0.262	C|C: 0.204	C|T: 0.534
ITU	T: 0.446	C: 0.554	T|T: 0.176	C|C: 0.284	C|T: 0.539
PJL	T: 0.531	C: 0.469	T|T: 0.333	C|C: 0.271	C|T: 0.396
STU	T: 0.456	C: 0.544	T|T: 0.225	C|C: 0.314	C|T: 0.461

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2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

3.ExAC Browser. (2016). Exome Aggregation Consortium. Retrieved March 12, 2017 from http://exac.broadinstitute.org/

Table 3.5: Gives an exampleof second studied SNP rs4833095

3.5 Determining Diseases Caused Archaic-like Single Nucleotide Polymorphisms

Dating between Archaic humans and modern humans resulted adaptation in their environment and local pathogens. Admixture of both homins were resulted the introgression of common alleles, therefore modern human gained adaptive immunity from archaic and survived as a result of natural selection. Archaic-like alleles regulate gene expression of *TLR* genes (Akira *et al.*, 2006). Additionally, these alleles are also associated with the microbial resistance and allergic diseases. Different alleles together with variety of gene expressions lead different disease phenotypes in modern humans. These archaic-like SNPs are responsible for some disease and disease susceptibility in the human genome. Our meta-analysis report listed each archaic-like SNP and its association with pathogenic disease (Table 3.6).

SNP ID	GWAS TRAIT
rs6841698	Self-reported allergy
rs10024216	Amyotrophic lateral sclerosis | Helicobacter pylori serologic status | Self-reported allergy
rs10008492	Endometriosis | Helicobacter pylori serologic status | Self-reported allergy
rs10470854	Self-reported allergy
rs4331786	Amyotrophic lateral sclerosis | Self-reported allergy | Blood Pressure
rs4513579	Self-reported allergy
rs10776482	Helicobacter pylori serologic status | Self-reported allergy
rs4129009	Helicobacter pylori serologic status | Self-reported allergy
rs10776483	Helicobacter pylori serologic status | Self-reported allergy
rs11466657	Self-reported allergy
rs11096955	Self-reported allergy
rs11096956	Helicobacter pylori serologic status | Self-reported allergy
rs11096957	Amyotrophic lateral sclerosis | Endometriosis | Self-reported allergy
rs4274855	Helicobacter pylori serologic status | Self-reported allergy
rs11466645	Helicobacter pylori serologic status | Self-reported allergy
rs11466640	Helicobacter pylori serologic status | Self-reported allergy
rs7694115	Self-reported allergy
rs11466617	Helicobacter pylori serologic status | Self-reported allergy
rs7653908	Helicobacter pylori serologic status | Self-reported allergy
rs7658893	Helicobacter pylori serologic status | Self-reported allergy
rs11725309	Helicobacter pylori serologic status | Self-reported allergy
rs10034903	Self-reported allergy
rs10004195	Helicobacter pylori serologic status | Self-reported allergy
rs12233670	Multiple complex diseases | Coronary Artery Disease | Lymphocyte counts | Helicobacter pylori serologic status | Self-reported allergy
rs6834581	Alcohol consumption
rs4833093	Alcohol consumption
rs6531663	Alcohol consumption
rs4543123	Amyotrophic lateral sclerosis | Paget`s disease | Helicobacter pylori serologic status | Alcohol consumption | Self-reported allergy
rs4624663	Panic disorder
rs4833095	Amyotrophic lateral sclerosis | Paget`s disease | Helicobacter pylori serologic status | Alcohol consumption | Self-reported allergy
rs5743604	Helicobacter pylori serologic status | Alcohol consumption | Self-reported allergy
rs5743596	Helicobacter pylori serologic status | Self-reported allergy
rs5743595	Helicobacter pylori serologic status | Self-reported allergy

rs5743594	Height
rs5743592	Helicobacter pylori serologic status | Self-reported allergy
rs5743571	Helicobacter pylori serologic status | Self-reported allergy
rs5743565	Helicobacter pylori serologic status | Self-reported allergy
rs5743563	Helicobacter pylori serologic status | Self-reported allergy
rs5743562	Helicobacter pylori serologic status | Self-reported allergy
rs5743557	Helicobacter pylori serologic status | Self-reported allergy
rs11722813	Helicobacter pylori serologic status
rs2101521	Helicobacter pylori serologic status | Self-reported allergy
rs17616434	Helicobacter pylori serologic status | Alcohol consumption | Self-reported allergy | Allergic sensitization
rs4833103	Helicobacter pylori serologic status | Self-reported allergy
rs6815814	Helicobacter pylori serologic status | Self-reported allergy
rs7696175	Breast cancer | Multiple complex diseases | Self-reported allergy
rs5743810	Self-reported allergy
rs1039559	Self-reported allergy
rs5743794	Suicide attempts in bipolar disorder | Helicobacter pylori serologic status | Self-reported allergy
rs5743788	Self-reported allergy
rs7665774	Self-reported allergy
rs7673348	Helicobacter pylori serologic status | Self-reported allergy
rs7687447	Helicobacter pylori serologic status | Self-reported allergy
rs6531672	Self-reported allergy
rs6531673	Self-reported allergy
rs7681628	Self-reported allergy
rs2174284	Helicobacter pylori serologic status | Self-reported allergy
rs3860069	Helicobacter pylori serologic status | Self-reported allergy
rs17582830	Helicobacter pylori serologic status | Self-reported allergy
rs2130296	Multiple complex diseases
rs721653	Self-reported allergy
rs902136	Self-reported allergy
rs11943027	Self-reported allergy
rs17582893	Suicide attempts in bipolar disorder | Helicobacter pylori serologic status | Self-reported allergy
rs2381345	Self-reported allergy
rs1873195	Helicobacter pylori serologic status | Self-reported allergy
rs17582921	Helicobacter pylori serologic status | Self-reported allergy
rs6851685	Helicobacter pylori serologic status | Self-reported allergy
rs6835514	Multiple complex diseases | Coronary Artery Disease | Helicobacter pylori serologic status | Self-reported allergy
rs1604834	Multiple complex diseases|Self-reported allergy
rs974734	Self-reported allergy
rs7688418	Self-reported allergy
rs7665932	Self-reported allergy
rs6531677	Self-reported allergy
rs12642243	Self-reported allergy
rs12641669	Self-reported allergy
rs1115259	Self-reported allergy
rs6824769	Multiple complex diseases | Self-reported allergy
rs7664107	Self-reported allergy

Table 3.6: Shows each listed archaic-like SNP and its associated disease. These archaic-like SNPs mainly cause self-reported allergies and helicobacter pylori serologic status

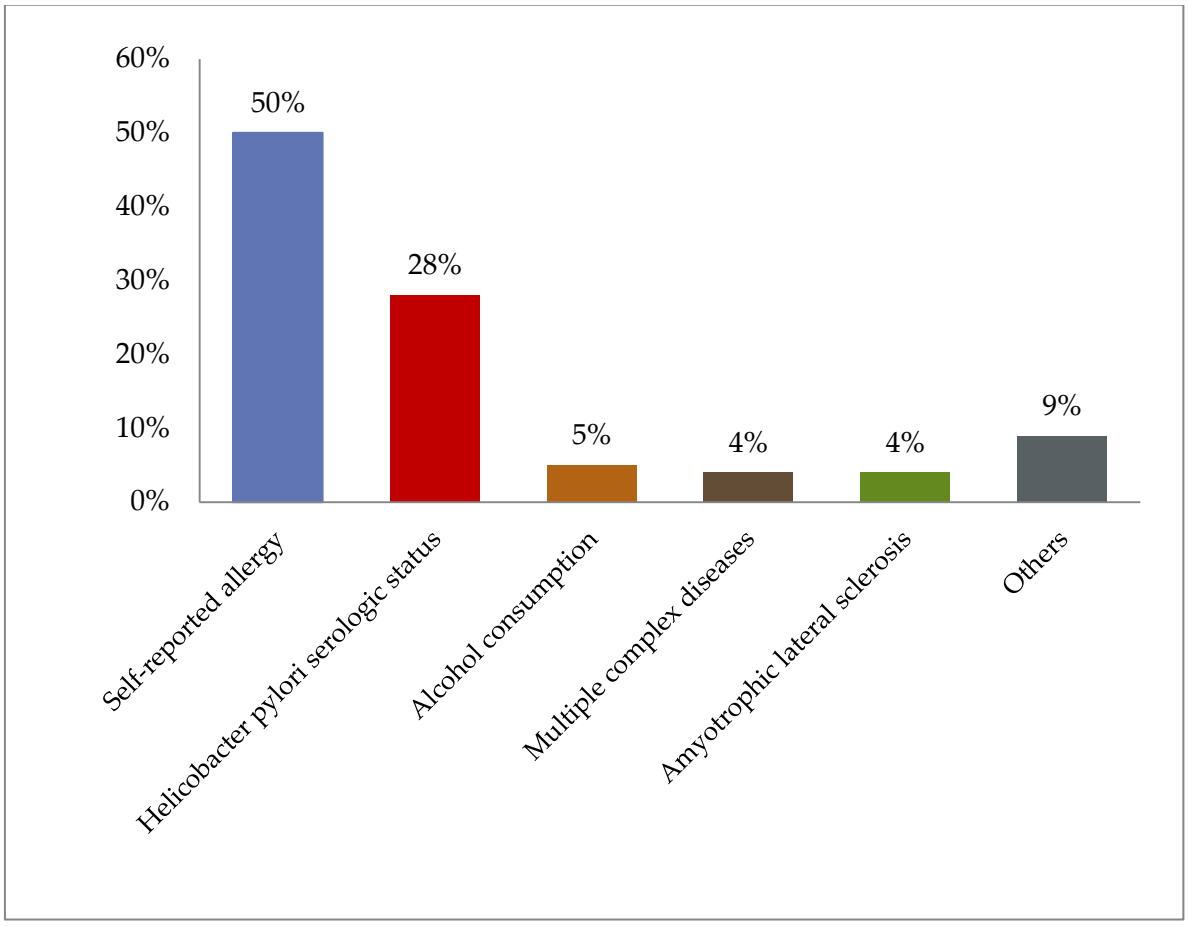


Figure 3.1: Illustrates the statistical calculation of most seen diseases that might caused by interested arhaic-like SNPs. Self-reported allergy is the most seen dieases and Helicobacter pylori serological status follows up secondly. Interestingly alcohol consumption and amylotrophic lateral sclerosis (ALS) had an association with arhaic-like SNPS (5% and 4%, respectively). The others that are seen less than 1% were endometricsis, blood pressure, coronary artery disease, lymphocyte counts, Paget's disease, height, allergic sensitization, breast cancer, suicide attempts in bipolar disorder and panic disorder

3.6 Discussion

In this chapter, meta-analysis of previous studies combined with genome browsers. As a first step, data is collected from previously identified archaic-like SNPs. Hereby, 79 archaic-like SNP were determined by Dannemann *et al.*, (2016). Then, 1000genome browser was used to check if those SNPs were registered and identified in the 1000genome population data. Moreover, other international genome databases were used to detect clinical significance of those SNPs. Three international browsers were selected to carry our meta-analysis: Ensembl genome (Ensembl, 2016), 1000genome (International Genome, 2016) and dbSNP (National Center for Biotechnology Information, 2014). Population genetics data, clinical data and allele frequency data were collected from these browsers for each SNP. Individual population genetic data was collected for each archaic-like SNPs.

Five populations and twenty-six sub-populations were used in this study. These populations were African, American, Eastern Asia, European and Southern Asia. The African sub-populations were Yoruba in Ibadan, African Caribbean in Barbados, Mende in Sierra Leone African Ancestry in Southwest US, Gambian in western division, Esan in Nigeria and Luhya in Webuye. Colombian in Medellin, Peruvian in Lima, Mexican ancestry in Los Angeles and Puerto Ricon in Puerto Rico were included to American population. Chinese Dai in Xishuangbanna, Kinth in Ho Chi Minh City, Han Chinese in Bejiing, Japanese in Tokyo and Southern Han Chinese were included to East Asian population. Toscani in Italy, Finnish in Finland, Utah residents with Northern and Western European ancestry, Iberian populations in Spain and Biritish in England and Scotland were included to European population. Lastly, Gujarati Indian in Houston Bengali in Bangladesh, Indian Telugu in the UK, Sri Lankan Tamil in the UK and Punjabi in Lahore were included to South Asian population. All those population genetics data merged with allele and genotype frequencies for each determined archaic–like single nucleotide polymorphisms.

Our data revealed that, self-reported allergy is the main disease that caused by the SNPs in our list (50%), meaning that half of the SNPs have an association with allergy. The main reason is relies on the fact of, *TLRs* provide natural immunity against to pathogens and they are an important defense against pathogens. As mentioned earlier, 1-4 percent of

archaic-like genome are located in the *TLR* gene clusters. Other associated diseases are helicobacter pylori serologic status (28%), alcohol consumption (5%), multiple complex diseases (4%), amyotrophic lateral sclerosis (4%), and others (9%), respectively. The others showed the frequency of 1: endometricsis, blood pressure, coronary artery disease, lymphocyte counts, Paget's disease, height, allergic sensitization, breast cancer, suicide attempts in bipolar disorder, and panic disorder, respectively (Table3.7 and figure 3.1).

Before our study, all significant information about archaic SNPs was distributed in different places and various genome browsers. In our study, we have merged all information in one place as the first stage of the study. Our merged meta-analysis data will help researchers and the clinicians for better understanding the mechanism and the background of the diseases. The second stage of the study, creating an *in silico* software, will be discussed in the next result chapter.

CHAPTER 4

COMPOSING THE ARCHAICS2PHENOTYPE.NEU.EDU.TR GENOME BROWSER: USEFUL TOOL FOR CLINICIANS AND RESEARCHERS

4.1 Introduction

A software based database was created to accumulate all necessary information in an easy accessible browser. Software is the name of the programs that enable the functions of electronic devices. Software was generated by programming languages. Different programming languages can be used for creating the software. C, C++, Java and pascal are examples of these programming languages. The database is storage of relevant information about one selected topic. In short, it ensures that related data are stored together inside of databases. Nowadays, databases have been using in every field, such as; industries, banks, health fields, and many other sectors. Users can easily access to the data via the internet. Databases are also be used to build infrastructure in computer systems.

Presently, C programming language is very popular programming language and was created in AT&T Bell Laboratories by Ken Thompson and Dennis Ritchie to develop the UNIX operating system. Although this programming language was developed in 1972, almost 95% of the operating systems are using it today, for instance; Microsoft Windows, GNU/Linux, BSD, and Minix (Deitel, P.and Deitel, H., 2010).

As mentioned in previous chapters, several well-known and common international genetic browsers (Ensembl, 1000genome, and dbSNP) were used to carry out the meta-analysis in this study.

The Ensembl genome database project was started in 1999 as cooperation between the European Bioinformatics Institute and The Wellcome Trust Sanger Institute. The purpose of this genetic database was to provide a source for researchers interested in examining our species, other vertebrates and model organisms. All data were stored in MySQL database. And, user can be free access to Ensembl genome databases via internet (Ensembl, 2016).

The 1000genome project was the research initiated project to create the most detailed catalogue of human variation in January 2008. The completion of this project made it possible to obtain data of population genetics and genetic diversity. The 1000genome database provides sources to genetic data for different populations in the world. This catalogue was aimed to estimate population frequencies for ethnic groups. The second aim was genotyping all different populations and the development of the human reference sequence. However, this database helps to understand the processes underlying the population variation, mutation and recombination (International Genome, 2016).

Last selected database, The Single Nucleotide Polymorphism Database (dbSNP), was created by National Center for Biotechnology Information (NCBI) in cooperation with National Human Genome Research Institute (NHGRI) in September 1998. This database does not only contain all SNP collections of different populations, moreover, it includes other variation types such as; Indels/DIPs, STRs, MNPs, heterozygous sequence and additionally, named variants. Also, dbSNP browser is accessible free via internet by the users (National Center for Biotechnology Information, 2014).

4.2 The archaics2phenotpe Software is Generated by C Language on Visual Studio C++ 2008 Edition

During the stage of the designing the database, C language on visual studio C++ 2008 edition was used and all program codes written in C language in Visual Studio. Nevertheless, all the given codes that belong to the software are enclosed in the appendix part of this thesis. The software of this study was basically divided into two parts (Figure 4.1).

In the first section, users can enter three different inputs independently or together .Meaning that, the software was designed to allow users search by SNP ID, chromosome location of the interested SNP or both (Figure 4.2). In the second section, outputs of searched input are display on the screen (Figure 4.3 and Figure 4.4). In this section, out accumulated data were used to create the *in silico* browser. After the necessary and required algorithms were created, all collected informative data about 79 archaic-like SNPs were combined with the new software. Therefore, the archaics2phenotpe software was generated.

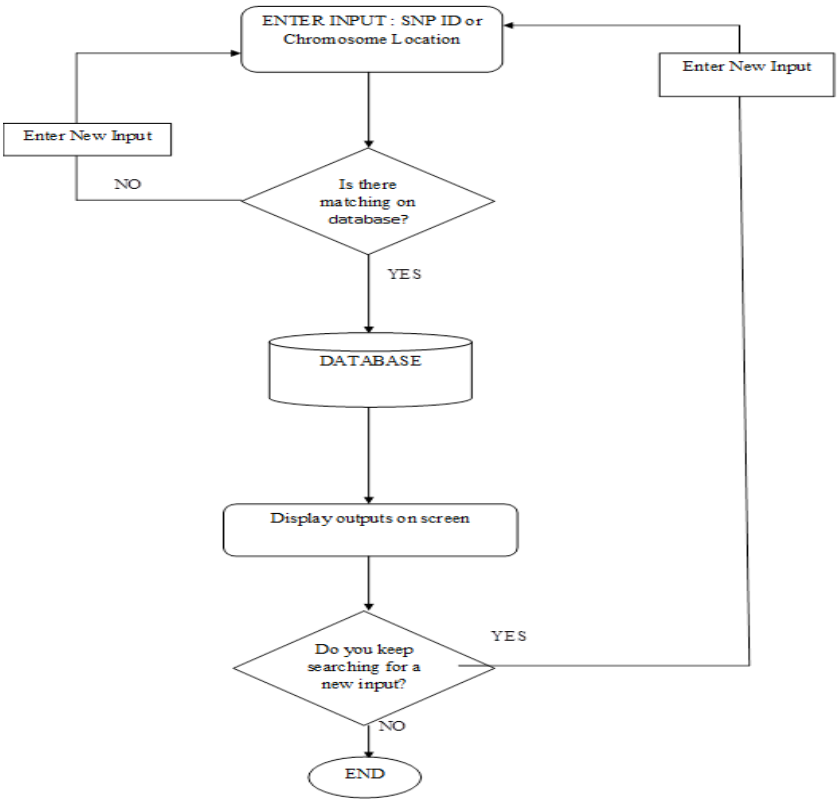


Figure 4.1: Flow chart of the generating the software. Firstly, users need to write necessary information to the search engine. However, users only can make a search with SNP ID or chromosome location of the interested SNP in the database. If their interested SNP is in our database, the full information will show up on the screen

Figure 4.2: Shows how inputs can be entered by user on Microsoft visual studio C++ 2008 edition. Users can enter the SNP ID such as above mentioned SNP rs6841698 or a chromosomal location of the SNP rs6841698 for example, 4:387600093

However, if there is a matching with given SNP ID or chromosome location in the database, user can obtain data outputs. The data outputs include the information of the ancestral allele, ambiguity code, minor allele frequency of the SNP, chromosomal location of SNP, SNP ID, genome-wide association study (GWAS) trait (Figure 4.3), allele frequencies and genotype frequencies of the SNP in all sequenced populations (Figure 4.4).

```
Enter SNP ID: rs6841698
Enter LOCATION: 4: -


 Alleles  G/A, Ancestral:G, Ambiguity code: R, MAF: 0.41 [2]
 Location: 4:38760093 [2]
 SNP ID: rs6841698 [1]
 GWAS Trait: Self-reported allergy [1]
 Archaic-like haplotype cluster: Not Known
 Clinical Assertion Description: Not Known
```

Figure 4.3: Gives an example of searching output of the archaic-like SNP rs6841698 that are responsible from self-reported allergy

Although, humans come from common ancestor, gene frequencies are different because of natural selection. Different environmental conditions affect to natural selection. For example, Gene frequencies of Cyprus and Nigeria populations are different. Thus, the frequency of the genes in the gene pool depends on the factors that have influenced the gene pool. Then, they carried these genes to their genotypes.

Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G:0.585	A:0.415	G|G: 0.348	A|A: 0.178	A|G: 0.474
AFRICAN	G:0,539	A:0.461	G|G: 0.289	A|A: 0.210	A|G: 0.501
ACB	G:0.474	A:0.526	G|G: 0.219	A|A: 0.271	A|G: 0.510
ASW	G:0.615	A:0.385	G|G: 0.393	A|A: 0.164	A|G: 0.443
ESN	G:0.566	A:0.434	G|G: 0.313	A|A: 0.182	A|G: 0.505
GWD	G:0.487	A:0.513	G|G: 0.204	A|A: 0.230	A|G: 0.566
LWK	G:0.606	A:0.394	G|G: 0.394	A|A: 0.182	A|G: 0.424
MSL	G:0.535	A:0.465	G|G: 0.271	A|A: 0.200	A|G: 0.529
YRI	G:0.528	A:0.472	G|G: 0.278	A|A: 0.222	A|G: 0.500
AMERICAN	G:0.576	A:0.424	G|G: 0.343	A|A: 0.190	A|G: 0.467
CLM	G:0.612	A:0.388	G|G: 0.383	A|A: 0.160	A|G: 0.457
MXL	G:0.523	A:0.477	G|G: 0.250	A|A: 0.203	A|G: 0.547
PEL	G:0.535	A:0.465	G|G: 0.306	A|A: 0.235	A|G: 0.459
PUR	G:0.611	A:0.389	G|G: 0.394	A|A: 0.173	A|G: 0.433
EAST ASIAN	G:0,599	A:0,401	G|G: 0.367	A|A: 0.169	A|G: 0.464
CDX	G:0.758	A:0.242	G|G: 0.581	A|A: 0.065	A|G: 0.355
CHB	G:0.534	A:0.466	G|G: 0.272	A|A: 0.204	A|G: 0.524
CHS	G:0.605	A:0.395	G|G: 0.343	A|A: 0.133	A|G: 0.524
JPT	G:0.375	A:0.625	G|G: 0.115	A|A: 0.365	A|G: 0.519
KHV	G:0.747	A:0.253	G|G: 0.566	A|A: 0.061	A|G: 0.384
EUROPEAN	G:0.645	A:0.355	G|G: 0.427	A|A: 0.137	A|G: 0.435
CEU	G:0.687	A:0.313	G|G: 0.444	A|A: 0.071	A|G: 0.485
FIN	G:0.667	A:0.333	G|G: 0.485	A|A: 0.152	A|G: 0.364
GBR	G:0.681	A:0.319	G|G: 0.451	A|A: 0.088	A|G: 0.462
IBS	G:0.612	A:0.388	G|G: 0.364	A|A: 0.140	A|G: 0.495
TSI	G:0.589	A:0.411	G|G: 0.402	A|A: 0.224	A|G: 0.374
SOUTH ASIAN	G:0,578	A:0,422	G|G: 0.331	A|A: 0.176	A|G: 0.493
BEB	G:0.610	A:0.390	G|G: 0.337	A|A: 0.116	A|G: 0.547
GIH	G:0.617	A:0.383	G|G: 0.388	A|A: 0.155	A|G: 0.456
ITU	G:0.564	A:0.436	G|G: 0.294	A|A: 0.167	A|G: 0.539
PJL	G:0.594	A:0.406	G|G: 0.385	A|A: 0.198	A|G: 0.417
STU	G:0.510	A:0.490	G|G: 0.255	A|A: 0.235	A|G: 0.510

Figure 4.4: Shows the population genetics data for rs6841698. Allele frequencies and genotype frequencies were given for twenty-six sub-populations within five main populations. Allele frequency is frequency of case of a specific allele in a population. But, genotype frequency is the number of individuals in a genotype to the ratio of individuals in the population

4.3 Creating *in-silico* genome browser: archaics2phenotype.neu.edu.tr

After created the software and the database, the final step of this study, the website, is generated. This created database combined to website for online access. The website is an information sharing platform, which is available online to users. The domain name and hosting are required to create the website.

Firstly, the domain, archaics2phenotype.neu.edu.tr, was created to setup the website for any internet browsers. Secondly, the hosting was created for activating the website. The hosting provides access to all data by users from the website. In addition, all data of 79 archaic-like SNP were stored in the hosting service. The created database by using

software was transferred into the hosting service. Then, the both domain name and hosting service were connected to each other and the website eventually was activated. As a final step, the interface of the website was designed. The appearance of the *in-silico* genome browser is important for easy use. After the database transferred to website for online access, archaics2phenotype.neu.edu.tr is freely opened to the globally public.

The figures below illustrate the use of the website step by step.

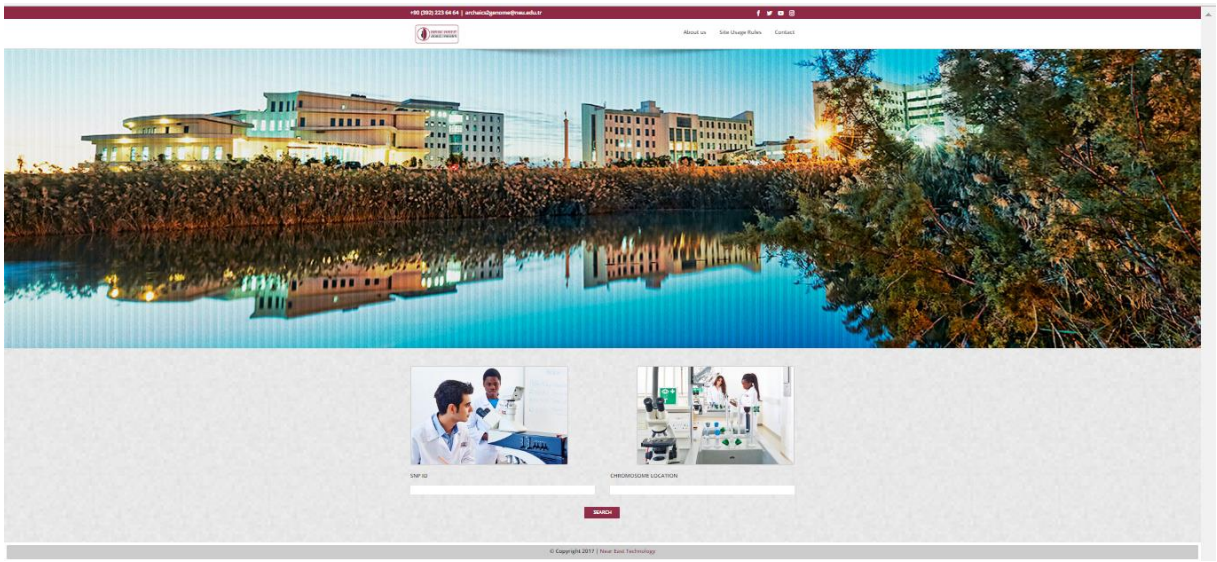


Figure 4.5: Homepage of archaics2phenotype.neu.edu.tr

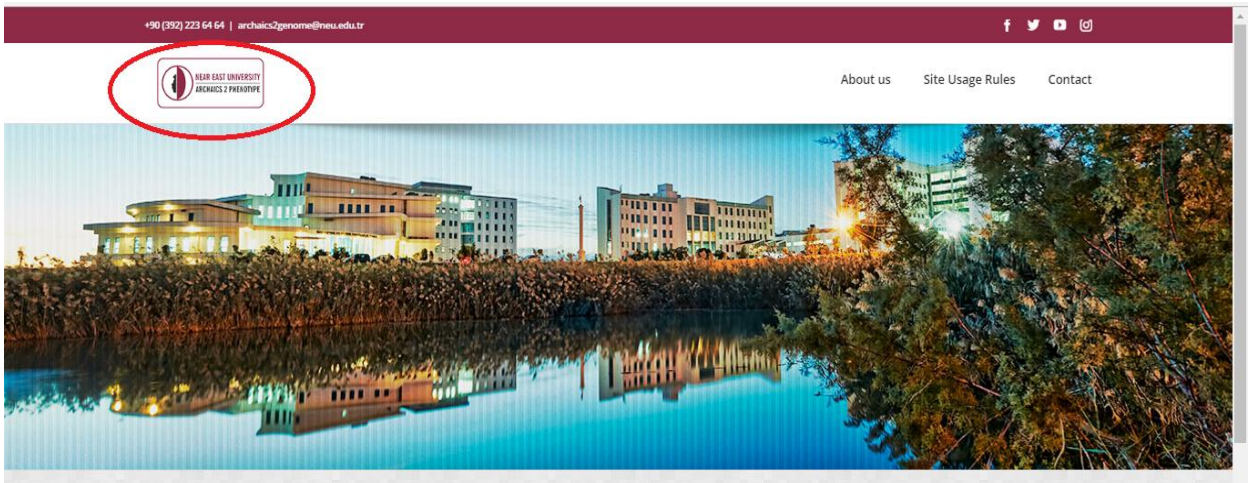


Figure 4.6: Designed Logo is located on the upper left corner at the homepage

Figure 4.7: There is a figure depicted an archaic homic on top of the logo

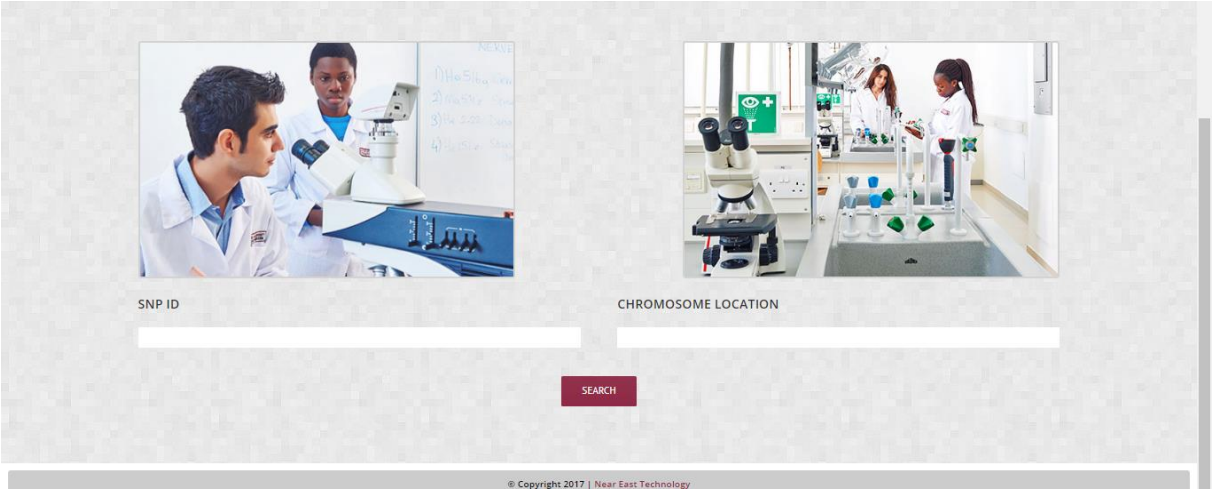
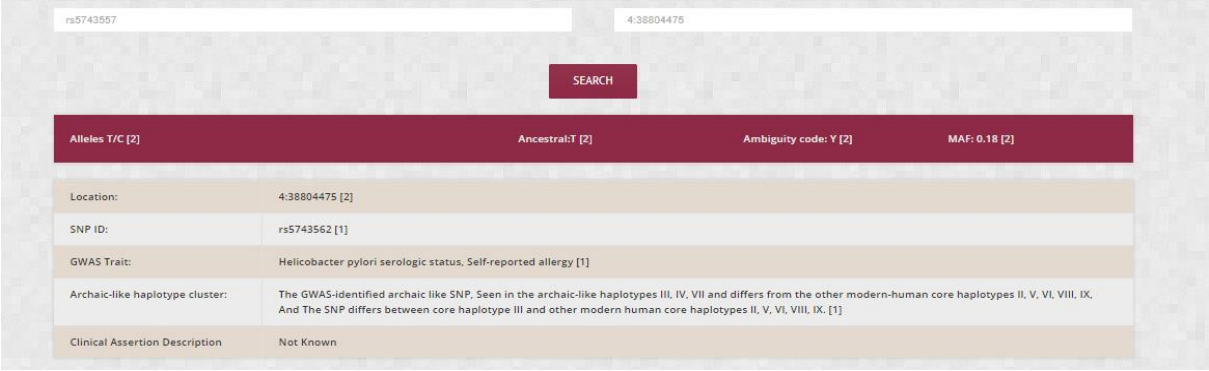


Figure 4.8: There different way of searching in the browser. Either the search can be run with the SNP ID or with the chrosomal location or both information can be entered. The search button must be clicked after entering the input. If there is a matching after clicking, the outputs will be reflected on the screen

After search of input (with SNP ID or Chromosome location), if there is any matching, user obtain data of SNPs from database.



rs5743557

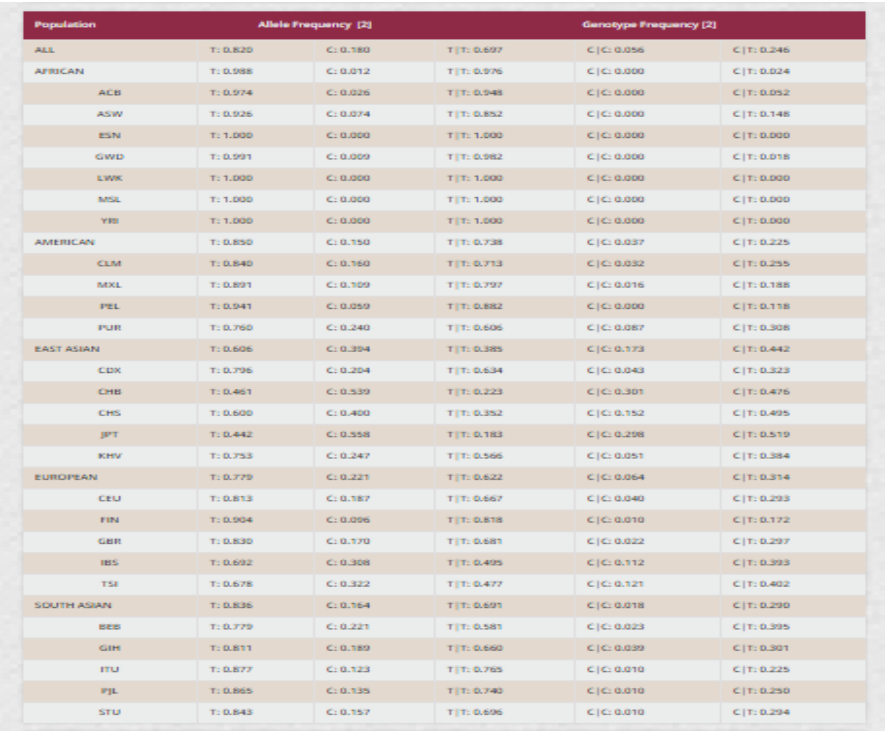
4:38804475

SEARCH

Alleles T/C [2]	Ancestral:T [2]	Ambiguity code: Y [2]	MAF: 0.18 [2]

Location:	4:38804475 [2]
SNP ID:	rs5743562 [1]
GWAS Trait:	Helicobacter pylori serologic status, Self-reported allergy [1]
Archaic-like haplotype cluster:	The GWAS-identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]
Clinical Assertion Description	Not Known

Figure 4.9: Shows searching results of archaic-like SNP rs5743562 that are responsible from helicobacter pylori serologic status and self-reported allergy. This figure was given as an example appearance of information on the archaics2phenotype.neu.edu.tr



Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.820	C: 0.180	T|T: 0.697	C|C: 0.056	C|T: 0.246
AFRICAN	T: 0.988	C: 0.012	T|T: 0.976	C|C: 0.000	C|T: 0.024
ACB	T: 0.974	C: 0.026	T|T: 0.948	C|C: 0.000	C|T: 0.052
ASW	T: 0.926	C: 0.074	T|T: 0.852	C|C: 0.000	C|T: 0.148
ESN	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
GWD	T: 0.991	C: 0.009	T|T: 0.982	C|C: 0.000	C|T: 0.018
LWK	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
MSL	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
YRI	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
AMERICAN	T: 0.850	C: 0.150	T|T: 0.738	C|C: 0.037	C|T: 0.225
CLM	T: 0.840	C: 0.160	T|T: 0.713	C|C: 0.032	C|T: 0.255
MXL	T: 0.891	C: 0.109	T|T: 0.797	C|C: 0.016	C|T: 0.188
PEL	T: 0.941	C: 0.059	T|T: 0.882	C|C: 0.000	C|T: 0.118
PUR	T: 0.760	C: 0.240	T|T: 0.606	C|C: 0.087	C|T: 0.308
EAST ASIAN	T: 0.606	C: 0.394	T|T: 0.385	C|C: 0.173	C|T: 0.442
CDX	T: 0.796	C: 0.204	T|T: 0.634	C|C: 0.043	C|T: 0.323
CHB	T: 0.461	C: 0.539	T|T: 0.223	C|C: 0.301	C|T: 0.476
CHS	T: 0.600	C: 0.400	T|T: 0.352	C|C: 0.152	C|T: 0.495
JPT	T: 0.442	C: 0.558	T|T: 0.183	C|C: 0.298	C|T: 0.519
KHV	T: 0.753	C: 0.247	T|T: 0.566	C|C: 0.051	C|T: 0.384
EUROPEAN	T: 0.779	C: 0.221	T|T: 0.622	C|C: 0.064	C|T: 0.314
CEU	T: 0.813	C: 0.187	T|T: 0.667	C|C: 0.040	C|T: 0.293
FIN	T: 0.904	C: 0.096	T|T: 0.818	C|C: 0.010	C|T: 0.172
GBR	T: 0.830	C: 0.170	T|T: 0.681	C|C: 0.022	C|T: 0.297
IBS	T: 0.692	C: 0.308	T|T: 0.495	C|C: 0.112	C|T: 0.393
TSI	T: 0.678	C: 0.322	T|T: 0.477	C|C: 0.121	C|T: 0.402
SOUTH ASIAN	T: 0.836	C: 0.164	T|T: 0.691	C|C: 0.018	C|T: 0.290
BEB	T: 0.779	C: 0.221	T|T: 0.581	C|C: 0.023	C|T: 0.395
GIH	T: 0.811	C: 0.189	T|T: 0.660	C|C: 0.039	C|T: 0.301
ITU	T: 0.877	C: 0.123	T|T: 0.765	C|C: 0.010	C|T: 0.225
PJL	T: 0.865	C: 0.135	T|T: 0.740	C|C: 0.010	C|T: 0.250
STU	T: 0.843	C: 0.157	T|T: 0.696	C|C: 0.010	C|T: 0.294

Figure 4.10: Shows information of the population genetics data for rs5743562 in all sequenced population by 1000genome. Allele frequencies and genotype frequencies were given for twenty-six sub-populations within five main populations. Allele frequency is frequency of case of a specific allele in a population. But, genotype frequency is the number of individuals in a genotype to the ratio of individuals in the population

ACB:	African Caribbean in Barbados
ASW:	African Ancestry in Southwest US
ESN:	Esan in Nigeria
GWD:	Gambian in Western Division, The Gambia
LWK:	Luhya in Webuye, Kenya
MSL:	Mende in Sierra Leone
YRI:	Yoruba in Ibadan, Nigeria
CLM:	Colombian in Medellin, Colombia
MXL:	Mexican Ancestry in Los Angeles, California
PEL:	Peruvian in Lima, Peru
PUR:	Puerto Rican in Puerto Rico
CDX:	Chinese Dai in Xishuangbanna, China
CHB:	Han Chinese in Bejing, China
CHS:	Southern Han Chinese, China
JPT:	Japanese in Tokyo, Japan
KHV:	Kinh in Ho Chi Minh City, Vietnam
CEU:	Utah residents with Northern and Western European ancestry
FIN:	Finnish in Finland
GBR:	British in England and Scotland
IBS:	Iberian Populations in Spain
TSI:	Toscani in Italy
BEB:	Bengali in Bangladesh
GIH:	Gujarati Indian in Houston, TX
ITU:	Indian Telugu in the UK
PJL:	Punjabi in Lahore, Pakistan
STU:	Sri Lankan Tamil in the UK

Figure 4.11: The abbreviation of the using populations were given in the database. Explanations of these abbreviations were given or researchers to easily understand the names of these populations

Figure 4.12: About us section of archaics2phenotype.neu.edu.tr. This section provides general information about the website.

Figure 4.13: User guide section of archaics2phenotype.neu.edu.tr. The user guide section explains how to use the website. In shortly, it provides guidance to users

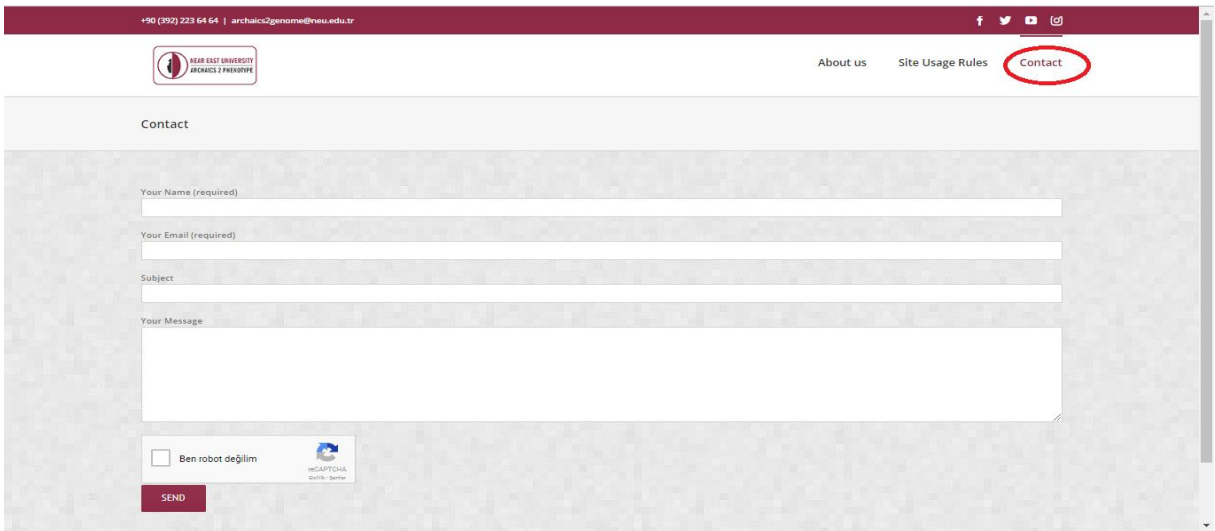


Figure 4.14: Contact section of archaics2phenotype.neu.edu.tr. This section provides communication with website administrator. If users want ask any question or make suggestion, they can send from contact part

4.4 Discussion

Primary work of this study was performing the meta-analysis and eventually, 79 archaic-like SNPs were determined. Moreover, data of these selected SNPs were collected from international genome browsers and wide-spectrum database was created with merging of accumulating information. Then, the genome browser was created to provide online access to researchers and clinicians.

Firstly, software was developed to create the database. The computer operating system that is used in this work was windows 10. The system processor was Intel Core i5 central processing unit and 2.53 GHz. Random access memory (RAM) was 3.00GB and memory of computer was 444GB. Software was generated by C programming language on

Microsoft visual studio C++ 2008 edition. This visual studio is software development platform and is developed by Microsoft in 2008 to create computer programs. All collected data of 79 archaic-like SNPs were transferred to this computer language to create the first archaic-like SNP database.

Secondly, the *in-silico* genome browser was created and transferred to the online platform. This generated genome browser provides online access to researchers and clinicians. After separately creating the domain name and hosting service, they were merged to create the website. As a result http://archaics2phenotype.neu.edu.tr has been become globally online free.

To conclude, this website was generated for researchers and clinicians. The created database will facilitate the work of researchers, because they can obtain all data with references via ours browser. Our developed *in-silico* model provides better understanding for the origin of the genetic diseases/traits that are association with archaic genomes. Moreover, it provides quick access to data for researchers and clinicians via genome browser.

CHAPTER 5

DISCUSSION

5.1 Introduction

Archeological and genetic studies show that ancestors of modern humans immigrated from Africa to other continents; especially, Europe and Asia. Africa is very rich for human genetic diversity. Therefore, there are various linguistic and cultural diversities. African populations exposed to divergent environments, climate, nutrition and pathogens because of their geographical and ethnic varieties (Beltrame *et al.*, 2016).

Archaic humans emigrated from Africa to Europe and West Asia. They lived here for over 200.000 years. They adapted to new environment and pathogens in the new continents (Green *et al.*, 2010). Archaic humans are subspecies of *Homo sapiens*. These subspecies are *Homo heidelbergensis, Homo rhodesiensis, Homo neanderthalensis* and *Homo antecessor*. Especially, we focused on *Homo neanderthalensis* in this study. They were spread to all regions between England and Siberia. They were short and strong hunters (Groucutt *et al.*, 2015). Thus, archaic humans hybridized with ancestors of modern humans. As result of this hybridization, Neanderthal genome was passed into modern humans' DNA. So, present-day human genome contains approximately between 1-4% Neanderthal genome. These Neanderhal-specific sequences provide predisposition or adaptive immunity to some diseases.

Toll-Like Receptors (*TLRs*) provide natural immunity and defense against to many pathogens (Dannemann *et al.*, 2016). In humans, the *TLR* gene family has 10 functional members (*TLR1–TLR10*, respectively) (Akira *et al*., 2006). *TLR3*, *TLR7*, *TLR8* and *TLR9* are found in intracellular compartments (Barreiro *et al*., 2009). However, *TLR1*, *TLR2*, *TLR4*, *TLR5* and *TLR6* are expressed on the cell surface (Quintana-Murci and Clarck, 2013). Recent studies are revealed that modern humans carry three distinct archaic haplotypes (1%) within a cluster of three Toll-like receptors (*TLR6-TLR1-TLR10*) are

located on chromosome 4. This provides strong evidence for recurrent adaptive introgression at the *TLR6-TLR1-TLR10* locus, resulting in differences in disease phenotypes in modern humans (Dannemann *et al.*, 2016).

5.2 Interbreeding Between Neanderthals and Ancestors of Present-day Humans

Genetic and archaeological studies showed that Neanderthals and modern humans were interbred 50,000 years ago. The fossil findings revealed the population of Neanderthals began to decline 40,000 years ago, and the generations of Neanderthal were exhausted 39,000 years ago. There were many factors for exhausted and many hypotheses about their generation (Harris and Nelsen, 2017). First possibility, rivalry for resources or direct warfare between Neanderthals and modern humans. Humans were more advanced technologically and they were best hunters than Neanderthals. So, humans had more advantages for survive. Second possibility, Neanderthals were adapted to cold climate. Their lives became harder as climates have changed and warmed up. Other possibility could be that pathogens and parasites in the environment (Harris and Nelsen, 2017).

A great portion of genetic diversity in humans occurs by ancient polymorphisms. So, Neanderthal and modern haplotypes are not more diverged than modern human sequences. Introgressed Neanderthal sequences were identified in modern human autosomes an X chromosomes. Nevertheless, Neanderthal mitochondrial genome sequences were not reporte within modern human genome. Y chromosome sequences of Neanderthal has not been characterized yet (Mendez *et al.*, 2016). In 2016 Mendez and colleagues said, full mitochomdrial DNA sequences available at eight individuals. These individuals from Spain, Germany, Crotia and Russia. But, relation of Y chromosome still does not known between Neanderthal and present-days human. They obtained Y chromosome from male Neanderthal in El Siron, Spain (Mendez *et al.*, 2016).

Gibbons (2016) conducted a study in the male Neanderthal who lived in Spain 49,000 years ago. Chromosome Y of this Neanderthal did not pass to modern humans. Europeans and Asians are missing chunks of Neanderthal DNA on their Y chromosomes. So to conclude, female modern humans and male Neanderthals are not exactly compatible. Therefore, they think that Neanderthals may have problem about sperm production. So,

they may did not produce many healthy male babies. As a result of this, Neanderthal population might be declined rapidly (Gibbons, 2016).

As a result of the hybridization of early human and Neanderthals between Europe and West Asia, non-African populations carry almost 1-4% Neanderthal DNA in their genome. Nevertheless, this Neanderthal DNA made both positive and negative effects to modern humans. In study of Dannemann and Kelso (2017), they agreed introgressed genomes provide genetic adaptation to new environments. Thus could be a positive effect introgression of Neandethal genome to humans. Thus, it provides natural immunity to new environments and pathogens. Neanderthal alleles often are not adaptive to modern human genome (Dannemann and Kelso, 2017).

5.3 Determining Diseases Caused Archaic-like Single Nucleotide Polymorphisms

Dannemann and Kelso (2017) were used UK Biobank or described the relationships between the positive selection signs between Neanderthal DNA and modern human traits. They have revealed Neanderthal DNA might affect skin tone, hair color, height, sleep pattern, mood and smoking status of today's Europeans.

In 2016, Dannemann and colleagues (2016) identified 79 archaic-like SNPs. In this thesis, first of all meta-analysis was performed to collect all previously identified archaic-like SNPs. Thus, we combined the results of multiple independent studies in our thesis. Additionally, we used three biggest international genome browsers and several important scientific articles for this meta-analysis. We picked 79 archaic-like SNPs from study of Dannemann *et al.* (2016). Then, 1000genome was used to check if those SNPs were registered and identified in the 1000genome populations. Lastly, we determined clinical significance of identified SNPs with using international genome browsers [Ensembl genome (Ensembl, 2016), 1000genome (International Genome, 2016) and dbSNP (National Center for Biotechnology Information, 2014)] and scitific papers. We obtained allele and genotype frequencies of each determined SNPs by by each population. Those population genetics information was obtained using Ensemble's 1000genome population data.

Our meta-analysis results revealed that, self-reported allergy is the main clinical pathogen (50%) that caused by Archaic SNP that introgressed in human genome thousand years ago. This means that half of the Archaic-like SNPs have an association with allergy and the main reason relies on the fact that *TLR*s provide natural immunity against to pathogens and they are an important defense against pathogens. Other related diseases are helicobacter pylori serologic status (28%), alcohol consumption (5%), multiple complex diseases (4%), amyotrophic lateral sclerosis (4%), and others (9%), respectively. The others include; endometricsis, blood pressure, coronary artery disease, lymphocyte counts, Paget's disease, height, allergic sensitization, breast cancer, suicide attempts in bipolar disorder, and panic disorder, respectively. This is the first study that combines the information about Archaic SNPs that are located in modern human genome, their population frequency data and clinical information.

5.4 Generating Software, Database and Creating *in-silico* Genome Browser

The archaics2phenotpe software is generated by C programming language on Microsoft visual studio C++ 2008 edition. Database was related with C programming language. Users need to write necessary information to the search engine on our generated software. Users only can make a search with SNP ID or chromosome location of the interested SNP on the database. If their interested SNP is in our database, the full information will show up on the screen.

After generated software and databases, it was time to build *in-silico* genome browser. Software and database combined to *in-silico* for online access. Domain and hosting service were setup with separately. And, they were merged to generate website. Domain is the name and address of browser (archaics2phenotype.neu.edu.tr). And, hosting service provides keep files and information of website and makes it available to users. It can be called web server. As result of this, archaics2phenotype.neu.edu.tr became active to online access for users. As the website is an information sharing platform, we opened access to our data to public especially for researchers and the clinicians.

CHAPTER 6

CONCLUSION

Meta-analysis was carried out to select archaic-like SNPs. Then, to determine diseases that are associated with those SNPs in modern humans. Additionally, population genetic data for each SNP have been merged using three different biggest online international genetic browsers.

Secondly, *in-silico* software has been developed for clinicinas and researchs to reach all those combined data. Besides all clinical significanc and population data, this software gives us clues about the origin of the diseases for present-day humans.

Finally, our developed *in silico* model will help health providers to find the possible correlations with the persons' phenotype and the disease. Therefore, clinicians will be able to provide better understanding to evaluate the underlying mechanisms of the diseases.

To conclude, the generated database will facilitate the work of researchers, because they can obtain all data with references via this website. Our developed *in-silico* model provides better understanding for the origin of the genetic diseases that are introgressed from archaic genomes. Furthermore, our genome browser provides quick online access to data for researchers, clinicians or anyone has an interested in this history of early human life.

6.1 Future Remarks

In the future, the computer software will be needed to develop to evaluate the percentage of Neanderthal delivered sequences in modern humans. Therefore, Neanderthals and modern human genomes will be compared by this software and we are aiming to evaluate genetic diseases that originally came from Neanderthals.

Finally, this developed software is planning to use *in vitro* diagnostic laboratories. Therefore, at the beginning Turkish Cypriot community will be used for estimating the percentage of Neanderthal DNA and to determine the relation with genetically diseases.

Cyprus has an important geological location where migrating of modern human from Africa to Europe and Asia. Therefore, allergy is observed in many Cypriots with different varieties (personal communication with Professor Nerin Onder Bahceciler (Pediatric Immunologist at Near East University, Faculty of Medicine). We think Neanderthal SNPs might play a significant role in Turkish Cypriot population.

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APPENDICES

APPENDIX 1

DATA OF DETERMINED 79 ARCHAIC-LIKE SNPs IN THE DATABASE

Alleles G/A [2]	Ancestral:A [2]	Ambiguity code: R [2]	MAF: 0.44 [2]		
Location: 4:38762491 [2]					
SNP ID: rs10024216 [1]					
GWAS Trait: Amyotrophic lateral sclerosis, Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.561	A: 0.439	G|G: 0.324	A|A: 0.203	A|G: 0.473
AFRICAN	G: 0.623	A: 0.377	G|G: 0.381	A|A: 0.135	A|G: 0.484
ACB	G: 0.552	A: 0.448	G|G: 0.312	A|A: 0.208	A|G: 0.479
ASW	G: 0.623	A: 0.377	G|G: 0.344	A|A: 0.098	A|G: 0.557
ESN	G: 0.692	A: 0.308	G|G: 0.444	A|A: 0.061	A|G: 0.495
GWD	G: 0.615	A: 0.385	G|G: 0.381	A|A: 0.150	A|G: 0.469
LWK	G: 0.621	A: 0.379	G|G: 0.384	A|A: 0.141	A|G: 0.475
MSL	G: 0.571	A: 0.429	G|G: 0.318	A|A: 0.176	A|G: 0.506
YRI	G: 0.676	A: 0.324	G|G: 0.454	A|A: 0.102	A|G: 0.444
AMERICAN	G: 0.597	A: 0.403	G|G: 0.354	A|A: 0.161	A|G: 0.484
CLM	G: 0.596	A: 0.404	G|G: 0.351	A|A: 0.160	A|G: 0.489
MXL	G: 0.594	A: 0.406	G|G: 0.344	A|A: 0.156	A|G: 0.500
PEL	G: 0.641	A: 0.359	G|G: 0.400	A|A: 0.118	A|G: 0.482
PUR	G: 0.562	A: 0.438	G|G: 0.327	A|A: 0.202	A|G: 0.471
EAST ASIAN	G: 0.433	A: 0.567	G|G: 0.204	A|A: 0.339	A|G: 0.456
CDX	G: 0.538	A: 0.462	G|G: 0.312	A|A: 0.237	A|G: 0.452
CHB	G: 0.364	A: 0.636	G|G: 0.146	A|A: 0.417	A|G: 0.437
CHS	G: 0.481	A: 0.519	G|G: 0.248	A|A: 0.286	A|G: 0.467
JPT	G: 0.284	A: 0.716	G|G: 0.067	A|A: 0.500	A|G: 0.433
KHV	G: 0.510	A: 0.490	G|G: 0.263	A|A: 0.242	A|G: 0.495
EUROPEAN	G: 0.608	A: 0.392	G|G: 0.388	A|A: 0.171	A|G: 0.441
CEU	G: 0.646	A: 0.354	G|G: 0.404	A|A: 0.111	A|G: 0.485
FIN	G: 0.646	A: 0.354	G|G: 0.465	A|A: 0.172	A|G: 0.364
GBR	G: 0.687	A: 0.313	G|G: 0.440	A|A: 0.066	A|G: 0.495
IBS	G: 0.519	A: 0.481	G|G: 0.280	A|A: 0.243	A|G: 0.477
TSI	G: 0.561	A: 0.439	G|G: 0.364	A|A: 0.243	A|G: 0.393
SOUTH ASIAN	G: 0.534	A: 0.466	G|G: 0.284	A|A: 0.217	A|G: 0.499
BEB	G: 0.547	A: 0.453	G|G: 0.291	A|A: 0.198	A|G: 0.512
GIH	G: 0.490	A: 0.510	G|G: 0.262	A|A: 0.282	A|G: 0.456
ITU	G: 0.583	A: 0.417	G|G: 0.343	A|A: 0.176	A|G: 0.480
PJL	G: 0.531	A: 0.469	G|G: 0.323	A|A: 0.260	A|G: 0.417
STU	G: 0.520	A: 0.480	G|G: 0.206	A|A: 0.167	A|G: 0.627

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Alleles C/T [2]	Ancestral:T [2]	Ambiguity code: Y [2]	MAF: 0.17 [2]		
Location: 4:38764099 [2]					
SNP ID: rs10008492 [1]					
GWAS Trait: Endometriosis, Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	C: 0.166	T: 0.834	C|C: 0.081	C|T: 0.170	T|T: 0.750
AFRICAN	C: 0.017	T: 0.983	C|C: 0.002	C|T: 0.030	T|T: 0.968
ACB	C: 0.068	T: 0.932	C|C: 0.010	C|T: 0.115	T|T: 0.875
ASW	C: 0.074	T: 0.926	C|C: 0.000	C|T: 0.148	T|T: 0.852
ESN	C: 0.000	T: 1.000	C|C: 0.000	C|T: 0.000	T|T: 1.000
GWD	C: 0.000	T: 1.000	C|C: 0.000	C|T: 0.000	T|T: 1.000
LWK	C: 0.000	T: 1.000	C|C: 0.000	C|T: 0.000	T|T: 1.000
MSL	C: 0.000	T: 1.000	C|C: 0.000	C|T: 0.000	T|T: 1.000
YRI	C: 0.000	T: 1.000	C|C: 0.000	C|T: 0.000	T|T: 1.000
AMERICAN	C: 0.249	T: 0.751	C|C: 0.089	C|T: 0.320	T|T: 0.591
CLM	C: 0.330	T: 0.670	C|C: 0.117	C|T: 0.426	T|T: 0.457
MXL	C: 0.133	T: 0.867	C|C: 0.031	C|T: 0.203	T|T: 0.766
PEL	C: 0.106	T: 0.894	C|C: 0.024	C|T: 0.165	T|T: 0.812
PUR	C: 0.365	T: 0.635	C|C: 0.154	C|T: 0.423	T|T: 0.423
EAST ASIAN	C: 0.001	T: 0.999	C|C: 0.000	C|T: 0.002	T|T: 0.998
CDX	C: 0.000	T: 1.000	C|C: 0.000	C|T: 0.000	T|T: 1.000
CHB	C: 0.000	T: 1.000	C|C: 0.000	C|T: 0.000	T|T: 1.000
CHS	C: 0.005	T: 0.995	C|C: 0.000	C|T: 0.010	T|T: 0.990
JPT	C: 0.000	T: 1.000	C|C: 0.000	C|T: 0.000	T|T: 1.000
KHV	C: 0.000	T: 1.000	C|C: 0.000	C|T: 0.000	T|T: 1.000
EUROPEAN	C: 0.566	T: 0.434	C|C: 0.334	C|T: 0.463	T|T: 0.203
CEU	C: 0.631	T: 0.369	C|C: 0.384	C|T: 0.495	T|T: 0.121
FIN	C: 0.626	T: 0.374	C|C: 0.434	C|T: 0.384	T|T: 0.182
GBR	C: 0.648	T: 0.352	C|C: 0.374	C|T: 0.549	T|T: 0.077
IBS	C: 0.458	T: 0.542	C|C: 0.215	C|T: 0.486	T|T: 0.299
TSI	C: 0.486	T: 0.514	C|C: 0.280	C|T: 0.411	T|T: 0.308
SOUTH ASIAN	C: 0.065	T: 0.935	C|C: 0.004	C|T: 0.123	T|T: 0.873

BEB	C: 0.070	T: 0.930	C|C: 0.000	C|T: 0.140	T|T: 0.860
GIH	C: 0.063	T: 0.937	C|C: 0.000	C|T: 0.126	T|T: 0.874
ITU	C: 0.054	T: 0.946	C|C: 0.010	C|T: 0.088	T|T: 0.902
PJL	C: 0.094	T: 0.906	C|C: 0.010	C|T: 0.167	T|T: 0.823
STU	C: 0.049	T: 0.951	C|C: 0.000	C|T: 0.098	T|T: 0.902

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2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/G [2]	Ancestral:G [2]	Ambiguity code: R [2]	MAF: 0.49 [2]		
Location: 4:38766912 [2]					
SNP ID: rs10470854 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.513	G: 0.487	A|A: 0.275	A|G: 0.476	G|G: 0.249
AFRICAN	A: 0.506	G: 0.494	A|A: 0.265	A|G: 0.483	G|G: 0.253
ACB	A: 0.448	G: 0.552	A|A: 0.219	A|G: 0.458	G|G: 0.323
ASW	A: 0.475	G: 0.525	A|A: 0.197	A|G: 0.557	G|G: 0.246
ESN	A: 0.606	G: 0.394	A|A: 0.354	A|G: 0.505	G|G: 0.141
GWD	A: 0.540	G: 0.460	A|A: 0.319	A|G: 0.442	G|G: 0.239
LWK	A: 0.480	G: 0.520	A|A: 0.273	A|G: 0.414	G|G: 0.313
MSL	A: 0.406	G: 0.594	A|A: 0.153	A|G: 0.506	G|G: 0.341
YRI	A: 0.551	G: 0.449	A|A: 0.287	A|G: 0.528	G|G: 0.185
AMERICAN	A: 0.585	G: 0.415	A|A: 0.337	A|G: 0.496	G|G: 0.167
CLM	A: 0.585	G: 0.415	A|A: 0.340	A|G: 0.489	G|G: 0.170
MXL	A: 0.594	G: 0.406	A|A: 0.328	A|G: 0.531	G|G: 0.141
PEL	A: 0.641	G: 0.359	A|A: 0.400	A|G: 0.482	G|G: 0.118
PUR	A: 0.534	G: 0.466	A|A: 0.288	A|G: 0.490	G|G: 0.221
EAST ASIAN	A: 0.445	G: 0.555	A|A: 0.218	A|G: 0.454	G|G: 0.327
CDX	A: 0.570	G: 0.430	A|A: 0.355	A|G: 0.430	G|G: 0.215
CHB	A: 0.374	G: 0.626	A|A: 0.136	A|G: 0.476	G|G: 0.388
CHS	A: 0.490	G: 0.510	A|A: 0.238	A|G: 0.505	G|G: 0.257
JPT	A: 0.269	G: 0.731	A|A: 0.087	A|G: 0.365	G|G: 0.548
KHV	A: 0.540	G: 0.460	A|A: 0.293	A|G: 0.495	G|G: 0.212
EUROPEAN	A: 0.602	G: 0.398	A|A: 0.378	A|G: 0.449	G|G: 0.173
CEU	A: 0.652	G: 0.348	A|A: 0.414	A|G: 0.475	G|G: 0.111
FIN	A: 0.631	G: 0.369	A|A: 0.434	A|G: 0.394	G|G: 0.172

GBR	A: 0.676	G: 0.324	A|A: 0.418	A|G: 0.516	G|G: 0.066
IBS	A: 0.514	G: 0.486	A|A: 0.271	A|G: 0.486	G|G: 0.243
TSI	A: 0.556	G: 0.444	A|A: 0.364	A|G: 0.383	G|G: 0.252
SOUTH ASIAN	A: 0.448	G: 0.552	A|A: 0.196	A|G: 0.503	G|G: 0.301
BEB	A: 0.465	G: 0.535	A|A: 0.221	A|G: 0.488	G|G: 0.291
GIH	A: 0.413	G: 0.587	A|A: 0.175	A|G: 0.476	G|G: 0.350
ITU	A: 0.490	G: 0.510	A|A: 0.225	A|G: 0.529	G|G: 0.245
PJL	A: 0.443	G: 0.557	A|A: 0.219	A|G: 0.448	G|G: 0.333
STU	A: 0.431	G: 0.569	A|A: 0.147	A|G: 0.569	G|G: 0.284

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2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles C/T [2]	Ancestral:T [2]	Ambiguity code: Y [2]	MAF: 0.49 [2]		
Location: 4:38767787 [2]					
SNP ID: rs4331786 [1]					
GWAS Trait: Amyotrophic lateral sclerosis, Self-reported allergy, Blood Pressure [1,2]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	C: 0.509	T: 0.491	C|C: 0.270	C|T: 0.478	T|T: 0.252
AFRICAN	C: 0.503	T: 0.497	C|C: 0.262	C|T: 0.483	T|T: 0.256
ACB	C: 0.448	T: 0.552	C|C: 0.219	C|T: 0.458	T|T: 0.323
ASW	C: 0.459	T: 0.541	C|C: 0.164	C|T: 0.590	T|T: 0.246
ESN	C: 0.601	T: 0.399	C|C: 0.354	C|T: 0.495	T|T: 0.152
GWD	C: 0.540	T: 0.460	C|C: 0.319	C|T: 0.442	T|T: 0.239
LWK	C: 0.480	T: 0.520	C|C: 0.273	C|T: 0.414	T|T: 0.313
MSL	C: 0.406	T: 0.594	C|C: 0.153	C|T: 0.506	T|T: 0.341
YRI	C: 0.546	T: 0.454	C|C: 0.287	C|T: 0.519	T|T: 0.194
AMERICAN	C: 0.585	T: 0.415	C|C: 0.337	C|T: 0.496	T|T: 0.167
CLM	C: 0.585	T: 0.415	C|C: 0.340	C|T: 0.489	T|T: 0.170
MXL	C: 0.594	T: 0.406	C|C: 0.328	C|T: 0.531	T|T: 0.141
PEL	C: 0.641	T: 0.359	C|C: 0.400	C|T: 0.482	T|T: 0.118
PUR	C: 0.534	T: 0.466	C|C: 0.288	C|T: 0.490	T|T: 0.221
EAST ASIAN	C: 0.421	T: 0.579	C|C: 0.200	C|T: 0.440	T|T: 0.359
CDX	C: 0.548	T: 0.452	C|C: 0.333	C|T: 0.430	T|T: 0.237
CHB	C: 0.364	T: 0.636	C|C: 0.136	C|T: 0.456	T|T: 0.408
CHS	C: 0.462	T: 0.538	C|C: 0.200	C|T: 0.524	T|T: 0.276
JPT	C: 0.236	T: 0.764	C|C: 0.067	C|T: 0.337	T|T: 0.596

KHV	C: 0.510	T: 0.490	C|C: 0.283	C|T: 0.455	T|T: 0.263
EUROPEAN	C: 0.602	T: 0.398	C|C: 0.378	C|T: 0.449	T|T: 0.173
CEU	C: 0.652	T: 0.348	C|C: 0.414	C|T: 0.475	T|T: 0.111
FIN	C: 0.631	T: 0.369	C|C: 0.434	C|T: 0.394	T|T: 0.172
GBR	C: 0.676	T: 0.324	C|C: 0.418	C|T: 0.516	T|T: 0.066
IBS	C: 0.514	T: 0.486	C|C: 0.271	C|T: 0.486	T|T: 0.243
TSI	C: 0.556	T: 0.444	C|C: 0.364	C|T: 0.383	T|T: 0.252
SOUTH ASIAN	C: 0.459	T: 0.541	C|C: 0.196	C|T: 0.526	T|T: 0.278
BEB	C: 0.471	T: 0.529	C|C: 0.209	C|T: 0.523	T|T: 0.267
GIH	C: 0.427	T: 0.573	C|C: 0.184	C|T: 0.485	T|T: 0.330
ITU	C: 0.495	T: 0.505	C|C: 0.225	C|T: 0.539	T|T: 0.235
PJL	C: 0.453	T: 0.547	C|C: 0.219	C|T: 0.469	T|T: 0.312
STU	C: 0.451	T: 0.549	C|C: 0.147	C|T: 0.608	T|T: 0.245

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1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/C [2]	Ancestral:C [2]	Ambiguity code: Y [2]	MAF: 0.30 [2]		
Location: 4:38772195 [2]					
SNP ID: rs4513579 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.701	C: 0.299	T|T: 0.506	C|C: 0.103	C|T: 0.390
AFRICAN	T: 0.787	C: 0.213	T|T: 0.620	C|C: 0.045	C|T: 0.334
ACB	T: 0.708	C: 0.292	T|T: 0.490	C|C: 0.073	C|T: 0.438
ASW	T: 0.779	C: 0.221	T|T: 0.607	C|C: 0.049	C|T: 0.344
ESN	T: 0.813	C: 0.187	T|T: 0.657	C|C: 0.030	C|T: 0.313
GWD	T: 0.792	C: 0.208	T|T: 0.619	C|C: 0.035	C|T: 0.345
LWK	T: 0.874	C: 0.126	T|T: 0.778	C|C: 0.030	C|T: 0.192
MSL	T: 0.729	C: 0.271	T|T: 0.529	C|C: 0.071	C|T: 0.400
YRI	T: 0.801	C: 0.199	T|T: 0.639	C|C: 0.037	C|T: 0.324
AMERICAN	T: 0.680	C: 0.320	T|T: 0.458	C|C: 0.098	C|T: 0.444
CLM	T: 0.697	C: 0.303	T|T: 0.479	C|C: 0.085	C|T: 0.436
MXL	T: 0.688	C: 0.312	T|T: 0.453	C|C: 0.078	C|T: 0.469
PEL	T: 0.694	C: 0.306	T|T: 0.482	C|C: 0.094	C|T: 0.424
PUR	T: 0.649	C: 0.351	T|T: 0.423	C|C: 0.125	C|T: 0.452
EAST ASIAN	T: 0.568	C: 0.432	T|T: 0.345	C|C: 0.208	C|T: 0.446

CDX	T: 0.742	C: 0.258	T|T: 0.591	C|C: 0.108	C|T: 0.301
CHB	T: 0.476	C: 0.524	T|T: 0.194	C|C: 0.243	C|T: 0.563
CHS	T: 0.600	C: 0.400	T|T: 0.362	C|C: 0.162	C|T: 0.476
JPT	T: 0.341	C: 0.659	T|T: 0.115	C|C: 0.433	C|T: 0.452
KHV	T: 0.707	C: 0.293	T|T: 0.495	C|C: 0.081	C|T: 0.424
EUROPEAN	T: 0.750	C: 0.250	T|T: 0.579	C|C: 0.078	C|T: 0.344
CEU	T: 0.778	C: 0.222	T|T: 0.596	C|C: 0.040	C|T: 0.364
FIN	T: 0.899	C: 0.101	T|T: 0.808	C|C: 0.010	C|T: 0.182
GBR	T: 0.797	C: 0.203	T|T: 0.615	C|C: 0.022	C|T: 0.363
IBS	T: 0.659	C: 0.341	T|T: 0.458	C|C: 0.140	C|T: 0.402
TSI	T: 0.640	C: 0.360	T|T: 0.439	C|C: 0.159	C|T: 0.402
SOUTH ASIAN	T: 0.687	C: 0.313	T|T: 0.479	C|C: 0.104	C|T: 0.417
BEB	T: 0.692	C: 0.308	T|T: 0.512	C|C: 0.128	C|T: 0.360
GIH	T: 0.641	C: 0.359	T|T: 0.408	C|C: 0.126	C|T: 0.466
ITU	T: 0.716	C: 0.284	T|T: 0.510	C|C: 0.078	C|T: 0.412
PJL	T: 0.693	C: 0.307	T|T: 0.510	C|C: 0.125	C|T: 0.365
STU	T: 0.696	C: 0.304	T|T: 0.461	C|C: 0.069	C|T: 0.471

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/G [2]	Ancestral:G [2]	Ambiguity code: R [2]	MAF: 0.30 [2]		
Location: 4:38773164 [2]					
SNP ID: rs10776482 [1]					
GWAS Trait: Helicobacter pylori setologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.701	G: 0.299	A|A: 0.506	A|G: 0.391	G|G: 0.103
AFRICAN	A: 0.787	G: 0.213	A|A: 0.620	A|G: 0.334	G|G: 0.045
ACB	A: 0.708	G: 0.292	A|A: 0.490	A|G: 0.438	G|G: 0.073
ASW	A: 0.779	G: 0.221	A|A: 0.607	A|G: 0.344	G|G: 0.049
ESN	A: 0.813	G: 0.187	A|A: 0.657	A|G: 0.313	G|G: 0.030
GWD	A: 0.792	G: 0.208	A|A: 0.619	A|G: 0.345	G|G: 0.035
LWK	A: 0.874	G: 0.126	A|A: 0.778	A|G: 0.192	G|G: 0.030
MSL	A: 0.729	G: 0.271	A|A: 0.529	A|G: 0.400	G|G: 0.071
YRI	A: 0.801	G: 0.199	A|A: 0.639	A|G: 0.324	G|G: 0.037
AMERICAN	A: 0.682	G: 0.318	A|A: 0.461	A|G: 0.441	G|G: 0.098
CLM	A: 0.702	G: 0.298	A|A: 0.489	A|G: 0.426	G|G: 0.085

MXL	A: 0.688	G: 0.312	A|A: 0.453	A|G: 0.469	G|G: 0.078
PEL	A: 0.694	G: 0.306	A|A: 0.482	A|G: 0.424	G|G: 0.094
PUR	A: 0.649	G: 0.351	A|A: 0.423	A|G: 0.452	G|G: 0.125
EAST ASIAN	A: 0.567	G: 0.433	A|A: 0.343	A|G: 0.448	G|G: 0.208
CDX	A: 0.742	G: 0.258	A|A: 0.591	A|G: 0.301	G|G: 0.108
CHB	A: 0.476	G: 0.524	A|A: 0.194	A|G: 0.563	G|G: 0.243
CHS	A: 0.600	G: 0.400	A|A: 0.362	A|G: 0.476	G|G: 0.162
JPT	A: 0.341	G: 0.659	A|A: 0.115	A|G: 0.452	G|G: 0.433
KHV	A: 0.702	G: 0.298	A|A: 0.485	A|G: 0.434	G|G: 0.081
EUROPEAN	A: 0.750	G: 0.250	A|A: 0.579	A|G: 0.344	G|G: 0.078
CEU	A: 0.778	G: 0.222	A|A: 0.596	A|G: 0.364	G|G: 0.040
FIN	A: 0.899	G: 0.101	A|A: 0.808	A|G: 0.182	G|G: 0.010
GBR	A: 0.797	G: 0.203	A|A: 0.615	A|G: 0.363	G|G: 0.022
IBS	A: 0.659	G: 0.341	A|A: 0.458	A|G: 0.402	G|G: 0.140
TSI	A: 0.640	G: 0.360	A|A: 0.439	A|G: 0.402	G|G: 0.159
SOUTH ASIAN	A: 0.686	G: 0.314	A|A: 0.476	A|G: 0.419	G|G: 0.104
BEB	A: 0.686	G: 0.314	A|A: 0.500	A|G: 0.372	G|G: 0.128
GIH	A: 0.641	G: 0.359	A|A: 0.408	A|G: 0.466	G|G: 0.126
ITU	A: 0.716	G: 0.284	A|A: 0.510	A|G: 0.412	G|G: 0.078
PJL	A: 0.693	G: 0.307	A|A: 0.510	A|G: 0.365	G|G: 0.125
STU	A: 0.696	G: 0.304	A|A: 0.461	A|G: 0.471	G|G: 0.069

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/A/C/G [2]	Ancestral:T [2]	Ambiguity code: N [2]	MAF: 0.15 [2]		
Location: 4:38773268 [2]					
SNP ID: rs4129009 [1]					
GWAS Trait: Helicobacter pylori setologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.853	C: 0.147	T|T: 0.743	C|C: 0.036	C|T: 0.220
AFRICAN	T: 0.989	C: 0.011	T|T: 0.979	C|C: 0.000	C|T: 0.021
ACB	T: 0.984	C: 0.016	T|T: 0.969	C|C: 0.000	C|T: 0.031
ASW	T: 0.926	C: 0.074	T|T: 0.852	C|C: 0.000	C|T: 0.148
ESN	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
GWD	T: 0.991	C: 0.009	T|T: 0.982	C|C: 0.000	C|T: 0.018
LWK	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000

MSL	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
YRI	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
AMERICAN	T: 0.860	C: 0.140	T|T: 0.752	C|C: 0.032	C|T: 0.216
CLM	T: 0.856	C: 0.144	T|T: 0.734	C|C: 0.021	C|T: 0.245
MXL	T: 0.914	C: 0.086	T|T: 0.844	C|C: 0.016	C|T: 0.141
PEL	T: 0.941	C: 0.059	T|T: 0.882	C|C: 0.000	C|T: 0.118
PUR	T: 0.764	C: 0.236	T|T: 0.606	C|C: 0.077	C|T: 0.317
EAST ASIAN	T: 0.731	C: 0.269	T|T: 0.550	C|C: 0.087	C|T: 0.363
CDX	T: 0.898	C: 0.102	T|T: 0.817	C|C: 0.022	C|T: 0.161
CHB	T: 0.636	C: 0.364	T|T: 0.388	C|C: 0.117	C|T: 0.495
CHS	T: 0.757	C: 0.243	T|T: 0.552	C|C: 0.038	C|T: 0.410
JPT	T: 0.500	C: 0.500	T|T: 0.240	C|C: 0.240	C|T: 0.519
KHV	T: 0.889	C: 0.111	T|T: 0.788	C|C: 0.010	C|T: 0.202
EUROPEAN	T: 0.793	C: 0.207	T|T: 0.640	C|C: 0.054	C|T: 0.306
CEU	T: 0.813	C: 0.187	T|T: 0.667	C|C: 0.040	C|T: 0.293
FIN	T: 0.914	C: 0.086	T|T: 0.838	C|C: 0.010	C|T: 0.152
GBR	T: 0.835	C: 0.165	T|T: 0.681	C|C: 0.011	C|T: 0.308
IBS	T: 0.724	C: 0.276	T|T: 0.542	C|C: 0.093	C|T: 0.364
TSI	T: 0.696	C: 0.304	T|T: 0.495	C|C: 0.103	C|T: 0.402
SOUTH ASIAN	T: 0.853	C: 0.147	T|T: 0.724	C|C: 0.018	C|T: 0.258
BEB	T: 0.802	C: 0.198	T|T: 0.628	C|C: 0.023	C|T: 0.349
GIH	T: 0.820	C: 0.180	T|T: 0.680	C|C: 0.039	C|T: 0.282
ITU	T: 0.897	C: 0.103	T|T: 0.804	C|C: 0.010	C|T: 0.186
PJL	T: 0.875	C: 0.125	T|T: 0.760	C|C: 0.010	C|T: 0.229
STU	T: 0.863	C: 0.137	T|T: 0.735	C|C: 0.010	C|T: 0.255

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/G [2]	Ancestral:A [2]	Ambiguity code: R [2]	MAF: 0.30 [2]		
Location: 4:38773419 [2]					
SNP ID: rs10776483 [1]					
GWAS Trait: Helicobacter pylori setologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.701	G: 0.299	A|A: 0.506	A|G: 0.391	G|G: 0.103
AFRICAN	A: 0.787	G: 0.213	A|A: 0.620	A|G: 0.334	G|G: 0.045
ACB	A: 0.708	G: 0.292	A|A: 0.490	A|G: 0.438	G|G: 0.073

ASW	A: 0.779	G: 0.221	A|A: 0.607	A|G: 0.344	G|G: 0.049
ESN	A: 0.813	G: 0.187	A|A: 0.657	A|G: 0.313	G|G: 0.030
GWD	A: 0.792	G: 0.208	A|A: 0.619	A|G: 0.345	G|G: 0.035
LWK	A: 0.874	G: 0.126	A|A: 0.778	A|G: 0.192	G|G: 0.030
MSL	A: 0.729	G: 0.271	A|A: 0.529	A|G: 0.400	G|G: 0.071
YRI	A: 0.801	G: 0.199	A|A: 0.639	A|G: 0.324	G|G: 0.037
AMERICAN	A: 0.682	G: 0.318	A|A: 0.461	A|G: 0.441	G|G: 0.098
CLM	A: 0.702	G: 0.298	A|A: 0.489	A|G: 0.426	G|G: 0.085
MXL	A: 0.688	G: 0.312	A|A: 0.453	A|G: 0.469	G|G: 0.078
PEL	A: 0.694	G: 0.306	A|A: 0.482	A|G: 0.424	G|G: 0.094
PUR	A: 0.649	G: 0.351	A|A: 0.423	A|G: 0.452	G|G: 0.125
EAST ASIAN	A: 0.567	G: 0.433	A|A: 0.343	A|G: 0.448	G|G: 0.208
CDX	A: 0.742	G: 0.258	A|A: 0.591	A|G: 0.301	G|G: 0.108
CHB	A: 0.476	G: 0.524	A|A: 0.194	A|G: 0.563	G|G: 0.243
CHS	A: 0.600	G: 0.400	A|A: 0.362	A|G: 0.476	G|G: 0.162
JPT	A: 0.341	G: 0.659	A|A: 0.115	A|G: 0.452	G|G: 0.433
KHV	A: 0.702	G: 0.298	A|A: 0.485	A|G: 0.434	G|G: 0.081
EUROPEAN	A: 0.750	G: 0.250	A|A: 0.579	A|G: 0.344	G|G: 0.078
CEU	A: 0.778	G: 0.222	A|A: 0.596	A|G: 0.364	G|G: 0.040
FIN	A: 0.899	G: 0.101	A|A: 0.808	A|G: 0.182	G|G: 0.010
GBR	A: 0.797	G: 0.203	A|A: 0.615	A|G: 0.363	G|G: 0.022
IBS	A: 0.659	G: 0.341	A|A: 0.458	A|G: 0.402	G|G: 0.140
TSI	A: 0.640	G: 0.360	A|A: 0.439	A|G: 0.402	G|G: 0.159
SOUTH ASIAN	A: 0.686	G: 0.314	A|A: 0.476	A|G: 0.419	G|G: 0.104
BEB	A: 0.686	G: 0.314	A|A: 0.500	A|G: 0.372	G|G: 0.128
GIH	A: 0.641	G: 0.359	A|A: 0.408	A|G: 0.466	G|G: 0.126
ITU	A: 0.716	G: 0.284	A|A: 0.510	A|G: 0.412	G|G: 0.078
PJL	A: 0.693	G: 0.307	A|A: 0.510	A|G: 0.365	G|G: 0.125
STU	A: 0.696	G: 0.304	A|A: 0.461	A|G: 0.471	G|G: 0.069

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/G [2]	Ancestral:A [2]	Ambiguity code: R [2]	MAF: 0.02 [2]		
Location: 4:38774173 [2]					
SNP ID: rs11466657 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.981	G: 0.019	A|A: 0.964	A|G: 0.034	G|G: 0.002
AFRICAN	A: 0.998	G: 0.002	A|A: 0.995	A|G: 0.005	G|G: 0.000
ACB	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
ASW	A: 0.992	G: 0.008	A|A: 0.984	A|G: 0.016	G|G: 0.000
ESN	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
GWD	A: 0.991	G: 0.009	A|A: 0.982	A|G: 0.018	G|G: 0.000
LWK	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
MSL	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
YRI	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
AMERICAN	A: 0.967	G: 0.033	A|A: 0.934	A|G: 0.066	G|G: 0.000
CLM	A: 0.952	G: 0.048	A|A: 0.904	A|G: 0.096	G|G: 0.000
MXL	A: 0.984	G: 0.016	A|A: 0.969	A|G: 0.031	G|G: 0.000
PEL	A: 0.988	G: 0.012	A|A: 0.976	A|G: 0.024	G|G: 0.000
PUR	A: 0.952	G: 0.048	A|A: 0.904	A|G: 0.096	G|G: 0.000
EAST ASIAN	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
CDX	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
CHB	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
CHS	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
JPT	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
KHV	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
EUROPEAN	A: 0.947	G: 0.053	A|A: 0.903	A|G: 0.089	G|G: 0.008
CEU	A: 0.970	G: 0.030	A|A: 0.939	A|G: 0.061	G|G: 0.000
FIN	A: 0.990	G: 0.010	A|A: 0.980	A|G: 0.020	G|G: 0.000
GBR	A: 0.962	G: 0.038	A|A: 0.923	A|G: 0.077	G|G: 0.000
IBS	A: 0.921	G: 0.079	A|A: 0.841	A|G: 0.159	G|G: 0.000
TSI	A: 0.902	G: 0.098	A|A: 0.841	A|G: 0.121	G|G: 0.000
SOUTH ASIAN	A: 0.986	G: 0.014	A|A: 0.971	A|G: 0.029	G|G: 0.037
BEB	A: 0.988	G: 0.012	A|A: 0.977	A|G: 0.023	G|G: 0.000
GIH	A: 0.981	G: 0.019	A|A: 0.961	A|G: 0.039	G|G: 0.000
ITU	A: 0.985	G: 0.015	A|A: 0.971	A|G: 0.029	G|G: 0.000
PJL	A: 0.990	G: 0.010	A|A: 0.979	A|G: 0.021	G|G: 0.000
STU	A: 0.985	G: 0.015	A|A: 0.971	A|G: 0.029	G|G: 0.000
REFERENCES					

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/C/G [2]	Ancestral:T [2]	Ambiguity code: B [2]	MAF: 0.50 [2]		
Location: 4:38774486 [2]					
SNP ID: rs11096955 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.500	G: 0.500	T|T: 0.262	G|G: 0.261	G|T: 0.478
AFRICAN	T: 0.453	G: 0.547	T|T: 0.215	G|G: 0.309	G|T: 0.477
ACB	T: 0.438	G: 0.562	T|T: 0.219	G|G: 0.344	G|T: 0.438
ASW	T: 0.410	G: 0.590	T|T: 0.164	G|G: 0.344	G|T: 0.492
ESN	T: 0.551	G: 0.449	T|T: 0.303	G|G: 0.202	G|T: 0.495
GWD	T: 0.465	G: 0.535	T|T: 0.248	G|G: 0.319	G|T: 0.434
LWK	T: 0.449	G: 0.551	T|T: 0.232	G|G: 0.333	G|T: 0.434
MSL	T: 0.365	G: 0.635	T|T: 0.094	G|G: 0.365	G|T: 0.541
YRI	T: 0.463	G: 0.537	T|T: 0.204	G|G: 0.278	G|T: 0.519
AMERICAN	T: 0.582	G: 0.418	T|T: 0.334	G|G: 0.170	G|T: 0.496
CLM	T: 0.580	G: 0.420	T|T: 0.340	G|G: 0.181	G|T: 0.479
MXL	T: 0.594	G: 0.406	T|T: 0.328	G|G: 0.141	G|T: 0.531
PEL	T: 0.641	G: 0.359	T|T: 0.400	G|G: 0.118	G|T: 0.482
PUR	T: 0.529	G: 0.471	T|T: 0.279	G|G: 0.221	G|T: 0.500
EAST ASIAN	T: 0.445	G: 0.555	T|T: 0.218	G|G: 0.327	G|T: 0.454
CDX	T: 0.570	G: 0.430	T|T: 0.355	G|G: 0.215	G|T: 0.430
CHB	T: 0.374	G: 0.626	T|T: 0.136	G|G: 0.388	G|T: 0.476
CHS	T: 0.490	G: 0.510	T|T: 0.238	G|G: 0.257	G|T: 0.505
JPT	T: 0.269	G: 0.731	T|T: 0.087	G|G: 0.548	G|T: 0.365
KHV	T: 0.540	G: 0.460	T|T: 0.293	G|G: 0.212	G|T: 0.495
EUROPEAN	T: 0.602	G: 0.398	T|T: 0.378	G|G: 0.173	G|T: 0.449
CEU	T: 0.652	G: 0.348	T|T: 0.414	G|G: 0.111	G|T: 0.475
FIN	T: 0.631	G: 0.369	T|T: 0.434	G|G: 0.172	G|T: 0.394
GBR	T: 0.676	G: 0.324	T|T: 0.418	G|G: 0.066	G|T: 0.516
IBS	T: 0.514	G: 0.486	T|T: 0.271	G|G: 0.243	G|T: 0.486
TSI	T: 0.556	G: 0.444	T|T: 0.364	G|G: 0.252	G|T: 0.383
SOUTH ASIAN	T: 0.458	G: 0.542	T|T: 0.198	G|G: 0.282	G|T: 0.519
BEB	T: 0.465	G: 0.535	T|T: 0.221	G|G: 0.291	G|T: 0.488
GIH	T: 0.427	G: 0.573	T|T: 0.184	G|G: 0.330	G|T: 0.485

ITU	T: 0.495	G: 0.505	T|T: 0.225	G|G: 0.235	G|T: 0.539
PJL	T: 0.453	G: 0.547	T|T: 0.219	G|G: 0.312	G|T: 0.469
STU	T: 0.451	G: 0.549	T|T: 0.147	G|G: 0.245	G|T: 0.608

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles C/A/T [2]	Ancestral:A [2]	Ambiguity code: H [2]	MAF: 0.30 [2]		
Location: 4:38774559 [2]					
SNP ID: rs11096956 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	C: 0.701	A: 0.299	C|C: 0.506	A|A: 0.103	A|C: 0.390
AFRICAN	C: 0.788	A: 0.212	C|C: 0.622	A|A: 0.045	A|C: 0.333
ACB	C: 0.714	A: 0.286	C|C: 0.500	A|A: 0.073	A|C: 0.427
ASW	C: 0.779	A: 0.221	C|C: 0.607	A|A: 0.049	A|C: 0.344
ESN	C: 0.813	A: 0.187	C|C: 0.657	A|A: 0.030	A|C: 0.313
GWD	C: 0.792	A: 0.208	C|C: 0.619	A|A: 0.035	A|C: 0.345
LWK	C: 0.874	A: 0.126	C|C: 0.778	A|A: 0.030	A|C: 0.192
MSL	C: 0.729	A: 0.271	C|C: 0.529	A|A: 0.071	A|C: 0.400
YRI	C: 0.801	A: 0.199	C|C: 0.639	A|A: 0.037	A|C: 0.324
AMERICAN	C: 0.682	A: 0.318	C|C: 0.461	A|A: 0.098	A|C: 0.441
CLM	C: 0.702	A: 0.298	C|C: 0.489	A|A: 0.085	A|C: 0.426
MXL	C: 0.688	A: 0.312	C|C: 0.453	A|A: 0.078	A|C: 0.469
PEL	C: 0.694	A: 0.306	C|C: 0.482	A|A: 0.094	A|C: 0.424
PUR	C: 0.649	A: 0.351	C|C: 0.423	A|A: 0.125	A|C: 0.452
EAST ASIAN	C: 0.567	A: 0.433	C|C: 0.343	A|A: 0.208	A|C: 0.448
CDX	C: 0.742	A: 0.258	C|C: 0.591	A|A: 0.108	A|C: 0.301
CHB	C: 0.476	A: 0.524	C|C: 0.194	A|A: 0.243	A|C: 0.563
CHS	C: 0.600	A: 0.400	C|C: 0.362	A|A: 0.162	A|C: 0.476
JPT	C: 0.341	A: 0.659	C|C: 0.115	A|A: 0.433	A|C: 0.452
KHV	C: 0.702	A: 0.298	C|C: 0.485	A|A: 0.081	A|C: 0.434
EUROPEAN	C: 0.750	A: 0.250	C|C: 0.579	A|A: 0.078	A|C: 0.344
CEU	C: 0.778	A: 0.222	C|C: 0.596	A|A: 0.040	A|C: 0.364
FIN	C: 0.899	A: 0.101	C|C: 0.808	A|A: 0.010	A|C: 0.182
GBR	C: 0.797	A: 0.203	C|C: 0.615	A|A: 0.022	A|C: 0.363
IBS	C: 0.659	A: 0.341	C|C: 0.458	A|A: 0.140	A|C: 0.402

TSI	C: 0.640	A: 0.360	C|C: 0.439	A|A: 0.159	A|C: 0.402
SOUTH ASIAN	C: 0.686	A: 0.314	C|C: 0.476	A|A: 0.104	A|C: 0.419
BEB	C: 0.686	A: 0.314	C|C: 0.500	A|A: 0.128	A|C: 0.372
GIH	C: 0.641	A: 0.359	C|C: 0.408	A|A: 0.126	A|C: 0.466
ITU	C: 0.716	A: 0.284	C|C: 0.510	A|A: 0.078	A|C: 0.412
PJL	C: 0.693	A: 0.307	C|C: 0.510	A|A: 0.125	A|C: 0.365
STU	C: 0.696	A: 0.304	C|C: 0.461	A|A: 0.069	A|C: 0.471

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1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/G [2]	Ancestral:T [2]	Ambiguity code: K [2]	MAF: 0.50 [2]		
Location: 4:38774870 [2]					
SNP ID: rs11096957 [1]					
GWAS Trait: Amyotrophic lateral sclerosis, Endometriosis, Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.500	G: 0.500	T|T: 0.260	G|G: 0.260	G|T: 0.479
AFRICAN	T: 0.451	G: 0.549	T|T: 0.210	G|G: 0.309	G|T: 0.481
ACB	T: 0.438	G: 0.562	T|T: 0.219	G|G: 0.344	G|T: 0.438
ASW	T: 0.410	G: 0.590	T|T: 0.164	G|G: 0.344	G|T: 0.492
ESN	T: 0.545	G: 0.455	T|T: 0.293	G|G: 0.202	G|T: 0.505
GWD	T: 0.456	G: 0.544	T|T: 0.230	G|G: 0.319	G|T: 0.451
LWK	T: 0.449	G: 0.551	T|T: 0.232	G|G: 0.333	G|T: 0.434
MSL	T: 0.365	G: 0.635	T|T: 0.094	G|G: 0.365	G|T: 0.541
YRI	T: 0.463	G: 0.537	T|T: 0.204	G|G: 0.278	G|T: 0.519
AMERICAN	T: 0.582	G: 0.418	T|T: 0.334	G|G: 0.170	G|T: 0.496
CLM	T: 0.580	G: 0.420	T|T: 0.340	G|G: 0.181	G|T: 0.479
MXL	T: 0.594	G: 0.406	T|T: 0.328	G|G: 0.141	G|T: 0.531
PEL	T: 0.641	G: 0.359	T|T: 0.400	G|G: 0.118	G|T: 0.482
PUR	T: 0.529	G: 0.471	T|T: 0.279	G|G: 0.221	G|T: 0.500
EAST ASIAN	T: 0.445	G: 0.555	T|T: 0.218	G|G: 0.327	G|T: 0.454
CDX	T: 0.570	G: 0.430	T|T: 0.355	G|G: 0.215	G|T: 0.430
CHB	T: 0.374	G: 0.626	T|T: 0.136	G|G: 0.388	G|T: 0.476
CHS	T: 0.490	G: 0.510	T|T: 0.238	G|G: 0.257	G|T: 0.505
JPT	T: 0.269	G: 0.731	T|T: 0.087	G|G: 0.548	G|T: 0.365
KHV	T: 0.540	G: 0.460	T|T: 0.293	G|G: 0.212	G|T: 0.495

EUROPEAN	T: 0.602	G: 0.398	T|T: 0.378	G|G: 0.173	G|T: 0.449
CEU	T: 0.652	G: 0.348	T|T: 0.414	G|G: 0.111	G|T: 0.475
FIN	T: 0.631	G: 0.369	T|T: 0.434	G|G: 0.172	G|T: 0.394
GBR	T: 0.676	G: 0.324	T|T: 0.418	G|G: 0.066	G|T: 0.516
IBS	T: 0.514	G: 0.486	T|T: 0.271	G|G: 0.243	G|T: 0.486
TSI	T: 0.556	G: 0.444	T|T: 0.364	G|G: 0.252	G|T: 0.383
SOUTH ASIAN	T: 0.459	G: 0.541	T|T: 0.198	G|G: 0.280	G|T: 0.521
BEB	T: 0.471	G: 0.529	T|T: 0.221	G|G: 0.279	G|T: 0.500
GIH	T: 0.427	G: 0.573	T|T: 0.184	G|G: 0.330	G|T: 0.485
ITU	T: 0.495	G: 0.505	T|T: 0.225	G|G: 0.235	G|T: 0.539
PJL	T: 0.453	G: 0.547	T|T: 0.219	G|G: 0.312	G|T: 0.469
STU	T: 0.451	G: 0.549	T|T: 0.147	G|G: 0.245	G|T: 0.608

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles G/A [2]	Ancestral:A [2]	Ambiguity code: R [2]	MAF: 0.43 [2]		
Location: 4:38775850 [2]					
SNP ID: rs4274855 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: The GWAS-identified archaic like SNP, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	C: 0.841	T: 0.159	C|C: 0.723	C|T: 0.235	T|T: 0.042
AFRICAN	C: 0.989	T: 0.011	C|C: 0.979	C|T: 0.021	T|T: 0.000
ACB	C: 0.984	T: 0.016	C|C: 0.969	C|T: 0.031	T|T: 0.000
ASW	C: 0.926	T: 0.074	C|C: 0.852	C|T: 0.148	T|T: 0.000
ESN	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
GWD	C: 0.991	T: 0.009	C|C: 0.982	C|T: 0.018	T|T: 0.000
LWK	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
MSL	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
YRI	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
AMERICAN	C: 0.860	T: 0.140	C|C: 0.752	C|T: 0.216	T|T: 0.032
CLM	C: 0.856	T: 0.144	C|C: 0.734	C|T: 0.245	T|T: 0.021
MXL	C: 0.914	T: 0.086	C|C: 0.844	C|T: 0.141	T|T: 0.016
PEL	C: 0.941	T: 0.059	C|C: 0.882	C|T: 0.118	T|T: 0.000
PUR	C: 0.764	T: 0.236	C|C: 0.606	C|T: 0.317	T|T: 0.077
EAST ASIAN	C: 0.676	T: 0.324	C|C: 0.464	C|T: 0.423	T|T: 0.113
CDX	C: 0.839	T: 0.161	C|C: 0.710	C|T: 0.258	T|T: 0.032

CHB	C: 0.568	T: 0.432	C|C: 0.301	C|T: 0.534	T|T: 0.165
CHS	C: 0.695	T: 0.305	C|C: 0.448	C|T: 0.495	T|T: 0.057
JPT	C: 0.471	T: 0.529	C|C: 0.212	C|T: 0.519	T|T: 0.269
KHV	C: 0.828	T: 0.172	C|C: 0.687	C|T: 0.283	T|T: 0.030
EUROPEAN	C: 0.793	T: 0.207	C|C: 0.640	C|T: 0.306	T|T: 0.054
CEU	C: 0.813	T: 0.187	C|C: 0.667	C|T: 0.293	T|T: 0.040
FIN	C: 0.914	T: 0.086	C|C: 0.838	C|T: 0.152	T|T: 0.010
GBR	C: 0.835	T: 0.165	C|C: 0.681	C|T: 0.308	T|T: 0.011
IBS	C: 0.724	T: 0.276	C|C: 0.542	C|T: 0.364	T|T: 0.093
TSI	C: 0.696	T: 0.304	C|C: 0.495	C|T: 0.402	T|T: 0.103
SOUTH ASIAN	C: 0.846	T: 0.154	C|C: 0.710	C|T: 0.272	T|T: 0.018
BEB	C: 0.802	T: 0.198	C|C: 0.628	C|T: 0.349	T|T: 0.023
GIH	C: 0.816	T: 0.184	C|C: 0.670	C|T: 0.291	T|T: 0.039
ITU	C: 0.892	T: 0.108	C|C: 0.794	C|T: 0.196	T|T: 0.010
PJL	C: 0.875	T: 0.125	C|C: 0.760	C|T: 0.229	T|T: 0.010
STU	C: 0.838	T: 0.162	C|C: 0.686	C|T: 0.304	T|T: 0.010

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/T [2]	Ancestral:A [2]	Ambiguity code: W [2]	MAF: 0.16 [2]		
Location: 4:38776582 [2]					
SNP ID: rs11466645 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.840	T: 0.160	A|A: 0.722	A|T: 0.236	T|T: 0.042
AFRICAN	A: 0.989	T: 0.011	A|A: 0.979	A|T: 0.021	T|T: 0.000
ACB	A: 0.984	T: 0.016	A|A: 0.969	A|T: 0.031	T|T: 0.000
ASW	A: 0.8926	T: 0.074	A|A: 0.852	A|T: 0.148	T|T: 0.000
ESN	A: 1.000	T: 0.000	A|A: 1.000	A|T: 0.000	T|T: 0.000
GWD	A: 0.991	T: 0.009	A|A: 0.982	A|T: 0.018	T|T: 0.000
LWK	A: 1.000	T: 0.000	A|A: 1.000	A|T: 0.000	T|T: 0.000
MSL	A: 1.000	T: 0.000	A|A: 1.000	A|T: 0.000	T|T: 0.000
YRI	A: 1.000	T: 0.000	A|A: 1.000	A|T: 0.000	T|T: 0.000
AMERICAN	A: 0.860	T: 0.140	A|A: 0.752	A|T: 0.216	T|T: 0.032
CLM	A: 0.856	T: 0.144	A|A: 0.734	A|T: 0.245	T|T: 0.021
MXL	A: 0.914	T: 0.086	A|A: 0.844	A|T: 0.141	T|T: 0.016

PEL	A: 0.941	T: 0.059	A|A: 0.882	A|T: 0.118	T|T: 0.000
PUR	A: 0.764	T: 0.236	A|A: 0.606	A|T: 0.317	T|T: 0.077
EAST ASIAN	A: 0.676	T: 0.324	A|A: 0.464	A|T: 0.423	T|T: 0.113
CDX	A: 0.839	T: 0.161	A|A: 0.710	A|T: 0.258	T|T: 0.032
CHB	A: 0.568	T: 0.432	A|A: 0.301	A|T: 0.534	T|T: 0.165
CHS	A: 0.695	T: 0.305	A|A: 0.448	A|T: 0.495	T|T: 0.057
JPT	A: 0.471	T: 0.529	A|A: 0.212	A|T: 0.519	T|T: 0.269
KHV	A: 0.828	T: 0.172	A|A: 0.687	A|T: 0.283	T|T: 0.030
EUROPEAN	A: 0.793	T: 0.207	A|A: 0.640	A|T: 0.306	T|T: 0.054
CEU	A: 0.813	T: 0.187	A|A: 0.667	A|T: 0.293	T|T: 0.040
FIN	A: 0.914	T: 0.086	A|A: 0.838	A|T: 0.152	T|T: 0.010
GBR	A: 0.835	T: 0.165	A|A: 0.681	A|T: 0.308	T|T: 0.011
IBS	A: 0.724	T: 0.276	A|A: 0.542	A|T: 0.364	T|T: 0.093
TSI	A: 0.696	T: 0.304	A|A: 0.495	A|T: 0.402	T|T: 0.103
SOUTH ASIAN	A: 0.844	T: 0.156	A|A: 0.706	A|T: 0.276	T|T: 0.018
BEB	A: 0.802	T: 0.198	A|A: 0.628	A|T: 0.349	T|T: 0.023
GIH	A: 0.816	T: 0.184	A|A: 0.670	A|T: 0.291	T|T: 0.039
ITU	A: 0.887	T: 0.113	A|A: 0.784	A|T: 0.206	T|T: 0.010
PJL	A: 0.875	T: 0.125	A|A: 0.760	A|T: 0.229	T|T: 0.010
STU	A: 0.833	T: 0.167	A|A: 0.676	A|T: 0.314	T|T: 0.010

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles G/A [2]	Ancestral:G [2]	Ambiguity code: R [2]	MAF: 0.16 [2]		
Location: 4:38777282 [2]					
SNP ID: rs11466640 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: The GWAS-identified archaic like SNP, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.841	A: 0.159	G|G: 0.723	A|A: 0.042	A|G: 0.235
AFRICAN	G: 0.989	A: 0.011	G|G: 0.979	A|A: 0.000	A|G: 0.021
ACB	G: 0.984	A: 0.016	G|G: 0.969	A|A: 0.000	A|G: 0.031
ASW	G: 0.926	A: 0.074	G|G: 0.852	A|A: 0.000	A|G: 0.148
ESN	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
GWD	G: 0.991	A: 0.009	G|G: 0.982	A|A: 0.000	A|G: 0.018
LWK	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
MSL	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000

YRI	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
AMERICAN	G: 0.860	A: 0.140	G|G: 0.752	A|A: 0.032	A|G: 0.216
CLM	G: 0.856	A: 0.144	G|G: 0.734	A|A: 0.021	A|G: 0.245
MXL	G: 0.914	A: 0.086	G|G: 0.844	A|A: 0.016	A|G: 0.141
PEL	G: 0.941	A: 0.059	G|G: 0.882	A|A: 0.000	A|G: 0.118
PUR	G: 0.764	A: 0.236	G|G: 0.606	A|A: 0.077	A|G: 0.317
EAST ASIAN	G: 0.676	A: 0.324	G|G: 0.464	A|A: 0.113	A|G: 0.423
CDX	G: 0.839	A: 0.161	G|G: 0.710	A|A: 0.032	A|G: 0.258
CHB	G: 0.568	A: 0.432	G|G: 0.301	A|A: 0.165	A|G: 0.534
CHS	G: 0.695	A: 0.305	G|G: 0.448	A|A: 0.057	A|G: 0.495
JPT	G: 0.471	A: 0.529	G|G: 0.212	A|A: 0.269	A|G: 0.519
KHV	G: 0.828	A: 0.172	G|G: 0.687	A|A: 0.030	A|G: 0.283
EUROPEAN	G: 0.793	A: 0.207	G|G: 0.640	A|A: 0.054	A|G: 0.306
CEU	G: 0.813	A: 0.187	G|G: 0.667	A|A: 0.040	A|G: 0.293
FIN	G: 0.914	A: 0.086	G|G: 0.838	A|A: 0.010	A|G: 0.152
GBR	G: 0.835	A: 0.165	G|G: 0.681	A|A: 0.011	A|G: 0.308
IBS	G: 0.724	A: 0.276	G|G: 0.542	A|A: 0.093	A|G: 0.364
TSI	G: 0.696	A: 0.304	G|G: 0.495	A|A: 0.103	A|G: 0.402
SOUTH ASIAN	G: 0.846	A: 0.154	G|G: 0.710	A|A: 0.018	A|G: 0.272
BEB	G: 0.802	A: 0.198	G|G: 0.628	A|A: 0.023	A|G: 0.349
GIH	G: 0.816	A: 0.184	G|G: 0.670	A|A: 0.039	A|G: 0.291
ITU	G: 0.892	A: 0.108	G|G: 0.794	A|A: 0.010	A|G: 0.196
PJL	G: 0.875	A: 0.125	G|G: 0.760	A|A: 0.010	A|G: 0.229
STU	G: 0.838	A: 0.162	G|G: 0.686	A|A: 0.010	A|G: 0.304

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/G [2]	Ancestral:G [2]	Ambiguity code: R [2]	MAF: 0.49 [2]		
Location: 4:38777473 [2]					
SNP ID: rs7694115 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.512	G: 0.488	A|A: 0.273	A|G: 0.479	G|G: 0.248
AFRICAN	A: 0.492	G: 0.508	A|A: 0.248	A|G: 0.489	G|G: 0.263
ACB	A: 0.458	G: 0.542	A|A: 0.219	A|G: 0.479	G|G: 0.302
ASW	A: 0.434	G: 0.566	A|A: 0.180	A|G: 0.508	G|G: 0.311
ESN	A: 0.566	G: 0.434	A|A: 0.313	A|G: 0.505	G|G: 0.182

GWD	A: 0.531	G: 0.469	A|A: 0.319	A|G: 0.425	G|G: 0.257
LWK	A: 0.475	G: 0.525	A|A: 0.263	A|G: 0.424	G|G: 0.313
MSL	A: 0.400	G: 0.600	A|A: 0.129	A|G: 0.541	G|G: 0.329
YRI	A: 0.537	G: 0.463	A|A: 0.259	A|G: 0.556	G|G: 0.185
AMERICAN	A: 0.588	G: 0.412	A|A: 0.343	A|G: 0.490	G|G: 0.167
CLM	A: 0.590	G: 0.410	A|A: 0.362	A|G: 0.457	G|G: 0.181
MXL	A: 0.594	G: 0.406	A|A: 0.328	A|G: 0.531	G|G: 0.141
PEL	A: 0.641	G: 0.359	A|A: 0.400	A|G: 0.482	G|G: 0.118
PUR	A: 0.538	G: 0.462	A|A: 0.288	A|G: 0.500	G|G: 0.212
EAST ASIAN	A: 0.445	G: 0.555	A|A: 0.218	A|G: 0.454	G|G: 0.327
CDX	A: 0.570	G: 0.430	A|A: 0.355	A|G: 0.430	G|G: 0.215
CHB	A: 0.374	G: 0.626	A|A: 0.136	A|G: 0.476	G|G: 0.388
CHS	A: 0.490	G: 0.510	A|A: 0.238	A|G: 0.505	G|G: 0.257
JPT	A: 0.269	G: 0.731	A|A: 0.087	A|G: 0.365	G|G: 0.548
KHV	A: 0.340	G: 0.460	A|A: 0.293	A|G: 0.495	G|G: 0.212
EUROPEAN	A: 0.605	G: 0.395	A|A: 0.384	A|G: 0.443	G|G: 0.173
CEU	A: 0.652	G: 0.348	A|A: 0.414	A|G: 0.475	G|G: 0.111
FIN	A: 0.646	G: 0.354	A|A: 0.465	A|G: 0.364	G|G: 0.172
GBR	A: 0.676	G: 0.324	A|A: 0.418	A|G: 0.516	G|G: 0.066
IBS	A: 0.514	G: 0.486	A|A: 0.271	A|G: 0.486	G|G: 0.243
TSI	A: 0.556	G: 0.444	A|A: 0.364	A|G: 0.383	G|G: 0.252
SOUTH ASIAN	A: 0.459	G: 0.541	A|A: 0.198	A|G: 0.521	G|G: 0.280
BEB	A: 0.471	G: 0.529	A|A: 0.221	A|G: 0.500	G|G: 0.279
GIH	A: 0.427	G: 0.573	A|A: 0.184	A|G: 0.485	G|G: 0.330
ITU	A: 0.495	G: 0.505	A|A: 0.225	A|G: 0.539	G|G: 0.235
PJL	A: 0.453	G: 0.547	A|A: 0.219	A|G: 0.469	G|G: 0.312
STU	A: 0.451	G: 0.549	A|A: 0.147	A|G: 0.608	G|G: 0.245

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/C [2]	Ancestral:T [2]	Ambiguity code: Y [2]	MAF: 0.16 [2]		
Location: 4:38778850 [2]					
SNP ID: rs11466617 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: The GWAS-identified archaic like SNP, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.840	C: 0.160	T|T: 0.722	C|C: 0.042	C|T: 0.236
AFRICAN	T: 0.989	C: 0.011	T|T: 0.979	C|C: 0.000	C|T: 0.021
ACB	T: 0.984	C: 0.016	T|T: 0.969	C|C: 0.000	C|T: 0.031
ASW	T: 0.926	C: 0.074	T|T: 0.852	C|C: 0.000	C|T: 0.148
ESN	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
GWD	T: 0.991	C: 0.009	T|T: 0.982	C|C: 0.000	C|T: 0.018
LWK	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
MSL	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
YRI	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
AMERICAN	T: 0.860	C: 0.140	T|T: 0.752	C|C: 0.032	C|T: 0.216
CLM	T: 0.856	C: 0.144	T|T: 0.734	C|C: 0.021	C|T: 0.245
MXL	T: 0.914	C: 0.086	T|T: 0.844	C|C: 0.016	C|T: 0.141
PEL	T: 0.941	C: 0.059	T|T: 0.882	C|C: 0.000	C|T: 0.118
PUR	T: 0.764	C: 0.236	T|T: 0.606	C|C: 0.077	C|T: 0.317
EAST ASIAN	T: 0.676	C: 0.324	T|T: 0.464	C|C: 0.113	C|T: 0.423
CDX	T: 0.839	C: 0.161	T|T: 0.710	C|C: 0.032	C|T: 0.258
CHB	T: 0.568	C: 0.432	T|T: 0.301	C|C: 0.165	C|T: 0.534
CHS	T: 0.695	C: 0.305	T|T: 0.448	C|C: 0.057	C|T: 0.495
JPT	T: 0.471	C: 0.529	T|T: 0.212	C|C: 0.269	C|T: 0.519
KHV	T: 0.828	C: 0.172	T|T: 0.687	C|C: 0.030	C|T: 0.283
EUROPEAN	T: 0.793	C: 0.207	T|T: 0.640	C|C: 0.054	C|T: 0.306

CEU	T: 0.813	C: 0.187	T|T: 0.667	C|C: 0.040	C|T: 0.293
FIN	T: 0.914	C: 0.086	T|T: 0.838	C|C: 0.010	C|T: 0.152
GBR	T: 0.835	C: 0.165	T|T: 0.681	C|C: 0.011	C|T: 0.308
IBS	T: 0.724	C: 0.276	T|T: 0.542	C|C: 0.093	C|T: 0.364
TSI	T: 0.696	C: 0.304	T|T: 0.495	C|C: 0.103	C|T: 0.402
SOUTH ASIAN	T: 0.844	C: 0.156	T|T: 0.706	C|C: 0.018	C|T: 0.276
BEB	T: 0.802	C: 0.198	T|T: 0.628	C|C: 0.023	C|T: 0.349
GIH	T: 0.816	C: 0.184	T|T: 0.670	C|C: 0.039	C|T: 0.291
ITU	T: 0.887	C: 0.113	T|T: 0.784	C|C: 0.010	C|T: 0.206
PJL	T: 0.875	C: 0.125	T|T: 0.760	C|C: 0.010	C|T: 0.229
STU	T: 0.833	C: 0.167	T|T: 0.676	C|C: 0.010	C|T: 0.314

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles G/C [2]	Ancestral:G [2]	Ambiguity code: S [2]	MAF: 0.26 [2]		
Location: 4:38780600 [2]					
SNP ID: rs7653908 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.743	C: 0.257	G|G: 0.563	C|C: 0.077	C|G: 0.359
AFRICAN	G: 0.710	C: 0.290	G|G: 0.507	C|C: 0.086	C|G: 0.407
ACB	G: 0.792	C: 0.208	G|G: 0.625	C|C: 0.042	C|G: 0.333
ASW	G: 0.689	C: 0.311	G|G: 0.459	C|C: 0.082	C|G: 0.459
ESN	G: 0.717	C: 0.283	G|G: 0.515	C|C: 0.081	C|G: 0.404
GWD	G: 0.735	C: 0.265	G|G: 0.575	C|C: 0.106	C|G: 0.319
LWK	G: 0.657	C: 0.343	G|G: 0.404	C|C: 0.091	C|G: 0.505
MSL	G: 0.729	C: 0.271	G|G: 0.541	C|C: 0.082	C|G: 0.376
YRI	G: 0.653	C: 0.347	G|G: 0.417	C|C: 0.111	C|G: 0.472
AMERICAN	G: 0.831	C: 0.169	G|G: 0.712	C|C: 0.049	C|G: 0.239
CLM	G: 0.840	C: 0.160	G|G: 0.713	C|C: 0.032	C|G: 0.255
MXL	G: 0.898	C: 0.102	G|G: 0.812	C|C: 0.016	C|G: 0.172
PEL	G: 0.929	C: 0.071	G|G: 0.871	C|C: 0.012	C|G: 0.118
PUR	G: 0.702	C: 0.298	G|G: 0.519	C|C: 0.115	C|G: 0.365
EAST ASIAN	G: 0.652	C: 0.348	G|G: 0.437	C|C: 0.133	C|G: 0.431
CDX	G: 0.801	C: 0.199	G|G: 0.656	C|C: 0.054	C|G: 0.290
CHB	G: 0.549	C: 0.451	G|G: 0.291	C|C: 0.194	C|G: 0.515
CHS	G: 0.690	C: 0.310	G|G: 0.448	C|C: 0.067	C|G: 0.486
JPT	G: 0.466	C: 0.534	G|G: 0.202	C|C: 0.269	C|G: 0.529
KHV	G: 0.773	C: 0.227	G|G: 0.616	C|C: 0.071	C|G: 0.313
EUROPEAN	G: 0.765	C: 0.235	G|G: 0.596	C|C: 0.066	C|G: 0.338

CEU	G: 0.798	C: 0.202	G|G: 0.646	C|C: 0.051	C|G: 0.303
FIN	G: 0.884	C: 0.116	G|G: 0.788	C|C: 0.020	C|G: 0.192
GBR	G: 0.819	C: 0.181	G|G: 0.648	C|C: 0.011	C|G: 0.341
IBS	G: 0.664	C: 0.336	G|G: 0.439	C|C: 0.112	C|G: 0.449
TSI	G: 0.682	C: 0.318	G|G: 0.486	C|C: 0.121	C|G: 0.393
SOUTH ASIAN	G: 0.797	C: 0.203	G|G: 0.632	C|C: 0.039	C|G: 0.329
BEB	G: 0.744	C: 0.256	G|G: 0.523	C|C: 0.035	C|G: 0.442
GIH	G: 0.796	C: 0.204	G|G: 0.641	C|C: 0.049	C|G: 0.311
ITU	G: 0.828	C: 0.172	G|G: 0.696	C|C: 0.039	C|G: 0.265
PJL	G: 0.828	C: 0.172	G|G: 0.698	C|C: 0.042	C|G: 0.260
STU	G: 0.779	C: 0.221	G|G: 0.588	C|C: 0.029	C|G: 0.382

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles G/A [2]	Ancestral:A [2]	Ambiguity code: R [2]	MAF: 0.43 [2]		
Location: 4:38780799 [2]					
SNP ID: rs7658893 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.568	A: 0.432	G|G: 0.346	A|A: 0.210	A|G: 0.444
AFRICAN	G: 0.466	A: 0.534	G|G: 0.224	A|A: 0.292	A|G: 0.484
ACB	G: 0.453	A: 0.547	G|G: 0.177	A|A: 0.271	A|G: 0.552
ASW	G: 0.418	A: 0.582	G|G: 0.197	A|A: 0.361	A|G: 0.443
ESN	G: 0.444	A: 0.556	G|G: 0.202	A|A: 0.313	A|G: 0.485
GWD	G: 0.509	A: 0.491	G|G: 0.265	A|A: 0.248	A|G: 0.487
LWK	G: 0.520	A: 0.480	G|G: 0.253	A|A: 0.212	A|G: 0.535
MSL	G: 0.435	A: 0.565	G|G: 0.212	A|A: 0.341	A|G: 0.447
YRI	G: 0.454	A: 0.546	G|G: 0.241	A|A: 0.333	A|G: 0.426
AMERICAN	G: 0.648	A: 0.352	G|G: 0.424	A|A: 0.127	A|G: 0.450
CLM	G: 0.660	A: 0.340	G|G: 0.447	A|A: 0.128	A|G: 0.426
MXL	G: 0.672	A: 0.328	G|G: 0.422	A|A: 0.078	A|G: 0.500
PEL	G: 0.682	A: 0.318	G|G: 0.471	A|A: 0.106	A|G: 0.424
PUR	G: 0.596	A: 0.404	G|G: 0.365	A|A: 0.173	A|G: 0.462
EAST ASIAN	G: 0.476	A: 0.524	G|G: 0.260	A|A: 0.308	A|G: 0.433
CDX	G: 0.618	A: 0.382	G|G: 0.430	A|A: 0.194	A|G: 0.376
CHB	G: 0.388	A: 0.612	G|G: 0.155	A|A: 0.379	A|G: 0.466

CHS	G: 0.495	A: 0.505	G|G: 0.257	A|A: 0.267	A|G: 0.476
JPT	G: 0.303	A: 0.697	G|G: 0.106	A|A: 0.500	A|G: 0.394
KHV	G: 0.596	A: 0.404	G|G: 0.374	A|A: 0.182	A|G: 0.444
EUROPEAN	G: 0.725	A: 0.275	G|G: 0.541	A|A: 0.091	A|G: 0.368
CEU	G: 0.763	A: 0.237	G|G: 0.576	A|A: 0.051	A|G: 0.374
FIN	G: 0.869	A: 0.131	G|G: 0.758	A|A: 0.020	A|G: 0.222
GBR	G: 0.780	A: 0.220	G|G: 0.582	A|A: 0.022	A|G: 0.396
IBS	G: 0.598	A: 0.402	G|G: 0.364	A|A: 0.168	A|G: 0.467
TSI	G: 0.636	A: 0.364	G|G: 0.449	A|A: 0.178	A|G: 0.374
SOUTH ASIAN	G: 0.583	A: 0.417	G|G: 0.346	A|A: 0.180	A|G: 0.474
BEB	G: 0.570	A: 0.430	G|G: 0.337	A|A: 0.198	A|G: 0.465
GIH	G: 0.573	A: 0.427	G|G: 0.340	A|A: 0.194	A|G: 0.466
ITU	G: 0.627	A: 0.373	G|G: 0.382	A|A: 0.127	A|G: 0.490
PJL	G: 0.594	A: 0.406	G|G: 0.396	A|A: 0.208	A|G: 0.396
STU	G: 0.549	A: 0.451	G|G: 0.275	A|A: 0.176	A|G: 0.549

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/C [2]	Ancestral:T [2]	Ambiguity code: Y [2]	MAF: 0.17 [2]		
Location: 4:38782227 [2]					
SNP ID: rs11725309 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: The GWAS-identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.826	C: 0.174	T|T: 0.704	C|C: 0.052	C|T: 0.244
AFRICAN	T: 0.989	C: 0.011	T|T: 0.977	C|C: 0.000	C|T: 0.023
ACB	T: 0.979	C: 0.021	T|T: 0.958	C|C: 0.000	C|T: 0.042
ASW	T: 0.926	C: 0.074	T|T: 0.852	C|C: 0.000	C|T: 0.148
ESN	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
GWD	T: 0.991	C: 0.009	T|T: 0.982	C|C: 0.000	C|T: 0.018
LWK	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
MSL	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
YRI	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
AMERICAN	T: 0.854	C: 0.146	T|T: 0.744	C|C: 0.035	C|T: 0.222
CLM	T: 0.856	C: 0.144	T|T: 0.734	C|C: 0.021	C|T: 0.245

MXL	T: 0.891	C: 0.109	T|T: 0.797	C|C: 0.016	C|T: 0.188
PEL	T: 0.941	C: 0.059	T|T: 0.882	C|C: 0.000	C|T: 0.118
PUR	T: 0.760	C: 0.240	T|T: 0.606	C|C: 0.087	C|T: 0.308
EAST ASIAN	T: 0.626	C: 0.374	T|T: 0.405	C|C: 0.153	C|T: 0.442
CDX	T: 0.796	C: 0.204	T|T: 0.634	C|C: 0.043	C|T: 0.323
CHB	T: 0.485	C: 0.515	T|T: 0.233	C|C: 0.262	C|T: 0.505
CHS	T: 0.633	C: 0.367	T|T: 0.390	C|C: 0.124	C|T: 0.486
JPT	T: 0.476	C: 0.524	T|T: 0.221	C|C: 0.269	C|T: 0.510
KHV	T: 0.763	C: 0.237	T|T: 0.576	C|C: 0.051	C|T: 0.374
EUROPEAN	T: 0.786	C: 0.214	T|T: 0.632	C|C: 0.060	C|T: 0.308
CEU	T: 0.813	C: 0.187	T|T: 0.667	C|C: 0.040	C|T: 0.293
FIN	T: 0.909	C: 0.091	T|T: 0.828	C|C: 0.010	C|T: 0.162
GBR	T: 0.835	C: 0.165	T|T: 0.692	C|C: 0.022	C|T: 0.286
IBS	T: 0.701	C: 0.299	T|T: 0.514	C|C: 0.112	C|T: 0.374
TSI	T: 0.692	C: 0.308	T|T: 0.486	C|C: 0.103	C|T: 0.411
SOUTH ASIAN	T: 0.834	C: 0.166	T|T: 0.689	C|C: 0.020	C|T: 0.290
BEB	T: 0.779	C: 0.221	T|T: 0.593	C|C: 0.035	C|T: 0.372
GIH	T: 0.820	C: 0.180	T|T: 0.680	C|C: 0.039	C|T: 0.282
ITU	T: 0.873	C: 0.127	T|T: 0.755	C|C: 0.010	C|T: 0.235
PJL	T: 0.870	C: 0.130	T|T: 0.750	C|C: 0.010	C|T: 0.240
STU	T: 0.824	C: 0.176	T|T: 0.657	C|C: 0.010	C|T: 0.333

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles C/G [2]	Ancestral:G [2]	Ambiguity code: S [2]	MAF: 0.44 [2]		
Location: 4:38783057 [2]					
SNP ID: rs10034903 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	C: 0.562	G: 0.438	C|C: 0.343	C|G: 0.437	G|G: 0.220
AFRICAN	C: 0.356	G: 0.644	C|C: 0.126	C|G: 0.461	G|G: 0.413
ACB	C: 0.375	G: 0.625	C|C: 0.115	C|G: 0.521	G|G: 0.365
ASW	C: 0.508	G: 0.492	C|C: 0.197	C|G: 0.623	G|G: 0.180
ESN	C: 0.374	G: 0.626	C|C: 0.152	C|G: 0.444	G|G: 0.404
GWD	C: 0.327	G: 0.673	C|C: 0.133	C|G: 0.389	G|G: 0.478
LWK	C: 0.343	G: 0.657	C|C: 0.131	C|G: 0.424	G|G: 0.444

MSL	C: 0.353	G: 0.647	C|C: 0.094	C|G: 0.518	G|G: 0.388
YRI	C: 0.282	G: 0.718	C|C: 0.083	C|G: 0.398	G|G: 0.519
AMERICAN	C: 0.749	G: 0.251	C|C: 0.585	C|G: 0.329	G|G: 0.086
CLM	C: 0.729	G: 0.271	C|C: 0.521	C|G: 0.415	G|G: 0.064
MXL	C: 0.812	G: 0.188	C|C: 0.656	C|G: 0.312	G|G: 0.031
PEL	C: 0.882	G: 0.118	C|C: 0.788	C|G: 0.188	G|G: 0.024
PUR	C: 0.620	G: 0.380	C|C: 0.433	C|G: 0.375	G|G: 0.192
EAST ASIAN	C: 0.519	G: 0.481	C|C: 0.278	C|G: 0.482	G|G: 0.240
CDX	C: 0.634	G: 0.366	C|C: 0.409	C|G: 0.452	G|G: 0.140
CHB	C: 0.403	G: 0.597	C|C: 0.155	C|G: 0.495	G|G: 0.350
CHS	C: 0.548	G: 0.452	C|C: 0.286	C|G: 0.524	G|G: 0.190
JPT	C: 0.399	G: 0.601	C|C: 0.154	C|G: 0.490	G|G: 0.356
KHV	C: 0.626	G: 0.374	C|C: 0.404	C|G: 0.444	G|G: 0.152
EUROPEAN	C: 0.722	G: 0.278	C|C: 0.541	C|G: 0.362	G|G: 0.097
CEU	C: 0.788	G: 0.212	C|C: 0.626	C|G: 0.323	G|G: 0.051
FIN	C: 0.854	G: 0.146	C|C: 0.747	C|G: 0.212	G|G: 0.040
GBR	C: 0.802	G: 0.198	C|C: 0.626	C|G: 0.352	G|G: 0.022
IBS	C: 0.575	G: 0.425	C|C: 0.336	C|G: 0.477	G|G: 0.187
TSI	C: 0.617	G: 0.383	C|C: 0.402	C|G: 0.430	G|G: 0.168
SOUTH ASIAN	C: 0.586	G: 0.414	C|C: 0.329	C|G: 0.513	G|G: 0.157
BEB	C: 0.564	G: 0.436	C|C: 0.302	C|G: 0.523	G|G: 0.174
GIH	C: 0.607	G: 0.393	C|C: 0.379	C|G: 0.456	G|G: 0.165
ITU	C: 0.574	G: 0.426	C|C: 0.284	C|G: 0.578	G|G: 0.137
PJL	C: 0.620	G: 0.380	C|C: 0.375	C|G: 0.490	G|G: 0.135
STU	C: 0.564	G: 0.436	C|C: 0.304	C|G: 0.520	G|G: 0.176

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/A [2]	Ancestral:A [2]	Ambiguity code: W [2]	MAF: 0.37 [2]		
Location: 4:38783103 [2]					
SNP ID: rs10004195 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1,2]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.626	A: 0.374	T|T: 0.403	A|A: 0.150	A|T: 0.447
AFRICAN	T: 0.592	A: 0.408	T|T: 0.340	A|A: 0.156	A|T: 0.504
ACB	T: 0.604	A: 0.396	T|T: 0.323	A|A: 0.115	A|T: 0.562
ASW	T: 0.689	A: 0.311	T|T: 0.443	A|A: 0.066	A|T: 0.492
ESN	T: 0.662	A: 0.338	T|T: 0.465	A|A: 0.141	A|T: 0.394
GWD	T: 0.558	A: 0.442	T|T: 0.310	A|A: 0.195	A|T: 0.496
LWK	T: 0.571	A: 0.429	T|T: 0.323	A|A: 0.182	A|T: 0.495
MSL	T: 0.565	A: 0.435	T|T: 0.247	A|A: 0.118	A|T: 0.635
YRI	T: 0.542	A: 0.458	T|T: 0.306	A|A: 0.222	A|T: 0.472
AMERICAN	T: 0.768	A: 0.232	T|T: 0.611	A|A: 0.075	A|T: 0.314
CLM	T: 0.734	A: 0.266	T|T: 0.532	A|A: 0.064	A|T: 0.404
MXL	T: 0.820	A: 0.180	T|T: 0.656	A|A: 0.016	A|T: 0.328

PEL	T: 0.888	A: 0.112	T|T: 0.800	A|A: 0.024	A|T: 0.176
PUR	T: 0.668	A: 0.332	T|T: 0.500	A|A: 0.163	A|T: 0.337
EAST ASIAN	T: 0.519	A: 0.481	T|T: 0.278	A|A: 0.240	A|T: 0.482
CDX	T: 0.634	A: 0.366	T|T: 0.409	A|A: 0.140	A|T: 0.452
CHB	T: 0.403	A: 0.597	T|T: 0.155	A|A: 0.350	A|T: 0.495
CHS	T: 0.548	A: 0.452	T|T: 0.286	A|A: 0.190	A|T: 0.524
JPT	T: 0.399	A: 0.601	T|T: 0.154	A|A: 0.356	A|T: 0.490
KHV	T: 0.626	A: 0.374	T|T: 0.404	A|A: 0.152	A|T: 0.444
EUROPEAN	T: 0.721	A: 0.279	T|T: 0.539	A|A: 0.097	A|T: 0.364
CEU	T: 0.788	A: 0.212	T|T: 0.626	A|A: 0.051	A|T: 0.323
FIN	T: 0.848	A: 0.152	T|T: 0.737	A|A: 0.040	A|T: 0.222
GBR	T: 0.802	A: 0.198	T|T: 0.626	A|A: 0.022	A|T: 0.352
IBS	T: 0.575	A: 0.425	T|T: 0.336	A|A: 0.187	A|T: 0.477
TSI	T: 0.617	A: 0.383	T|T: 0.402	A|A: 0.168	A|T: 0.430
SOUTH ASIAN	T: 0.586	A: 0.414	T|T: 0.329	A|A: 0.157	A|T: 0.513
BEB	T: 0.564	A: 0.436	T|T: 0.302	A|A: 0.174	A|T: 0.523
GIH	T: 0.607	A: 0.393	T|T: 0.379	A|A: 0.165	A|T: 0.456
ITU	T: 0.574	A: 0.426	T|T: 0.284	A|A: 0.137	A|T: 0.578
PJL	T: 0.620	A: 0.380	T|T: 0.375	A|A: 0.135	A|T: 0.490
STU	T: 0.564	A: 0.436	T|T: 0.304	A|A: 0.176	A|T: 0.520

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles C/T [2]	Ancestral:T [2]	Ambiguity code: Y [2]	MAF: 0.41 [2]		
Location: 38785595 [2]					
SNP ID: rs12233670 [1]					
GWAS Trait: Multiple complex diseases, Coronary Artery Disease, Lymphocyte counts, Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	C: 0.592	T: 0.408	C|C: 0.369	C|T: 0.446	T|T: 0.185
AFRICAN	C: 0.464	T: 0.536	C|C: 0.215	C|T: 0.498	T|T: 0.287
ACB	C: 0.526	T: 0.474	C|C: 0.250	C|T: 0.552	T|T: 0.198
ASW	C: 0.549	T: 0.451	C|C: 0.262	C|T: 0.574	T|T: 0.164
ESN	C: 0.500	T: 0.500	C|C: 0.242	C|T: 0.515	T|T: 0.242
GWD	C: 0.482	T: 0.518	C|C: 0.239	C|T: 0.487	T|T: 0.274
LWK	C: 0.384	T: 0.616	C|C: 0.172	C|T: 0.424	T|T: 0.404

MSL	C: 0.429	T: 0.571	C|C: 0.153	C|T: 0.553	T|T: 0.294
YRI	C: 0.407	T: 0.593	C|C: 0.194	C|T: 0.426	T|T: 0.380
AMERICAN	C: 0.761	T: 0.239	C|C: 0.599	C|T: 0.323	T|T: 0.078
CLM	C: 0.729	T: 0.271	C|C: 0.521	C|T: 0.415	T|T: 0.064
MXL	C: 0.820	T: 0.180	C|C: 0.656	C|T: 0.328	T|T: 0.016
PEL	C: 0.888	T: 0.112	C|C: 0.800	C|T: 0.176	T|T: 0.024
PUR	C: 0.649	T: 0.351	C|C: 0.471	C|T: 0.356	T|T: 0.173
EAST ASIAN	C: 0.519	T: 0.481	C|C: 0.278	C|T: 0.482	T|T: 0.240
CDX	C: 0.634	T: 0.366	C|C: 0.409	C|T: 0.452	T|T: 0.140
CHB	C: 0.403	T: 0.597	C|C: 0.155	C|T: 0.495	T|T: 0.350
CHS	C: 0.548	T: 0.452	C|C: 0.286	C|T: 0.524	T|T: 0.190
JPT	C: 0.399	T: 0.601	C|C: 0.154	C|T: 0.490	T|T: 0.356
KHV	C: 0.626	T: 0.374	C|C: 0.404	C|T: 0.444	T|T: 0.152
EUROPEAN	C: 0.722	T: 0.278	C|C: 0.541	C|T: 0.362	T|T: 0.097
CEU	C: 0.788	T: 0.212	C|C: 0.626	C|T: 0.323	T|T: 0.051
FIN	C: 0.854	T: 0.146	C|C: 0.747	C|T: 0.212	T|T: 0.040
GBR	C: 0.802	T: 0.198	C|C: 0.626	C|T: 0.352	T|T: 0.022
IBS	C: 0.575	T: 0.425	C|C: 0.336	C|T: 0.477	T|T: 0.187
TSI	C: 0.617	T: 0.383	C|C: 0.402	C|T: 0.430	T|T: 0.168
SOUTH ASIAN	C: 0.586	T: 0.414	C|C: 0.329	C|T: 0.513	T|T: 0.157
BEB	C: 0.564	T: 0.436	C|C: 0.302	C|T: 0.523	T|T: 0.174
GIH	C: 0.607	T: 0.393	C|C: 0.379	C|T: 0.456	T|T: 0.165
ITU	C: 0.574	T: 0.426	C|C: 0.284	C|T: 0.578	T|T: 0.137
PJL	C: 0.620	T: 0.380	C|C: 0.375	C|T: 0.490	T|T: 0.135
STU	C: 0.564	T: 0.436	C|C: 0.304	C|T: 0.520	T|T: 0.176

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/C [2]	Ancestral:T [2]	Ambiguity code: Y [2]	MAF: 0.44 [2]		
Location: 38786613 [2]					
SNP ID: rs6834581 [1]					
GWAS Trait: Alcohol consumption [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.556	C: 0.444	T|T: 0.339	C|C: 0.227	C|T: 0.433
AFRICAN	T: 0.337	C: 0.663	T|T: 0.115	C|C: 0.442	C|T: 0.443
ACB	T: 0.344	C: 0.656	T|T: 0.115	C|C: 0.427	C|T: 0.458
ASW	T: 0.467	C: 0.533	T|T: 0.180	C|C: 0.246	C|T: 0.574
ESN	T: 0.359	C: 0.641	T|T: 0.141	C|C: 0.424	C|T: 0.434
GWD	T: 0.314	C: 0.686	T|T: 0.115	C|C: 0.487	C|T: 0.398

LWK	T: 0.333	C: 0.667	T|T: 0.131	C|C: 0.465	C|T: 0.404
MSL	T: 0.324	C: 0.676	T|T: 0.059	C|C: 0.412	C|T: 0.529
YRI	T: 0.273	C: 0.727	T|T: 0.083	C|C: 0.537	C|T: 0.380
AMERICAN	T: 0.746	C: 0.254	T|T: 0.579	C|C: 0.086	C|T: 0.334
CLM	T: 0.718	C: 0.282	T|T: 0.500	C|C: 0.064	C|T: 0.436
MXL	T: 0.812	C: 0.188	T|T: 0.656	C|C: 0.031	C|T: 0.312
PEL	T: 0.882	C: 0.118	T|T: 0.788	C|C: 0.024	C|T: 0.188
PUR	T: 0.620	C: 0.380	T|T: 0.433	C|C: 0.192	C|T: 0.375
EAST ASIAN	T: 0.519	C: 0.481	T|T: 0.278	C|C: 0.240	C|T: 0.482
CDX	T: 0.634	C: 0.366	T|T: 0.409	C|C: 0.140	C|T: 0.452
CHB	T: 0.403	C: 0.597	T|T: 0.155	C|C: 0.350	C|T: 0.495
CHS	T: 0.548	C: 0.452	T|T: 0.286	C|C: 0.190	C|T: 0.524
JPT	T: 0.399	C: 0.601	T|T: 0.154	C|C: 0.356	C|T: 0.490
KHV	T: 0.626	C: 0.374	T|T: 0.404	C|C: 0.152	C|T: 0.444
EUROPEAN	T: 0.722	C: 0.278	T|T: 0.541	C|C: 0.097	C|T: 0.362
CEU	T: 0.788	C: 0.212	T|T: 0.626	C|C: 0.051	C|T: 0.323
FIN	T: 0.854	C: 0.146	T|T: 0.747	C|C: 0.040	C|T: 0.212
GBR	T: 0.802	C: 0.198	T|T: 0.626	C|C: 0.022	C|T: 0.352
IBS	T: 0.575	C: 0.425	T|T: 0.336	C|C: 0.187	C|T: 0.477
TSI	T: 0.617	C: 0.383	T|T: 0.402	C|C: 0.168	C|T: 0.430
SOUTH ASIAN	T: 0.586	C: 0.414	T|T: 0.329	C|C: 0.157	C|T: 0.513
BEB	T: 0.564	C: 0.436	T|T: 0.302	C|C: 0.174	C|T: 0.523
GIH	T: 0.607	C: 0.393	T|T: 0.379	C|C: 0.165	C|T: 0.456
ITU	T: 0.574	C: 0.426	T|T: 0.284	C|C: 0.137	C|T: 0.578
PJL	T: 0.620	C: 0.380	T|T: 0.375	C|C: 0.135	C|T: 0.490
STU	T: 0.564	C: 0.436	T|T: 0.304	C|C: 0.176	C|T: 0.520

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles G/T [2]	Ancestral:T [2]	Ambiguity code: K [2]	MAF: 0.40 [2]		
Location: 38788119 [2]					
SNP ID: rs4833093 [1]					
GWAS Trait: Alcohol consumption [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.597	T: 0.403	G|G: 0.373	G|T: 0.446	T|T: 0.180
AFRICAN	G: 0.464	T: 0.536	G|G: 0.215	G|T: 0.498	T|T: 0.287

ACB	G: 0.521	T: 0.479	G|G: 0.240	G|T: 0.562	T|T: 0.198
ASW	G: 0.557	T: 0.443	G|G: 0.279	G|T: 0.557	T|T: 0.164
ESN	G: 0.500	T: 0.500	G|G: 0.242	G|T: 0.515	T|T: 0.242
GWD	G: 0.482	T: 0.518	G|G: 0.239	G|T: 0.487	T|T: 0.274
LWK	G: 0.389	T: 0.611	G|G: 0.172	G|T: 0.434	T|T: 0.394
MSL	G: 0.429	T: 0.571	G|G: 0.153	G|T: 0.553	T|T: 0.294
YRI	G: 0.403	T: 0.597	G|G: 0.194	G|T: 0.417	T|T: 0.389
AMERICAN	G: 0.765	T: 0.235	G|G: 0.608	G|T: 0.314	T|T: 0.078
CLM	G: 0.739	T: 0.261	G|G: 0.543	G|T: 0.394	T|T: 0.064
MXL	G: 0.828	T: 0.172	G|G: 0.672	G|T: 0.312	T|T: 0.016
PEL	G: 0.888	T: 0.112	G|G: 0.800	G|T: 0.176	T|T: 0.024
PUR	G: 0.649	T: 0.351	G|G: 0.471	G|T: 0.356	T|T: 0.173
EAST ASIAN	G: 0.520	T: 0.480	G|G: 0.278	G|T: 0.484	T|T: 0.238
CDX	G: 0.640	T: 0.360	G|G: 0.409	G|T: 0.462	T|T: 0.129
CHB	G: 0.403	T: 0.597	G|G: 0.155	G|T: 0.495	T|T: 0.350
CHS	G: 0.548	T: 0.452	G|G: 0.286	G|T: 0.524	T|T: 0.190
JPT	G: 0.399	T: 0.601	G|G: 0.154	G|T: 0.490	T|T: 0.356
KHV	G: 0.626	T: 0.374	G|G: 0.404	G|T: 0.444	T|T: 0.152
EUROPEAN	G: 0.721	T: 0.279	G|G: 0.539	G|T: 0.364	T|T: 0.097
CEU	G: 0.788	T: 0.212	G|G: 0.626	G|T: 0.323	T|T: 0.051
FIN	G: 0.854	T: 0.146	G|G: 0.747	G|T: 0.212	T|T: 0.040
GBR	G: 0.802	T: 0.198	G|G: 0.626	G|T: 0.352	T|T: 0.022
IBS	G: 0.575	T: 0.425	G|G: 0.336	G|T: 0.477	T|T: 0.187
TSI	G: 0.612	T: 0.388	G|G: 0.393	G|T: 0.439	T|T: 0.168
SOUTH ASIAN	G: 0.608	T: 0.392	G|G: 0.350	G|T: 0.517	T|T: 0.133
BEB	G: 0.576	T: 0.424	G|G: 0.326	G|T: 0.500	T|T: 0.174
GIH	G: 0.665	T: 0.335	G|G: 0.447	G|T: 0.437	T|T: 0.117
ITU	G: 0.593	T: 0.407	G|G: 0.284	G|T: 0.618	T|T: 0.098
PJL	G: 0.630	T: 0.370	G|G: 0.375	G|T: 0.510	T|T: 0.115
STU	G: 0.574	T: 0.426	G|G: 0.314	G|T: 0.520	T|T: 0.167

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/C [2]	Ancestral:C [2]	Ambiguity code: Y [2]	MAF: 0.45 [2]		
Location: 38790719 [2]					
SNP ID: rs6531663 [1]					
GWAS Trait: Alcohol consumption [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.548	C: 0.452	T|T: 0.334	C|C: 0.239	C|T: 0.427
AFRICAN	T: 0.304	C: 0.696	T|T: 0.094	C|C: 0.486	C|T: 0.421
ACB	T: 0.323	C: 0.677	T|T: 0.094	C|C: 0.448	C|T: 0.458
ASW	T: 0.410	C: 0.590	T|T: 0.148	C|C: 0.328	C|T: 0.525
ESN	T: 0.348	C: 0.652	T|T: 0.141	C|C: 0.444	C|T: 0.414
GWD	T: 0.288	C: 0.712	T|T: 0.097	C|C: 0.522	C|T: 0.381
LWK	T: 0.283	C: 0.717	T|T: 0.061	C|C: 0.495	C|T: 0.444
MSL	T: 0.271	C: 0.729	T|T: 0.059	C|C: 0.518	C|T: 0.424
YRI	T: 0.250	C: 0.750	T|T: 0.074	C|C: 0.574	C|T: 0.352
AMERICAN	T: 0.748	C: 0.252	T|T: 0.582	C|C: 0.086	C|T: 0.331
CLM	T: 0.729	C: 0.271	T|T: 0.521	C|C: 0.064	C|T: 0.415
MXL	T: 0.820	C: 0.180	T|T: 0.672	C|C: 0.031	C|T: 0.297
PEL	T: 0.882	C: 0.118	T|T: 0.788	C|C: 0.024	C|T: 0.188
PUR	T: 0.611	C: 0.389	T|T: 0.413	C|C: 0.192	C|T: 0.394
EAST ASIAN	T: 0.520	C: 0.480	T|T: 0.280	C|C: 0.240	C|T: 0.480
CDX	T: 0.640	C: 0.360	T|T: 0.419	C|C: 0.140	C|T: 0.441
CHB	T: 0.408	C: 0.592	T|T: 0.155	C|C: 0.340	C|T: 0.505
CHS	T: 0.543	C: 0.457	T|T: 0.286	C|C: 0.200	C|T: 0.514
JPT	T: 0.399	C: 0.601	T|T: 0.154	C|C: 0.356	C|T: 0.490
KHV	T: 0.626	C: 0.374	T|T: 0.404	C|C: 0.152	C|T: 0.444
EUROPEAN	T: 0.721	C: 0.279	T|T: 0.539	C|C: 0.097	C|T: 0.364
CEU	T: 0.788	C: 0.212	T|T: 0.626	C|C: 0.051	C|T: 0.323
FIN	T: 0.854	C: 0.146	T|T: 0.747	C|C: 0.040	C|T: 0.212
GBR	T: 0.802	C: 0.198	T|T: 0.626	C|C: 0.022	C|T: 0.352
IBS	T: 0.575	C: 0.425	T|T: 0.336	C|C: 0.187	C|T: 0.477
TSI	T: 0.612	C: 0.388	T|T: 0.393	C|C: 0.168	C|T: 0.439
SOUTH ASIAN	T: 0.586	C: 0.414	T|T: 0.329	C|C: 0.157	C|T: 0.513
BEB	T: 0.564	C: 0.436	T|T: 0.302	C|C: 0.174	C|T: 0.523
GIH	T: 0.607	C: 0.393	T|T: 0.379	C|C: 0.165	C|T: 0.456
ITU	T: 0.574	C: 0.426	T|T: 0.284	C|C: 0.137	C|T: 0.578
PJL	T: 0.620	C: 0.380	T|T: 0.375	C|C: 0.135	C|T: 0.490
STU	T: 0.564	C: 0.436	T|T: 0.304	C|C: 0.176	C|T: 0.520
REFERENCES					
1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33					
2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html					

Alleles A/G [2]	Ancestral:G [2]	Ambiguity code: R [2]	MAF: 0.37 [2]		
Location: 4:38790903 [2]					
SNP ID: rs4543123 [1]					
GWAS Trait: Amyotrophic lateral sclerosis, PAget's disease, Helicobacter pylori serologic status, Alcohol consumption, Self-reported allergy [1,2]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.632	G: 0.368	A|A: 0.416	A|G: 0.433	G|G: 0.151
AFRICAN	A: 0.467	G: 0.533	A|A: 0.201	A|G: 0.533	G|G: 0.266
ACB	A: 0.458	G: 0.542	A|A: 0.167	A|G: 0.583	G|G: 0.250
ASW	A: 0.566	G: 0.434	A|A: 0.262	A|G: 0.607	G|G: 0.131
ESN	A: 0.455	G: 0.545	A|A: 0.192	A|G: 0.525	G|G: 0.283
GWD	A: 0.429	G: 0.571	A|A: 0.159	A|G: 0.540	G|G: 0.301
LWK	A: 0.515	G: 0.485	A|A: 0.273	A|G: 0.485	G|G: 0.242

MSL	A: 0.447	G: 0.553	A|A: 0.176	A|G: 0.541	G|G: 0.282
YRI	A: 0.444	G: 0.556	A|A: 0.204	A|G: 0.481	G|G: 0.315
AMERICAN	A: 0.775	G: 0.225	A|A: 0.631	A|G: 0.288	G|G: 0.081
CLM	A: 0.771	G: 0.229	A|A: 0.606	A|G: 0.330	G|G: 0.064
MXL	A: 0.836	G: 0.164	A|A: 0.703	A|G: 0.266	G|G: 0.031
PEL	A: 0.906	G: 0.094	A|A: 0.824	A|G: 0.165	G|G: 0.012
PUR	A: 0.635	G: 0.365	A|A: 0.452	A|G: 0.365	G|G: 0.183
EAST ASIAN	A: 0.591	G: 0.409	A|A: 0.353	A|G: 0.476	G|G: 0.171
CDX	A: 0.720	G: 0.280	A|A: 0.505	A|G: 0.430	G|G: 0.065
CHB	A: 0.466	G: 0.534	A|A: 0.214	A|G: 0.505	G|G: 0.282
CHS	A: 0.629	G: 0.371	A|A: 0.390	A|G: 0.476	G|G: 0.133
JPT	A: 0.462	G: 0.538	A|A: 0.202	A|G: 0.519	G|G: 0.279
KHV	A: 0.697	G: 0.303	A|A: 0.475	A|G: 0.444	G|G: 0.081
EUROPEAN	A: 0.733	G: 0.267	A|A: 0.555	A|G: 0.356	G|G: 0.089
CEU	A: 0.788	G: 0.212	A|A: 0.626	A|G: 0.323	G|G: 0.051
FIN	A: 0.854	G: 0.146	A|A: 0.747	A|G: 0.212	G|G: 0.040
GBR	A: 0.808	G: 0.192	A|A: 0.637	A|G: 0.341	G|G: 0.022
IBS	A: 0.603	G: 0.397	A|A: 0.383	A|G: 0.439	G|G: 0.178
TSI	A: 0.636	G: 0.364	A|A: 0.411	A|G: 0.449	G|G: 0.140
SOUTH ASIAN	A: 0.692	G: 0.308	A|A: 0.474	A|G: 0.436	G|G: 0.090
BEB	A: 0.640	G: 0.360	A|A: 0.419	A|G: 0.442	G|G: 0.140
GIH	A: 0.699	G: 0.301	A|A: 0.505	A|G: 0.388	G|G: 0.107
ITU	A: 0.706	G: 0.294	A|A: 0.471	A|G: 0.471	G|G: 0.059
PJL	A: 0.719	G: 0.281	A|A: 0.521	A|G: 0.396	G|G: 0.083
STU	A: 0.691	G: 0.309	A|A: 0.451	A|G: 0.480	G|G: 0.069

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/C [2]	Ancestral:T [2]	Ambiguity code: Y [2]	MAF: 0.03 [2]		
Location: 4:38796255 [2]					
SNP ID: rs4624663 [1]					
GWAS Trait: Panic disorder [1]					
Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.970	C: 0.030	T|T: 0.943	C|C: 0.003	C|T: 0.054
AFRICAN	T: 0.921	C: 0.079	T|T: 0.849	C|C: 0.006	C|T: 0.145
ACB	T: 0.917	C: 0.083	T|T: 0.844	C|C: 0.010	C|T: 0.146
ASW	T: 0.918	C: 0.082	T|T: 0.836	C|C: 0.000	C|T: 0.164
ESN	T: 0.924	C: 0.076	T|T: 0.848	C|C: 0.000	C|T: 0.152
GWD	T: 0.920	C: 0.080	T|T: 0.850	C|C: 0.009	C|T: 0.142
LWK	T: 0.934	C: 0.066	T|T: 0.879	C|C: 0.010	C|T: 0.111
MSL	T: 0.924	C: 0.076	T|T: 0.859	C|C: 0.012	C|T: 0.129
YRI	T: 0.912	C: 0.088	T|T: 0.824	C|C: 0.000	C|T: 0.176
AMERICAN	T: 0.980	C: 0.020	T|T: 0.960	C|C: 0.000	C|T: 0.040
CLM	T: 0.968	C: 0.032	T|T: 0.936	C|C: 0.000	C|T: 0.064
MXL	T: 0.984	C: 0.016	T|T: 0.969	C|C: 0.000	C|T: 0.031
PEL	T: 0.994	C: 0.006	T|T: 0.988	C|C: 0.000	C|T: 0.012

PUR	T: 0.976	C: 0.024	T|T: 0.952	C|C: 0.000	C|T: 0.048
EAST ASIAN	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
CDX	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
CHB	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
CHS	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
JPT	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
KHV	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
EUROPEAN	T: 0.975	C: 0.025	T|T: 0.954	C|C: 0.004	C|T: 0.042
CEU	T: 0.990	C: 0.010	T|T: 0.980	C|C: 0.000	C|T: 0.020
FIN	T: 0.970	C: 0.030	T|T: 0.949	C|C: 0.010	C|T: 0.040
GBR	T: 0.978	C: 0.022	T|T: 0.956	C|C: 0.000	C|T: 0.044
IBS	T: 0.949	C: 0.051	T|T: 0.907	C|C: 0.009	C|T: 0.084
TSI	T: 0.991	C: 0.009	T|T: 0.981	C|C: 0.000	C|T: 0.019
SOUTH ASIAN	T: 0.993	C: 0.007	T|T: 0.988	C|C: 0.002	C|T: 0.010
BEB	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
GIH	T: 0.990	C: 0.010	T|T: 0.981	C|C: 0.000	C|T: 0.019
ITU	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
PJL	T: 0.979	C: 0.021	T|T: 0.969	C|C: 0.010	C|T: 0.021
STU	T: 0.995	C: 0.005	T|T: 0.990	C|C: 0.000	C|T: 0.010

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/G [2]	Ancestral:G [2]	Ambiguity code: R [2]	MAF: 0.47 [2]		
Location: 4:38798089 [2]					
SNP ID: rs5743604 [1]					
GWAS Trait: Helicobacter pylori serologic status, Alcohol consumption, Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.532	G: 0.468	A|A: 0.306	A|G: 0.451	G|G: 0.243
AFRICAN	A: 0.377	G: 0.623	A|A: 0.142	A|G: 0.469	G|G: 0.389
ACB	A: 0.438	G: 0.562	A|A: 0.177	A|G: 0.521	G|G: 0.302
ASW	A: 0.393	G: 0.607	A|A: 0.148	A|G: 0.492	G|G: 0.361
ESN	A: 0.318	G: 0.682	A|A: 0.081	A|G: 0.475	G|G: 0.444
GWD	A: 0.482	G: 0.518	A|A: 0.230	A|G: 0.504	G|G: 0.265
LWK	A: 0.283	G: 0.717	A|A: 0.051	A|G: 0.465	G|G: 0.485
MSL	A: 0.324	G: 0.676	A|A: 0.106	A|G: 0.435	G|G: 0.459
YRI	A: 0.384	G: 0.616	A|A: 0.185	A|G: 0.398	G|G: 0.417
AMERICAN	A: 0.563	G: 0.437	A|A: 0.326	A|G: 0.476	G|G: 0.199

CLM	A: 0.596	G: 0.404	A|A: 0.362	A|G: 0.468	G|G: 0.170
MXL	A: 0.523	G: 0.477	A|A: 0.266	A|G: 0.516	G|G: 0.219
PEL	A: 0.524	G: 0.476	A|A: 0.282	A|G: 0.482	G|G: 0.235
PUR	A: 0.591	G: 0.409	A|A: 0.365	A|G: 0.452	G|G: 0.183
EAST ASIAN	A: 0.472	G: 0.528	A|A: 0.224	A|G: 0.496	G|G: 0.280
CDX	A: 0.565	G: 0.435	A|A: 0.323	A|G: 0.484	G|G: 0.194
CHB	A: 0.374	G: 0.626	A|A: 0.136	A|G: 0.476	G|G: 0.388
CHS	A: 0.486	G: 0.514	A|A: 0.219	A|G: 0.533	G|G: 0.248
JPT	A: 0.365	G: 0.635	A|A: 0.125	A|G: 0.481	G|G: 0.394
KHV	A: 0.586	G: 0.414	A|A: 0.333	A|G: 0.505	G|G: 0.162
EUROPEAN	A: 0.726	G: 0.274	A|A: 0.545	A|G: 0.362	G|G: 0.093
CEU	A: 0.788	G: 0.212	A|A: 0.636	A|G: 0.303	G|G: 0.061
FIN	A: 0.854	G: 0.146	A|A: 0.747	A|G: 0.212	G|G: 0.040
GBR	A: 0.808	G: 0.192	A|A: 0.637	A|G: 0.341	G|G: 0.022
IBS	A: 0.579	G: 0.421	A|A: 0.346	A|G: 0.467	G|G: 0.187
TSI	A: 0.626	G: 0.374	A|A: 0.393	A|G: 0.467	G|G: 0.140
SOUTH ASIAN	A: 0.580	G: 0.420	A|A: 0.352	A|G: 0.456	G|G: 0.192
BEB	A: 0.552	G: 0.448	A|A: 0.314	A|G: 0.477	G|G: 0.209
GIH	A: 0.621	G: 0.379	A|A: 0.379	A|G: 0.485	G|G: 0.136
ITU	A: 0.539	G: 0.461	A|A: 0.294	A|G: 0.490	G|G: 0.216
PJL	A: 0.620	G: 0.380	A|A: 0.448	A|G: 0.344	G|G: 0.208
STU	A: 0.564	G: 0.436	A|A: 0.324	A|G: 0.480	G|G: 0.196

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles G/A [2]	Ancestral:G [2]	Ambiguity code: R [2]	MAF: 0.14 [2]		
Location: 4:38800907 [2]					
SNP ID: rs5743596 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.861	A: 0.139	G|G: 0.760	A|A: 0.038	A|G: 0.202
AFRICAN	G: 0.990	A: 0.010	G|G: 0.980	A|A: 0.000	A|G: 0.020
ACB	G: 0.984	A: 0.016	G|G: 0.969	A|A: 0.000	A|G: 0.031
ASW	G: 0.934	A: 0.066	G|G: 0.869	A|A: 0.000	A|G: 0.131
ESN	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
GWD	G: 0.991	A: 0.009	G|G: 0.982	A|A: 0.000	A|G: 0.018
LWK	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000

MSL	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
YRI	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
AMERICAN	G: 0.879	A: 0.121	G|G: 0.790	A|A: 0.032	A|G: 0.179
CLM	G: 0.878	A: 0.122	G|G: 0.766	A|A: 0.011	A|G: 0.223
MXL	G: 0.930	A: 0.070	G|G: 0.875	A|A: 0.016	A|G: 0.109
PEL	G: 0.947	A: 0.053	G|G: 0.894	A|A: 0.000	A|G: 0.106
PUR	G: 0.793	A: 0.207	G|G: 0.673	A|A: 0.087	A|G: 0.240
EAST ASIAN	G: 0.723	A: 0.277	G|G: 0.550	A|A: 0.103	A|G: 0.347
CDX	G: 0.898	A: 0.102	G|G: 0.817	A|A: 0.022	A|G: 0.161
CHB	G: 0.612	A: 0.388	G|G: 0.379	A|A: 0.155	A|G: 0.466
CHS	G: 0.724	A: 0.276	G|G: 0.524	A|A: 0.076	A|G: 0.400
JPT	G: 0.514	A: 0.486	G|G: 0.269	A|A: 0.240	A|G: 0.490
KHV	G: 0.894	A: 0.106	G|G: 0.798	A|A: 0.010	A|G: 0.192
EUROPEAN	G: 0.824	A: 0.176	G|G: 0.694	A|A: 0.046	A|G: 0.260
CEU	G: 0.828	A: 0.172	G|G: 0.697	A|A: 0.040	A|G: 0.263
FIN	G: 0.944	A: 0.056	G|G: 0.899	A|A: 0.010	A|G: 0.091
GBR	G: 0.868	A: 0.132	G|G: 0.747	A|A: 0.011	A|G: 0.242
IBS	G: 0.748	A: 0.252	G|G: 0.570	A|A: 0.075	A|G: 0.355
TSI	G: 0.748	A: 0.252	G|G: 0.579	A|A: 0.084	A|G: 0.336
SOUTH ASIAN	G: 0.855	A: 0.145	G|G: 0.728	A|A: 0.018	A|G: 0.254
BEB	G: 0.808	A: 0.192	G|G: 0.640	A|A: 0.023	A|G: 0.337
GIH	G: 0.820	A: 0.180	G|G: 0.680	A|A: 0.039	A|G: 0.282
ITU	G: 0.902	A: 0.098	G|G: 0.814	A|A: 0.010	A|G: 0.176
PJL	G: 0.885	A: 0.115	G|G: 0.781	A|A: 0.010	A|G: 0.208
STU	G: 0.853	A: 0.147	G|G: 0.716	A|A: 0.010	A|G: 0.275

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/G [2]	Ancestral:A [2]	Ambiguity code: R [2]	MAF: 0.18 [2]		
Location: 4:38801023 [2]					
SNP ID: rs5743595 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.821	G: 0.179	A|A: 0.698	A|G: 0.246	G|G: 0.056
AFRICAN	A: 0.988	G: 0.012	A|A: 0.976	A|G: 0.024	G|G: 0.000
ACB	A: 0.974	G: 0.026	A|A: 0.948	A|G: 0.052	G|G: 0.000
ASW	A: 0.926	G: 0.074	A|A: 0.852	A|G: 0.148	G|G: 0.000
ESN	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000

GWD	A: 0.991	G: 0.009	A|A: 0.982	A|G: 0.018	G|G: 0.000
LWK	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
MSL	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
YRI	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
AMERICAN	A: 0.854	G: 0.146	A|A: 0.744	A|G: 0.222	G|G: 0.035
CLM	A: 0.856	G: 0.144	A|A: 0.734	A|G: 0.245	G|G: 0.021
MXL	A: 0.891	G: 0.109	A|A: 0.797	A|G: 0.188	G|G: 0.016
PEL	A: 0.941	G: 0.059	A|A: 0.882	A|G: 0.118	G|G: 0.000
PUR	A: 0.760	G: 0.240	A|A: 0.606	A|G: 0.308	G|G: 0.087
EAST ASIAN	A: 0.606	G: 0.394	A|A: 0.385	A|G: 0.442	G|G: 0.173
CDX	A: 0.796	G: 0.204	A|A: 0.634	A|G: 0.323	G|G: 0.043
CHB	A: 0.461	G: 0.539	A|A: 0.223	A|G: 0.476	G|G: 0.301
CHS	A: 0.605	G: 0.395	A|A: 0.352	A|G: 0.505	G|G: 0.143
JPT	A: 0.442	G: 0.558	A|A: 0.183	A|G: 0.519	G|G: 0.298
KHV	A: 0.753	G: 0.247	A|A: 0.566	A|G: 0.374	G|G: 0.061
EUROPEAN	A: 0.781	G: 0.219	A|A: 0.626	A|G: 0.310	G|G: 0.064
CEU	A: 0.813	G: 0.187	A|A: 0.667	A|G: 0.293	G|G: 0.040
FIN	A: 0.909	G: 0.091	A|A: 0.828	A|G: 0.162	G|G: 0.010
GBR	A: 0.830	G: 0.170	A|A: 0.681	A|G: 0.297	G|G: 0.022
IBS	A: 0.696	G: 0.304	A|A: 0.505	A|G: 0.383	G|G: 0.112
TSI	A: 0.678	G: 0.322	A|A: 0.477	A|G: 0.402	G|G: 0.121
SOUTH ASIAN	A: 0.835	G: 0.165	A|A: 0.689	A|G: 0.292	G|G: 0.018
BEB	A: 0.785	G: 0.215	A|A: 0.593	A|G: 0.384	G|G: 0.023
GIH	A: 0.811	G: 0.189	A|A: 0.660	A|G: 0.301	G|G: 0.039
ITU	A: 0.882	G: 0.118	A|A: 0.775	A|G: 0.216	G|G: 0.010
PJL	A: 0.865	G: 0.135	A|A: 0.740	A|G: 0.250	G|G: 0.010
STU	A: 0.828	G: 0.172	A|A: 0.667	A|G: 0.324	G|G: 0.010

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles G/A [2]	Ancestral:G [2]	Ambiguity code: R [2]	MAF: 0.05 [2]		
Location: 4:38801130 [2]					
SNP ID: rs5743594 [1]					
GWAS Trait: Height [1,2]					
Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.949	A: 0.051	G|G: 0.903	A|A: 0.005	A|G: 0.092

AFRICAN	G: 0.995	A: 0.005	G|G: 0.992	A|A: 0.002	A|G: 0.006
ACB	G: 0.969	A: 0.031	G|G: 0.948	A|A: 0.010	A|G: 0.042
ASW	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
ESN	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
GWD	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
LWK	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
MSL	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
YRI	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
AMERICAN	G: 0.929	A: 0.071	G|G: 0.862	A|A: 0.003	A|G: 0.135
CLM	G: 0.904	A: 0.096	G|G: 0.809	A|A: 0.000	A|G: 0.191
MXL	G: 0.992	A: 0.008	G|G: 0.984	A|A: 0.000	A|G: 0.016
PEL	G: 0.971	A: 0.029	G|G: 0.941	A|A: 0.000	A|G: 0.059
PUR	G: 0.880	A: 0.120	G|G: 0.769	A|A: 0.010	A|G: 0.221
EAST ASIAN	G: 0.999	A: 0.001	G|G: 0.998	A|A: 0.000	A|G: 0.002
CDX	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
CHB	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
CHS	G: 0.995	A: 0.005	G|G: 0.990	A|A: 0.000	A|G: 0.010
JPT	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
KHV	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
EUROPEAN	G: 0.843	A: 0.157	G|G: 0.702	A|A: 0.016	A|G: 0.282
CEU	G: 0.833	A: 0.167	G|G: 0.687	A|A: 0.020	A|G: 0.293
FIN	G: 0.828	A: 0.172	G|G: 0.667	A|A: 0.010	A|G: 0.323
GBR	G: 0.797	A: 0.203	G|G: 0.626	A|A: 0.033	A|G: 0.341
IBS	G: 0.902	A: 0.098	G|G: 0.804	A|A: 0.000	A|G: 0.196
TSI	G: 0.846	A: 0.154	G|G: 0.710	A|A: 0.019	A|G: 0.271
SOUTH ASIAN	G: 0.958	A: 0.042	G|G: 0.920	A|A: 0.004	A|G: 0.076
BEB	G: 0.965	A: 0.035	G|G: 0.930	A|A: 0.000	A|G: 0.070
GIH	G: 0.961	A: 0.039	G|G: 0.922	A|A: 0.000	A|G: 0.078
ITU	G: 0.956	A: 0.044	G|G: 0.922	A|A: 0.010	A|G: 0.069
PJL	G: 0.938	A: 0.062	G|G: 0.885	A|A: 0.010	A|G: 0.104
STU	G: 0.971	A: 0.029	G|G: 0.941	A|A: 0.000	A|G: 0.059

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/G [2]	Ancestral:G [2]	Ambiguity code: R [2]	MAF: 0.18 [2]		
Location: 4:38801442 [2]					
SNP ID: rs5743592 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: The GWAS-identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.818	G: 0.182	A|A: 0.694	A|G: 0.249	G|G: 0.058
AFRICAN	A: 0.988	G: 0.012	A|A: 0.976	A|G: 0.024	G|G: 0.000
ACB	A: 0.974	G: 0.026	A|A: 0.948	A|G: 0.052	G|G: 0.000
ASW	A: 0.926	G: 0.074	A|A: 0.852	A|G: 0.148	G|G: 0.000
ESN	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000

GWD	A: 0.991	G: 0.009	A|A: 0.982	A|G: 0.018	G|G: 0.000
LWK	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
MSL	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
YRI	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
AMERICAN	A: 0.850	G: 0.150	A|A: 0.738	A|G: 0.225	G|G: 0.037
CLM	A: 0.840	G: 0.160	A|A: 0.713	A|G: 0.255	G|G: 0.032
MXL	A: 0.891	G: 0.109	A|A: 0.797	A|G: 0.188	G|G: 0.016
PEL	A: 0.941	G: 0.059	A|A: 0.882	A|G: 0.118	G|G: 0.000
PUR	A: 0.760	G: 0.240	A|A: 0.606	A|G: 0.308	G|G: 0.087
EAST ASIAN	A: 0.595	G: 0.405	A|A: 0.369	A|G: 0.452	G|G: 0.179
CDX	A: 0.790	G: 0.210	A|A: 0.624	A|G: 0.333	G|G: 0.043
CHB	A: 0.442	G: 0.558	A|A: 0.194	A|G: 0.495	G|G: 0.311
CHS	A: 0.576	G: 0.424	A|A: 0.314	A|G: 0.524	G|G: 0.162
JPT	A: 0.438	G: 0.562	A|A: 0.183	A|G: 0.510	G|G: 0.308
KHV	A: 0.758	G: 0.242	A|A: 0.566	A|G: 0.384	G|G: 0.051
EUROPEAN	A: 0.779	G: 0.221	A|A: 0.622	A|G: 0.314	G|G: 0.064
CEU	A: 0.813	G: 0.187	A|A: 0.667	A|G: 0.293	G|G: 0.040
FIN	A: 0.909	G: 0.091	A|A: 0.828	A|G: 0.162	G|G: 0.010
GBR	A: 0.830	G: 0.170	A|A: 0.681	A|G: 0.297	G|G: 0.022
IBS	A: 0.692	G: 0.308	A|A: 0.495	A|G: 0.393	G|G: 0.112
TSI	A: 0.673	G: 0.327	A|A: 0.467	A|G: 0.411	G|G: 0.121
SOUTH ASIAN	A: 0.835	G: 0.165	A|A: 0.689	A|G: 0.292	G|G: 0.018
BEB	A: 0.779	G: 0.221	A|A: 0.581	A|G: 0.395	G|G: 0.023
GIH	A: 0.806	G: 0.194	A|A: 0.650	A|G: 0.311	G|G: 0.039
ITU	A: 0.877	G: 0.123	A|A: 0.765	A|G: 0.225	G|G: 0.010
PJL	A: 0.865	G: 0.135	A|A: 0.740	A|G: 0.250	G|G: 0.010
STU	A: 0.843	G: 0.157	A|A: 0.696	A|G: 0.294	G|G: 0.010

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles C/T [2]	Ancestral:C [2]	Ambiguity code: Y [2]	MAF: 0.18 [2]		
Location: 4:38803868 [2]					
SNP ID: rs5743571 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: The GWAS-identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	C: 0.821	T: 0.179	C|C: 0.698	C|T: 0.246	T|T: 0.056

AFRICAN	C: 0.988	T: 0.012	C|C: 0.976	C|T: 0.024	T|T: 0.000
ACB	C: 0.974	T: 0.026	C|C: 0.948	C|T: 0.052	T|T: 0.000
ASW	C: 0.926	T: 0.074	C|C: 0.852	C|T: 0.148	T|T: 0.000
ESN	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
GWD	C: 0.991	T: 0.009	C|C: 0.982	C|T: 0.018	T|T: 0.000
LWK	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
MSL	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
YRI	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
AMERICAN	C: 0.850	T: 0.150	C|C: 0.738	C|T: 0.225	T|T: 0.037
CLM	C: 0.840	T: 0.160	C|C: 0.713	C|T: 0.255	T|T: 0.032
MXL	C: 0.891	T: 0.109	C|C: 0.797	C|T: 0.188	T|T: 0.016
PEL	C: 0.941	T: 0.059	C|C: 0.882	C|T: 0.118	T|T: 0.000
PUR	C: 0.760	T: 0.240	C|C: 0.606	C|T: 0.308	T|T: 0.087
EAST ASIAN	C: 0.606	T: 0.394	C|C: 0.385	C|T: 0.442	T|T: 0.173
CDX	C: 0.796	T: 0.204	C|C: 0.634	C|T: 0.323	T|T: 0.043
CHB	C: 0.461	T: 0.539	C|C: 0.223	C|T: 0.476	T|T: 0.301
CHS	C: 0.600	T: 0.400	C|C: 0.352	C|T: 0.495	T|T: 0.152
JPT	C: 0.442	T: 0.558	C|C: 0.183	C|T: 0.519	T|T: 0.298
KHV	C: 0.758	T: 0.242	C|C: 0.566	C|T: 0.384	T|T: 0.051
EUROPEAN	C: 0.780	T: 0.220	C|C: 0.624	C|T: 0.312	T|T: 0.064
CEU	C: 0.813	T: 0.187	C|C: 0.667	C|T: 0.293	T|T: 0.040
FIN	C: 0.909	T: 0.091	C|C: 0.828	C|T: 0.162	T|T: 0.010
GBR	C: 0.830	T: 0.170	C|C: 0.681	C|T: 0.297	T|T: 0.022
IBS	C: 0.692	T: 0.308	C|C: 0.495	C|T: 0.393	T|T: 0.112
TSI	C: 0.678	T: 0.322	C|C: 0.477	C|T: 0.402	T|T: 0.121
SOUTH ASIAN	C: 0.836	T: 0.164	C|C: 0.691	C|T: 0.290	T|T: 0.018
BEB	C: 0.779	T: 0.221	C|C: 0.581	C|T: 0.395	T|T: 0.023
GIH	C: 0.811	T: 0.189	C|C: 0.660	C|T: 0.301	T|T: 0.039
ITU	C: 0.877	T: 0.123	C|C: 0.765	C|T: 0.225	T|T: 0.010
PJL	C: 0.865	T: 0.135	C|C: 0.740	C|T: 0.250	T|T: 0.010
STU	C: 0.843	T: 0.157	C|C: 0.696	C|T: 0.294	T|T: 0.010

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/C [2]	Ancestral:T [2]	Ambiguity code: Y [2]	MAF: 0.18 [2]

Location: 4:38804362 [2]

SNP ID: rs5743565 [1]

GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]

Archaic-like haplotype cluster: The GWAS-identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]

Clinical Assertion Description: Not Known

Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.820	C: 0.180	T|T: 0.697	C|C: 0.057	C|T: 0.246
AFRICAN	T: 0.988	C: 0.012	T|T: 0.976	C|C: 0.000	C|T: 0.024
ACB	T: 0.974	C: 0.026	T|T: 0.948	C|C: 0.000	C|T: 0.052
ASW	T: 0.926	C: 0.074	T|T: 0.852	C|C: 0.000	C|T: 0.148

ESN	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
GWD	T: 0.991	C: 0.009	T|T: 0.982	C|C: 0.000	C|T: 0.018
LWK	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
MSL	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
YRI	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
AMERICAN	T: 0.850	C: 0.150	T|T: 0.738	C|C: 0.037	C|T: 0.225
CLM	T: 0.840	C: 0.160	T|T: 0.713	C|C: 0.032	C|T: 0.255
MXL	T: 0.891	C: 0.109	T|T: 0.797	C|C: 0.016	C|T: 0.188
PEL	T: 0.941	C: 0.059	T|T: 0.882	C|C: 0.000	C|T: 0.118
PUR	T: 0.760	C: 0.240	T|T: 0.606	C|C: 0.087	C|T: 0.308
EAST ASIAN	T: 0.605	C: 0.395	T|T: 0.385	C|C: 0.175	C|T: 0.440
CDX	T: 0.796	C: 0.204	T|T: 0.634	C|C: 0.043	C|T: 0.323
CHB	T: 0.461	C: 0.539	T|T: 0.223	C|C: 0.301	C|T: 0.476
CHS	T: 0.600	C: 0.400	T|T: 0.352	C|C: 0.152	C|T: 0.495
JPT	T: 0.442	C: 0.558	T|T: 0.183	C|C: 0.298	C|T: 0.519
KHV	T: 0.753	C: 0.247	T|T: 0.566	C|C: 0.061	C|T: 0.374
EUROPEAN	T: 0.779	C: 0.221	T|T: 0.622	C|C: 0.064	C|T: 0.314
CEU	T: 0.813	C: 0.187	T|T: 0.667	C|C: 0.040	C|T: 0.293
FIN	T: 0.904	C: 0.096	T|T: 0.818	C|C: 0.010	C|T: 0.172
GBR	T: 0.830	C: 0.170	T|T: 0.681	C|C: 0.022	C|T: 0.297
IBS	T: 0.692	C: 0.308	T|T: 0.495	C|C: 0.112	C|T: 0.393
TSI	T: 0.678	C: 0.322	T|T: 0.477	C|C: 0.121	C|T: 0.402
SOUTH ASIAN	T: 0.835	C: 0.165	T|T: 0.691	C|C: 0.020	C|T: 0.288
BEB	T: 0.779	C: 0.221	T|T: 0.581	C|C: 0.023	C|T: 0.395
GIH	T: 0.811	C: 0.189	T|T: 0.660	C|C: 0.039	C|T: 0.301
ITU	T: 0.877	C: 0.123	T|T: 0.765	C|C: 0.010	C|T: 0.225
PJL	T: 0.859	C: 0.141	T|T: 0.740	C|C: 0.021	C|T: 0.240
STU	T: 0.843	C: 0.157	T|T: 0.696	C|C: 0.010	C|T: 0.294

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/G [2]	Ancestral:G [2]	Ambiguity code: R [2]	MAF: 0.18 [2]		
Location: 4:38804398 [2]					
SNP ID: rs5743563 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: The GWAS-identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.820	G: 0.180	A|A: 0.697	A|G: 0.246	G|G: 0.057
AFRICAN	A: 0.988	G: 0.012	A|A: 0.976	A|G: 0.024	G|G: 0.000

ACB	A: 0.974	G: 0.026	A|A: 0.948	A|G: 0.052	G|G: 0.000
ASW	A: 0.926	G: 0.074	A|A: 0.852	A|G: 0.148	G|G: 0.000
ESN	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
GWD	A: 0.991	G: 0.009	A|A: 0.982	A|G: 0.018	G|G: 0.000
LWK	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
MSL	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
YRI	A: 1.000	G: 0.000	A|A: 1.000	A|G: 0.000	G|G: 0.000
AMERICAN	A: 0.850	G: 0.150	A|A: 0.738	A|G: 0.225	G|G: 0.037
CLM	A: 0.840	G: 0.160	A|A: 0.713	A|G: 0.255	G|G: 0.032
MXL	A: 0.891	G: 0.109	A|A: 0.797	A|G: 0.188	G|G: 0.016
PEL	A: 0.941	G: 0.059	A|A: 0.882	A|G: 0.118	G|G: 0.000
PUR	A: 0.760	G: 0.240	A|A: 0.606	A|G: 0.308	G|G: 0.087
EAST ASIAN	A: 0.605	G: 0.395	A|A: 0.385	A|G: 0.440	G|G: 0.175
CDX	A: 0.796	G: 0.204	A|A: 0.634	A|G: 0.323	G|G: 0.043
CHB	A: 0.461	G: 0.539	A|A: 0.223	A|G: 0.476	G|G: 0.301
CHS	A: 0.600	G: 0.400	A|A: 0.352	A|G: 0.495	G|G: 0.152
JPT	A: 0.442	G: 0.558	A|A: 0.183	A|G: 0.519	G|G: 0.298
KHV	A: 0.753	G: 0.247	A|A: 0.566	A|G: 0.374	G|G: 0.061
EUROPEAN	A: 0.779	G: 0.221	A|A: 0.622	A|G: 0.314	G|G: 0.064
CEU	A: 0.813	G: 0.187	A|A: 0.667	A|G: 0.293	G|G: 0.040
FIN	A: 0.904	G: 0.096	A|A: 0.818	A|G: 0.172	G|G: 0.010
GBR	A: 0.830	G: 0.170	A|A: 0.681	A|G: 0.297	G|G: 0.022
IBS	A: 0.692	G: 0.308	A|A: 0.495	A|G: 0.393	G|G: 0.112
TSI	A: 0.678	G: 0.322	A|A: 0.477	A|G: 0.402	G|G: 0.121
SOUTH ASIAN	A: 0.835	G: 0.165	A|A: 0.691	A|G: 0.288	G|G: 0.020
BEB	A: 0.779	G: 0.221	A|A: 0.581	A|G: 0.395	G|G: 0.023
GIH	A: 0.811	G: 0.189	A|A: 0.660	A|G: 0.301	G|G: 0.039
ITU	A: 0.877	G: 0.123	A|A: 0.765	A|G: 0.225	G|G: 0.010
PJL	A: 0.859	G: 0.141	A|A: 0.740	A|G: 0.240	G|G: 0.021
STU	A: 0.843	G: 0.157	A|A: 0.696	A|G: 0.294	G|G: 0.010

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/C [2]	Ancestral:T [2]	Ambiguity code: Y [2]	MAF: 0.18 [2]
Location: 4:38804475 [2]			
SNP ID: rs5743562 [1]			
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]			
Archaic-like haplotype cluster: The GWAS-identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]			
Clinical Assertion Description: Not Known			

Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.820	C: 0.180	T|T: 0.697	C|C: 0.056	C|T: 0.246
AFRICAN	T: 0.988	C: 0.012	T|T: 0.976	C|C: 0.000	C|T: 0.024
ACB	T: 0.974	C: 0.026	T|T: 0.948	C|C: 0.000	C|T: 0.052
ASW	T: 0.926	C: 0.074	T|T: 0.852	C|C: 0.000	C|T: 0.148
ESN	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
GWD	T: 0.991	C: 0.009	T|T: 0.982	C|C: 0.000	C|T: 0.018
LWK	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
MSL	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
YRI	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
AMERICAN	T: 0.850	C: 0.150	T|T: 0.738	C|C: 0.037	C|T: 0.225
CLM	T: 0.840	C: 0.160	T|T: 0.713	C|C: 0.032	C|T: 0.255
MXL	T: 0.891	C: 0.109	T|T: 0.797	C|C: 0.016	C|T: 0.188
PEL	T: 0.941	C: 0.059	T|T: 0.882	C|C: 0.000	C|T: 0.118
PUR	T: 0.760	C: 0.240	T|T: 0.606	C|C: 0.087	C|T: 0.308
EAST ASIAN	T: 0.606	C: 0.394	T|T: 0.385	C|C: 0.173	C|T: 0.442
CDX	T: 0.796	C: 0.204	T|T: 0.634	C|C: 0.043	C|T: 0.323
CHB	T: 0.461	C: 0.539	T|T: 0.223	C|C: 0.301	C|T: 0.476
CHS	T: 0.600	C: 0.400	T|T: 0.352	C|C: 0.152	C|T: 0.495
JPT	T: 0.442	C: 0.558	T|T: 0.183	C|C: 0.298	C|T: 0.519
KHV	T: 0.758	C: 0.242	T|T: 0.566	C|C: 0.051	C|T: 0.384
EUROPEAN	T: 0.779	C: 0.221	T|T: 0.622	C|C: 0.064	C|T: 0.314
CEU	T: 0.813	C: 0.187	T|T: 0.667	C|C: 0.040	C|T: 0.293
FIN	T: 0.904	C: 0.096	T|T: 0.818	C|C: 0.010	C|T: 0.172
GBR	T: 0.830	C: 0.170	T|T: 0.681	C|C: 0.022	C|T: 0.297
IBS	T: 0.692	C: 0.308	T|T: 0.495	C|C: 0.112	C|T: 0.393
TSI	T: 0.678	C: 0.322	T|T: 0.477	C|C: 0.121	C|T: 0.402
SOUTH ASIAN	T: 0.836	C: 0.164	T|T: 0.691	C|C: 0.018	C|T: 0.290
BEB	T: 0.779	C: 0.221	T|T: 0.581	C|C: 0.023	C|T: 0.395
GIH	T: 0.811	C: 0.189	T|T: 0.660	C|C: 0.039	C|T: 0.301
ITU	T: 0.877	C: 0.123	T|T: 0.765	C|C: 0.010	C|T: 0.225
PJL	T: 0.865	C: 0.135	T|T: 0.740	C|C: 0.010	C|T: 0.250
STU	T: 0.843	C: 0.157	T|T: 0.696	C|C: 0.010	C|T: 0.294

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles C/T [2]	Ancestral:T [2]	Ambiguity code: Y [2]	MAF: 0.18 [2]		
Location: 4:38809148 [2]					
SNP ID: rs11722813 [1]					
GWAS Trait: Helicobacter pylori serologic status [1]					
Archaic-like haplotype cluster: The GWAS-identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	C: 0.821	T: 0.179	C|C: 0.697	C|T: 0.247	T|T: 0.056
AFRICAN	C: 0.988	T: 0.012	C|C: 0.976	C|T: 0.024	T|T: 0.000
ACB	C: 0.974	T: 0.026	C|C: 0.948	C|T: 0.052	T|T: 0.000
ASW	C: 0.926	T: 0.074	C|C: 0.852	C|T: 0.148	T|T: 0.000
ESN	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
GWD	C: 0.991	T: 0.009	C|C: 0.982	C|T: 0.018	T|T: 0.000
LWK	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
MSL	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
YRI	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
AMERICAN	C: 0.850	T: 0.150	C|C: 0.738	C|T: 0.225	T|T: 0.037
CLM	C: 0.840	T: 0.160	C|C: 0.713	C|T: 0.255	T|T: 0.032
MXL	C: 0.891	T: 0.109	C|C: 0.797	C|T: 0.188	T|T: 0.016
PEL	C: 0.941	T: 0.059	C|C: 0.882	C|T: 0.118	T|T: 0.000
PUR	C: 0.760	T: 0.240	C|C: 0.606	C|T: 0.308	T|T: 0.087
EAST ASIAN	C: 0.605	T: 0.395	C|C: 0.383	C|T: 0.444	T|T: 0.173
CDX	C: 0.796	T: 0.204	C|C: 0.634	C|T: 0.323	T|T: 0.043
CHB	C: 0.461	T: 0.539	C|C: 0.223	C|T: 0.476	T|T: 0.301
CHS	C: 0.600	T: 0.400	C|C: 0.352	C|T: 0.495	T|T: 0.152
JPT	C: 0.438	T: 0.562	C|C: 0.173	C|T: 0.529	T|T: 0.298
KHV	C: 0.758	T: 0.242	C|C: 0.566	C|T: 0.384	T|T: 0.051
EUROPEAN	C: 0.782	T: 0.218	C|C: 0.626	C|T: 0.312	T|T: 0.062
CEU	C: 0.813	T: 0.187	C|C: 0.667	C|T: 0.293	T|T: 0.040
FIN	C: 0.904	T: 0.096	C|C: 0.818	C|T: 0.172	T|T: 0.010
GBR	C: 0.835	T: 0.165	C|C: 0.692	C|T: 0.286	T|T: 0.022
IBS	C: 0.692	T: 0.308	C|C: 0.495	C|T: 0.393	T|T: 0.112
TSI	C: 0.687	T: 0.313	C|C: 0.486	C|T: 0.402	T|T: 0.112
SOUTH ASIAN	C: 0.835	T: 0.165	C|C: 0.689	C|T: 0.292	T|T: 0.018
BEB	C: 0.779	T: 0.221	C|C: 0.581	C|T: 0.395	T|T: 0.023
GIH	C: 0.811	T: 0.189	C|C: 0.660	C|T: 0.301	T|T: 0.039
ITU	C: 0.873	T: 0.127	C|C: 0.755	C|T: 0.235	T|T: 0.010
PJL	C: 0.865	T: 0.135	C|C: 0.740	C|T: 0.250	T|T: 0.010
STU	C: 0.843	T: 0.157	C|C: 0.696	C|T: 0.294	T|T: 0.010

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles G/A [2]	Ancestral:A [2]	Ambiguity code: R [2]	MAF: 0.48 [2]		
Location: 4:38809930 [2]					
SNP ID: rs2101521 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1,2]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.525	A: 0.475	G|G: 0.306	A|A: 0.256	A|G: 0.438
AFRICAN	G: 0.336	A: 0.664	G|G: 0.113	A|A: 0.442	A|G: 0.445
ACB	G: 0.385	A: 0.615	G|G: 0.135	A|A: 0.365	A|G: 0.500
ASW	G: 0.410	A: 0.590	G|G: 0.180	A|A: 0.361	A|G: 0.459
ESN	G: 0.348	A: 0.652	G|G: 0.131	A|A: 0.434	A|G: 0.434
GWD	G: 0.420	A: 0.580	G|G: 0.168	A|A: 0.327	A|G: 0.504
LWK	G: 0.232	A: 0.768	G|G: 0.030	A|A: 0.566	A|G: 0.404
MSL	G: 0.253	A: 0.747	G|G: 0.094	A|A: 0.588	A|G: 0.318
YRI	G: 0.310	A: 0.690	G|G: 0.074	A|A: 0.454	A|G: 0.472
AMERICAN	G: 0.581	A: 0.419	G|G: 0.346	A|A: 0.184	A|G: 0.470
CLM	G: 0.612	A: 0.388	G|G: 0.372	A|A: 0.149	A|G: 0.479
MXL	G: 0.531	A: 0.469	G|G: 0.266	A|A: 0.203	A|G: 0.531
PEL	G: 0.524	A: 0.476	G|G: 0.294	A|A: 0.247	A|G: 0.459
PUR	G: 0.630	A: 0.370	G|G: 0.413	A|A: 0.154	A|G: 0.433
EAST ASIAN	G: 0.421	A: 0.579	G|G: 0.183	A|A: 0.341	A|G: 0.476
CDX	G: 0.565	A: 0.435	G|G: 0.301	A|A: 0.172	A|G: 0.527
CHB	G: 0.320	A: 0.680	G|G: 0.087	A|A: 0.447	A|G: 0.466
CHS	G: 0.386	A: 0.614	G|G: 0.152	A|A: 0.381	A|G: 0.467
JPT	G: 0.284	A: 0.716	G|G: 0.048	A|A: 0.481	A|G: 0.471
KHV	G: 0.571	A: 0.429	G|G: 0.343	A|A: 0.202	A|G: 0.455
EUROPEAN	G: 0.741	A: 0.259	G|G: 0.565	A|A: 0.083	A|G: 0.352
CEU	G: 0.803	A: 0.197	G|G: 0.657	A|A: 0.051	A|G: 0.293
FIN	G: 0.859	A: 0.141	G|G: 0.747	A|A: 0.030	A|G: 0.222
GBR	G: 0.808	A: 0.192	G|G: 0.637	A|A: 0.022	A|G: 0.341
IBS	G: 0.617	A: 0.383	G|G: 0.393	A|A: 0.159	A|G: 0.449
TSI	G: 0.640	A: 0.360	G|G: 0.421	A|A: 0.140	A|G: 0.439
SOUTH ASIAN	G: 0.626	A: 0.374	G|G: 0.397	A|A: 0.145	A|G: 0.458
BEB	G: 0.622	A: 0.378	G|G: 0.360	A|A: 0.116	A|G: 0.523
GIH	G: 0.626	A: 0.374	G|G: 0.398	A|A: 0.146	A|G: 0.456
ITU	G: 0.618	A: 0.382	G|G: 0.373	A|A: 0.137	A|G: 0.490
PJL	G: 0.672	A: 0.328	G|G: 0.500	A|A: 0.156	A|G: 0.344
STU	G: 0.593	A: 0.407	G|G: 0.353	A|A: 0.167	A|G: 0.480

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/C [2]	Ancestral:C [2]	Ambiguity code: Y [2]	MAF: 0.43 [2]		
Location: 4:38811255 [2]					
SNP ID: rs17616434 [1]					
GWAS Trait: Helicobacter pylori serologic status, Alcohol consumption, Self-reported allergy, Allergic sensitization [1,2]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.427	C: 0.573	T|T: 0.238	C|C: 0.385	C|T: 0.376
AFRICAN	T: 0.103	C: 0.897	T|T: 0.017	C|C: 0.811	C|T: 0.172
ACB	T: 0.167	C: 0.833	T|T: 0.010	C|C: 0.677	C|T: 0.312
ASW	T: 0.254	C: 0.746	T|T: 0.098	C|C: 0.590	C|T: 0.311
ESN	T: 0.106	C: 0.894	T|T: 0.020	C|C: 0.808	C|T: 0.172
GWD	T: 0.044	C: 0.956	T|T: 0.009	C|C: 0.920	C|T: 0.071
LWK	T: 0.076	C: 0.924	T|T: 0.010	C|C: 0.859	C|T: 0.131
MSL	T: 0.035	C: 0.965	T|T: 0.000	C|C: 0.929	C|T: 0.071
YRI	T: 0.097	C: 0.903	T|T: 0.000	C|C: 0.806	C|T: 0.194
AMERICAN	T: 0.530	C: 0.470	T|T: 0.297	C|C: 0.236	C|T: 0.467
CLM	T: 0.574	C: 0.426	T|T: 0.340	C|C: 0.191	C|T: 0.468
MXL	T: 0.500	C: 0.500	T|T: 0.234	C|C: 0.234	C|T: 0.531
PEL	T: 0.494	C: 0.506	T|T: 0.271	C|C: 0.282	C|T: 0.447
PUR	T: 0.538	C: 0.462	T|T: 0.317	C|C: 0.240	C|T: 0.442
EAST ASIAN	T: 0.396	C: 0.604	T|T: 0.155	C|C: 0.363	C|T: 0.482
CDX	T: 0.516	C: 0.484	T|T: 0.237	C|C: 0.204	C|T: 0.559
CHB	T: 0.306	C: 0.694	T|T: 0.078	C|C: 0.466	C|T: 0.456
CHS	T: 0.381	C: 0.619	T|T: 0.162	C|C: 0.400	C|T: 0.438
JPT	T: 0.274	C: 0.726	T|T: 0.048	C|C: 0.500	C|T: 0.452
KHV	T: 0.520	C: 0.480	T|T: 0.263	C|C: 0.222	C|T: 0.515
EUROPEAN	T: 0.716	C: 0.284	T|T: 0.533	C|C: 0.101	C|T: 0.366
CEU	T: 0.788	C: 0.212	T|T: 0.626	C|C: 0.051	C|T: 0.323
FIN	T: 0.843	C: 0.157	T|T: 0.727	C|C: 0.040	C|T: 0.232
GBR	T: 0.802	C: 0.198	T|T: 0.626	C|C: 0.022	C|T: 0.352
IBS	T: 0.575	C: 0.425	T|T: 0.346	C|C: 0.196	C|T: 0.458
TSI	T: 0.598	C: 0.402	T|T: 0.374	C|C: 0.178	C|T: 0.449
SOUTH ASIAN	T: 0.525	C: 0.475	T|T: 0.280	C|C: 0.231	C|T: 0.489
BEB	T: 0.529	C: 0.471	T|T: 0.279	C|C: 0.221	C|T: 0.500
GIH	T: 0.539	C: 0.461	T|T: 0.262	C|C: 0.184	C|T: 0.553
ITU	T: 0.475	C: 0.525	T|T: 0.186	C|C: 0.235	C|T: 0.578
PJL	T: 0.573	C: 0.427	T|T: 0.396	C|C: 0.250	C|T: 0.354
STU	T: 0.510	C: 0.490	T|T: 0.284	C|C: 0.265	C|T: 0.451

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/C [2]	Ancestral:C [2]	Ambiguity code: M [2]	MAF: 0.14 [2]		
Location: 4:38813881 [2]					
SNP ID: rs4833103 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.138	C: 0.862	A|A: 0.062	A|C: 0.153	C|C: 0.786
AFRICAN	A: 0.018	C: 0.982	A|A: 0.003	A|C: 0.030	C|C: 0.967
ACB	A: 0.042	C: 0.958	A|A: 0.000	A|C: 0.083	C|C: 0.917
ASW	A: 0.131	C: 0.869	A|A: 0.033	A|C: 0.197	C|C: 0.770
ESN	A: 0.000	C: 1.000	A|A: 0.000	A|C: 0.000	C|C: 1.000
GWD	A: 0.000	C: 1.000	A|A: 0.000	A|C: 0.000	C|C: 1.000
LWK	A: 0.000	C: 1.000	A|A: 0.000	A|C: 0.000	C|C: 1.000
MSL	A: 0.000	C: 1.000	A|A: 0.000	A|C: 0.000	C|C: 1.000
YRI	A: 0.000	C: 1.000	A|A: 0.000	A|C: 0.000	C|C: 1.000
AMERICAN	A: 0.207	C: 0.793	A|A: 0.058	A|C: 0.300	C|C: 0.643
CLM	A: 0.266	C: 0.734	A|A: 0.106	A|C: 0.319	C|C: 0.574
MXL	A: 0.164	C: 0.836	A|A: 0.031	A|C: 0.266	C|C: 0.703
PEL	A: 0.094	C: 0.906	A|A: 0.000	A|C: 0.188	C|C: 0.812
PUR	A: 0.274	C: 0.726	A|A: 0.077	A|C: 0.394	C|C: 0.529
EAST ASIAN	A: 0.000	C: 1.000	A|A: 0.000	A|C: 0.000	C|C: 1.000
CDX	A: 0.000	C: 1.000	A|A: 0.000	A|C: 0.000	C|C: 1.000
CHB	A: 0.000	C: 1.000	A|A: 0.000	A|C: 0.000	C|C: 1.000
CHS	A: 0.000	C: 1.000	A|A: 0.000	A|C: 0.000	C|C: 1.000
JPT	A: 0.000	C: 1.000	A|A: 0.000	A|C: 0.000	C|C: 1.000
KHV	A: 0.000	C: 1.000	A|A: 0.000	A|C: 0.000	C|C: 1.000
EUROPEAN	A: 0.505	C: 0.495	A|A: 0.262	A|C: 0.485	C|C: 0.252
CEU	A: 0.586	C: 0.414	A|A: 0.333	A|C: 0.505	C|C: 0.162
FIN	A: 0.657	C: 0.343	A|A: 0.444	A|C: 0.424	C|C: 0.131
GBR	A: 0.549	C: 0.451	A|A: 0.253	A|C: 0.593	C|C: 0.154
IBS	A: 0.383	C: 0.617	A|A: 0.140	A|C: 0.486	C|C: 0.374
TSI	A: 0.374	C: 0.626	A|A: 0.159	A|C: 0.430	C|C: 0.411
SOUTH ASIAN	A: 0.014	C: 0.986	A|A: 0.000	A|C: 0.029	C|C: 0.971
BEB	A: 0.012	C: 0.988	A|A: 0.000	A|C: 0.023	C|C: 0.977
GIH	A: 0.024	C: 0.976	A|A: 0.000	A|C: 0.049	C|C: 0.951
ITU	A: 0.005	C: 0.995	A|A: 0.000	A|C: 0.010	C|C: 0.990
PJL	A: 0.021	C: 0.979	A|A: 0.000	A|C: 0.042	C|C: 0.958
STU	A: 0.010	C: 0.990	A|A: 0.000	A|C: 0.020	C|C: 0.980
REFERENCES					
1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33					
2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html					

Alleles A/C [2]	Ancestral:C [2]	Ambiguity code: M [2]	MAF: 0.44 [2]		
Location: 4:38814717 [2]					
SNP ID: rs6815814 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.436	C: 0.564	A|A: 0.250	A|C: 0.371	C|C: 0.378
AFRICAN	A: 0.103	C: 0.897	A|A: 0.017	A|C: 0.172	C|C: 0.811
ACB	A: 0.161	C: 0.839	A|A: 0.010	A|C: 0.302	C|C: 0.688
ASW	A: 0.262	C: 0.738	A|A: 0.098	A|C: 0.328	C|C: 0.574
ESN	A: 0.106	C: 0.894	A|A: 0.020	A|C: 0.172	C|C: 0.808

GWD	A: 0.044	C: 0.956	A|A: 0.009	A|C: 0.071	C|C: 0.920
LWK	A: 0.076	C: 0.924	A|A: 0.010	A|C: 0.131	C|C: 0.859
MSL	A: 0.035	C: 0.965	A|A: 0.000	A|C: 0.071	C|C: 0.929
YRI	A: 0.097	C: 0.903	A|A: 0.000	A|C: 0.194	C|C: 0.806
AMERICAN	A: 0.612	C: 0.388	A|A: 0.398	A|C: 0.429	C|C: 0.173
CLM	A: 0.649	C: 0.351	A|A: 0.447	A|C: 0.404	C|C: 0.149
MXL	A: 0.656	C: 0.344	A|A: 0.406	A|C: 0.500	C|C: 0.094
PEL	A: 0.629	C: 0.371	A|A: 0.435	A|C: 0.388	C|C: 0.176
PUR	A: 0.538	C: 0.462	A|A: 0.317	A|C: 0.442	C|C: 0.240
EAST ASIAN	A: 0.416	C: 0.584	A|A: 0.177	A|C: 0.478	C|C: 0.345
CDX	A: 0.548	C: 0.452	A|A: 0.280	A|C: 0.538	C|C: 0.183
CHB	A: 0.320	C: 0.680	A|A: 0.087	A|C: 0.466	C|C: 0.447
CHS	A: 0.400	C: 0.600	A|A: 0.171	A|C: 0.457	C|C: 0.371
JPT	A: 0.288	C: 0.712	A|A: 0.067	A|C: 0.442	C|C: 0.490
KHV	A: 0.540	C: 0.460	A|A: 0.293	A|C: 0.495	C|C: 0.212
EUROPEAN	A: 0.710	C: 0.290	A|A: 0.529	A|C: 0.362	C|C: 0.109
CEU	A: 0.793	C: 0.207	A|A: 0.636	A|C: 0.313	C|C: 0.051
FIN	A: 0.843	C: 0.157	A|A: 0.727	A|C: 0.232	C|C: 0.040
GBR	A: 0.802	C: 0.198	A|A: 0.626	A|C: 0.352	C|C: 0.022
IBS	A: 0.556	C: 0.444	A|A: 0.327	A|C: 0.458	C|C: 0.215
TSI	A: 0.584	C: 0.416	A|A: 0.364	A|C: 0.439	C|C: 0.196
SOUTH ASIAN	A: 0.501	C: 0.499	A|A: 0.252	A|C: 0.499	C|C: 0.249
BEB	A: 0.517	C: 0.483	A|A: 0.279	A|C: 0.477	C|C: 0.244
GIH	A: 0.500	C: 0.500	A|A: 0.204	A|C: 0.592	C|C: 0.204
ITU	A: 0.451	C: 0.549	A|A: 0.176	A|C: 0.549	C|C: 0.275
PJL	A: 0.552	C: 0.448	A|A: 0.354	A|C: 0.396	C|C: 0.250
STU	A: 0.490	C: 0.510	A|A: 0.255	A|C: 0.471	C|C: 0.275

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/C [2]	Ancestral: C [2]	Ambiguity code: Y [2]	MAF: 0.22 [2]

Location: 4:38819365 [2]

SNP ID: rs7696175 [1]

GWAS Trait: Breast cancer, Multiple complex diseases, Self-reported allergy, Breast Neoplasms [1,2]

Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]

Clinical Assertion Description: Not Known

Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.217	C: 0.783	T|T: 0.075	C|C: 0.641	C|T: 0.284
AFRICAN	T: 0.018	C: 0.982	T|T: 0.002	C|C: 0.965	C|T: 0.033
ACB	T: 0.036	C: 0.964	T|T: 0.000	C|C: 0.927	C|T: 0.073
ASW	T: 0.098	C: 0.902	T|T: 0.016	C|C: 0.820	C|T: 0.164
ESN	T: 0.000	C: 1.000	T|T: 0.000	C|C: 1.000	C|T: 0.000
GWD	T: 0.013	C: 0.987	T|T: 0.000	C|C: 0.973	C|T: 0.027
LWK	T: 0.010	C: 0.990	T|T: 0.000	C|C: 0.980	C|T: 0.020
MSL	T: 0.000	C: 1.000	T|T: 0.000	C|C: 1.000	C|T: 0.000
YRI	T: 0.000	C: 1.000	T|T: 0.000	C|C: 1.000	C|T: 0.000
AMERICAN	T: 0.343	C: 0.657	T|T: 0.133	C|C: 0.447	C|T: 0.421
CLM	T: 0.388	C: 0.612	T|T: 0.213	C|C: 0.436	C|T: 0.351
MXL	T: 0.406	C: 0.594	T|T: 0.141	C|C: 0.328	C|T: 0.531
PEL	T: 0.282	C: 0.718	T|T: 0.071	C|C: 0.506	C|T: 0.424
PUR	T: 0.312	C: 0.688	T|T: 0.106	C|C: 0.481	C|T: 0.413
EAST ASIAN	T: 0.152	C: 0.848	T|T: 0.024	C|C: 0.720	C|T: 0.256
CDX	T: 0.177	C: 0.823	T|T: 0.043	C|C: 0.688	C|T: 0.269
CHB	T: 0.117	C: 0.883	T|T: 0.000	C|C: 0.767	C|T: 0.233
CHS	T: 0.186	C: 0.814	T|T: 0.048	C|C: 0.676	C|T: 0.276
JPT	T: 0.087	C: 0.913	T|T: 0.000	C|C: 0.827	C|T: 0.173

KHV	T: 0.197	C: 0.803	T|T: 0.030	C|C: 0.636	C|T: 0.333
EUROPEAN	T: 0.427	C: 0.573	T|T: 0.197	C|C: 0.342	C|T: 0.461
CEU	T: 0.490	C: 0.510	T|T: 0.253	C|C: 0.273	C|T: 0.475
FIN	T: 0.434	C: 0.566	T|T: 0.222	C|C: 0.354	C|T: 0.424
GBR	T: 0.467	C: 0.533	T|T: 0.154	C|C: 0.220	C|T: 0.626
IBS	T: 0.402	C: 0.598	T|T: 0.168	C|C: 0.364	C|T: 0.467
TSI	T: 0.355	C: 0.645	T|T: 0.187	C|C: 0.477	C|T: 0.336
SOUTH ASIAN	T: 0.247	C: 0.753	T|T: 0.061	C|C: 0.566	C|T: 0.372
BEB	T: 0.279	C: 0.721	T|T: 0.093	C|C: 0.535	C|T: 0.372
GIH	T: 0.248	C: 0.752	T|T: 0.049	C|C: 0.553	C|T: 0.398
ITU	T: 0.211	C: 0.789	T|T: 0.049	C|C: 0.627	C|T: 0.324
PJL	T: 0.276	C: 0.724	T|T: 0.062	C|C: 0.510	C|T: 0.427
STU	T: 0.230	C: 0.770	T|T: 0.059	C|C: 0.598	C|T: 0.343

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/G [2]	Ancestral:G [2]	Ambiguity code: R [2]	MAF: 0.12 [2]		
Location: 4:38828729 [2]					
SNP ID: rs5743810 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.115	G: 0.885	A|A: 0.042	A|G: 0.146	G|G: 0.812
AFRICAN	A: 0.017	G: 0.983	A|A: 0.002	A|G: 0.030	G|G: 0.968
ACB	A: 0.036	G: 0.964	A|A: 0.010	A|G: 0.052	G|G: 0.938
ASW	A: 0.074	G: 0.926	A|A: 0.000	A|G: 0.148	G|G: 0.852
ESN	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
GWD	A: 0.013	G: 0.987	A|A: 0.000	A|G: 0.027	G|G: 0.973
LWK	A: 0.015	G: 0.985	A|A: 0.000	A|G: 0.030	G|G: 0.970
MSL	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
YRI	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
AMERICAN	A: 0.183	G: 0.817	A|A: 0.049	A|G: 0.268	G|G: 0.683
CLM	A: 0.255	G: 0.745	A|A: 0.096	A|G: 0.319	G|G: 0.585
MXL	A: 0.141	G: 0.859	A|A: 0.031	A|G: 0.219	G|G: 0.750
PEL	A: 0.082	G: 0.918	A|A: 0.000	A|G: 0.165	G|G: 0.835
PUR	A: 0.226	G: 0.774	A|A: 0.058	A|G: 0.337	G|G: 0.606
EAST ASIAN	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
CDX	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
CHB	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
CHS	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
JPT	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
KHV	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
EUROPEAN	A: 0.409	G: 0.591	A|A: 0.175	A|G: 0.467	G|G: 0.358
CEU	A: 0.485	G: 0.515	A|A: 0.242	A|G: 0.485	G|G: 0.273
FIN	A: 0.424	G: 0.576	A|A: 0.222	A|G: 0.404	G|G: 0.374
GBR	A: 0.451	G: 0.549	A|A: 0.143	A|G: 0.615	G|G: 0.242
IBS	A: 0.355	G: 0.645	A|A: 0.121	A|G: 0.467	G|G: 0.411
TSI	A: 0.341	G: 0.659	A|A: 0.150	A|G: 0.383	G|G: 0.467
SOUTH ASIAN	A: 0.017	G: 0.983	A|A: 0.000	A|G: 0.035	G|G: 0.965
BEB	A: 0.017	G: 0.983	A|A: 0.000	A|G: 0.035	G|G: 0.965
GIH	A: 0.029	G: 0.971	A|A: 0.000	A|G: 0.058	G|G: 0.942
ITU	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
PJL	A: 0.036	G: 0.964	A|A: 0.000	A|G: 0.073	G|G: 0.927
STU	A: 0.005	G: 0.995	A|A: 0.000	A|G: 0.010	G|G: 0.990

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles G/A [2]	Ancestral:A [2]	Ambiguity code: R [2]	MAF: 0.33 [2]		
Location: 4:38829975 [2]					
SNP ID: rs1039559 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.332	A: 0.668	G|G: 0.140	A|A: 0.475	A|G: 0.385
AFRICAN	G: 0.120	A: 0.880	G|G: 0.012	A|A: 0.772	A|G: 0.216
ACB	G: 0.135	A: 0.865	G|G: 0.021	A|A: 0.750	A|G: 0.229
ASW	G: 0.172	A: 0.828	G|G: 0.016	A|A: 0.672	A|G: 0.311
ESN	G: 0.131	A: 0.869	G|G: 0.010	A|A: 0.747	A|G: 0.242
GWD	G: 0.124	A: 0.876	G|G: 0.009	A|A: 0.761	A|G: 0.230
LWK	G: 0.061	A: 0.939	G|G: 0.000	A|A: 0.879	A|G: 0.121
MSL	G: 0.124	A: 0.876	G|G: 0.012	A|A: 0.765	A|G: 0.224
YRI	G: 0.116	A: 0.884	G|G: 0.019	A|A: 0.787	A|G: 0.194
AMERICAN	G: 0.513	A: 0.487	G|G: 0.282	A|A: 0.256	A|G: 0.461
CLM	G: 0.495	A: 0.505	G|G: 0.298	A|A: 0.309	A|G: 0.394
MXL	G: 0.602	A: 0.398	G|G: 0.328	A|A: 0.125	A|G: 0.547
PEL	G: 0.594	A: 0.406	G|G: 0.376	A|A: 0.188	A|G: 0.435
PUR	G: 0.409	A: 0.591	G|G: 0.163	A|A: 0.346	A|G: 0.490
EAST ASIAN	G: 0.272	A: 0.728	G|G: 0.085	A|A: 0.542	A|G: 0.373
CDX	G: 0.323	A: 0.677	G|G: 0.097	A|A: 0.452	A|G: 0.452
CHB	G: 0.189	A: 0.811	G|G: 0.029	A|A: 0.650	A|G: 0.320
CHS	G: 0.281	A: 0.719	G|G: 0.124	A|A: 0.562	A|G: 0.314
JPT	G: 0.245	A: 0.755	G|G: 0.067	A|A: 0.577	A|G: 0.356
KHV	G: 0.328	A: 0.672	G|G: 0.111	A|A: 0.455	A|G: 0.434
EUROPEAN	G: 0.456	A: 0.544	G|G: 0.219	A|A: 0.306	A|G: 0.475
CEU	G: 0.530	A: 0.470	G|G: 0.273	A|A: 0.212	A|G: 0.515
FIN	G: 0.455	A: 0.545	G|G: 0.242	A|A: 0.333	A|G: 0.424
GBR	G: 0.511	A: 0.489	G|G: 0.220	A|A: 0.198	A|G: 0.582
IBS	G: 0.416	A: 0.584	G|G: 0.168	A|A: 0.336	A|G: 0.495
TSI	G: 0.383	A: 0.617	G|G: 0.196	A|A: 0.430	A|G: 0.374
SOUTH ASIAN	G: 0.425	A: 0.575	G|G: 0.186	A|A: 0.335	A|G: 0.479
BEB	G: 0.442	A: 0.558	G|G: 0.209	A|A: 0.326	A|G: 0.465
GIH	G: 0.471	A: 0.529	G|G: 0.175	A|A: 0.233	A|G: 0.592
ITU	G: 0.353	A: 0.647	G|G: 0.098	A|A: 0.392	A|G: 0.510
PJL	G: 0.427	A: 0.573	G|G: 0.240	A|A: 0.385	A|G: 0.375
STU	G: 0.436	A: 0.564	G|G: 0.216	A|A: 0.343	A|G: 0.441
REFERENCES					
1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33					
2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html					

Alleles C/T [2]	Ancestral:C [2]	Ambiguity code: Y [2]	MAF: 0.18 [2]		
Location: 4:38831106 [2]					
SNP ID: rs5743794 [1]					
GWAS Trait: Suicide attempts in bipolar disorder, Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	C: 0.824	T: 0.176	C|C: 0.696	C|T: 0.256	T|T: 0.048
AFRICAN	C: 0.986	T: 0.014	C|C: 0.971	C|T: 0.029	T|T: 0.000

ACB	C: 0.969	T: 0.031	C|C: 0.938	C|T: 0.062	T|T: 0.000
ASW	C: 0.926	T: 0.074	C|C: 0.852	C|T: 0.148	T|T: 0.000
ESN	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
GWD	C: 0.991	T: 0.009	C|C: 0.982	C|T: 0.018	T|T: 0.000
LWK	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
MSL	C: 0.994	T: 0.006	C|C: 0.988	C|T: 0.012	T|T: 0.000
YRI	C: 0.995	T: 0.005	C|C: 0.991	C|T: 0.009	T|T: 0.000
AMERICAN	C: 0.840	T: 0.160	C|C: 0.715	C|T: 0.251	T|T: 0.035
CLM	C: 0.819	T: 0.181	C|C: 0.670	C|T: 0.298	T|T: 0.032
MXL	C: 0.891	T: 0.109	C|C: 0.797	C|T: 0.188	T|T: 0.016
PEL	C: 0.929	T: 0.071	C|C: 0.859	C|T: 0.141	T|T: 0.000
PUR	C: 0.755	T: 0.245	C|C: 0.587	C|T: 0.337	T|T: 0.077
EAST ASIAN	C: 0.667	T: 0.333	C|C: 0.454	C|T: 0.425	T|T: 0.121
CDX	C: 0.833	T: 0.167	C|C: 0.699	C|T: 0.269	T|T: 0.032
CHB	C: 0.534	T: 0.466	C|C: 0.282	C|T: 0.505	T|T: 0.214
CHS	C: 0.676	T: 0.324	C|C: 0.429	C|T: 0.495	T|T: 0.076
JPT	C: 0.505	T: 0.495	C|C: 0.260	C|T: 0.490	T|T: 0.250
KHV	C: 0.808	T: 0.192	C|C: 0.636	C|T: 0.343	T|T: 0.020
EUROPEAN	C: 0.771	T: 0.229	C|C: 0.606	C|T: 0.330	T|T: 0.064
CEU	C: 0.808	T: 0.192	C|C: 0.657	C|T: 0.303	T|T: 0.040
FIN	C: 0.909	T: 0.091	C|C: 0.828	C|T: 0.162	T|T: 0.010
GBR	C: 0.830	T: 0.170	C|C: 0.670	C|T: 0.319	T|T: 0.011
IBS	C: 0.673	T: 0.327	C|C: 0.458	C|T: 0.430	T|T: 0.112
TSI	C: 0.659	T: 0.341	C|C: 0.449	C|T: 0.421	T|T: 0.131
SOUTH ASIAN	C: 0.813	T: 0.187	C|C: 0.654	C|T: 0.317	T|T: 0.029
BEB	C: 0.767	T: 0.233	C|C: 0.558	C|T: 0.419	T|T: 0.023
GIH	C: 0.791	T: 0.209	C|C: 0.631	C|T: 0.320	T|T: 0.049
ITU	C: 0.843	T: 0.157	C|C: 0.706	C|T: 0.275	T|T: 0.020
PJL	C: 0.828	T: 0.172	C|C: 0.688	C|T: 0.281	T|T: 0.031
STU	C: 0.828	T: 0.172	C|C: 0.676	C|T: 0.304	T|T: 0.020

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles C/G [2]	Ancestral:G [2]	Ambiguity code: S [2]	MAF: 0.39 [2]		
Location: 4:38831586 [2]					
SNP ID: rs5743788 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	C: 0.388	G: 0.612	C|C: 0.165	C|G: 0.446	G|G: 0.389
AFRICAN	C: 0.286	G: 0.714	C|C: 0.071	C|G: 0.430	G|G: 0.499
ACB	C: 0.271	G: 0.729	C|C: 0.073	C|G: 0.396	G|G: 0.531
ASW	C: 0.287	G: 0.713	C|C: 0.049	C|G: 0.475	G|G: 0.475
ESN	C: 0.273	G: 0.727	C|C: 0.040	C|G: 0.465	G|G: 0.495
GWD	C: 0.367	G: 0.633	C|C: 0.115	C|G: 0.504	G|G: 0.381
LWK	C: 0.202	G: 0.798	C|C: 0.040	C|G: 0.323	G|G: 0.636
MSL	C: 0.276	G: 0.724	C|C: 0.059	C|G: 0.435	G|G: 0.506
YRI	C: 0.310	G: 0.690	C|C: 0.102	C|G: 0.417	G|G: 0.481
AMERICAN	C: 0.539	G: 0.461	C|C: 0.300	C|G: 0.478	G|G: 0.222
CLM	C: 0.521	G: 0.479	C|C: 0.330	C|G: 0.383	G|G: 0.287
MXL	C: 0.602	G: 0.398	C|C: 0.328	C|G: 0.547	G|G: 0.125
PEL	C: 0.612	G: 0.388	C|C: 0.400	C|G: 0.424	G|G: 0.176
PUR	C: 0.457	G: 0.543	C|C: 0.173	C|G: 0.567	G|G: 0.260
EAST ASIAN	C: 0.272	G: 0.728	C|C: 0.085	C|G: 0.373	G|G: 0.542
CDX	C: 0.323	G: 0.677	C|C: 0.097	C|G: 0.452	G|G: 0.452
CHB	C: 0.194	G: 0.806	C|C: 0.029	C|G: 0.330	G|G: 0.641
CHS	C: 0.281	G: 0.719	C|C: 0.124	C|G: 0.314	G|G: 0.562
JPT	C: 0.240	G: 0.760	C|C: 0.067	C|G: 0.346	G|G: 0.587

KHV	C: 0.328	G: 0.672	C|C: 0.111	C|G: 0.434	G|G: 0.455
EUROPEAN	C: 0.487	G: 0.513	C|C: 0.250	C|G: 0.473	G|G: 0.276
CEU	C: 0.540	G: 0.460	C|C: 0.273	C|G: 0.535	G|G: 0.192
FIN	C: 0.505	G: 0.495	C|C: 0.303	C|G: 0.404	G|G: 0.293
GBR	C: 0.533	G: 0.467	C|C: 0.264	C|G: 0.538	G|G: 0.198
IBS	C: 0.463	G: 0.537	C|C: 0.215	C|G: 0.495	G|G: 0.290
TSI	C: 0.407	G: 0.593	C|C: 0.206	C|G: 0.402	G|G: 0.393
SOUTH ASIAN	C: 0.437	G: 0.563	C|C: 0.190	C|G: 0.493	G|G: 0.317
BEB	C: 0.453	G: 0.547	C|C: 0.209	C|G: 0.488	G|G: 0.302
GIH	C: 0.476	G: 0.524	C|C: 0.175	C|G: 0.602	G|G: 0.223
ITU	C: 0.353	G: 0.647	C|C: 0.098	C|G: 0.510	G|G: 0.392
PJL	C: 0.464	G: 0.536	C|C: 0.260	C|G: 0.406	G|G: 0.333
STU	C: 0.441	G: 0.559	C|C: 0.216	C|G: 0.451	G|G: 0.333
REFERENCES					
1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33					
2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html					

Alleles G/C [2]	Ancestral:C [2]	Ambiguity code: S [2]	MAF: 0.34 [2]		
Location: 4:38842128 [2]					
SNP ID: rs7665774 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.344	C: 0.656	G|G: 0.144	C|C: 0.455	C|G: 0.401
AFRICAN	G: 0.130	C: 0.870	G|G: 0.017	C|C: 0.756	C|G: 0.227
ACB	G: 0.146	C: 0.854	G|G: 0.021	C|C: 0.729	C|G: 0.250
ASW	G: 0.164	C: 0.836	G|G: 0.016	C|C: 0.689	C|G: 0.295
ESN	G: 0.146	C: 0.854	G|G: 0.030	C|C: 0.737	C|G: 0.232
GWD	G: 0.142	C: 0.858	G|G: 0.018	C|C: 0.735	C|G: 0.248
LWK	G: 0.061	C: 0.939	G|G: 0.000	C|C: 0.879	C|G: 0.121
MSL	G: 0.135	C: 0.865	G|G: 0.012	C|C: 0.741	C|G: 0.247
YRI	G: 0.130	C: 0.870	G|G: 0.019	C|C: 0.759	C|G: 0.222
AMERICAN	G: 0.468	C: 0.532	G|G: 0.219	C|C: 0.282	C|G: 0.499
CLM	G: 0.468	C: 0.532	G|G: 0.266	C|C: 0.330	C|G: 0.404
MXL	G: 0.555	C: 0.445	G|G: 0.281	C|C: 0.172	C|G: 0.547
PEL	G: 0.518	C: 0.482	G|G: 0.235	C|C: 0.200	C|G: 0.565
PUR	G: 0.375	C: 0.625	G|G: 0.125	C|C: 0.375	C|G: 0.500
EAST ASIAN	G: 0.287	C: 0.713	G|G: 0.093	C|C: 0.520	C|G: 0.387
CDX	G: 0.371	C: 0.629	G|G: 0.129	C|C: 0.387	C|G: 0.484
CHB	G: 0.189	C: 0.811	G|G: 0.029	C|C: 0.650	C|G: 0.320
CHS	G: 0.267	C: 0.733	G|G: 0.105	C|C: 0.571	C|G: 0.324
JPT	G: 0.255	C: 0.745	G|G: 0.067	C|C: 0.558	C|G: 0.375
KHV	G: 0.364	C: 0.636	G|G: 0.141	C|C: 0.414	C|G: 0.444
EUROPEAN	G: 0.461	C: 0.539	G|G: 0.221	C|C: 0.298	C|G: 0.481
CEU	G: 0.535	C: 0.465	G|G: 0.283	C|C: 0.212	C|G: 0.505
FIN	G: 0.460	C: 0.540	G|G: 0.242	C|C: 0.323	C|G: 0.434
GBR	G: 0.522	C: 0.478	G|G: 0.220	C|C: 0.176	C|G: 0.604
IBS	G: 0.421	C: 0.579	G|G: 0.168	C|C: 0.327	C|G: 0.505
TSI	G: 0.383	C: 0.617	G|G: 0.196	C|C: 0.430	C|G: 0.374
SOUTH ASIAN	G: 0.486	C: 0.514	G|G: 0.237	C|C: 0.266	C|G: 0.497
BEB	G: 0.494	C: 0.506	G|G: 0.221	C|C: 0.233	C|G: 0.547
GIH	G: 0.563	C: 0.437	G|G: 0.272	C|C: 0.146	C|G: 0.583
ITU	G: 0.431	C: 0.569	G|G: 0.206	C|C: 0.343	C|G: 0.451
PJL	G: 0.464	C: 0.536	G|G: 0.260	C|C: 0.333	C|G: 0.406
STU	G: 0.475	C: 0.525	G|G: 0.225	C|C: 0.275	C|G: 0.500
REFERENCES					

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles G/A [2]	Ancestral:A [2]	Ambiguity code: R [2]	MAF: 0.46 [2]	
Location: 4:38843577 [2]				
SNP ID: rs7673348 [1]				
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]				
Archaic-like haplotype cluster: Not Known				
Clinical Assertion Description: Not Known				
Population	Allele Frequency [2]		Genotype Frequency [2]	
ALL	G: 0.456	A: 0.544	G|G: 0.252	A|A: 0.340	A|G: 0.408
AFRICAN	G: 0.200	A: 0.800	G|G: 0.035	A|A: 0.634	A|G: 0.331
ACB	G: 0.219	A: 0.781	G|G: 0.031	A|A: 0.594	A|G: 0.375
ASW	G: 0.238	A: 0.762	G|G: 0.115	A|A: 0.639	A|G: 0.246
ESN	G: 0.207	A: 0.793	G|G: 0.040	A|A: 0.626	A|G: 0.333
GWD	G: 0.208	A: 0.792	G|G: 0.027	A|A: 0.611	A|G: 0.363
LWK	G: 0.136	A: 0.864	G|G: 0.010	A|A: 0.737	A|G: 0.253
MSL	G: 0.182	A: 0.818	G|G: 0.012	A|A: 0.647	A|G: 0.341
YRI	G: 0.222	A: 0.778	G|G: 0.037	A|A: 0.593	A|G: 0.370
AMERICAN	G: 0.572	A: 0.428	G|G: 0.331	A|A: 0.187	A|G: 0.481
CLM	G: 0.606	A: 0.394	G|G: 0.415	A|A: 0.202	A|G: 0.383
MXL	G: 0.594	A: 0.406	G|G: 0.344	A|A: 0.156	A|G: 0.500
PEL	G: 0.559	A: 0.441	G|G: 0.282	A|A: 0.165	A|G: 0.553
PUR	G: 0.538	A: 0.462	G|G: 0.288	A|A: 0.212	A|G: 0.500
EAST ASIAN	G: 0.312	A: 0.688	G|G: 0.099	A|A: 0.474	A|G: 0.427
CDX	G: 0.398	A: 0.602	G|G: 0.140	A|A: 0.344	A|G: 0.516
CHB	G: 0.252	A: 0.748	G|G: 0.049	A|A: 0.544	A|G: 0.408
CHS	G: 0.300	A: 0.700	G|G: 0.105	A|A: 0.505	A|G: 0.390
JPT	G: 0.260	A: 0.740	G|G: 0.067	A|A: 0.548	A|G: 0.385
KHV	G: 0.364	A: 0.636	G|G: 0.141	A|A: 0.414	A|G: 0.444
EUROPEAN	G: 0.735	A: 0.265	G|G: 0.559	A|A: 0.089	A|G: 0.352
CEU	G: 0.798	A: 0.202	G|G: 0.636	A|A: 0.040	A|G: 0.323
FIN	G: 0.884	A: 0.116	G|G: 0.788	A|A: 0.020	A|G: 0.192
GBR	G: 0.824	A: 0.176	G|G: 0.659	A|A: 0.011	A|G: 0.330
IBS	G: 0.593	A: 0.407	G|G: 0.355	A|A: 0.168	A|G: 0.477
TSI	G: 0.603	A: 0.397	G|G: 0.393	A|A: 0.187	A|G: 0.421
SOUTH ASIAN	G: 0.579	A: 0.421	G|G: 0.329	A|A: 0.172	A|G: 0.499
BEB	G: 0.570	A: 0.430	G|G: 0.279	A|A: 0.140	A|G: 0.581
GIH	G: 0.626	A: 0.374	G|G: 0.350	A|A: 0.097	A|G: 0.553
ITU	G: 0.544	A: 0.456	G|G: 0.314	A|A: 0.225	A|G: 0.461
PJL	G: 0.604	A: 0.396	G|G: 0.396	A|A: 0.188	A|G: 0.417
STU	G: 0.549	A: 0.451	G|G: 0.304	A|A: 0.206	A|G: 0.490
REFERENCES				
1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33				
2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html				

Alleles C/G [2]	Ancestral:G [2]	Ambiguity code: S [2]	MAF: 0.49 [2]
Location: 4:38845358 [2]			
SNP ID: rs7687447 [1]			
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]			
Archaic-like haplotype cluster: Not Known			
Clinical Assertion Description: Not Known			
Population	Allele Frequency [2]		Genotype Frequency [2]

ALL	C: 0.489	G: 0.511	C|C: 0.274	C|G: 0.430	G|G: 0.296
AFRICAN	C: 0.272	G: 0.728	C|C: 0.071	C|G: 0.402	G|G: 0.526
ACB	C: 0.318	G: 0.682	C|C: 0.094	C|G: 0.448	G|G: 0.458
ASW	C: 0.295	G: 0.705	C|C: 0.131	C|G: 0.328	G|G: 0.541
ESN	C: 0.268	G: 0.732	C|C: 0.081	C|G: 0.374	G|G: 0.545
GWD	C: 0.265	G: 0.735	C|C: 0.053	C|G: 0.425	G|G: 0.522
LWK	C: 0.232	G: 0.768	C|C: 0.061	C|G: 0.343	G|G: 0.596
MSL	C: 0.259	G: 0.741	C|C: 0.035	C|G: 0.447	G|G: 0.518
YRI	C: 0.278	G: 0.722	C|C: 0.065	C|G: 0.426	G|G: 0.509
AMERICAN	C: 0.575	G: 0.425	C|C: 0.334	C|G: 0.481	G|G: 0.184
CLM	C: 0.612	G: 0.388	C|C: 0.415	C|G: 0.394	G|G: 0.191
MXL	C: 0.594	G: 0.406	C|C: 0.344	C|G: 0.500	G|G: 0.156
PEL	C: 0.559	G: 0.441	C|C: 0.282	C|G: 0.553	G|G: 0.165
PUR	C: 0.543	G: 0.457	C|C: 0.298	C|G: 0.490	G|G: 0.212
EAST ASIAN	C: 0.367	G: 0.633	C|C: 0.141	C|G: 0.452	G|G: 0.407
CDX	C: 0.462	G: 0.538	C|C: 0.204	C|G: 0.516	G|G: 0.280
CHB	C: 0.335	G: 0.665	C|C: 0.107	C|G: 0.456	G|G: 0.437
CHS	C: 0.333	G: 0.667	C|C: 0.124	C|G: 0.419	G|G: 0.457
JPT	C: 0.279	G: 0.721	C|C: 0.087	C|G: 0.385	G|G: 0.529
KHV	C: 0.439	G: 0.561	C|C: 0.192	C|G: 0.495	G|G: 0.313
EUROPEAN	C: 0.736	G: 0.264	C|C: 0.561	C|G: 0.350	G|G: 0.089
CEU	C: 0.798	G: 0.202	C|C: 0.636	C|G: 0.323	G|G: 0.040
FIN	C: 0.884	G: 0.116	C|C: 0.788	C|G: 0.192	G|G: 0.020
GBR	C: 0.824	G: 0.176	C|C: 0.659	C|G: 0.330	G|G: 0.011
IBS	C: 0.598	G: 0.402	C|C: 0.364	C|G: 0.467	G|G: 0.168
TSI	C: 0.603	G: 0.397	C|C: 0.393	C|G: 0.421	G|G: 0.187
SOUTH ASIAN	C: 0.592	G: 0.408	C|C: 0.348	C|G: 0.489	G|G: 0.164
BEB	C: 0.587	G: 0.413	C|C: 0.302	C|G: 0.570	G|G: 0.128
GIH	C: 0.631	G: 0.369	C|C: 0.359	C|G: 0.544	G|G: 0.097
ITU	C: 0.564	G: 0.436	C|C: 0.333	C|G: 0.461	G|G: 0.206
PJL	C: 0.615	G: 0.385	C|C: 0.417	C|G: 0.396	G|G: 0.188
STU	C: 0.564	G: 0.436	C|C: 0.324	C|G: 0.480	G|G: 0.196

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/C [2]	Ancestral:C [2]	Ambiguity code: Y [2]	MAF: 0.33 [2]		
Location: 4:38845390 [2]					
SNP ID: rs6531672 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.331	C: 0.669	T|T: 0.133	C|C: 0.470	C|T: 0.397
AFRICAN	T: 0.120	C: 0.880	T|T: 0.012	C|C: 0.772	C|T: 0.216
ACB	T: 0.135	C: 0.865	T|T: 0.021	C|C: 0.750	C|T: 0.229
ASW	T: 0.164	C: 0.836	T|T: 0.016	C|C: 0.689	C|T: 0.295
ESN	T: 0.136	C: 0.864	T|T: 0.010	C|C: 0.737	C|T: 0.253
GWD	T: 0.124	C: 0.876	T|T: 0.009	C|C: 0.761	C|T: 0.230
LWK	T: 0.061	C: 0.939	T|T: 0.000	C|C: 0.879	C|T: 0.121
MSL	T: 0.124	C: 0.876	T|T: 0.012	C|C: 0.765	C|T: 0.224
YRI	T: 0.116	C: 0.884	T|T: 0.019	C|C: 0.787	C|T: 0.194
AMERICAN	T: 0.463	C: 0.537	T|T: 0.210	C|C: 0.285	C|T: 0.504
CLM	T: 0.463	C: 0.537	T|T: 0.255	C|C: 0.330	C|T: 0.415
MXL	T: 0.539	C: 0.461	T|T: 0.266	C|C: 0.188	C|T: 0.547
PEL	T: 0.512	C: 0.488	T|T: 0.224	C|C: 0.200	C|T: 0.576
PUR	T: 0.375	C: 0.625	T|T: 0.125	C|C: 0.375	C|T: 0.500

EAST ASIAN	T: 0.287	C: 0.713	T|T: 0.091	C|C: 0.518	C|T: 0.391
CDX	T: 0.366	C: 0.634	T|T: 0.129	C|C: 0.398	C|T: 0.473
CHB	T: 0.209	C: 0.791	T|T: 0.039	C|C: 0.621	C|T: 0.340
CHS	T: 0.281	C: 0.719	T|T: 0.105	C|C: 0.543	C|T: 0.352
JPT	T: 0.240	C: 0.760	T|T: 0.058	C|C: 0.577	C|T: 0.365
KHV	T: 0.348	C: 0.652	T|T: 0.131	C|C: 0.434	C|T: 0.434
EUROPEAN	T: 0.458	C: 0.542	T|T: 0.221	C|C: 0.304	C|T: 0.475
CEU	T: 0.535	C: 0.465	T|T: 0.283	C|C: 0.212	C|T: 0.505
FIN	T: 0.460	C: 0.540	T|T: 0.242	C|C: 0.323	C|T: 0.434
GBR	T: 0.511	C: 0.489	T|T: 0.220	C|C: 0.198	C|T: 0.582
IBS	T: 0.421	C: 0.579	T|T: 0.168	C|C: 0.327	C|T: 0.505
TSI	T: 0.379	C: 0.621	T|T: 0.196	C|C: 0.439	C|T: 0.364
SOUTH ASIAN	T: 0.439	C: 0.561	T|T: 0.194	C|C: 0.317	C|T: 0.489
BEB	T: 0.436	C: 0.564	T|T: 0.198	C|C: 0.326	C|T: 0.477
GIH	T: 0.515	C: 0.485	T|T: 0.214	C|C: 0.184	C|T: 0.602
ITU	T: 0.363	C: 0.637	T|T: 0.118	C|C: 0.392	C|T: 0.490
PJL	T: 0.432	C: 0.568	T|T: 0.229	C|C: 0.365	C|T: 0.406
STU	T: 0.446	C: 0.554	T|T: 0.216	C|C: 0.324	C|T: 0.461

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/C [2]	Ancestral:C [2]	Ambiguity code: Y [2]	MAF: 0.36 [2]		
Location: 4:38846296 [2]					
SNP ID: rs6531673 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.359	C: 0.641	T|T: 0.153	C|C: 0.434	C|T: 0.413
AFRICAN	T: 0.139	C: 0.861	T|T: 0.017	C|C: 0.738	C|T: 0.245
ACB	T: 0.156	C: 0.844	T|T: 0.021	C|C: 0.708	C|T: 0.271
ASW	T: 0.164	C: 0.836	T|T: 0.016	C|C: 0.689	C|T: 0.295
ESN	T: 0.157	C: 0.843	T|T: 0.030	C|C: 0.717	C|T: 0.253
GWD	T: 0.142	C: 0.858	T|T: 0.018	C|C: 0.735	C|T: 0.248
LWK	T: 0.091	C: 0.909	T|T: 0.000	C|C: 0.818	C|T: 0.182
MSL	T: 0.135	C: 0.865	T|T: 0.012	C|C: 0.741	C|T: 0.247
YRI	T: 0.139	C: 0.861	T|T: 0.019	C|C: 0.741	C|T: 0.241
AMERICAN	T: 0.480	C: 0.520	T|T: 0.225	C|C: 0.265	C|T: 0.510
CLM	T: 0.484	C: 0.516	T|T: 0.287	C|C: 0.319	C|T: 0.394
MXL	T: 0.555	C: 0.445	T|T: 0.281	C|C: 0.172	C|T: 0.547
PEL	T: 0.524	C: 0.476	T|T: 0.235	C|C: 0.188	C|T: 0.576
PUR	T: 0.394	C: 0.606	T|T: 0.125	C|C: 0.337	C|T: 0.538
EAST ASIAN	T: 0.303	C: 0.697	T|T: 0.099	C|C: 0.494	C|T: 0.407
CDX	T: 0.398	C: 0.602	T|T: 0.140	C|C: 0.344	C|T: 0.516
CHB	T: 0.223	C: 0.777	T|T: 0.049	C|C: 0.602	C|T: 0.350
CHS	T: 0.286	C: 0.714	T|T: 0.105	C|C: 0.533	C|T: 0.362
JPT	T: 0.255	C: 0.745	T|T: 0.067	C|C: 0.558	C|T: 0.375
KHV	T: 0.364	C: 0.636	T|T: 0.141	C|C: 0.414	C|T: 0.444
EUROPEAN	T: 0.490	C: 0.510	T|T: 0.252	C|C: 0.272	C|T: 0.475
CEU	T: 0.545	C: 0.455	T|T: 0.283	C|C: 0.192	C|T: 0.525
FIN	T: 0.510	C: 0.490	T|T: 0.303	C|C: 0.283	C|T: 0.414
GBR	T: 0.544	C: 0.456	T|T: 0.264	C|C: 0.176	C|T: 0.560
IBS	T: 0.463	C: 0.537	T|T: 0.215	C|C: 0.290	C|T: 0.495
TSI	T: 0.402	C: 0.598	T|T: 0.206	C|C: 0.402	C|T: 0.393
SOUTH ASIAN	T: 0.496	C: 0.504	T|T: 0.239	C|C: 0.247	C|T: 0.513
BEB	T: 0.506	C: 0.494	T|T: 0.221	C|C: 0.209	C|T: 0.570
GIH	T: 0.563	C: 0.437	T|T: 0.262	C|C: 0.136	C|T: 0.602

ITU	T: 0.431	C: 0.569	T|T: 0.206	C|C: 0.343	C|T: 0.451
PJL	T: 0.500	C: 0.500	T|T: 0.281	C|C: 0.281	C|T: 0.438
STU	T: 0.480	C: 0.520	T|T: 0.225	C|C: 0.265	C|T: 0.510
REFERENCES					
1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33					
2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html					

Alleles G/A [2]	Ancestral:A [2]	Ambiguity code: R [2]	MAF: 0.36 [2]		
Location: 4:38854763 [2]					
SNP ID: rs7681628 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.362	A: 0.638	G|G: 0.154	A|A: 0.431	A|G: 0.415
AFRICAN	G: 0.150	A: 0.850	G|G: 0.020	A|A: 0.720	A|G: 0.260
ACB	G: 0.172	A: 0.828	G|G: 0.021	A|A: 0.677	A|G: 0.302
ASW	G: 0.164	A: 0.836	G|G: 0.016	A|A: 0.689	A|G: 0.295
ESN	G: 0.167	A: 0.833	G|G: 0.030	A|A: 0.697	A|G: 0.273
GWD	G: 0.146	A: 0.854	G|G: 0.018	A|A: 0.726	A|G: 0.257
LWK	G: 0.096	A: 0.904	G|G: 0.000	A|A: 0.808	A|G: 0.192
MSL	G: 0.159	A: 0.841	G|G: 0.024	A|A: 0.706	A|G: 0.271
YRI	G: 0.153	A: 0.847	G|G: 0.028	A|A: 0.722	A|G: 0.250
AMERICAN	G: 0.480	A: 0.520	G|G: 0.225	A|A: 0.265	A|G: 0.510
CLM	G: 0.484	A: 0.516	G|G: 0.287	A|A: 0.319	A|G: 0.394
MXL	G: 0.555	A: 0.445	G|G: 0.281	A|A: 0.172	A|G: 0.547
PEL	G: 0.524	A: 0.476	G|G: 0.235	A|A: 0.188	A|G: 0.576
PUR	G: 0.394	A: 0.606	G|G: 0.125	A|A: 0.337	A|G: 0.538
EAST ASIAN	G: 0.303	A: 0.697	G|G: 0.099	A|A: 0.494	A|G: 0.407
CDX	G: 0.398	A: 0.602	G|G: 0.140	A|A: 0.344	A|G: 0.516
CHB	G: 0.223	A: 0.777	G|G: 0.049	A|A: 0.602	A|G: 0.350
CHS	G: 0.286	A: 0.714	G|G: 0.105	A|A: 0.533	A|G: 0.362
JPT	G: 0.255	A: 0.745	G|G: 0.067	A|A: 0.558	A|G: 0.375
KHV	G: 0.364	A: 0.636	G|G: 0.141	A|A: 0.414	A|G: 0.444
EUROPEAN	G: 0.489	A: 0.511	G|G: 0.254	A|A: 0.276	A|G: 0.469
CEU	G: 0.545	A: 0.455	G|G: 0.283	A|A: 0.192	A|G: 0.525
FIN	G: 0.505	A: 0.495	G|G: 0.303	A|A: 0.293	A|G: 0.404
GBR	G: 0.544	A: 0.456	G|G: 0.264	A|A: 0.176	A|G: 0.560
IBS	G: 0.467	A: 0.533	G|G: 0.224	A|A: 0.290	A|G: 0.486
TSI	G: 0.397	A: 0.603	G|G: 0.206	A|A: 0.411	A|G: 0.383
SOUTH ASIAN	G: 0.494	A: 0.506	G|G: 0.239	A|A: 0.252	A|G: 0.509
BEB	G: 0.494	A: 0.506	G|G: 0.221	A|A: 0.233	A|G: 0.547
GIH	G: 0.563	A: 0.437	G|G: 0.262	A|A: 0.136	A|G: 0.602
ITU	G: 0.431	A: 0.569	G|G: 0.206	A|A: 0.343	A|G: 0.451
PJL	G: 0.500	A: 0.500	G|G: 0.281	A|A: 0.281	A|G: 0.438
STU	G: 0.480	A: 0.520	G|G: 0.225	A|A: 0.265	A|G: 0.510
REFERENCES					
1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33					
2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html					

Alleles C/T [2]	Ancestral:G [2]	Ambiguity code: Y [2]	MAF: 0.16 [2]		
Location: 4:38857718 [2]					
SNP ID: rs2174284 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	C: 0.839	T: 0.161	C|C: 0.720	C|T: 0.238	T|T: 0.042
AFRICAN	C: 0.989	T: 0.011	C|C: 0.977	C|T: 0.023	T|T: 0.000
ACB	C: 0.974	T: 0.026	C|C: 0.948	C|T: 0.052	T|T: 0.000
ASW	C: 0.934	T: 0.066	C|C: 0.869	C|T: 0.131	T|T: 0.000
ESN	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
GWD	C: 0.991	T: 0.009	C|C: 0.982	C|T: 0.018	T|T: 0.000
LWK	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
MSL	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
YRI	C: 1.000	T: 0.000	C|C: 1.000	C|T: 0.000	T|T: 0.000
AMERICAN	C: 0.840	T: 0.160	C|C: 0.718	C|T: 0.245	T|T: 0.037
CLM	C: 0.824	T: 0.176	C|C: 0.681	C|T: 0.287	T|T: 0.032
MXL	C: 0.891	T: 0.109	C|C: 0.797	C|T: 0.188	T|T: 0.016
PEL	C: 0.929	T: 0.071	C|C: 0.859	C|T: 0.141	T|T: 0.000
PUR	C: 0.750	T: 0.250	C|C: 0.587	C|T: 0.327	T|T: 0.087
EAST ASIAN	C: 0.728	T: 0.272	C|C: 0.546	C|T: 0.365	T|T: 0.089
CDX	C: 0.892	T: 0.108	C|C: 0.796	C|T: 0.194	T|T: 0.011
CHB	C: 0.621	T: 0.379	C|C: 0.379	C|T: 0.485	T|T: 0.136
CHS	C: 0.724	T: 0.276	C|C: 0.505	C|T: 0.438	T|T: 0.057
JPT	C: 0.538	T: 0.462	C|C: 0.298	C|T: 0.481	T|T: 0.221
KHV	C: 0.889	T: 0.111	C|C: 0.788	C|T: 0.202	T|T: 0.010
EUROPEAN	C: 0.770	T: 0.230	C|C: 0.606	C|T: 0.328	T|T: 0.066
CEU	C: 0.813	T: 0.187	C|C: 0.667	C|T: 0.293	T|T: 0.040
FIN	C: 0.909	T: 0.091	C|C: 0.828	C|T: 0.162	T|T: 0.010
GBR	C: 0.830	T: 0.170	C|C: 0.670	C|T: 0.319	T|T: 0.011
IBS	C: 0.678	T: 0.322	C|C: 0.458	C|T: 0.439	T|T: 0.103
TSI	C: 0.645	T: 0.355	C|C: 0.439	C|T: 0.411	T|T: 0.150
SOUTH ASIAN	C: 0.822	T: 0.178	C|C: 0.671	C|T: 0.303	T|T: 0.027
BEB	C: 0.779	T: 0.221	C|C: 0.581	C|T: 0.395	T|T: 0.023
GIH	C: 0.796	T: 0.204	C|C: 0.641	C|T: 0.311	T|T: 0.049
ITU	C: 0.858	T: 0.142	C|C: 0.735	C|T: 0.245	T|T: 0.020
PJL	C: 0.833	T: 0.167	C|C: 0.698	C|T: 0.271	T|T: 0.031
STU	C: 0.838	T: 0.162	C|C: 0.686	C|T: 0.304	T|T: 0.010
REFERENCES					
1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33					
2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html					

Alleles A/C [2]	Ancestral:A [2]	Ambiguity code: M [2]	MAF: 0.46 [2]		
Location: 4:38860500 [2]					
SNP ID: rs3860069 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.543	C: 0.457	A|A: 0.313	A|C: 0.458	C|C: 0.228
AFRICAN	A: 0.393	C: 0.607	A|A: 0.151	A|C: 0.483	C|C: 0.366
ACB	A: 0.422	C: 0.578	A|A: 0.188	A|C: 0.469	C|C: 0.344
ASW	A: 0.467	C: 0.533	A|A: 0.246	A|C: 0.443	C|C: 0.311
ESN	A: 0.379	C: 0.621	A|A: 0.141	A|C: 0.475	C|C: 0.384
GWD	A: 0.354	C: 0.646	A|A: 0.124	A|C: 0.460	C|C: 0.416
LWK	A: 0.414	C: 0.586	A|A: 0.162	A|C: 0.505	C|C: 0.333
MSL	A: 0.394	C: 0.606	A|A: 0.165	A|C: 0.459	C|C: 0.376

YRI	A: 0.356	C: 0.644	A|A: 0.083	A|C: 0.546	C|C: 0.370
AMERICAN	A: 0.588	C: 0.412	A|A: 0.354	A|C: 0.467	C|C: 0.179
CLM	A: 0.617	C: 0.383	A|A: 0.426	A|C: 0.383	C|C: 0.191
MXL	A: 0.602	C: 0.398	A|A: 0.359	A|C: 0.484	C|C: 0.156
PEL	A: 0.571	C: 0.429	A|A: 0.294	A|C: 0.553	C|C: 0.153
PUR	A: 0.567	C: 0.433	A|A: 0.337	A|C: 0.462	C|C: 0.202
EAST ASIAN	A: 0.446	C: 0.554	A|A: 0.196	A|C: 0.500	C|C: 0.304
CDX	A: 0.548	C: 0.452	A|A: 0.280	A|C: 0.538	C|C: 0.183
CHB	A: 0.379	C: 0.621	A|A: 0.136	A|C: 0.485	C|C: 0.379
CHS	A: 0.433	C: 0.567	A|A: 0.190	A|C: 0.486	C|C: 0.324
JPT	A: 0.346	C: 0.654	A|A: 0.135	A|C: 0.423	C|C: 0.442
KHV	A: 0.540	C: 0.460	A|A: 0.253	A|C: 0.576	C|C: 0.172
EUROPEAN	A: 0.736	C: 0.264	A|A: 0.563	A|C: 0.346	C|C: 0.091
CEU	A: 0.798	C: 0.202	A|A: 0.636	A|C: 0.323	C|C: 0.040
FIN	A: 0.884	C: 0.116	A|A: 0.788	A|C: 0.192	C|C: 0.020
GBR	A: 0.830	C: 0.170	A|A: 0.670	A|C: 0.319	C|C: 0.011
IBS	A: 0.593	C: 0.407	A|A: 0.364	A|C: 0.458	C|C: 0.178
TSI	A: 0.603	C: 0.397	A|A: 0.393	A|C: 0.421	C|C: 0.187
SOUTH ASIAN	A: 0.615	C: 0.385	A|A: 0.368	A|C: 0.493	C|C: 0.139
BEB	A: 0.593	C: 0.407	A|A: 0.314	A|C: 0.558	C|C: 0.128
GIH	A: 0.646	C: 0.354	A|A: 0.388	A|C: 0.515	C|C: 0.097
ITU	A: 0.593	C: 0.407	A|A: 0.333	A|C: 0.520	C|C: 0.147
PJL	A: 0.646	C: 0.354	A|A: 0.438	A|C: 0.417	C|C: 0.146
STU	A: 0.593	C: 0.407	A|A: 0.363	A|C: 0.461	C|C: 0.176

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/G [2]	Ancestral:A [2]	Ambiguity code: R [2]	MAF: 0.21 [2]		
Location: 4:38865806 [2]					
SNP ID: rs17582830 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.794	G: 0.206	A|A: 0.645	A|G: 0.300	G|G: 0.056
AFRICAN	A: 0.923	G: 0.077	A|A: 0.850	A|G: 0.145	G|G: 0.005
ACB	A: 0.880	G: 0.120	A|A: 0.781	A|G: 0.198	G|G: 0.021
ASW	A: 0.885	G: 0.115	A|A: 0.770	A|G: 0.230	G|G: 0.000
ESN	A: 0.934	G: 0.066	A|A: 0.869	A|G: 0.131	G|G: 0.000
GWD	A: 0.960	G: 0.040	A|A: 0.920	A|G: 0.080	G|G: 0.000
LWK	A: 0.874	G: 0.126	A|A: 0.747	A|G: 0.253	G|G: 0.000
MSL	A: 0.947	G: 0.053	A|A: 0.894	A|G: 0.106	G|G: 0.000
YRI	A: 0.958	G: 0.042	A|A: 0.926	A|G: 0.065	G|G: 0.009
AMERICAN	A: 0.820	G: 0.180	A|A: 0.686	A|G: 0.268	G|G: 0.046
CLM	A: 0.798	G: 0.202	A|A: 0.638	A|G: 0.319	G|G: 0.043
MXL	A: 0.875	G: 0.125	A|A: 0.766	A|G: 0.219	G|G: 0.016
PEL	A: 0.912	G: 0.088	A|A: 0.824	A|G: 0.176	G|G: 0.000
PUR	A: 0.731	G: 0.269	A|A: 0.567	A|G: 0.327	G|G: 0.106
EAST ASIAN	A: 0.661	G: 0.339	A|A: 0.437	A|G: 0.448	G|G: 0.115
CDX	A: 0.801	G: 0.199	A|A: 0.634	A|G: 0.333	G|G: 0.032
CHB	A: 0.534	G: 0.466	A|A: 0.272	A|G: 0.524	G|G: 0.204
CHS	A: 0.681	G: 0.319	A|A: 0.438	A|G: 0.486	G|G: 0.076
JPT	A: 0.510	G: 0.490	A|A: 0.250	A|G: 0.519	G|G: 0.231
KHV	A: 0.798	G: 0.202	A|A: 0.616	A|G: 0.364	G|G: 0.020
EUROPEAN	A: 0.766	G: 0.234	A|A: 0.604	A|G: 0.324	G|G: 0.072
CEU	A: 0.813	G: 0.187	A|A: 0.667	A|G: 0.293	G|G: 0.040
FIN	A: 0.909	G: 0.091	A|A: 0.828	A|G: 0.162	G|G: 0.010

GBR	A: 0.813	G: 0.187	A|A: 0.648	A|G: 0.330	G|G: 0.022
IBS	A: 0.678	G: 0.322	A|A: 0.458	A|G: 0.439	G|G: 0.103
TSI	A: 0.640	G: 0.360	A|A: 0.449	A|G: 0.383	G|G: 0.168
SOUTH ASIAN	A: 0.769	G: 0.231	A|A: 0.593	A|G: 0.352	G|G: 0.055
BEB	A: 0.709	G: 0.291	A|A: 0.500	A|G: 0.419	G|G: 0.081
GIH	A: 0.752	G: 0.248	A|A: 0.573	A|G: 0.359	G|G: 0.068
ITU	A: 0.775	G: 0.225	A|A: 0.598	A|G: 0.353	G|G: 0.049
PJL	A: 0.807	G: 0.193	A|A: 0.656	A|G: 0.302	G|G: 0.042
STU	A: 0.794	G: 0.206	A|A: 0.627	A|G: 0.333	G|G: 0.039

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/G [2]	Ancestral:G [2]	Ambiguity code: R [2]	MAF: 0.20 [2]		
Location: 4:38873181 [2]					
SNP ID: rs2130296 [1]					
GWAS Trait: Multiple complex diseases [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.796	G: 0.204	A|A: 0.658	A|G: 0.275	G|G: 0.067
AFRICAN	A: 0.603	G: 0.397	A|A: 0.366	A|G: 0.474	G|G: 0.160
ACB	A: 0.583	G: 0.417	A|A: 0.375	A|G: 0.417	G|G: 0.208
ASW	A: 0.615	G: 0.385	A|A: 0.361	A|G: 0.508	G|G: 0.131
ESN	A: 0.646	G: 0.354	A|A: 0.374	A|G: 0.545	G|G: 0.081
GWD	A: 0.575	G: 0.425	A|A: 0.336	A|G: 0.478	G|G: 0.186
LWK	A: 0.616	G: 0.384	A|A: 0.394	A|G: 0.444	G|G: 0.162
MSL	A: 0.629	G: 0.371	A|A: 0.400	A|G: 0.459	G|G: 0.141
YRI	A: 0.569	G: 0.431	A|A: 0.333	A|G: 0.472	G|G: 0.194
AMERICAN	A: 0.862	G: 0.138	A|A: 0.744	A|G: 0.236	G|G: 0.020
CLM	A: 0.819	G: 0.181	A|A: 0.660	A|G: 0.319	G|G: 0.021
MXL	A: 0.945	G: 0.055	A|A: 0.891	A|G: 0.109	G|G: 0.000
PEL	A: 0.935	G: 0.065	A|A: 0.871	A|G: 0.129	G|G: 0.000
PUR	A: 0.788	G: 0.212	A|A: 0.625	A|G: 0.327	G|G: 0.048
EAST ASIAN	A: 0.986	G: 0.014	A|A: 0.972	A|G: 0.028	G|G: 0.000
CDX	A: 0.995	G: 0.005	A|A: 0.989	A|G: 0.011	G|G: 0.000
CHB	A: 0.966	G: 0.034	A|A: 0.932	A|G: 0.068	G|G: 0.000
CHS	A: 0.990	G: 0.010	A|A: 0.981	A|G: 0.019	G|G: 0.000
JPT	A: 0.995	G: 0.005	A|A: 0.990	A|G: 0.010	G|G: 0.000
KHV	A: 0.985	G: 0.015	A|A: 0.970	A|G: 0.030	G|G: 0.000
EUROPEAN	A: 0.726	G: 0.274	A|A: 0.545	A|G: 0.362	G|G: 0.093
CEU	A: 0.737	G: 0.263	A|A: 0.545	A|G: 0.384	G|G: 0.071
FIN	A: 0.581	G: 0.419	A|A: 0.354	A|G: 0.455	G|G: 0.192
GBR	A: 0.698	G: 0.302	A|A: 0.495	A|G: 0.407	G|G: 0.099
IBS	A: 0.827	G: 0.173	A|A: 0.692	A|G: 0.271	G|G: 0.037
TSI	A: 0.771	G: 0.229	A|A: 0.617	A|G: 0.308	G|G: 0.075
SOUTH ASIAN	A: 0.885	G: 0.115	A|A: 0.785	A|G: 0.200	G|G: 0.014
BEB	A: 0.907	G: 0.093	A|A: 0.814	A|G: 0.186	G|G: 0.000
GIH	A: 0.913	G: 0.087	A|A: 0.825	A|G: 0.175	G|G: 0.000
ITU	A: 0.858	G: 0.142	A|A: 0.735	A|G: 0.245	G|G: 0.020
PJL	A: 0.849	G: 0.151	A|A: 0.750	A|G: 0.198	G|G: 0.052
STU	A: 0.902	G: 0.098	A|A: 0.804	A|G: 0.196	G|G: 0.000

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/C [2]	Ancestral:C [2]	Ambiguity code: Y [2]	MAF: 0.45 [2]		
Location: 4:38876573 [2]					
SNP ID: rs721653 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.552	C: 0.448	T|T: 0.313	C|C: 0.209	C|T: 0.478
AFRICAN	T: 0.491	C: 0.509	T|T: 0.238	C|C: 0.256	C|T: 0.507
ACB	T: 0.464	C: 0.536	T|T: 0.250	C|C: 0.323	C|T: 0.427
ASW	T: 0.410	C: 0.590	T|T: 0.115	C|C: 0.295	C|T: 0.590
ESN	T: 0.566	C: 0.434	T|T: 0.313	C|C: 0.182	C|T: 0.505
GWD	T: 0.518	C: 0.482	T|T: 0.248	C|C: 0.212	C|T: 0.540
LWK	T: 0.424	C: 0.576	T|T: 0.152	C|C: 0.303	C|T: 0.545
MSL	T: 0.524	C: 0.476	T|T: 0.306	C|C: 0.259	C|T: 0.435
YRI	T: 0.500	C: 0.500	T|T: 0.241	C|C: 0.241	C|T: 0.519
AMERICAN	T: 0.599	C: 0.401	T|T: 0.378	C|C: 0.179	C|T: 0.444
CLM	T: 0.569	C: 0.431	T|T: 0.287	C|C: 0.149	C|T: 0.564
MXL	T: 0.641	C: 0.359	T|T: 0.438	C|C: 0.156	C|T: 0.406
PEL	T: 0.700	C: 0.300	T|T: 0.529	C|C: 0.129	C|T: 0.341
PUR	T: 0.519	C: 0.481	T|T: 0.298	C|C: 0.260	C|T: 0.442
EAST ASIAN	T: 0.574	C: 0.426	T|T: 0.345	C|C: 0.196	C|T: 0.458
CDX	T: 0.710	C: 0.290	T|T: 0.484	C|C: 0.065	C|T: 0.452
CHB	T: 0.456	C: 0.544	T|T: 0.204	C|C: 0.291	C|T: 0.505
CHS	T: 0.581	C: 0.419	T|T: 0.362	C|C: 0.200	C|T: 0.438
JPT	T: 0.447	C: 0.553	T|T: 0.212	C|C: 0.317	C|T: 0.471
KHV	T: 0.697	C: 0.303	T|T: 0.485	C|C: 0.091	C|T: 0.424
EUROPEAN	T: 0.490	C: 0.510	T|T: 0.249	C|C: 0.268	C|T: 0.483
CEU	T: 0.551	C: 0.449	T|T: 0.303	C|C: 0.202	C|T: 0.495
FIN	T: 0.485	C: 0.515	T|T: 0.253	C|C: 0.283	C|T: 0.465
GBR	T: 0.511	C: 0.489	T|T: 0.220	C|C: 0.198	C|T: 0.582
IBS	T: 0.505	C: 0.495	T|T: 0.234	C|C: 0.224	C|T: 0.542
TSI	T: 0.407	C: 0.593	T|T: 0.234	C|C: 0.421	C|T: 0.346
SOUTH ASIAN	T: 0.642	C: 0.358	T|T: 0.403	C|C: 0.119	C|T: 0.479
BEB	T: 0.605	C: 0.395	T|T: 0.360	C|C: 0.151	C|T: 0.488
GIH	T: 0.660	C: 0.340	T|T: 0.437	C|C: 0.117	C|T: 0.447
ITU	T: 0.632	C: 0.368	T|T: 0.392	C|C: 0.127	C|T: 0.480
PJL	T: 0.620	C: 0.380	T|T: 0.375	C|C: 0.135	C|T: 0.490
STU	T: 0.686	C: 0.314	T|T: 0.441	C|C: 0.069	C|T: 0.490
REFERENCES					
1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33					
2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html					

Alleles C/A/G [2]	Ancestral:A [2]	Ambiguity code: V [2]	MAF: 0.45 [2]		
Location: 4:38878692 [2]					
SNP ID: rs902136 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	C: 0.555	A: 0.445	C|C: 0.314	A|A: 0.204	A|C: 0.482
AFRICAN	C: 0.467	A: 0.533	C|C: 0.209	A|A: 0.275	A|C: 0.516
ACB	C: 0.458	A: 0.542	C|C: 0.229	A|A: 0.312	A|C: 0.458
ASW	C: 0.402	A: 0.598	C|C: 0.115	A|A: 0.311	A|C: 0.574
ESN	C: 0.551	A: 0.449	C|C: 0.293	A|A: 0.192	A|C: 0.515
GWD	C: 0.509	A: 0.491	C|C: 0.239	A|A: 0.221	A|C: 0.540
LWK	C: 0.343	A: 0.657	C|C: 0.081	A|A: 0.394	A|C: 0.525
MSL	C: 0.482	A: 0.518	C|C: 0.235	A|A: 0.271	A|C: 0.494
YRI	C: 0.491	A: 0.509	C|C: 0.231	A|A: 0.250	A|C: 0.519

AMERICAN	C: 0.607	A: 0.393	C|C: 0.372	A|A: 0.159	A|C: 0.470
CLM	C: 0.585	A: 0.415	C|C: 0.309	A|A: 0.138	A|C: 0.553
MXL	C: 0.656	A: 0.344	C|C: 0.438	A|A: 0.125	A|C: 0.438
PEL	C: 0.712	A: 0.288	C|C: 0.541	A|A: 0.118	A|C: 0.341
PUR	C: 0.510	A: 0.490	C|C: 0.250	A|A: 0.231	A|C: 0.519
EAST ASIAN	C: 0.573	A: 0.427	C|C: 0.343	A|A: 0.196	A|C: 0.460
CDX	C: 0.710	A: 0.290	C|C: 0.484	A|A: 0.065	A|C: 0.452
CHB	C: 0.456	A: 0.544	C|C: 0.204	A|A: 0.291	A|C: 0.505
CHS	C: 0.581	A: 0.419	C|C: 0.362	A|A: 0.200	A|C: 0.438
JPT	C: 0.447	A: 0.553	C|C: 0.212	A|A: 0.317	A|C: 0.471
KHV	C: 0.692	A: 0.308	C|C: 0.475	A|A: 0.091	A|C: 0.434
EUROPEAN	C: 0.516	A: 0.484	C|C: 0.276	A|A: 0.245	A|C: 0.479
CEU	C: 0.561	A: 0.439	C|C: 0.303	A|A: 0.182	A|C: 0.515
FIN	C: 0.515	A: 0.485	C|C: 0.303	A|A: 0.273	A|C: 0.424
GBR	C: 0.544	A: 0.456	C|C: 0.264	A|A: 0.176	A|C: 0.560
IBS	C: 0.547	A: 0.453	C|C: 0.280	A|A: 0.187	A|C: 0.533
TSI	C: 0.421	A: 0.579	C|C: 0.234	A|A: 0.393	A|C: 0.374
SOUTH ASIAN	C: 0.658	A: 0.342	C|C: 0.423	A|A: 0.106	A|C: 0.470
BEB	C: 0.605	A: 0.395	C|C: 0.360	A|A: 0.151	A|C: 0.488
GIH	C: 0.684	A: 0.316	C|C: 0.456	A|A: 0.087	A|C: 0.456
ITU	C: 0.647	A: 0.353	C|C: 0.412	A|A: 0.118	A|C: 0.471
PJL	C: 0.646	A: 0.354	C|C: 0.417	A|A: 0.125	A|C: 0.458
STU	C: 0.701	A: 0.299	C|C: 0.461	A|A: 0.059	A|C: 0.480

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles G/C [2]	Ancestral:C [2]	Ambiguity code: S [2]	MAF: 0.12 [2]		
Location: 4:38880267 [2]					
SNP ID: rs11943027 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.118	C: 0.882	G|G: 0.044	C|C: 0.808	C|G: 0.148
AFRICAN	G: 0.018	C: 0.982	G|G: 0.003	C|C: 0.967	C|G: 0.030
ACB	G: 0.042	C: 0.958	G|G: 0.010	C|C: 0.927	C|G: 0.062
ASW	G: 0.074	C: 0.926	G|G: 0.016	C|C: 0.869	C|G: 0.115
ESN	G: 0.000	C: 1.000	G|G: 0.000	C|C: 1.000	C|G: 0.000
GWD	G: 0.018	C: 0.982	G|G: 0.000	C|C: 0.965	C|G: 0.035
LWK	G: 0.015	C: 0.985	G|G: 0.000	C|C: 0.970	C|G: 0.030
MSL	G: 0.000	C: 1.000	G|G: 0.000	C|C: 1.000	C|G: 0.000
YRI	G: 0.000	C: 1.000	G|G: 0.000	C|C: 1.000	C|G: 0.000
AMERICAN	G: 0.189	C: 0.811	G|G: 0.052	C|C: 0.674	C|G: 0.274
CLM	G: 0.261	C: 0.739	G|G: 0.096	C|C: 0.574	C|G: 0.330
MXL	G: 0.133	C: 0.867	G|G: 0.031	C|C: 0.766	C|G: 0.203
PEL	G: 0.082	C: 0.918	G|G: 0.000	C|C: 0.835	C|G: 0.165
PUR	G: 0.245	C: 0.755	G|G: 0.067	C|C: 0.577	C|G: 0.356
EAST ASIAN	G: 0.000	C: 1.000	G|G: 0.000	C|C: 1.000	C|G: 0.000
CDX	G: 0.000	C: 1.000	G|G: 0.000	C|C: 1.000	C|G: 0.000
CHB	G: 0.000	C: 1.000	G|G: 0.000	C|C: 1.000	C|G: 0.000
CHS	G: 0.000	C: 1.000	G|G: 0.000	C|C: 1.000	C|G: 0.000
JPT	G: 0.000	C: 1.000	G|G: 0.000	C|C: 1.000	C|G: 0.000
KHV	G: 0.000	C: 1.000	G|G: 0.000	C|C: 1.000	C|G: 0.000
EUROPEAN	G: 0.408	C: 0.592	G|G: 0.179	C|C: 0.364	C|G: 0.457
CEU	G: 0.490	C: 0.510	G|G: 0.242	C|C: 0.263	C|G: 0.495

FIN	G: 0.429	C: 0.571	G|G: 0.222	C|C: 0.364	C|G: 0.414
GBR	G: 0.445	C: 0.555	G|G: 0.143	C|C: 0.253	C|G: 0.604
IBS	G: 0.360	C: 0.640	G|G: 0.131	C|C: 0.411	C|G: 0.458
TSI	G: 0.327	C: 0.673	G|G: 0.159	C|C: 0.505	C|G: 0.336
SOUTH ASIAN	G: 0.027	C: 0.973	G|G: 0.000	C|C: 0.947	C|G: 0.053
BEB	G: 0.041	C: 0.959	G|G: 0.000	C|C: 0.919	C|G: 0.081
GIH	G: 0.029	C: 0.971	G|G: 0.000	C|C: 0.942	C|G: 0.058
ITU	G: 0.000	C: 1.000	G|G: 0.000	C|C: 1.000	C|G: 0.000
PJL	G: 0.052	C: 0.948	G|G: 0.000	C|C: 0.896	C|G: 0.104
STU	G: 0.015	C: 0.985	G|G: 0.000	C|C: 0.971	C|G: 0.029

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles G/A [2]	Ancestral:G [2]	Ambiguity code: R [2]	MAF: 0.17 [2]		
Location: 4:38884799 [2]					
SNP ID: rs17582893 [1]					
GWAS Trait: Suicide attempts in bipolar disorder, Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: The GWAS-identified archaic like SNP, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.830	A: 0.170	G|G: 0.706	A|A: 0.045	A|G: 0.249
AFRICAN	G: 0.989	A: 0.011	G|G: 0.977	A|A: 0.000	A|G: 0.023
ACB	G: 0.974	A: 0.026	G|G: 0.948	A|A: 0.000	A|G: 0.052
ASW	G: 0.934	A: 0.066	G|G: 0.869	A|A: 0.000	A|G: 0.131
ESN	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
GWD	G: 0.991	A: 0.009	G|G: 0.982	A|A: 0.000	A|G: 0.018
LWK	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
MSL	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
YRI	G: 1.000	A: 0.000	G|G: 1.000	A|A: 0.000	A|G: 0.000
AMERICAN	G: 0.839	A: 0.161	G|G: 0.720	A|A: 0.043	A|G: 0.236
CLM	G: 0.830	A: 0.170	G|G: 0.691	A|A: 0.032	A|G: 0.277
MXL	G: 0.883	A: 0.117	G|G: 0.797	A|A: 0.031	A|G: 0.172
PEL	G: 0.929	A: 0.071	G|G: 0.859	A|A: 0.000	A|G: 0.141
PUR	G: 0.745	A: 0.255	G|G: 0.587	A|A: 0.096	A|G: 0.317
EAST ASIAN	G: 0.692	A: 0.308	G|G: 0.484	A|A: 0.099	A|G: 0.417
CDX	G: 0.839	A: 0.161	G|G: 0.699	A|A: 0.022	A|G: 0.280
CHB	G: 0.549	A: 0.451	G|G: 0.301	A|A: 0.204	A|G: 0.495
CHS	G: 0.695	A: 0.305	G|G: 0.457	A|A: 0.067	A|G: 0.476
JPT	G: 0.591	A: 0.409	G|G: 0.356	A|A: 0.173	A|G: 0.471
KHV	G: 0.808	A: 0.192	G|G: 0.636	A|A: 0.020	A|G: 0.343
EUROPEAN	G: 0.771	A: 0.229	G|G: 0.608	A|A: 0.066	A|G: 0.326
CEU	G: 0.813	A: 0.187	G|G: 0.677	A|A: 0.051	A|G: 0.273
FIN	G: 0.909	A: 0.091	G|G: 0.828	A|A: 0.010	A|G: 0.162
GBR	G: 0.835	A: 0.165	G|G: 0.681	A|A: 0.011	A|G: 0.308
IBS	G: 0.678	A: 0.322	G|G: 0.449	A|A: 0.093	A|G: 0.458
TSI	G: 0.645	A: 0.355	G|G: 0.439	A|A: 0.150	A|G: 0.411
SOUTH ASIAN	G: 0.813	A: 0.187	G|G: 0.656	A|A: 0.031	A|G: 0.313
BEB	G: 0.767	A: 0.233	G|G: 0.558	A|A: 0.023	A|G: 0.419
GIH	G: 0.801	A: 0.199	G|G: 0.641	A|A: 0.039	A|G: 0.320
ITU	G: 0.838	A: 0.162	G|G: 0.716	A|A: 0.039	A|G: 0.245
PJL	G: 0.823	A: 0.177	G|G: 0.677	A|A: 0.031	A|G: 0.292
STU	G: 0.828	A: 0.172	G|G: 0.676	A|A: 0.020	A|G: 0.304

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-

like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles C/T [2]	Ancestral:T [2]	Ambiguity code: Y [2]	MAF: 0.43 [2]		
Location: 4:38885730 [2]					
SNP ID: rs2381345 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	C: 0.568	T: 0.432	C|C: 0.331	C|T: 0.474	T|T: 0.194
AFRICAN	C: 0.499	T: 0.501	C|C: 0.248	C|T: 0.502	T|T: 0.250
ACB	C: 0.469	T: 0.531	C|C: 0.240	C|T: 0.458	T|T: 0.302
ASW	C: 0.426	T: 0.574	C|C: 0.148	C|T: 0.557	T|T: 0.295
ESN	C: 0.571	T: 0.429	C|C: 0.323	C|T: 0.495	T|T: 0.182
GWD	C: 0.518	T: 0.482	C|C: 0.248	C|T: 0.540	T|T: 0.212
LWK	C: 0.455	T: 0.545	C|C: 0.202	C|T: 0.505	T|T: 0.293
MSL	C: 0.524	T: 0.476	C|C: 0.306	C|T: 0.435	T|T: 0.259
YRI	C: 0.505	T: 0.495	C|C: 0.241	C|T: 0.528	T|T: 0.231
AMERICAN	C: 0.615	T: 0.385	C|C: 0.389	C|T: 0.452	T|T: 0.159
CLM	C: 0.585	T: 0.415	C|C: 0.309	C|T: 0.553	T|T: 0.138
MXL	C: 0.656	T: 0.344	C|C: 0.438	C|T: 0.438	T|T: 0.125
PEL	C: 0.712	T: 0.288	C|C: 0.541	C|T: 0.341	T|T: 0.118
PUR	C: 0.538	T: 0.462	C|C: 0.308	C|T: 0.462	T|T: 0.231
EAST ASIAN	C: 0.590	T: 0.410	C|C: 0.363	C|T: 0.454	T|T: 0.183
CDX	C: 0.699	T: 0.301	C|C: 0.462	C|T: 0.473	T|T: 0.065
CHB	C: 0.466	T: 0.534	C|C: 0.223	C|T: 0.485	T|T: 0.291
CHS	C: 0.590	T: 0.410	C|C: 0.362	C|T: 0.457	T|T: 0.181
JPT	C: 0.514	T: 0.486	C|C: 0.298	C|T: 0.433	T|T: 0.269
KHV	C: 0.697	T: 0.303	C|C: 0.485	C|T: 0.424	T|T: 0.091
EUROPEAN	C: 0.518	T: 0.482	C|C: 0.278	C|T: 0.479	T|T: 0.243
CEU	C: 0.566	T: 0.434	C|C: 0.313	C|T: 0.505	T|T: 0.182
FIN	C: 0.515	T: 0.485	C|C: 0.303	C|T: 0.424	T|T: 0.273
GBR	C: 0.544	T: 0.456	C|C: 0.264	C|T: 0.560	T|T: 0.176
IBS	C: 0.547	T: 0.453	C|C: 0.280	C|T: 0.533	T|T: 0.187
TSI	C: 0.425	T: 0.575	C|C: 0.234	C|T: 0.383	T|T: 0.383
SOUTH ASIAN	C: 0.657	T: 0.343	C|C: 0.423	C|T: 0.468	T|T: 0.108
BEB	C: 0.605	T: 0.395	C|C: 0.360	C|T: 0.488	T|T: 0.151
GIH	C: 0.684	T: 0.316	C|C: 0.456	C|T: 0.456	T|T: 0.087
ITU	C: 0.642	T: 0.358	C|C: 0.412	C|T: 0.461	T|T: 0.127
PJL	C: 0.646	T: 0.354	C|C: 0.417	C|T: 0.458	T|T: 0.125
STU	C: 0.701	T: 0.299	C|C: 0.461	C|T: 0.480	T|T: 0.059
REFERENCES					

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles C/T [2]	Ancestral:C [2]	Ambiguity code: Y [2]	MAF: 0.20 [2]		
Location: 4:38889552 [2]					
SNP ID: rs1873195 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	C: 0.803	T: 0.197	C|C: 0.653	C|T: 0.301	T|T: 0.047
AFRICAN	C: 0.896	T: 0.104	C|C: 0.800	C|T: 0.192	T|T: 0.008
ACB	C: 0.901	T: 0.099	C|C: 0.812	C|T: 0.177	T|T: 0.010
ASW	C: 0.869	T: 0.131	C|C: 0.754	C|T: 0.230	T|T: 0.016
ESN	C: 0.904	T: 0.096	C|C: 0.818	C|T: 0.172	T|T: 0.010
GWD	C: 0.938	T: 0.062	C|C: 0.876	C|T: 0.124	T|T: 0.000
LWK	C: 0.793	T: 0.207	C|C: 0.606	C|T: 0.374	T|T: 0.020
MSL	C: 0.912	T: 0.088	C|C: 0.824	C|T: 0.176	T|T: 0.000
YRI	C: 0.940	T: 0.060	C|C: 0.880	C|T: 0.120	T|T: 0.000
AMERICAN	C: 0.823	T: 0.177	C|C: 0.692	C|T: 0.262	T|T: 0.046
CLM	C: 0.814	T: 0.186	C|C: 0.660	C|T: 0.309	T|T: 0.032
MXL	C: 0.891	T: 0.109	C|C: 0.797	C|T: 0.188	T|T: 0.016
PEL	C: 0.918	T: 0.082	C|C: 0.835	C|T: 0.165	T|T: 0.000
PUR	C: 0.712	T: 0.288	C|C: 0.538	C|T: 0.346	T|T: 0.115
EAST ASIAN	C: 0.692	T: 0.308	C|C: 0.484	C|T: 0.417	T|T: 0.099
CDX	C: 0.839	T: 0.161	C|C: 0.699	C|T: 0.280	T|T: 0.022
CHB	C: 0.549	T: 0.451	C|C: 0.301	C|T: 0.495	T|T: 0.204
CHS	C: 0.695	T: 0.305	C|C: 0.457	C|T: 0.476	T|T: 0.067
JPT	C: 0.591	T: 0.409	C|C: 0.356	C|T: 0.471	T|T: 0.173
KHV	C: 0.808	T: 0.192	C|C: 0.636	C|T: 0.343	T|T: 0.020
EUROPEAN	C: 0.771	T: 0.229	C|C: 0.604	C|T: 0.334	T|T: 0.062
CEU	C: 0.818	T: 0.182	C|C: 0.677	C|T: 0.283	T|T: 0.040
FIN	C: 0.909	T: 0.091	C|C: 0.828	C|T: 0.162	T|T: 0.010
GBR	C: 0.835	T: 0.165	C|C: 0.681	C|T: 0.308	T|T: 0.011
IBS	C: 0.673	T: 0.327	C|C: 0.439	C|T: 0.467	T|T: 0.093
TSI	C: 0.645	T: 0.355	C|C: 0.430	C|T: 0.430	T|T: 0.140
SOUTH ASIAN	C: 0.809	T: 0.191	C|C: 0.648	C|T: 0.321	T|T: 0.031
BEB	C: 0.767	T: 0.233	C|C: 0.558	C|T: 0.419	T|T: 0.023
GIH	C: 0.801	T: 0.199	C|C: 0.641	C|T: 0.320	T|T: 0.039
ITU	C: 0.828	T: 0.172	C|C: 0.696	C|T: 0.265	T|T: 0.039
PJL	C: 0.823	T: 0.177	C|C: 0.677	C|T: 0.292	T|T: 0.031
STU	C: 0.819	T: 0.181	C|C: 0.657	C|T: 0.324	T|T: 0.020
REFERENCES					
1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33					
2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html					

Alleles T/C [2]	Ancestral:C [2]	Ambiguity code: Y [2]	MAF: 0.17 [2]		
Location: 4:38891028 [2]					
SNP ID: rs17582921 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: The GWAS-identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.830	C: 0.170	T|T: 0.704	C|C: 0.044	C|T: 0.252
AFRICAN	T: 0.989	C: 0.011	T|T: 0.977	C|C: 0.000	C|T: 0.023
ACB	T: 0.974	C: 0.026	T|T: 0.948	C|C: 0.000	C|T: 0.052
ASW	T: 0.934	C: 0.066	T|T: 0.869	C|C: 0.000	C|T: 0.131

ESN	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
GWD	T: 0.991	C: 0.009	T|T: 0.982	C|C: 0.000	C|T: 0.018
LWK	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
MSL	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
YRI	T: 1.000	C: 0.000	T|T: 1.000	C|C: 0.000	C|T: 0.000
AMERICAN	T: 0.843	C: 0.157	T|T: 0.723	C|C: 0.037	C|T: 0.239
CLM	T: 0.840	C: 0.160	T|T: 0.702	C|C: 0.021	C|T: 0.277
MXL	T: 0.891	C: 0.109	T|T: 0.797	C|C: 0.016	C|T: 0.188
PEL	T: 0.929	C: 0.071	T|T: 0.859	C|C: 0.000	C|T: 0.141
PUR	T: 0.745	C: 0.255	T|T: 0.587	C|C: 0.096	C|T: 0.317
EAST ASIAN	T: 0.692	C: 0.308	T|T: 0.484	C|C: 0.099	C|T: 0.417
CDX	T: 0.839	C: 0.161	T|T: 0.699	C|C: 0.022	C|T: 0.280
CHB	T: 0.549	C: 0.451	T|T: 0.301	C|C: 0.204	C|T: 0.495
CHS	T: 0.695	C: 0.305	T|T: 0.457	C|C: 0.067	C|T: 0.476
JPT	T: 0.591	C: 0.409	T|T: 0.356	C|C: 0.173	C|T: 0.471
KHV	T: 0.808	C: 0.192	T|T: 0.636	C|C: 0.020	C|T: 0.343
EUROPEAN	T: 0.772	C: 0.228	T|T: 0.608	C|C: 0.064	C|T: 0.328
CEU	T: 0.818	C: 0.182	T|T: 0.677	C|C: 0.040	C|T: 0.283
FIN	T: 0.909	C: 0.091	T|T: 0.828	C|C: 0.010	C|T: 0.162
GBR	T: 0.835	C: 0.165	T|T: 0.681	C|C: 0.011	C|T: 0.308
IBS	T: 0.673	C: 0.327	T|T: 0.449	C|C: 0.103	C|T: 0.449
TSI	T: 0.650	C: 0.350	T|T: 0.439	C|C: 0.140	C|T: 0.421
SOUTH ASIAN	T: 0.809	C: 0.191	T|T: 0.648	C|C: 0.031	C|T: 0.321
BEB	T: 0.767	C: 0.233	T|T: 0.558	C|C: 0.023	C|T: 0.419
GIH	T: 0.801	C: 0.199	T|T: 0.641	C|C: 0.039	C|T: 0.320
ITU	T: 0.828	C: 0.172	T|T: 0.696	C|C: 0.039	C|T: 0.265
PJL	T: 0.818	C: 0.182	T|T: 0.667	C|C: 0.031	C|T: 0.302
STU	T: 0.824	C: 0.176	T|T: 0.667	C|C: 0.020	C|T: 0.314

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles G/T [2]	Ancestral:T [2]	Ambiguity code: K [2]	MAF: 0.24 [2]		
Location: 4:38892222 [2]					
SNP ID: rs6851685 [1]					
GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.755	T: 0.245	G|G: 0.581	G|T: 0.348	T|T: 0.071
AFRICAN	G: 0.787	T: 0.213	G|G: 0.620	G|T: 0.334	T|T: 0.045
ACB	G: 0.797	T: 0.203	G|G: 0.656	G|T: 0.281	T|T: 0.062
ASW	G: 0.779	T: 0.221	G|G: 0.607	G|T: 0.344	T|T: 0.049
ESN	G: 0.823	T: 0.177	G|G: 0.667	G|T: 0.313	T|T: 0.020
GWD	G: 0.726	T: 0.274	G|G: 0.522	G|T: 0.407	T|T: 0.071
LWK	G: 0.803	T: 0.197	G|G: 0.636	G|T: 0.333	T|T: 0.030
MSL	G: 0.824	T: 0.176	G|G: 0.682	G|T: 0.282	T|T: 0.035
YRI	G: 0.773	T: 0.227	G|G: 0.593	G|T: 0.361	T|T: 0.046
AMERICAN	G: 0.797	T: 0.203	G|G: 0.657	G|T: 0.280	T|T: 0.063
CLM	G: 0.798	T: 0.202	G|G: 0.628	G|T: 0.340	T|T: 0.032
MXL	G: 0.875	T: 0.125	G|G: 0.766	G|T: 0.219	T|T: 0.016
PEL	G: 0.900	T: 0.100	G|G: 0.812	G|T: 0.176	T|T: 0.012
PUR	G: 0.663	T: 0.337	G|G: 0.490	G|T: 0.346	T|T: 0.163
EAST ASIAN	G: 0.741	T: 0.259	G|G: 0.562	G|T: 0.359	T|T: 0.079
CDX	G: 0.892	T: 0.108	G|G: 0.796	G|T: 0.194	T|T: 0.011
CHB	G: 0.626	T: 0.374	G|G: 0.388	G|T: 0.476	T|T: 0.136
CHS	G: 0.733	T: 0.267	G|G: 0.524	G|T: 0.419	T|T: 0.057
JPT	G: 0.601	T: 0.399	G|G: 0.375	G|T: 0.452	T|T: 0.173

KHV	G: 0.874	T: 0.126	G|G: 0.758	G|T: 0.232	T|T: 0.010
EUROPEAN	G: 0.717	T: 0.283	G|G: 0.541	G|T: 0.352	T|T: 0.107
CEU	G: 0.798	T: 0.202	G|G: 0.646	G|T: 0.303	T|T: 0.051
FIN	G: 0.843	T: 0.157	G|G: 0.737	G|T: 0.212	T|T: 0.051
GBR	G: 0.797	T: 0.203	G|G: 0.604	G|T: 0.385	T|T: 0.011
IBS	G: 0.579	T: 0.421	G|G: 0.355	G|T: 0.449	T|T: 0.196
TSI	G: 0.593	T: 0.407	G|G: 0.393	G|T: 0.402	T|T: 0.206
SOUTH ASIAN	G: 0.736	T: 0.264	G|G: 0.536	G|T: 0.401	T|T: 0.063
BEB	G: 0.733	T: 0.267	G|G: 0.500	G|T: 0.465	T|T: 0.035
GIH	G: 0.718	T: 0.282	G|G: 0.534	G|T: 0.369	T|T: 0.097
ITU	G: 0.750	T: 0.250	G|G: 0.549	G|T: 0.402	T|T: 0.049
PJL	G: 0.714	T: 0.286	G|G: 0.521	G|T: 0.385	T|T: 0.094
STU	G: 0.765	T: 0.235	G|G: 0.569	G|T: 0.392	T|T: 0.039

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/G [2]	Ancestral:G [2]	Ambiguity code: R [2]	MAF: 0.37 [2]		
Location: 4:38892759 [2]					
SNP ID: rs6835514 [1]					
GWAS Trait: Multiple complex diseases, Coronary Artery Disease, Helicobacter pylori serologic status, Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.631	G: 0.369	A|A: 0.415	A|G: 0.432	G|G: 0.153
AFRICAN	A: 0.570	G: 0.430	A|A: 0.339	A|G: 0.461	G|G: 0.200
ACB	A: 0.573	G: 0.427	A|A: 0.354	A|G: 0.438	G|G: 0.208
ASW	A: 0.566	G: 0.434	A|A: 0.328	A|G: 0.475	G|G: 0.197
ESN	A: 0.631	G: 0.369	A|A: 0.384	A|G: 0.495	G|G: 0.121
GWD	A: 0.580	G: 0.420	A|A: 0.372	A|G: 0.416	G|G: 0.212
LWK	A: 0.434	G: 0.566	A|A: 0.182	A|G: 0.505	G|G: 0.313
MSL	A: 0.582	G: 0.418	A|A: 0.376	A|G: 0.412	G|G: 0.212
YRI	A: 0.616	G: 0.384	A|A: 0.370	A|G: 0.491	G|G: 0.139
AMERICAN	A: 0.683	G: 0.317	A|A: 0.490	A|G: 0.386	G|G: 0.124
CLM	A: 0.702	G: 0.298	A|A: 0.468	A|G: 0.468	G|G: 0.064
MXL	A: 0.695	G: 0.305	A|A: 0.516	A|G: 0.359	G|G: 0.125
PEL	A: 0.741	G: 0.259	A|A: 0.565	A|G: 0.353	G|G: 0.082
PUR	A: 0.611	G: 0.389	A|A: 0.433	A|G: 0.356	G|G: 0.212
EAST ASIAN	A: 0.594	G: 0.406	A|A: 0.359	A|G: 0.470	G|G: 0.171
CDX	A: 0.688	G: 0.312	A|A: 0.441	A|G: 0.495	G|G: 0.065
CHB	A: 0.495	G: 0.505	A|A: 0.233	A|G: 0.524	G|G: 0.243
CHS	A: 0.595	G: 0.405	A|A: 0.371	A|G: 0.448	G|G: 0.181
JPT	A: 0.519	G: 0.481	A|A: 0.298	A|G: 0.442	G|G: 0.260
KHV	A: 0.687	G: 0.313	A|A: 0.465	A|G: 0.444	G|G: 0.091
EUROPEAN	A: 0.711	G: 0.289	A|A: 0.533	A|G: 0.356	G|G: 0.111
CEU	A: 0.798	G: 0.202	A|A: 0.646	A|G: 0.303	G|G: 0.051
FIN	A: 0.838	G: 0.162	A|A: 0.727	A|G: 0.222	G|G: 0.051
GBR	A: 0.786	G: 0.214	A|A: 0.593	A|G: 0.385	G|G: 0.022
IBS	A: 0.575	G: 0.425	A|A: 0.346	A|G: 0.458	G|G: 0.196
TSI	A: 0.584	G: 0.416	A|A: 0.383	A|G: 0.402	G|G: 0.215
SOUTH ASIAN	A: 0.634	G: 0.366	A|A: 0.403	A|G: 0.462	G|G: 0.135
BEB	A: 0.605	G: 0.395	A|A: 0.360	A|G: 0.488	G|G: 0.151
GIH	A: 0.646	G: 0.354	A|A: 0.417	A|G: 0.456	G|G: 0.126
ITU	A: 0.618	G: 0.382	A|A: 0.392	A|G: 0.451	G|G: 0.157
PJL	A: 0.625	G: 0.375	A|A: 0.396	A|G: 0.458	G|G: 0.146
STU	A: 0.672	G: 0.328	A|A: 0.441	A|G: 0.461	G|G: 0.098

REFERENCES
1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33
2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles G/A [2]	Ancestral:A [2]	Ambiguity code: R [2]	MAF: 0.44 [2]		
Location: 4:38895633 [2]					
SNP ID: rs1604834 [1]					
GWAS Trait: Multiple complex diseases, Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.561	A: 0.439	G|G: 0.323	A|A: 0.200	A|G: 0.476
AFRICAN	G: 0.567	A: 0.433	G|G: 0.313	A|A: 0.180	A|G: 0.507
ACB	G: 0.568	A: 0.432	G|G: 0.312	A|A: 0.177	A|G: 0.510
ASW	G: 0.557	A: 0.443	G|G: 0.295	A|A: 0.180	A|G: 0.525
ESN	G: 0.606	A: 0.394	G|G: 0.323	A|A: 0.111	A|G: 0.566
GWD	G: 0.531	A: 0.469	G|G: 0.310	A|A: 0.248	A|G: 0.442
LWK	G: 0.480	A: 0.520	G|G: 0.232	A|A: 0.273	A|G: 0.495
MSL	G: 0.618	A: 0.382	G|G: 0.376	A|A: 0.141	A|G: 0.482
YRI	G: 0.611	A: 0.389	G|G: 0.343	A|A: 0.120	A|G: 0.537
AMERICAN	G: 0.611	A: 0.389	G|G: 0.386	A|A: 0.164	A|G: 0.450
CLM	G: 0.606	A: 0.394	G|G: 0.330	A|A: 0.117	A|G: 0.553
MXL	G: 0.656	A: 0.344	G|G: 0.469	A|A: 0.156	A|G: 0.375
PEL	G: 0.700	A: 0.300	G|G: 0.518	A|A: 0.118	A|G: 0.365
PUR	G: 0.514	A: 0.486	G|G: 0.279	A|A: 0.250	A|G: 0.471
EAST ASIAN	G: 0.596	A: 0.404	G|G: 0.361	A|A: 0.169	A|G: 0.470
CDX	G: 0.715	A: 0.285	G|G: 0.473	A|A: 0.043	A|G: 0.484
CHB	G: 0.476	A: 0.524	G|G: 0.223	A|A: 0.272	A|G: 0.505
CHS	G: 0.605	A: 0.395	G|G: 0.371	A|A: 0.162	A|G: 0.467
JPT	G: 0.510	A: 0.490	G|G: 0.288	A|A: 0.269	A|G: 0.442
KHV	G: 0.692	A: 0.308	G|G: 0.465	A|A: 0.081	A|G: 0.455
EUROPEAN	G: 0.493	A: 0.507	G|G: 0.268	A|A: 0.282	A|G: 0.449
CEU	G: 0.561	A: 0.439	G|G: 0.313	A|A: 0.192	A|G: 0.495
FIN	G: 0.495	A: 0.505	G|G: 0.293	A|A: 0.303	A|G: 0.404
GBR	G: 0.527	A: 0.473	G|G: 0.264	A|A: 0.209	A|G: 0.527
IBS	G: 0.500	A: 0.500	G|G: 0.271	A|A: 0.271	A|G: 0.458
TSI	G: 0.393	A: 0.607	G|G: 0.206	A|A: 0.421	A|G: 0.374
SOUTH ASIAN	G: 0.533	A: 0.447	G|G: 0.309	A|A: 0.202	A|G: 0.489
BEB	G: 0.523	A: 0.477	G|G: 0.291	A|A: 0.244	A|G: 0.465
GIH	G: 0.592	A: 0.408	G|G: 0.340	A|A: 0.155	A|G: 0.505
ITU	G: 0.505	A: 0.495	G|G: 0.265	A|A: 0.255	A|G: 0.480
PJL	G: 0.536	A: 0.464	G|G: 0.302	A|A: 0.229	A|G: 0.469
STU	G: 0.603	A: 0.397	G|G: 0.343	A|A: 0.137	A|G: 0.520

REFERENCES
1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33
2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles G/C [2]	Ancestral:G [2]	Ambiguity code: S [2]	MAF: 0.45 [2]		
Location: 4:38896848 [2]					
SNP ID: rs974734 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	G: 0.552	C: 0.448	G|G: 0.311	C|C: 0.207	C|G: 0.482
AFRICAN	G: 0.533	C: 0.467	G|G: 0.275	C|C: 0.209	C|G: 0.516
ACB	G: 0.516	C: 0.484	G|G: 0.250	C|C: 0.219	C|G: 0.531
ASW	G: 0.525	C: 0.475	G|G: 0.279	C|C: 0.230	C|G: 0.492
ESN	G: 0.586	C: 0.414	G|G: 0.313	C|C: 0.141	C|G: 0.545
GWD	G: 0.535	C: 0.465	G|G: 0.265	C|C: 0.195	C|G: 0.540
LWK	G: 0.449	C: 0.551	G|G: 0.202	C|C: 0.303	C|G: 0.495
MSL	G: 0.529	C: 0.471	G|G: 0.318	C|C: 0.259	C|G: 0.424
YRI	G: 0.583	C: 0.417	G|G: 0.306	C|C: 0.139	C|G: 0.556
AMERICAN	G: 0.610	C: 0.390	G|G: 0.380	C|C: 0.161	C|G: 0.458
CLM	G: 0.596	C: 0.404	G|G: 0.309	C|C: 0.117	C|G: 0.574
MXL	G: 0.656	C: 0.344	G|G: 0.469	C|C: 0.156	C|G: 0.375
PEL	G: 0.700	C: 0.300	G|G: 0.518	C|C: 0.118	C|G: 0.365
PUR	G: 0.519	C: 0.481	G|G: 0.279	C|C: 0.240	C|G: 0.481
EAST ASIAN	G: 0.595	C: 0.405	G|G: 0.359	C|C: 0.169	C|G: 0.472
CDX	G: 0.710	C: 0.290	G|G: 0.462	C|C: 0.043	C|G: 0.495
CHB	G: 0.476	C: 0.524	G|G: 0.223	C|C: 0.272	C|G: 0.505
CHS	G: 0.605	C: 0.395	G|G: 0.371	C|C: 0.162	C|G: 0.467
JPT	G: 0.510	C: 0.490	G|G: 0.288	C|C: 0.269	C|G: 0.442
KHV	G: 0.692	C: 0.308	G|G: 0.465	C|C: 0.081	C|G: 0.455
EUROPEAN	G: 0.493	C: 0.507	G|G: 0.266	C|C: 0.280	C|G: 0.453
CEU	G: 0.561	C: 0.439	G|G: 0.313	C|C: 0.192	C|G: 0.495
FIN	G: 0.495	C: 0.505	G|G: 0.293	C|C: 0.303	C|G: 0.404
GBR	G: 0.527	C: 0.473	G|G: 0.264	C|C: 0.209	C|G: 0.527
IBS	G: 0.495	C: 0.505	G|G: 0.262	C|C: 0.271	C|G: 0.467
TSI	G: 0.397	C: 0.603	G|G: 0.206	C|C: 0.411	C|G: 0.383
SOUTH ASIAN	G: 0.551	C: 0.449	G|G: 0.305	C|C: 0.202	C|G: 0.493
BEB	G: 0.523	C: 0.477	G|G: 0.291	C|C: 0.244	C|G: 0.465
GIH	G: 0.592	C: 0.408	G|G: 0.340	C|C: 0.155	C|G: 0.505
ITU	G: 0.505	C: 0.495	G|G: 0.265	C|C: 0.255	C|G: 0.480
PJL	G: 0.526	C: 0.474	G|G: 0.281	C|C: 0.229	C|G: 0.490
STU	G: 0.603	C: 0.397	G|G: 0.343	C|C: 0.137	C|G: 0.520
REFERENCES					
1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33					
2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html					

Alleles C/G [2]	Ancestral:C [2]	Ambiguity code: S [2]	MAF: 0.32 [2]		
Location: 4:38898436 [2]					
SNP ID: rs7688418 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	C: 0.678	G: 0.322	C|C: 0.470	C|G: 0.416	G|G: 0.115
AFRICAN	C: 0.703	G: 0.297	C|C: 0.478	C|G: 0.449	G|G: 0.073
ACB	C: 0.703	G: 0.297	C|C: 0.510	C|G: 0.385	G|G: 0.104
ASW	C: 0.697	G: 0.303	C|C: 0.443	C|G: 0.508	G|G: 0.049
ESN	C: 0.747	G: 0.253	C|C: 0.515	C|G: 0.465	G|G: 0.020
GWD	C: 0.735	G: 0.265	C|C: 0.540	C|G: 0.389	G|G: 0.071
LWK	C: 0.667	G: 0.333	C|C: 0.444	C|G: 0.444	G|G: 0.111

MSL	C: 0.694	G: 0.306	C|C: 0.447	C|G: 0.494	G|G: 0.059
YRI	C: 0.671	G: 0.329	C|C: 0.426	C|G: 0.491	G|G: 0.083
AMERICAN	C: 0.725	G: 0.275	C|C: 0.548	C|G: 0.354	G|G: 0.098
CLM	C: 0.686	G: 0.314	C|C: 0.479	C|G: 0.415	G|G: 0.106
MXL	C: 0.844	G: 0.156	C|C: 0.719	C|G: 0.250	G|G: 0.031
PEL	C: 0.876	G: 0.124	C|C: 0.776	C|G: 0.200	G|G: 0.024
PUR	C: 0.562	G: 0.438	C|C: 0.317	C|G: 0.490	G|G: 0.192
EAST ASIAN	C: 0.736	G: 0.264	C|C: 0.563	C|G: 0.345	G|G: 0.091
CDX	C: 0.909	G: 0.091	C|C: 0.817	C|G: 0.183	G|G: 0.000
CHB	C: 0.592	G: 0.408	C|C: 0.369	C|G: 0.447	G|G: 0.184
CHS	C: 0.729	G: 0.271	C|C: 0.524	C|G: 0.410	G|G: 0.067
JPT	C: 0.596	G: 0.404	C|C: 0.375	C|G: 0.442	G|G: 0.183
KHV	C: 0.879	G: 0.121	C|C: 0.768	C|G: 0.222	G|G: 0.010
EUROPEAN	C: 0.523	G: 0.477	C|C: 0.284	C|G: 0.477	G|G: 0.239
CEU	C: 0.571	G: 0.429	C|C: 0.323	C|G: 0.495	G|G: 0.182
FIN	C: 0.515	G: 0.485	C|C: 0.313	C|G: 0.404	G|G: 0.283
GBR	C: 0.555	G: 0.445	C|C: 0.275	C|G: 0.560	G|G: 0.165
IBS	C: 0.542	G: 0.458	C|C: 0.280	C|G: 0.523	G|G: 0.196
TSI	C: 0.439	G: 0.561	C|C: 0.234	C|G: 0.411	G|G: 0.355
SOUTH ASIAN	C: 0.709	G: 0.291	C|C: 0.497	C|G: 0.423	G|G: 0.080
BEB	C: 0.674	G: 0.326	C|C: 0.453	C|G: 0.442	G|G: 0.105
GIH	C: 0.728	G: 0.272	C|C: 0.524	C|G: 0.408	G|G: 0.068
ITU	C: 0.716	G: 0.284	C|C: 0.539	C|G: 0.353	G|G: 0.108
PJL	C: 0.677	G: 0.323	C|C: 0.458	C|G: 0.438	G|G: 0.104
STU	C: 0.740	G: 0.260	C|C: 0.500	C|G: 0.480	G|G: 0.020

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/C [2]	Ancestral:A [2]	Ambiguity code: M [2]	MAF: 0.35 [2]		
Location: 4:38898512 [2]					
SNP ID: rs7665932 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.647	C: 0.353	A|A: 0.426	A|C: 0.442	C|C: 0.132
AFRICAN	A: 0.675	C: 0.325	A|A: 0.448	A|C: 0.455	C|C: 0.097
ACB	A: 0.688	C: 0.312	A|A: 0.500	A|C: 0.375	C|C: 0.125
ASW	A: 0.680	C: 0.320	A|A: 0.443	A|C: 0.475	C|C: 0.082
ESN	A: 0.722	C: 0.278	A|A: 0.475	A|C: 0.495	C|C: 0.030
GWD	A: 0.695	C: 0.305	A|A: 0.496	A|C: 0.398	C|C: 0.106
LWK	A: 0.626	C: 0.374	A|A: 0.404	A|C: 0.444	C|C: 0.152
MSL	A: 0.665	C: 0.335	A|A: 0.412	A|C: 0.506	C|C: 0.082
YRI	A: 0.653	C: 0.347	A|A: 0.398	A|C: 0.509	C|C: 0.093
AMERICAN	A: 0.723	C: 0.277	A|A: 0.542	A|C: 0.363	C|C: 0.095
CLM	A: 0.686	C: 0.314	A|A: 0.479	A|C: 0.415	C|C: 0.106
MXL	A: 0.852	C: 0.148	A|A: 0.719	A|C: 0.266	C|C: 0.016
PEL	A: 0.876	C: 0.124	A|A: 0.776	A|C: 0.200	C|C: 0.024

PUR	A: 0.553	C: 0.447	A|A: 0.298	A|C: 0.510	C|C: 0.192
EAST ASIAN	A: 0.664	C: 0.336	A|A: 0.446	A|C: 0.435	C|C: 0.119
CDX	A: 0.801	C: 0.199	A|A: 0.624	A|C: 0.355	C|C: 0.022
CHB	A: 0.510	C: 0.490	A|A: 0.282	A|C: 0.456	C|C: 0.262
CHS	A: 0.690	C: 0.310	A|A: 0.457	A|C: 0.467	C|C: 0.076
JPT	A: 0.572	C: 0.428	A|A: 0.337	A|C: 0.471	C|C: 0.192
KHV	A: 0.763	C: 0.237	A|A: 0.556	A|C: 0.414	C|C: 0.030
EUROPEAN	A: 0.522	C: 0.478	A|A: 0.284	A|C: 0.475	C|C: 0.241
CEU	A: 0.571	C: 0.429	A|A: 0.323	A|C: 0.495	C|C: 0.182
FIN	A: 0.515	C: 0.485	A|A: 0.313	A|C: 0.404	C|C: 0.283
GBR	A: 0.549	C: 0.451	A|A: 0.275	A|C: 0.549	C|C: 0.176
IBS	A: 0.542	C: 0.458	A|A: 0.280	A|C: 0.523	C|C: 0.196
TSI	A: 0.439	C: 0.561	A|A: 0.234	A|C: 0.411	C|C: 0.355
SOUTH ASIAN	A: 0.666	C: 0.334	A|A: 0.440	A|C: 0.452	C|C: 0.108
BEB	A: 0.610	C: 0.390	A|A: 0.384	A|C: 0.453	C|C: 0.163
GIH	A: 0.699	C: 0.301	A|A: 0.476	A|C: 0.447	C|C: 0.078
ITU	A: 0.652	C: 0.348	A|A: 0.441	A|C: 0.422	C|C: 0.137
PJL	A: 0.651	C: 0.349	A|A: 0.417	A|C: 0.469	C|C: 0.115
STU	A: 0.706	C: 0.294	A|A: 0.471	A|C: 0.471	C|C: 0.059

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/G [2]	Ancestral:G [2]	Ambiguity code: R [2]	MAF: 0.11 [2]		
Location: 4:38898776 [2]					
SNP ID: rs6531677 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.114	G: 0.886	A|A: 0.042	A|G: 0.144	G|G: 0.814
AFRICAN	A: 0.018	G: 0.982	A|A: 0.002	A|G: 0.033	G|G: 0.965
ACB	A: 0.042	G: 0.958	A|A: 0.010	A|G: 0.062	G|G: 0.297
ASW	A: 0.074	G: 0.926	A|A: 0.000	A|G: 0.148	G|G: 0.852
ESN	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
GWD	A: 0.018	G: 0.982	A|A: 0.000	A|G: 0.035	G|G: 0.965
LWK	A: 0.015	G: 0.985	A|A: 0.000	A|G: 0.030	G|G: 0.970
MSL	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
YRI	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
AMERICAN	A: 0.180	G: 0.820	A|A: 0.043	A|G: 0.274	G|G: 0.683

CLM	A: 0.255	G: 0.745	A|A: 0.085	A|G: 0.340	G|G: 0.574
MXL	A: 0.141	G: 0.859	A|A: 0.031	A|G: 0.219	G|G: 0.750
PEL	A: 0.076	G: 0.924	A|A: 0.000	A|G: 0.153	G|G: 0.847
PUR	A: 0.221	G: 0.779	A|A: 0.048	A|G: 0.346	G|G: 0.606
EAST ASIAN	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
CDX	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
CHB	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
CHS	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
JPT	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
KHV	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
EUROPEAN	A: 0.405	G: 0.595	A|A: 0.179	A|G: 0.451	G|G: 0.370
CEU	A: 0.500	G: 0.500	A|A: 0.263	A|G: 0.475	G|G: 0.263
FIN	A: 0.424	G: 0.576	A|A: 0.222	A|G: 0.404	G|G: 0.374
GBR	A: 0.440	G: 0.560	A|A: 0.143	A|G: 0.593	G|G: 0.264
IBS	A: 0.355	G: 0.645	A|A: 0.131	A|G: 0.449	G|G: 0.421
TSI	A: 0.318	G: 0.682	A|A: 0.140	A|G: 0.355	G|G: 0.505
SOUTH ASIAN	A: 0.016	G: 0.984	A|A: 0.000	A|G: 0.033	G|G: 0.967
BEB	A: 0.017	G: 0.983	A|A: 0.000	A|G: 0.035	G|G: 0.965
GIH	A: 0.024	G: 0.976	A|A: 0.000	A|G: 0.049	G|G: 0.951
ITU	A: 0.000	G: 1.000	A|A: 0.000	A|G: 0.000	G|G: 1.000
PJL	A: 0.036	G: 0.964	A|A: 0.000	A|G: 0.073	G|G: 0.927
STU	A: 0.005	G: 0.995	A|A: 0.000	A|G: 0.010	G|G: 0.990

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/A [2]	Ancestral:A [2]	Ambiguity code: W [2]	MAF: 0.47 [2]		
Location: 4:38899908 [2]					
SNP ID: rs12642243 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.533	A: 0.467	T|T: 0.293	A|A: 0.227	A|T: 0.480
AFRICAN	T: 0.474	A: 0.526	T|T: 0.218	A|A: 0.271	A|T: 0.511
ACB	T: 0.479	A: 0.521	T|T: 0.219	A|A: 0.260	A|T: 0.521
ASW	T: 0.467	A: 0.533	T|T: 0.213	A|A: 0.279	A|T: 0.508
ESN	T: 0.545	A: 0.455	T|T: 0.253	A|A: 0.162	A|T: 0.586
GWD	T: 0.482	A: 0.518	T|T: 0.230	A|A: 0.265	A|T: 0.504
LWK	T: 0.338	A: 0.662	T|T: 0.101	A|A: 0.424	A|T: 0.475

MSL	T: 0.476	A: 0.524	T|T: 0.259	A|A: 0.306	A|T: 0.435
YRI	T: 0.519	A: 0.481	T|T: 0.250	A|A: 0.213	A|T: 0.537
AMERICAN	T: 0.595	A: 0.405	T|T: 0.372	A|A: 0.182	A|T: 0.447
CLM	T: 0.580	A: 0.420	T|T: 0.309	A|A: 0.149	A|T: 0.543
MXL	T: 0.656	A: 0.344	T|T: 0.469	A|A: 0.156	A|T: 0.375
PEL	T: 0.700	A: 0.300	T|T: 0.518	A|A: 0.118	A|T: 0.365
PUR	T: 0.486	A: 0.514	T|T: 0.250	A|A: 0.279	A|T: 0.471
EAST ASIAN	T: 0.592	A: 0.408	T|T: 0.355	A|A: 0.171	A|T: 0.474
CDX	T: 0.710	A: 0.290	T|T: 0.462	A|A: 0.043	A|T: 0.495
CHB	T: 0.476	A: 0.524	T|T: 0.223	A|A: 0.272	A|T: 0.505
CHS	T: 0.605	A: 0.395	T|T: 0.371	A|A: 0.162	A|T: 0.467
JPT	T: 0.510	A: 0.490	T|T: 0.288	A|A: 0.269	A|T: 0.442
KHV	T: 0.677	A: 0.323	T|T: 0.444	A|A: 0.091	A|T: 0.465
EUROPEAN	T: 0.491	A: 0.509	T|T: 0.264	A|A: 0.282	A|T: 0.453
CEU	T: 0.561	A: 0.439	T|T: 0.313	A|A: 0.192	A|T: 0.495
FIN	T: 0.495	A: 0.505	T|T: 0.293	A|A: 0.303	A|T: 0.404
GBR	T: 0.527	A: 0.473	T|T: 0.264	A|A: 0.209	A|T: 0.527
IBS	T: 0.491	A: 0.509	T|T: 0.252	A|A: 0.271	A|T: 0.477
TSI	T: 0.393	A: 0.607	T|T: 0.206	A|A: 0.421	A|T: 0.374
SOUTH ASIAN	T: 0.551	A: 0.449	T|T: 0.305	A|A: 0.202	A|T: 0.493
BEB	T: 0.523	A: 0.477	T|T: 0.291	A|A: 0.244	A|T: 0.465
GIH	T: 0.592	A: 0.408	T|T: 0.340	A|A: 0.155	A|T: 0.505
ITU	T: 0.505	A: 0.495	T|T: 0.265	A|A: 0.255	A|T: 0.480
PJL	T: 0.526	A: 0.474	T|T: 0.281	A|A: 0.229	A|T: 0.490
STU	T: 0.603	A: 0.397	T|T: 0.343	A|A: 0.137	A|T: 0.520

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2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/C [2]	Ancestral:C [2]	Ambiguity code: M [2]	MAF: 0.48 [2]		
Location: 4:38900148 [2]					
SNP ID: rs12641669 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	A: 0.517	C: 0.483	A|A: 0.278	A|C: 0.478	C|C: 0.244
AFRICAN	A: 0.417	C: 0.583	A|A: 0.168	A|C: 0.498	C|C: 0.334
ACB	A: 0.417	C: 0.583	A|A: 0.177	A|C: 0.479	C|C: 0.344
ASW	A: 0.402	C: 0.598	A|A: 0.148	A|C: 0.508	C|C: 0.344

ESN	A: 0.515	C: 0.485	A|A: 0.222	A|C: 0.586	C|C: 0.192
GWD	A: 0.425	C: 0.575	A|A: 0.150	A|C: 0.549	C|C: 0.301
LWK	A: 0.293	C: 0.707	A|A: 0.081	A|C: 0.424	C|C: 0.495
MSL	A: 0.406	C: 0.594	A|A: 0.188	A|C: 0.435	C|C: 0.376
YRI	A: 0.449	C: 0.551	A|A: 0.204	A|C: 0.491	C|C: 0.306
AMERICAN	A: 0.589	C: 0.411	A|A: 0.360	A|C: 0.458	C|C: 0.182
CLM	A: 0.564	C: 0.436	A|A: 0.277	A|C: 0.574	C|C: 0.149
MXL	A: 0.648	C: 0.352	A|A: 0.453	A|C: 0.391	C|C: 0.156
PEL	A: 0.700	C: 0.300	A|A: 0.518	A|C: 0.365	C|C: 0.118
PUR	A: 0.486	C: 0.514	A|A: 0.250	A|C: 0.471	C|C: 0.279
EAST ASIAN	A: 0.591	C: 0.409	A|A: 0.353	A|C: 0.476	C|C: 0.171
CDX	A: 0.710	C: 0.290	A|A: 0.462	A|C: 0.495	C|C: 0.043
CHB	A: 0.476	C: 0.524	A|A: 0.223	A|C: 0.505	C|C: 0.272
CHS	A: 0.605	C: 0.395	A|A: 0.371	A|C: 0.467	C|C: 0.162
JPT	A: 0.510	C: 0.490	A|A: 0.288	A|C: 0.442	C|C: 0.269
KHV	A: 0.672	C: 0.328	A|A: 0.434	A|C: 0.475	C|C: 0.091
EUROPEAN	A: 0.491	C: 0.509	A|A: 0.264	A|C: 0.453	C|C: 0.282
CEU	A: 0.561	C: 0.439	A|A: 0.313	A|C: 0.495	C|C: 0.192
FIN	A: 0.495	C: 0.505	A|A: 0.293	A|C: 0.404	C|C: 0.303
GBR	A: 0.527	C: 0.473	A|A: 0.264	A|C: 0.527	C|C: 0.209
IBS	A: 0.491	C: 0.509	A|A: 0.252	A|C: 0.477	C|C: 0.271
TSI	A: 0.393	C: 0.607	A|A: 0.206	A|C: 0.374	C|C: 0.421
SOUTH ASIAN	A: 0.551	C: 0.449	A|A: 0.305	A|C: 0.493	C|C: 0.202
BEB	A: 0.523	C: 0.477	A|A: 0.291	A|C: 0.465	C|C: 0.244
GIH	A: 0.592	C: 0.408	A|A: 0.340	A|C: 0.505	C|C: 0.155
ITU	A: 0.505	C: 0.495	A|A: 0.265	A|C: 0.480	C|C: 0.255
PJL	A: 0.526	C: 0.474	A|A: 0.281	A|C: 0.490	C|C: 0.229
STU	A: 0.603	C: 0.397	A|A: 0.343	A|C: 0.520	C|C: 0.137

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Alleles C/A/T [2]	Ancestral:C [2]	Ambiguity code: H [2]	MAF: 0.48 [2]		
Location: 4:38900512 [2]					
SNP ID: rs1115259 [1]					
GWAS Trait: Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	C: 0.517	T: 0.483	C|C: 0.278	C|T: 0.477	T|T: 0.245
AFRICAN	C: 0.416	T: 0.584	C|C: 0.168	C|T: 0.496	T|T: 0.336

ACB	C: 0.417	T: 0.583	C|C: 0.177	C|T: 0.479	T|T: 0.344
ASW	C: 0.402	T: 0.598	C|C: 0.148	C|T: 0.508	T|T: 0.344
ESN	C: 0.510	T: 0.490	C|C: 0.222	C|T: 0.576	T|T: 0.202
GWD	C: 0.425	T: 0.575	C|C: 0.150	C|T: 0.549	T|T: 0.301
LWK	C: 0.293	T: 0.707	C|C: 0.081	C|T: 0.424	T|T: 0.495
MSL	C: 0.406	T: 0.594	C|C: 0.188	C|T: 0.435	T|T: 0.376
YRI	C: 0.449	T: 0.551	C|C: 0.204	C|T: 0.491	T|T: 0.306
AMERICAN	C: 0.589	T: 0.411	C|C: 0.360	C|T: 0.458	T|T: 0.182
CLM	C: 0.564	T: 0.436	C|C: 0.277	C|T: 0.574	T|T: 0.149
MXL	C: 0.648	T: 0.352	C|C: 0.453	C|T: 0.391	T|T: 0.156
PEL	C: 0.700	T: 0.300	C|C: 0.518	C|T: 0.365	T|T: 0.118
PUR	C: 0.486	T: 0.514	C|C: 0.250	C|T: 0.471	T|T: 0.279
EAST ASIAN	C: 0.591	T: 0.409	C|C: 0.355	C|T: 0.472	T|T: 0.173
CDX	C: 0.710	T: 0.290	C|C: 0.462	C|T: 0.495	T|T: 0.043
CHB	C: 0.476	T: 0.524	C|C: 0.223	C|T: 0.505	T|T: 0.272
CHS	C: 0.605	T: 0.395	C|C: 0.371	C|T: 0.467	T|T: 0.162
JPT	C: 0.510	T: 0.490	C|C: 0.288	C|T: 0.442	T|T: 0.269
KHV	C: 0.672	T: 0.328	C|C: 0.444	C|T: 0.455	T|T: 0.101
EUROPEAN	C: 0.491	T: 0.509	C|C: 0.264	C|T: 0.453	T|T: 0.282
CEU	C: 0.561	T: 0.439	C|C: 0.313	C|T: 0.495	T|T: 0.192
FIN	C: 0.495	T: 0.505	C|C: 0.293	C|T: 0.404	T|T: 0.303
GBR	C: 0.527	T: 0.473	C|C: 0.264	C|T: 0.527	T|T: 0.209
IBS	C: 0.491	T: 0.509	C|C: 0.252	C|T: 0.477	T|T: 0.271
TSI	C: 0.393	T: 0.607	C|C: 0.206	C|T: 0.374	T|T: 0.421
SOUTH ASIAN	C: 0.551	T: 0.449	C|C: 0.305	C|T: 0.493	T|T: 0.202
BEB	C: 0.523	T: 0.477	C|C: 0.291	C|T: 0.465	T|T: 0.244
GIH	C: 0.592	T: 0.408	C|C: 0.340	C|T: 0.505	T|T: 0.155
ITU	C: 0.505	T: 0.495	C|C: 0.265	C|T: 0.480	T|T: 0.255
PJL	C: 0.526	T: 0.474	C|C: 0.281	C|T: 0.490	T|T: 0.229
STU	C: 0.603	T: 0.397	C|C: 0.343	C|T: 0.520	T|T: 0.137

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2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles T/C [2]	Ancestral:C [2]	Ambiguity code: Y [2]	MAF: 0.49 [2]		
Location: 4:38902960 [2]					
SNP ID: rs6824769 [1]					
GWAS Trait: Multiple complex diseases, Self-reported allergy [1]					
Archaic-like haplotype cluster: Not Known					
Clinical Assertion Description: Not Known					
Population	Allele Frequency [2]		Genotype Frequency [2]		
ALL	T: 0.514	C: 0.486	T|T: 0.277	C|C: 0.248	C|T: 0.475
AFRICAN	T: 0.408	C: 0.592	T|T: 0.166	C|C: 0.349	C|T: 0.484
ACB	T: 0.411	C: 0.589	T|T: 0.177	C|C: 0.354	C|T: 0.469
ASW	T: 0.385	C: 0.615	T|T: 0.148	C|C: 0.377	C|T: 0.475
ESN	T: 0.515	C: 0.485	T|T: 0.222	C|C: 0.192	C|T: 0.586
GWD	T: 0.403	C: 0.597	T|T: 0.150	C|C: 0.345	C|T: 0.504
LWK	T: 0.293	C: 0.707	T|T: 0.081	C|C: 0.495	C|T: 0.424
MSL	T: 0.394	C: 0.606	T|T: 0.176	C|C: 0.388	C|T: 0.435
YRI	T: 0.444	C: 0.556	T|T: 0.204	C|C: 0.315	C|T: 0.481
AMERICAN	T: 0.586	C: 0.414	T|T: 0.354	C|C: 0.182	C|T: 0.464
CLM	T: 0.564	C: 0.436	T|T: 0.277	C|C: 0.149	C|T: 0.574
MXL	T: 0.648	C: 0.352	T|T: 0.453	C|C: 0.156	C|T: 0.391
PEL	T: 0.694	C: 0.306	T|T: 0.506	C|C: 0.118	C|T: 0.376
PUR	T: 0.481	C: 0.519	T|T: 0.240	C|C: 0.279	C|T: 0.481
EAST ASIAN	T: 0.591	C: 0.409	T|T: 0.353	C|C: 0.171	C|T: 0.476
CDX	T: 0.710	C: 0.290	T|T: 0.462	C|C: 0.043	C|T: 0.495
CHB	T: 0.476	C: 0.524	T|T: 0.223	C|C: 0.272	C|T: 0.505
CHS	T: 0.605	C: 0.395	T|T: 0.371	C|C: 0.162	C|T: 0.467
JPT	T: 0.510	C: 0.490	T|T: 0.288	C|C: 0.269	C|T: 0.442
KHV	T: 0.672	C: 0.328	T|T: 0.434	C|C: 0.091	C|T: 0.475
EUROPEAN	T: 0.491	C: 0.509	T|T: 0.264	C|C: 0.282	C|T: 0.453
CEU	T: 0.561	C: 0.439	T|T: 0.313	C|C: 0.192	C|T: 0.495
FIN	T: 0.495	C: 0.505	T|T: 0.293	C|C: 0.303	C|T: 0.404
GBR	T: 0.527	C: 0.473	T|T: 0.264	C|C: 0.209	C|T: 0.527
IBS	T: 0.491	C: 0.509	T|T: 0.252	C|C: 0.271	C|T: 0.477
TSI	T: 0.393	C: 0.607	T|T: 0.206	C|C: 0.421	C|T: 0.374
SOUTH ASIAN	T: 0.551	C: 0.449	T|T: 0.305	C|C: 0.202	C|T: 0.493
BEB	T: 0.523	C: 0.477	T|T: 0.291	C|C: 0.244	C|T: 0.465
GIH	T: 0.592	C: 0.408	T|T: 0.340	C|C: 0.155	C|T: 0.505
ITU	T: 0.505	C: 0.495	T|T: 0.265	C|C: 0.255	C|T: 0.480
PJL	T: 0.526	C: 0.474	T|T: 0.281	C|C: 0.229	C|T: 0.490
STU	T: 0.603	C: 0.397	T|T: 0.343	C|C: 0.137	C|T: 0.520

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

Alleles A/T [2]	Ancestral:T [2]	Ambiguity code: W [2]	MAF: 0.47 [2]
Location: 4:38903573 [2]			
SNP ID: rs7664107 [1]			
GWAS Trait: Self-reported allergy [1]			
Archaic-like haplotype cluster: Not Known			
Clinical Assertion Description: Not Known			

Population	Allele Frequency [2]			Genotype Frequency [2]			
ALL	A: 0.532	ATT: 0.001	T: 0.467	A|A: 0.292	A|ATT: 0.001	A|T: 0.480	T|T: 0.227
AFRICAN	A: 0.473	ATT: 0.000	T: 0.527	A|A: 0.216	A|ATT: 0.000	A|T: 0.513	T|T: 0.271
ACB	A: 0.484	ATT: 0.000	T: 0.516	A|A: 0.229	A|ATT: 0.000	A|T: 0.510	T|T: 0.260
ASW	A: 0.451	ATT: 0.000	T: 0.549	A|A: 0.180	A|ATT: 0.000	A|T: 0.541	T|T: 0.279
ESN	A: 0.535	ATT: 0.000	T: 0.465	A|A: 0.253	A|ATT: 0.000	A|T: 0.566	T|T: 0.182
GWD	A: 0.482	ATT: 0.000	T: 0.518	A|A: 0.230	A|ATT: 0.000	A|T: 0.504	T|T: 0.265
LWK	A: 0.359	ATT: 0.000	T: 0.641	A|A: 0.111	A|ATT: 0.000	A|T: 0.495	T|T: 0.394
MSL	A: 0.471	ATT: 0.000	T: 0.529	A|A: 0.247	A|ATT: 0.000	A|T: 0.447	T|T: 0.306
YRI	A: 0.514	ATT: 0.000	T: 0.486	A|A: 0.250	A|ATT: 0.000	A|T: 0.528	T|T: 0.222
AMERICAN	A: 0.594	ATT: 0.000	T: 0.406	A|A: 0.369	A|ATT: 0.000	A|T: 0.450	T|T: 0.182
CLM	A: 0.585	ATT: 0.000	T: 0.415	A|A: 0.319	A|ATT: 0.000	A|T: 0.532	T|T: 0.149
MXL	A: 0.656	ATT: 0.000	T: 0.344	A|A: 0.469	A|ATT: 0.000	A|T: 0.375	T|T: 0.156
PEL	A: 0.694	ATT: 0.000	T: 0.306	A|A: 0.506	A|ATT: 0.000	A|T: 0.376	T|T: 0.118
PUR	A: 0.481	ATT: 0.000	T: 0.519	A|A: 0.240	A|ATT: 0.000	A|T: 0.481	T|T: 0.279
EAST ASIAN	A: 0.591	ATT: 0.003	T: 0.406	A|A: 0.353	A|ATT: 0.006	A|T: 0.470	T|T: 0.171
CDX	A: 0.710	ATT: 0.000	T: 0.290	A|A: 0.462	A|ATT: 0.000	A|T: 0.495	T|T: 0.043
CHB	A: 0.476	ATT: 0.000	T: 0.524	A|A: 0.223	A|ATT: 0.000	A|T: 0.505	T|T: 0.272
CHS	A: 0.605	ATT: 0.010	T: 0.386	A|A: 0.371	A|ATT: 0.019	A|T: 0.448	T|T: 0.162
JPT	A: 0.510	ATT: 0.000	T: 0.490	A|A: 0.288	A|ATT: 0.000	A|T: 0.442	T|T: 0.269
KHV	A: 0.672	ATT: 0.005	T: 0.323	A|A: 0.434	A|ATT: 0.010	A|T: 0.465	T|T: 0.091
EUROPEAN	A: 0.491	ATT: 0.000	T: 0.509	A|A: 0.264	A|ATT: 0.000	A|T: 0.453	T|T: 0.282
CEU	A: 0.561	ATT: 0.000	T: 0.439	A|A: 0.313	A|ATT: 0.000	A|T: 0.495	T|T: 0.192
FIN	A: 0.495	ATT: 0.000	T: 0.505	A|A: 0.293	A|ATT: 0.000	A|T: 0.404	T|T: 0.303
GBR	A: 0.527	ATT: 0.000	T: 0.473	A|A: 0.264	A|ATT: 0.000	A|T: 0.527	T|T: 0.209
IBS	A: 0.491	ATT: 0.000	T: 0.509	A|A: 0.252	A|ATT: 0.000	A|T: 0.477	T|T: 0.271
TSI	A: 0.393	ATT: 0.000	T: 0.607	A|A: 0.206	A|ATT: 0.000	A|T: 0.374	T|T: 0.421
SOUTH ASIAN	A: 0.551	ATT: 0.000	T: 0.449	A|A: 0.305	A|ATT: 0.000	A|T: 0.493	T|T: 0.202

BEB	A: 0.523	ATT: 0.000	T: 0.477	A|A: 0.291	A|ATT: 0.000	A|T: 0.465	T|T: 0.244
GIH	A: 0.592	ATT: 0.000	T: 0.408	A|A: 0.340	A|ATT: 0.000	A|T: 0.505	T|T: 0.155
ITU	A: 0.505	ATT: 0.000	T: 0.495	A|A: 0.265	A|ATT: 0.000	A|T: 0.480	T|T: 0.255
PJL	A: 0.526	ATT: 0.000	T: 0.474	A|A: 0.281	A|ATT: 0.000	A|T: 0.490	T|T: 0.229
STU	A: 0.603	ATT: 0.000	T: 0.397	A|A: 0.343	A|ATT: 0.000	A|T: 0.520	T|T: 0.137

REFERENCES

1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33

2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html

APPENDIX 2

C PROGRAMING CODES OF SOFTWARE

```
#include <stdio.h>
#include <stdlib.h>
int main()
{
        int snp,gene,chr;
  printf("Enter SNP ID: rs");
  scanf("%d", &snp);
        printf("Enter LOCATION: 4: ");
  scanf("%d", &chr);
if ((chr==38760093)|| (snp==6841698))
{
        printf(" \n\n Alleles  G/A, Ancestral:G, Ambiguity code: R, MAF: 0.41 [2]\n Location: 4:38760093 [2] \n SNP ID: rs6841698
[1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known
\n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL     \tG:0.585  A:0.415\tG|G: 0.348  A|A: 0.178  A|G: 0.474
\n\n AFRICAN  \tG:0,539  A:0.461\tG|G: 0.289  A|A: 0.210  A|G: 0.501  \n\tACB \tG:0.474  A:0.526\tG|G: 0.219  A|A: 0.271  A|G:
0.510  \n\tASW \tG:0.615  A:0.385\tG|G: 0.393  A|A: 0.164  A|G: 0.443  \n\tESN \tG:0.566  A:0.434\tG|G: 0.313  A|A: 0.182  A|G:
0.505  \n\tGWD \tG:0.487  A:0.513\tG|G: 0.204  A|A: 0.230  A|G: 0.566  \n\tLWK \tG:0.606  A:0.394\tG|G: 0.394  A|A: 0.182  A|G:
0.424  \n\tMSL \tG:0.535  A:0.465\tG|G: 0.271  A|A: 0.200  A|G: 0.529  \n\tYRI \tG:0.528  A:0.472\tG|G: 0.278  A|A: 0.222  A|G:
0.500  \n\n AMERICAN \tG:0.576  A:0.424\tG|G: 0.343  A|A: 0.190  A|G: 0.467  \n\tCLM \tG:0.612  A:0.388\tG|G: 0.383  A|A: 0.160
A|G: 0.457  \n\tMXL \tG:0.523  A:0.477\tG|G: 0.250  A|A: 0.203  A|G: 0.547  \n\tPEL \tG:0.535  A:0.465\tG|G: 0.306  A|A: 0.235  A|G:
0.459  \n\tPUR \tG:0.611  A:0.389\tG|G: 0.394  A|A: 0.173  A|G: 0.433  \n\n EAST ASIAN\tG:0,599  A:0,401\tG|G: 0.367  A|A: 0.169
A|G: 0.464  \n\tCDX \tG:0.758  A:0.242\tG|G: 0.581  A|A: 0.065  A|G: 0.355  \n\tCHB \tG:0.534  A:0.466\tG|G: 0.272  A|A: 0.204
A|G: 0.524  \n\tCHS \tG:0.605  A:0.395\tG|G: 0.343  A|A: 0.133  A|G: 0.524  \n\tJPT \tG:0.375  A:0.625\tG|G: 0.115  A|A: 0.365  A|G:
0.519  \n\tKHV \tG:0.747  A:0.253\tG|G: 0.566  A|A: 0.061  A|G: 0.384  \n\n EUROPEAN \tG:0.645  A:0.355 \tG|G: 0.427  A|A: 0.137
A|G: 0.435  \n\tCEU \tG:0.687  A:0.313\tG|G: 0.444  A|A: 0.071  A|G: 0.485  \n\tFIN \tG:0.667  A:0.333\tG|G: 0.485  A|A: 0.152  A|G:
0.364  \n\tGBR \tG:0.681  A:0.319\tG|G: 0.451  A|A: 0.088  A|G: 0.462  \n\tIBS \tG:0.612  A:0.388\tG|G: 0.364  A|A: 0.140  A|G: 0.495
\n\tTSI \tG:0.589  A:0.411\tG|G: 0.402  A|A: 0.224  A|G: 0.374  \n\n SOUTH ASIAN\tG:0,578  A:0,422\tG|G: 0.331  A|A: 0.176  A|G:
0.493  \n\tBEB \tG:0.610  A:0.390\tG|G: 0.337  A|A: 0.116  A|G: 0.547  \n\tGIH \tG:0.617  A:0.383\tG|G: 0.388  A|A: 0.155  A|G: 0.456
\n\tITU \tG:0.564  A:0.436\tG|G: 0.294  A|A: 0.167  A|G: 0.539  \n\tPJL \tG:0.594  A:0.406\tG|G: 0.385  A|A: 0.198  A|G: 0.417
\n\tSTU \tG:0.510  A:0.490\tG|G: 0.255  A|A: 0.235  A|G: 0.510  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
```

```
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38762491)|| (snp==10024216))
{
        printf(" \n\n Alleles  G/A, Ancestral:A, Ambiguity code: R, MAF: 0.44 [2]\n Location: 4:38762491 [2] \n SNP ID: rs10024216 [1] \n GWAS Trait: Amyotrophic lateral sclerosis, Helicobacter pylori serologic status, Self-reported allergy [1]\n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tG:0.561  A:0.439\tG|G: 0.324  A|A: 0.203  A|G: 0.473 \n\n AFRICAN  \tG:0.623  A:0.377\tG|G: 0.381  A|A: 0.135  A|G: 0.484  \n\tACB \tG:0.552  A:0.448\tG|G: 0.312  A|A: 0.208  A|G: 0.479  \n\tASW \tG:0.623  A:0.377\tG|G: 0.344  A|A: 0.098  A|G: 0.557  \n\tESN \tG:0.692  A:0.308\tG|G: 0.444  A|A: 0.061  A|G: 0.495  \n\tGWD \tG:0.615  A:0.385\tG|G: 0.381  A|A: 0.150  A|G: 0.469  \n\tLWK \tG:0.621  A:0.379\tG|G: 0.384  A|A: 0.141  A|G: 0.475  \n\tMSL \tG:0.571  A:0.429\tG|G: 0.318  A|A: 0.176  A|G: 0.506  \n\tYRI \tG:0.676  A:0.324\tG|G: 0.454  A|A: 0.102  A|G: 0.444  \n\n AMERICAN \tG:0.597  A:0.403\tG|G: 0.354  A|A: 0.161  A|G: 0.484  \n\tCLM \tG:0.596  A:0.404\tG|G: 0.351  A|A: 0.160  A|G: 0.489  \n\tMXL \tG:0.594  A:0.406\tG|G: 0.344  A|A: 0.156  A|G: 0.500  \n\tPEL \tG:0.641  A:0.359\tG|G: 0.400  A|A: 0.118  A|G: 0.482  \n\tPUR \tG:0.562  A:0.438 \tG|G: 0.327  A|A: 0.202  A|G: 0.471  \n\n EAST ASIAN\tG:0.433  A:0.567\tG|G: 0.204  A|A: 0.339  A|G: 0.456  \n\tCDX \tG:0.538  A:0.462\tG|G: 0.312  A|A: 0.237  A|G: 0.452  \n\tCHB \tG:0.364  A:0.636\tG|G: 0.146  A|A: 0.417  A|G: 0.437  \n\tCHS \tG:0.481  A:0.519\tG|G: 0.248  A|A: 0.286  A|G: 0.467  \n\tJPT \tG:0.284  A:0.716\tG|G: 0.067  A|A: 0.500  A|G: 0.433  \n\tKHV \tG:0.510  A:0.490\tG|G: 0.263  A|A: 0.242  A|G: 0.495  \n\n EUROPEAN \tG:0.608  A:0.392 \tG|G: 0.388  A|A: 0.171  A|G: 0.441  \n\tCEU \tG:0.646  A:0.354\tG|G: 0.404  A|A: 0.111  A|G: 0.485  \n\tFIN \tG:0.646  A:0.354\tG|G: 0.465  A|A: 0.172  A|G: 0.364  \n\tGBR \tG:0.687  A:0.313\tG|G: 0.440  A|A: 0.066  A|G: 0.495  \n\tIBS \tG:0.519  A:0.481\tG|G: 0.280  A|A: 0.243  A|G: 0.477  \n\tTSI \tG:0.561  A:0.439\tG|G: 0.364  A|A: 0.243  A|G: 0.393  \n\n SOUTH ASIAN\tG:0.534  A:0.466\tG|G: 0.284  A|A: 0.217  A|G: 0.499  \n\tBEB \tG:0.547  A:0.453\tG|G: 0.291  A|A: 0.198  A|G: 0.512  \n\tGIH \tG:0.490  A:0.510\tG|G: 0.262  A|A: 0.282  A|G: 0.456  \n\tITU \tG:0.583  A:0.417\tG|G: 0.343  A|A: 0.176  A|G: 0.480  \n\tPJL \tG:0.531  A:0.469\tG|G: 0.323  A|A: 0.260  A|G: 0.417  \n\tSTU \tG:0.520  A:0.480\tG|G: 0.206  A|A: 0.167  A|G: 0.627  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38764099)|| (snp==10008492))
{
        printf(" \n\n Alleles  C/T, Ancestral: T, Ambiguity code: Y, MAF: 0.17 [2]\n Location: 4:38764099 [2] \n SNP ID: rs10008492 [1] \n GWAS Trait: Endometriosis, Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tC:0.166  T:0.834\tC|C: 0.081  C|T: 0.170  T|T: 0.750 \n\n AFRICAN  \tC:0.017  T:0.983\tC|C: 0.002  C|T: 0.030  T|T: 0.968  \n\tACB \tC:0.068  T:0.932\tC|C: 0.010  C|T: 0.115  T|T: 0.875  \n\tASW \tC:0.074  T:0.926\tC|C: 0.000  C|T: 0.148  T|T: 0.852  \n\tESN \tC:0.000  T:1.000\tC|C: 0.000  C|T: 0.000  T|T: 1.000  \n\tGWD \tC:0.000  T:1.000\tC|C: 0.000  C|T: 0.000  T|T: 1.000  \n\tLWK \tC:0.000  T:1.000\tC|C: 0.000  C|T: 0.000  T|T: 1.000  \n\tMSL \tC:0.000  T:1.000\tC|C: 0.000  C|T: 0.000  T|T: 1.000  \n\tYRI \tC:0.000  T:1.000\tC|C: 0.000  C|T: 0.000  T|T: 1.000   \n\n AMERICAN \tC:0.249  T:0.751\tC|C: 0.089  C|T: 0.320  T|T: 0.591  \n\tCLM \tC:0.330  T:0.670\tC|C: 0.117  C|T: 0.426  T|T: 0.457  \n\tMXL \tC:0.133  T:0.867\tC|C: 0.031  C|T: 0.203  T|T: 0.766  \n\tPEL \tC:0.106  T:0.894\tC|C: 0.024  C|T: 0.165  T|T: 0.812  \n\tPUR \tC:0.365  T:0.635\tC|C: 0.154  C|T: 0.423  T|T: 0.423  \n\n EAST ASIAN\tC:0.001  T:0.999\tC|C: 0.000  C|T: 0.002  T|T: 0.998  \n\tCDX \tC:0.000  T:1.000\tC|C: 0.000  C|T: 0.000  T|T: 1.000  \n\tCHB \tC:0.000  T:1.000\tC|C: 0.000  C|T: 0.000  T|T: 1.000  \n\tCHS \tC:0.005  T:0.995\tC|C: 0.000  C|T: 0.010  T|T: 0.990  \n\tJPT \tC:0.000  T:1.000\tC|C: 0.000  C|T: 0.000  T|T: 1.000  \n\tKHV \tC:0.000  T:1.000\tC|C: 0.000  C|T: 0.000  T|T: 1.000   \n\n EUROPEAN \tC:0.566  T:0.434 \tC|C: 0.334  C|T: 0.463  T|T: 0.203  \n\tCEU \tC:0.631  T:0.369\tC|C: 0.384  C|T: 0.495  T|T: 0.121  \n\tFIN \tC:0.626  T:0.374\tC|C: 0.434  C|T: 0.384  T|T: 0.182  \n\tGBR \tC:0.648  T:0.352\tC|C: 0.374  C|T: 0.549  T|T: 0.077  \n\tIBS \tC:0.458  T:0.542\tC|C: 0.215  C|T: 0.486  T|T: 0.299  \n\tTSI \tC:0.486  T:0.514\tC|C: 0.280  C|T: 0.411  T|T: 0.308  \n\n SOUTH ASIAN\tC:0.065  T:0.935\tC|C: 0.004  C|T: 0.123  T|T: 0.873  \n\tBEB \tC:0.070  T:0.930\tC|C: 0.000  C|T: 0.140  T|T: 0.860  \n\tGIH \tC:0.063  T:0.937\tC|C: 0.000  C|T: 0.126  T|T: 0.874  \n\tITU \tC:0.054  T:0.946\tC|C: 0.010  C|T: 0.088  T|T: 0.902  \n\tPJL \tC:0.094  T:0.906\tC|C: 0.010  C|T: 0.167  T|T: 0.823  \n\tSTU \tC:0.049  T:0.951\tC|C: 0.000  C|T: 0.098  T|T: 0.902  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
```

```
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38766912)|| (snp==10470854))
{
            printf(" \n\n Alleles  A/G, Ancestral:G, Ambiguity code: R, MAF: 0.49 [2]\n Location: 4:38766912 [2] \n SNP ID: rs10470854 [1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tA:0.513  G:0.487\tA|A: 0.275  A|G: 0.476  G|G: 0.249 \n\n AFRICAN  \tA:0.506  G:0.494\tA|A: 0.265  A|G: 0.483  G|G: 0.253  \n\tACB \tA:0.448  G:0.552\tA|A: 0.219  A|G: 0.458  G|G: 0.323  \n\tASW \tA:0.475  G:0.525\tA|A: 0.197  A|G: 0.557  G|G: 0.246  \n\tESN \tA:0.606  G:0.394\tA|A: 0.354  A|G: 0.505  G|G: 0.141  \n\tGWD \tA:0.540  G:0.460\tA|A: 0.319  A|G: 0.442  G|G: 0.239  \n\tLWK \tA:0.480  G:0.520\tA|A: 0.273  A|G: 0.414  G|G: 0.313  \n\tMSL \tA:0.406  G:0.594\tA|A: 0.153  A|G: 0.506  G|G: 0.341  \n\tYRI \tA:0.551  G:0.449\tA|A: 0.287  A|G: 0.528  G|G: 0.185  \n\n AMERICAN \tA:0.585  G:0.415\tA|A: 0.337  A|G: 0.496  G|G: 0.167  \n\tCLM \tA:0.585  G:0.415\tA|A: 0.340  A|G: 0.489  G|G: 0.170  \n\tMXL \tA:0.594  G:0.406\tA|A: 0.328  A|G: 0.531  G|G: 0.141  \n\tPEL \tA:0.641  G:0.359\tA|A: 0.400  A|G: 0.482  G|G: 0.118  \n\tPUR \tA:0.534  G:0.466\tA|A: 0.288  A|G: 0.490  G|G: 0.221  \n\n EAST ASIAN\tA:0.445  G:0.555\tA|A: 0.218  A|G: 0.454  G|G: 0.327  \n\tCDX \tA:0.570  G:0.430\tA|A: 0.355  A|G: 0.430  G|G: 0.215  \n\tCHB \tA:0.374  G:0.626\tA|A: 0.136  A|G: 0.476  G|G: 0.388  \n\tCHS \tA:0.490  G:0.510\tA|A: 0.238  A|G: 0.505  G|G: 0.257  \n\tJPT \tA:0.269  G:0.731\tA|A: 0.087  A|G: 0.365  G|G: 0.548  \n\tKHV \tA:0.540  G:0.460\tA|A: 0.293  A|G: 0.495  G|G: 0.212  \n\n EUROPEAN \tA:0.602  G:0.398 \tA|A: 0.378  A|G: 0.449  G|G: 0.173  \n\tCEU \tA:0.652  G:0.348\tA|A: 0.414  A|G: 0.475  G|G: 0.111  \n\tFIN \tA:0.631  G:0.369\tA|A: 0.434  A|G: 0.394  G|G: 0.172  \n\tGBR \tA:0.676  G:0.324\tA|A: 0.418  A|G: 0.516  G|G: 0.066  \n\tIBS \tA:0.514  G:0.486\tA|A: 0.271  A|G: 0.486  G|G: 0.243  \n\tTSI \tA:0.556  G:0.444\tA|A: 0.364  A|G: 0.383  G|G: 0.252  \n\n SOUTH ASIAN\tA:0,448  G:0.552\tA|A: 0.196  A|G: 0.503  G|G: 0.301  \n\tBEB \tA:0.465  G:0.535\tA|A: 0.221  A|G: 0.488  G|G: 0.291  \n\tGIH \tA:0.413  G:0.587\tA|A: 0.175  A|G: 0.476  G|G: 0.350  \n\tITU \tA:0.490  G:0.510\tA|A: 0.225  A|G: 0.529  G|G: 0.245  \n\tPJL \tA:0.443  G:0.557\tA|A: 0.219  A|G: 0.448  G|G: 0.333  \n\tSTU \tA:0.431  G:0.569\tA|A: 0.147  A|G: 0.569  G|G: 0.284  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38767787)|| (snp==4331786))
{
            printf(" \n\n Alleles  C/T, Ancestral: T, Ambiguity code: Y, MAF: 0.49 [2]\n Location: 4:38767787 [2] \n SNP ID: rs4331786 [1] \n GWAS Trait: Amyotrophic lateral sclerosis, Self-reported allergy, Blood Pressure [1,2] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL  \tC:0.509  T:0.491\tC|C: 0.270  C|T: 0.478  T|T: 0.252 \n\n AFRICAN  \tC:0.503  T:0.497\tC|C: 0.262  C|T: 0.483  T|T: 0.256  \n\tACB  \tC:0.448  T:0.552\tC|C: 0.219  C|T: 0.458  T|T: 0.323  \n\tASW \tC:0.459  T:0.541\tC|C: 0.164  C|T: 0.590  T|T: 0.246  \n\tESN  \tC:0.601  T:0.399\tC|C: 0.354  C|T: 0.495  T|T: 0.152  \n\tGWD \tC:0.540  T:0.460\tC|C: 0.319  C|T: 0.442  T|T: 0.239  \n\tLWK  \tC:0.480  T:0.520\tC|C: 0.273  C|T: 0.414  T|T: 0.313  \n\tMSL \tC:0.406  T:0.594\tC|C: 0.153  C|T: 0.506  T|T: 0.341  \n\tYRI  \tC:0.546  T:0.454\tC|C: 0.287  C|T: 0.519  T|T: 0.194   \n\n AMERICAN \tC:0.585  T:0.415\tC|C: 0.337  C|T: 0.496  T|T: 0.167  \n\tCLM \tC:0.585  T:0.415\tC|C: 0.340  C|T: 0.489  T|T: 0.170  \n\tMXL \tC:0.594  T:0.406\tC|C: 0.328  C|T: 0.531  T|T: 0.141  \n\tPEL \tC:0.641  T:0.359\tC|C: 0.400  C|T: 0.482  T|T: 0.118  \n\tPUR \tC:0.534  T:0.466\tC|C: 0.288  C|T: 0.490  T|T: 0.221  \n\n EAST ASIAN\tC:0.421  T:0.579\tC|C: 0.200  C|T: 0.440  T|T: 0.359  \n\tCDX \tC:0.548  T:0.452\tC|C: 0.333  C|T: 0.430  T|T: 0.237  \n\tCHB \tC:0.364  T:0.636\tC|C: 0.136  C|T: 0.456  T|T: 0.408  \n\tCHS \tC:0.462  T:0.538\tC|C: 0.200  C|T: 0.524  T|T: 0.276  \n\tJPT  \tC:0.236  T:0.764\tC|C: 0.067  C|T: 0.337  T|T: 0.596  \n\tKHV \tC:0.510  T:0.490\tC|C: 0.283  C|T: 0.455  T|T: 0.263   \n\n EUROPEAN \tC:0.602  T:0.398 \tC|C: 0.378  C|T: 0.449  T|T: 0.173  \n\tCEU \tC:0.652  T:0.348\tC|C: 0.414  C|T: 0.475  T|T: 0.111  \n\tFIN \tC:0.631  T:0.369\tC|C: 0.434  C|T: 0.394  T|T: 0.172  \n\tGBR \tC:0.676  T:0.324\tC|C: 0.418  C|T: 0.516  T|T: 0.066  \n\tIBS  \tC:0.514  T:0.486\tC|C: 0.271  C|T: 0.486  T|T: 0.243  \n\tTSI \tC:0.556  T:0.444\tC|C: 0.364  C|T: 0.383  T|T: 0.252  \n\n SOUTH ASIAN\tC:0.459  T:0.541\tC|C: 0.196  C|T: 0.526  T|T: 0.278  \n\tBEB \tC:0.471  T:0.529\tC|C: 0.209  C|T: 0.523  T|T: 0.267  \n\tGIH  \tC:0.427  T:0.573\tC|C: 0.184  C|T: 0.485  T|T: 0.330  \n\tITU \tC:0.495  T:0.505\tC|C: 0.225  C|T: 0.539  T|T: 0.235  \n\tPJL \tC:0.453  T:0.547\tC|C: 0.219  C|T: 0.469  T|T: 0.312  \n\tSTU \tC:0.451  T:0.549\tC|C: 0.147  C|T: 0.608  T|T: 0.245  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
```

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printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38772195)|| (snp==4513579))
{
            printf(" \n\n Alleles  T/C, Ancestral: C, Ambiguity code: Y, MAF: 0.30 [2]\n Location: 4:38772195 [2] \n SNP ID: rs4512579
[1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known
\n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tT:0.701  C:0.299\tT|T: 0.506  C|C: 0.103  C|T: 0.390
\n\n AFRICAN  \tT:0.787  C:0.213\tT|T: 0.620  C|C: 0.045  C|T: 0.334  \n\tACB \tT:0.708  C:0.292\tT|T: 0.490  C|C: 0.073  C|T: 0.438
\n\tASW \tT:0.779  C:0.221\tT|T: 0.607  C|C: 0.049  C|T: 0.344  \n\tESN \tT:0.813  C:0.187\tT|T: 0.657  C|C: 0.030  C|T: 0.313
\n\tGWD \tT:0.792  C:0.208\tT|T: 0.619  C|C: 0.035  C|T: 0.345  \n\tLWK \tT:0.874  C:0.126\tT|T: 0.778  C|C: 0.030  C|T: 0.192
\n\tMSL \tT:0.729  C:0.271\tT|T: 0.529  C|C: 0.071  C|T: 0.400  \n\tYRI \tT:0.801  C:0.199\tT|T: 0.639  C|C: 0.037  C|T: 0.324    \n\n
AMERICAN \tT:0.680  C:0.320\tT|T: 0.458  C|C: 0.098  C|T: 0.444  \n\tCLM \tT:0.697  C:0.303\tT|T: 0.479  C|C: 0.085  C|T: 0.436
\n\tMXL \tT:0.688  C:0.312\tT|T: 0.453  C|C: 0.078  C|T: 0.469  \n\tPEL \tT:0.694  C:0.306\tT|T: 0.482  C|C: 0.094  C|T: 0.424  \n\tPUR
\tT:0.649  C:0.351\tT|T: 0.423  C|C: 0.125  C|T: 0.452  \n\n EAST ASIAN\tT:0.568  C:0.432\tT|T: 0.345  C|C: 0.208  C|T: 0.446
\n\tCDX \tT:0.742  C:0.258\tT|T: 0.591  C|C: 0.108  C|T: 0.301  \n\tCHB \tT:0.476  C:0.524\tT|T: 0.194  C|C: 0.243  C|T: 0.563
\n\tCHS \tT:0.600  C:0.400\tT|T: 0.362  C|C: 0.162  C|T: 0.476  \n\tJPT \tT:0.341  C:0.659\tT|T: 0.115  C|C: 0.433  C|T: 0.452  \n\tKHV
\tT:0.707  C:0.293\tT|T: 0.495  C|C: 0.081  C|T: 0.424    \n\n EUROPEAN \tT:0.750  C:0.250 \tT|T: 0.579  C|C: 0.078  C|T: 0.344
\n\tCEU \tT:0.778  C:0.222\tT|T: 0.596  C|C: 0.040  C|T: 0.364  \n\tFIN \tT:0.899  C:0.101\tT|T: 0.808  C|C: 0.010  C|T: 0.182  \n\tGBR
\tT:0.797  C:0.203\tT|T: 0.615  C|C: 0.022  C|T: 0.363  \n\tIBS \tT:0.659  C:0.341\tT|T: 0.458  C|C: 0.140  C|T: 0.402  \n\tTSI \tT:0.640
C:0.360\tT|T: 0.439  C|C: 0.159  C|T: 0.402  \n\n SOUTH ASIAN\tT:0.687  C:0.313\tT|T: 0.479  C|C: 0.104  C|T: 0.417  \n\tBEB
\tT:0.692  C:0.308\tT|T: 0.512  C|C: 0.128  C|T: 0.360  \n\tGIH \tT:0.641  C:0.359\tT|T: 0.408  C|C: 0.126  C|T: 0.466  \n\tITU \tT:0.716
C:0.284\tT|T: 0.510  C|C: 0.078  C|T: 0.412  \n\tPJL \tT:0.693  C:0.307\tT|T: 0.510  C|C: 0.125  C|T: 0.365  \n\tSTU \tT:0.696
C:0.304\tT|T: 0.461  C|C: 0.069  C|T: 0.471  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
 else if ((chr==38773164)|| (snp==10776482))
{
            printf(" \n\n Alleles  A/G, Ancestral:G, Ambiguity code: R, MAF: 0.30 [2]\n Location: 4:38773164 [2] \n SNP ID:
rs10776482 [1] \n GWAS Trait: Helicobacter pylori setologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: Not
Known\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL
\tA:0.701  G:0.299\tA|A: 0.506  A|G: 0.391  G|G: 0.103 \n\n AFRICAN  \tA:0.787  G:0.213\tA|A: 0.620  A|G: 0.334  G|G: 0.045
\n\tACB \tA:0.708  G:0.292\tA|A: 0.490  A|G: 0.438  G|G: 0.073  \n\tASW \tA:0.779  G:0.221\tA|A: 0.607  A|G: 0.344  G|G: 0.049
\n\tESN \tA:0.813  G:0.187\tA|A: 0.657  A|G: 0.313  G|G: 0.030  \n\tGWD \tA:0.792  G:0.208\tA|A: 0.619  A|G: 0.345  G|G: 0.035
\n\tLWK \tA:0.874  G:0.126\tA|A: 0.778  A|G: 0.192  G|G: 0.030  \n\tMSL \tA:0.729  G:0.271\tA|A: 0.529  A|G: 0.400  G|G: 0.071
\n\tYRI \tA:0.801  G:0.199\tA|A: 0.639  A|G: 0.324  G|G: 0.037  \n\n AMERICAN \tA:0.682  G:0.318\tA|A: 0.461  A|G: 0.441  G|G:
0.098  \n\tCLM \tA:0.702  G:0.298\tA|A: 0.489  A|G: 0.426  G|G: 0.085  \n\tMXL \tA:0.688  G:0.312\tA|A: 0.453  A|G: 0.469  G|G:
0.078  \n\tPEL \tA:0.694  G:0.306\tA|A: 0.482  A|G: 0.424  G|G: 0.094  \n\tPUR \tA:0.649  G:0.351\tA|A: 0.423  A|G: 0.452  G|G: 0.125
\n\n EAST ASIAN\tA:0.567  G:0.433\tA|A: 0.343  A|G: 0.448  G|G: 0.208  \n\tCDX \tA:0.742  G:0.258\tA|A: 0.591  A|G: 0.301  G|G:
0.108  \n\tCHB \tA:0.476  G:0.524\tA|A: 0.194  A|G: 0.563  G|G: 0.243  \n\tCHS \tA:0.600  G:0.400\tA|A: 0.362  A|G: 0.476  G|G:
0.162  \n\tJPT \tA:0.341  G:0.659\tA|A: 0.115  A|G: 0.452  G|G: 0.433  \n\tKHV \tA:0.702  G:0.298\tA|A: 0.485  A|G: 0.434  G|G: 0.081
\n\n EUROPEAN \tA:0.750  G:0.250 \tA|A: 0.579  A|G: 0.344  G|G: 0.078  \n\tCEU \tA:0.778  G:0.222\tA|A: 0.596  A|G: 0.364  G|G:
0.040  \n\tFIN \tA:0.899  G:0.101\tA|A: 0.808  A|G: 0.182  G|G: 0.010  \n\tGBR \tA:0.797  G:0.203\tA|A: 0.615  A|G: 0.363  G|G: 0.022
\n\tIBS \tA:0.659  G:0.341\tA|A: 0.458  A|G: 0.402  G|G: 0.140  \n\tTSI \tA:0.640  G:0.360\tA|A: 0.439  A|G: 0.402  G|G: 0.159  \n\n
SOUTH ASIAN\tA:0.686  G:0.314\tA|A: 0.476  A|G: 0.419  G|G: 0.104  \n\tBEB \tA:0.686  G:0.314\tA|A: 0.500  A|G: 0.372  G|G:
0.128  \n\tGIH \tA:0.641  G:0.359\tA|A: 0.408  A|G: 0.466  G|G: 0.126  \n\tITU \tA:0.716  G:0.284\tA|A: 0.510  A|G: 0.412  G|G: 0.078
\n\tPJL \tA:0.693  G:0.307\tA|A: 0.510  A|G: 0.365  G|G: 0.125  \n\tSTU \tA:0.696  G:0.304\tA|A: 0.461  A|G: 0.471  G|G: 0.069
\n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
```

```
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38773268)|| (snp==4129009))
{
            printf(" \n\n Alleles  T/A/C/G, Ancestral: T, Ambiguity code: N, MAF: 0.15 [2]\n Location: 4:38773268 [2] \n SNP ID: rs4129009 [1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tT:0.853  C:0.147\tT|T: 0.743  C|C: 0.036  C|T: 0.220 \n\n AFRICAN  \tT:0.989  C:0.011\tT|T: 0.979  C|C: 0.000  C|T: 0.021  \n\tACB \tT:0.984  C:0.016\tT|T: 0.969  C|C: 0.000  C|T: 0.031  \n\tASW \tT:0.926  C:0.074\tT|T: 0.852  C|C: 0.000  C|T: 0.148  \n\tESN \tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tGWD \tT:0.991  C:0.009\tT|T: 0.982  C|C: 0.000  C|T: 0.018  \n\tLWK \tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tMSL \tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tYRI \tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000      \n\n AMERICAN \tT:0.860  C:0.140\tT|T: 0.752  C|C: 0.032  C|T: 0.216  \n\tCLM \tT:0.856  C:0.144\tT|T: 0.734  C|C: 0.021  C|T: 0.245  \n\tMXL \tT:0.914  C:0.086\tT|T: 0.844  C|C: 0.016  C|T: 0.141  \n\tPEL \tT:0.941  C:0.059\tT|T: 0.882  C|C: 0.000  C|T: 0.118  \n\tPUR \tT:0.764  C:0.236\tT|T: 0.606  C|C: 0.077  C|T: 0.317  \n\n EAST ASIAN\tT:0.731  C:0.269\tT|T: 0.550  C|C: 0.087  C|T: 0.363  \n\tCDX \tT:0.898  C:0.102\tT|T: 0.817  C|C: 0.022  C|T: 0.161  \n\tCHB \tT:0.636  C:0.364\tT|T: 0.388  C|C: 0.117  C|T: 0.495  \n\tCHS \tT:0.757  C:0.243\tT|T: 0.552  C|C: 0.038  C|T: 0.410  \n\tJPT \tT:0.500  C:0.500\tT|T: 0.240  C|C: 0.240  C|T: 0.519  \n\tKHV \tT:0.889  C:0.111\tT|T: 0.788  C|C: 0.010  C|T: 0.202    \n\n EUROPEAN \tT:0.793  C:0.207 \tT|T: 0.640  C|C: 0.054  C|T: 0.306  \n\tCEU \tT:0.813  C:0.187\tT|T: 0.667  C|C: 0.040  C|T: 0.293  \n\tFIN \tT:0.914  C:0.086\tT|T: 0.838  C|C: 0.010  C|T: 0.152  \n\tGBR \tT:0.835  C:0.165\tT|T: 0.681  C|C: 0.011  C|T: 0.308  \n\tIBS \tT:0.724  C:0.276\tT|T: 0.542  C|C: 0.093  C|T: 0.364  \n\tTSI \tT:0.696  C:0.304\tT|T: 0.495  C|C: 0.103  C|T: 0.402  \n\n SOUTH ASIAN\tT:0.853  C:0.147\tT|T: 0.724  C|C: 0.018  C|T: 0.258  \n\tBEB \tT:0.802  C:0.198\tT|T: 0.628  C|C: 0.023  C|T: 0.349  \n\tGIH \tT:0.820  C:0.180\tT|T: 0.680  C|C: 0.039  C|T: 0.282  \n\tITU \tT:0.897  C:0.103\tT|T: 0.804  C|C: 0.010  C|T: 0.186  \n\tPJL \tT:0.875  C:0.125\tT|T: 0.760  C|C: 0.010  C|T: 0.229  \n\tSTU \tT:0.863  C:0.137\tT|T: 0.735  C|C: 0.010  C|T: 0.255  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
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printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
 }
else if ((chr==38773419)|| (snp==10776483))
{
            printf(" \n\n Alleles  A/G, Ancestral:A, Ambiguity code: R, MAF: 0.30 [2]\n Location: 4:38773419 [2] \n SNP ID: rs10776483 [1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL  \tA:0.701  G:0.299\tA|A: 0.506  A|G: 0.391  G|G: 0.103 \n\n AFRICAN  \tA:0.787  G:0.213\tA|A: 0.620  A|G: 0.334  G|G: 0.045  \n\tACB \tA:0.708  G:0.292\tA|A: 0.490  A|G: 0.438  G|G: 0.073  \n\tASW \tA:0.779  G:0.221\tA|A: 0.607  A|G: 0.344  G|G: 0.049  \n\tESN \tA:0.813  G:0.187\tA|A: 0.657  A|G: 0.313  G|G: 0.030  \n\tGWD \tA:0.792  G:0.208\tA|A: 0.619  A|G: 0.345  G|G: 0.035  \n\tLWK \tA:0.874  G:0.126\tA|A: 0.778  A|G: 0.192  G|G: 0.030  \n\tMSL \tA:0.729  G:0.271\tA|A: 0.529  A|G: 0.400  G|G: 0.071  \n\tYRI \tA:0.801  G:0.199\tA|A: 0.639  A|G: 0.324  G|G: 0.037  \n\n AMERICAN \tA:0.682  G:0.318\tA|A: 0.461  A|G: 0.441  G|G: 0.098  \n\tCLM \tA:0.702  G:0.298\tA|A: 0.489  A|G: 0.426  G|G: 0.085  \n\tMXL \tA:0.688  G:0.312\tA|A: 0.453  A|G: 0.469  G|G: 0.078  \n\tPEL \tA:0.694  G:0.306\tA|A: 0.482  A|G: 0.424  G|G: 0.094  \n\tPUR \tA:0.649  G:0.351\tA|A: 0.423  A|G: 0.452  G|G: 0.125  \n\n EAST ASIAN\tA:0.567  G:0.433\tA|A: 0.343  A|G: 0.448  G|G: 0.208  \n\tCDX \tA:0.742  G:0.258\tA|A: 0.591  A|G: 0.301  G|G: 0.108  \n\tCHB \tA:0.476  G:0.524\tA|A: 0.194  A|G: 0.563  G|G: 0.243  \n\tCHS \tA:0.600  G:0.400\tA|A: 0.362  A|G: 0.476  G|G: 0.162  \n\tJPT \tA:0.341  G:0.659\tA|A: 0.115  A|G: 0.452  G|G: 0.433  \n\tKHV \tA:0.702  G:0.298\tA|A: 0.485  A|G: 0.434  G|G: 0.081  \n\n EUROPEAN \tA:0.750  G:0.250 \tA|A: 0.579  A|G: 0.344  G|G: 0.078  \n\tCEU \tA:0.778  G:0.222\tA|A: 0.596  A|G: 0.364  G|G: 0.040  \n\tFIN \tA:0.899  G:0.101\tA|A: 0.808  A|G: 0.182  G|G: 0.010  \n\tGBR \tA:0.797  G:0.203\tA|A: 0.615  A|G: 0.363  G|G: 0.022  \n\tIBS \tA:0.659  G:0.341\tA|A: 0.458  A|G: 0.402  G|G: 0.140  \n\tTSI \tA:0.640  G:0.360\tA|A: 0.439  A|G: 0.402  G|G: 0.159  \n\n SOUTH ASIAN\tA:0.686  G:0.314\tA|A: 0.476  A|G: 0.419  G|G: 0.104  \n\tBEB \tA:0.686  G:0.314\tA|A: 0.500  A|G: 0.372  G|G: 0.128  \n\tGIH \tA:0.641  G:0.359\tA|A: 0.408  A|G: 0.466  G|G: 0.126  \n\tITU \tA:0.716  G:0.284\tA|A: 0.510  A|G: 0.412  G|G: 0.078  \n\tPJL \tA:0.693  G:0.307\tA|A: 0.510  A|G: 0.365  G|G: 0.125  \n\tSTU \tA:0.696  G:0.304\tA|A: 0.461  A|G: 0.471  G|G: 0.069  \n\n");
```

```
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
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printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38774173)|| (snp==11466657))
{
        printf(" \n\n Alleles  A/G, Ancestral:A, Ambiguity code: R, MAF: 0.02 [2]\n Location: 4:38774173 [2] \n SNP ID: rs11466657 [1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tA:0.981  G:0.019\tA|A: 0.964  A|G: 0.034  G|G: 0.002 \n\n AFRICAN  \tA:0.998  G:0.002\tA|A: 0.995  A|G: 0.005  G|G: 0.000  \n\tACB \tA:1.000  G:0.000\tA|A: 0.995  A|G: 0.005  G|G: 0.000  \n\tASW \tA:0.992  G:0.008\tA|A: 0.984  A|G: 0.016  G|G: 0.000  \n\tESN \tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\tGWD \tA:0.991  G:0.009\tA|A: 0.982  A|G: 0.018  G|G: 0.000  \n\tLWK \tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\tMSL \tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\tYRI \tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000   \n\n AMERICAN  \tA:0.967  G:0.033\tA|A: 0.934  A|G: 0.066  G|G: 0.000  \n\tCLM \tA:0.952  G:0.048\tA|A: 0.904  A|G: 0.096  G|G: 0.000  \n\tMXL  \tA:0.984  G:0.016\tA|A: 0.969  A|G: 0.031  G|G: 0.000  \n\tPEL \tA:0.988  G:0.012\tA|A: 0.976  A|G: 0.024  G|G: 0.000  \n\tPUR  \tA:0.952  G:0.048\tA|A: 0.904  A|G: 0.096  G|G: 0.000  \n\n EAST ASIAN\tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\tCDX \tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\tCHB \tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\tCHS \tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\tJPT \tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\tKHV \tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\n EUROPEAN \tA:0.947  G:0.053 \tA|A: 0.903  A|G: 0.089  G|G: 0.008  \n\tCEU \tA:0.970  G:0.030\tA|A: 0.939  A|G: 0.061  G|G: 0.000  \n\tFIN \tA:0.990  G:0.010\tA|A: 0.980  A|G: 0.020  G|G: 0.000  \n\tGBR \tA:0.962  G:0.038\tA|A: 0.923  A|G: 0.077  G|G: 0.000  \n\tIBS \tA:0.921  G:0.079\tA|A: 0.841  A|G: 0.159  G|G: 0.000  \n\tTSI \tA:0.902  G:0.098\tA|A: 0.841  A|G: 0.121  G|G: 0.037  \n\n SOUTH ASIAN\tA:0.986  G:0.014\tA|A: 0.971  A|G: 0.029  G|G: 0.000  \n\tBEB \tA:0.988  G:0.012\tA|A: 0.977  A|G: 0.023  G|G: 0.000  \n\tGIH \tA:0.981  G:0.019\tA|A: 0.961  A|G: 0.039  G|G: 0.000  \n\tITU \tA:0.985  G:0.015\tA|A: 0.971  A|G: 0.029  G|G: 0.000  \n\tPJL \tA:0.990  G:0.010\tA|A: 0.979  A|G: 0.021  G|G: 0.000  \n\tSTU \tA:0.985  G:0.015\tA|A: 0.971  A|G: 0.029  G|G: 0.000  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
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printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
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printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38774486)|| (snp==11096955))
{
        printf(" \n\n Alleles  T/C/G, Ancestral:T, Ambiguity code: B, MAF: 0.50 [2]\n Location: 4:38774486 [2] \n SNP ID: rs11096955 [1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tT:0.500  G:0.500\tT|T: 0.262  G|G: 0.261  G|T: 0.478 \n\n AFRICAN  \tT:0.453  G:0.547\tT|T: 0.215  G|G: 0.309  G|T: 0.477  \n\tACB \tT:0.438  G:0.562\tT|T: 0.219  G|G: 0.344  G|T: 0.438  \n\tASW \tT:0.410  G:0.590\tT|T: 0.164  G|G: 0.344  G|T: 0.492  \n\tESN \tT:0.551  G:0.449\tT|T: 0.303  G|G: 0.202  G|T: 0.495  \n\tGWD \tT:0.465  G:0.535\tT|T: 0.248  G|G: 0.319  G|T: 0.434  \n\tLWK \tT:0.449  G:0.551\tT|T: 0.232  G|G: 0.333  G|T: 0.434  \n\tMSL \tT:0.365  G:0.635\tT|T: 0.094  G|G: 0.365  G|T: 0.541  \n\tYRI \tT:0.463  G:0.537\tT|T: 0.204  G|G: 0.278  G|T: 0.519  \n\n AMERICAN \tT:0.582  G:0.418\tT|T: 0.334  G|G: 0.170  G|T: 0.496  \n\tCLM \tT:0.580  G:0.420\tT|T: 0.340  G|G: 0.181  G|T: 0.479  \n\tMXL \tT:0.594  G:0.406\tT|T: 0.328  G|G: 0.141  G|T: 0.531  \n\tPEL \tT:0.641  G:0.359\tT|T: 0.400  G|G: 0.118  G|T: 0.482  \n\tPUR \tT:0.529  G:0.471\tT|T: 0.279  G|G: 0.221  G|T: 0.500  \n\n EAST ASIAN\tT:0.445  G:0.555\tT|T: 0.218  G|G: 0.327  G|T: 0.454  \n\tCDX \tT:0.570  G:0.430\tT|T: 0.355  G|G: 0.215  G|T: 0.430  \n\tCHB \tT:0.374  G:0.626\tT|T: 0.136  G|G: 0.388  G|T: 0.476  \n\tCHS \tT:0.490  G:0.510\tT|T: 0.238  G|G: 0.257  G|T: 0.505  \n\tJPT \tT:0.269  G:0.731\tT|T: 0.087  G|G: 0.548  G|T: 0.365  \n\tKHV \tT:0.540  G:0.460\tT|T: 0.293  G|G: 0.212  G|T: 0.495  \n\n EUROPEAN \tT:0.602  G:0.398 \tT|T: 0.378  G|G: 0.173  G|T: 0.449  \n\tCEU \tT:0.652  G:0.348\tT|T: 0.414  G|G: 0.111  G|T: 0.475  \n\tFIN \tT:0.631  G:0.369\tT|T: 0.434  G|G: 0.172  G|T: 0.394  \n\tGBR \tT:0.676  G:0.324\tT|T: 0.418  G|G: 0.066  G|T: 0.516  \n\tIBS \tT:0.514  G:0.486\tT|T: 0.271  G|G: 0.243  G|T: 0.486  \n\tTSI \tT:0.556  G:0.444\tT|T: 0.364  G|G: 0.252  G|T: 0.383  \n\n SOUTH ASIAN\tT:0.458  G:0.542\tT|T: 0.198  G|G: 0.282  G|T: 0.519
```

```
\n\tBEB \tT:0.465  G:0.535\tT|T: 0.221  G|G: 0.291  G|T: 0.488  \n\tGIH \tT:0.427  G:0.573\tT|T: 0.184  G|G: 0.330  G|T: 0.485  \n\tITU
\tT:0.495  G:0.505\tT|T: 0.225  G|G: 0.235  G|T: 0.539  \n\tPJL \tT:0.453  G:0.547\tT|T: 0.219  G|G: 0.312  G|T: 0.469  \n\tSTU
\tT:0.451  G:0.549\tT|T: 0.147  G|G: 0.245  G|T: 0.608  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38774559)|| (snp==11096956))
{
        printf(" \n\n Alleles  C/A/T, Ancestral:A, Ambiguity code: H, MAF: 0.30 [2]\n Location: 4:38774559 [2] \n SNP ID:
rs11096956 [1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: Not
Known\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL
\tC:0.701  A:0.299\tC|C: 0.506  A|A: 0.103  A|C: 0.390 \n\n AFRICAN  \tC:0.788  A:0.212\tC|C: 0.622  A|A: 0.045  A|C: 0.333
\n\tACB \tC:0.714  A:0.286\tC|C: 0.500  A|A: 0.073  A|C: 0.427  \n\tASW \tC:0.779  A:0.221\tC|C: 0.607  A|A: 0.049  A|C: 0.344
\n\tESN \tC:0.813  A:0.187\tC|C: 0.657  A|A: 0.030  A|C: 0.313  \n\tGWD \tC:0.792  A:0.208\tC|C: 0.619  A|A: 0.035  A|C: 0.345
\n\tLWK \tC:0.874  A:0.126\tC|C: 0.778  A|A: 0.030  A|C: 0.192  \n\tMSL \tC:0.729  A:0.271\tC|C: 0.529  A|A: 0.071  A|C: 0.400
\n\tYRI \tC:0.801  A:0.199\tC|C: 0.639  A|A: 0.037  A|C: 0.324  \n\n AMERICAN \tC:0.682  A:0.318\tC|C: 0.461  A|A: 0.098  A|C:
0.441  \n\tCLM \tC:0.702  A:0.298\tC|C: 0.489  A|A: 0.085  A|C: 0.426  \n\tMXL \tC:0.688  A:0.312\tC|C: 0.453  A|A: 0.078  A|C:
0.469  \n\tPEL \tC:0.694  A:0.306\tC|C: 0.482  A|A: 0.094  A|C: 0.424  \n\tPUR \tC:0.649  A:0.351\tC|C: 0.423  A|A: 0.125  A|C: 0.452
\n\n EAST ASIAN\tC:0.567  A:0.433\tC|C: 0.343  A|A: 0.208  A|C: 0.448  \n\tCDX \tC:0.742  A:0.258\tC|C: 0.591  A|A: 0.108  A|C:
0.301  \n\tCHB \tC:0.476  A:0.524\tC|C: 0.194  A|A: 0.243  A|C: 0.563  \n\tCHS \tC:0.600  A:0.400\tC|C: 0.362  A|A: 0.162  A|C: 0.476
\n\tJPT \tC:0.341  A:0.659\tC|C: 0.115  A|A: 0.433  A|C: 0.452  \n\tKHV \tC:0.702  A:0.298\tC|C: 0.485  A|A: 0.081  A|C: 0.434  \n\n
EUROPEAN \tC:0.750  A:0.250 \tC|C: 0.579  A|A: 0.078  A|C: 0.344  \n\tCEU \tC:0.778  A:0.222\tC|C: 0.596  A|A: 0.040  A|C: 0.364
\n\tFIN \tC:0.899  A:0.101\tC|C: 0.808  A|A: 0.010  A|C: 0.182  \n\tGBR \tC:0.797  A:0.203\tC|C: 0.615  A|A: 0.022  A|C: 0.363
\n\tIBS \tC:0.659  A:0.341\tC|C: 0.458  A|A: 0.140  A|C: 0.402  \n\tTSI \tC:0.640  A:0.360\tC|C: 0.439  A|A: 0.159  A|C: 0.402  \n\n
SOUTH ASIAN\tC:0.686  A:0.314\tC|C: 0.476  A|A: 0.104  A|C: 0.419  \n\tBEB \tC:0.686  A:0.314\tC|C: 0.500  A|A: 0.128  A|C:
0.372  \n\tGIH \tC:0.641  A:0.359\tC|C: 0.408  A|A: 0.126  A|C: 0.466  \n\tITU \tC:0.716  A:0.284\tC|C: 0.510  A|A: 0.078  A|C: 0.412
\n\tPJL \tC:0.693  A:0.307\tC|C: 0.510  A|A: 0.125  A|C: 0.365  \n\tSTU \tC:0.696  A:0.304\tC|C: 0.461  A|A: 0.069  A|C: 0.471  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38774870)|| (snp==11096957))
{
        printf(" \n\n Alleles  T/G, Ancestral:T, Ambiguity code: K, MAF: 0.50 [2]\n Location: 4:38774870 [2] \n SNP ID:
rs11096957 [1] \n GWAS Trait: Amyotrophic lateral sclerosis, Endometriosis, Self-reported allergy [1] \n Archaic-like haplotype
cluster: Not Known\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2]
\n\n ALL      \tT:0.500  G:0.500\tT|T: 0.260  G|G: 0.260  G|T: 0.479 \n\n AFRICAN  \tT:0.451  G:0.549\tT|T: 0.210  G|G: 0.309  G|T:
0.481  \n\tACB \tT:0.438  G:0.562\tT|T: 0.219  G|G: 0.344  G|T: 0.438  \n\tASW \tT:0.410  G:0.590\tT|T: 0.164  G|G: 0.344  G|T: 0.492
\n\tESN \tT:0.545  G:0.455\tT|T: 0.293  G|G: 0.202  G|T: 0.505  \n\tGWD \tT:0.456  G:0.544\tT|T: 0.230  G|G: 0.319  G|T: 0.451
\n\tLWK \tT:0.449  G:0.551\tT|T: 0.232  G|G: 0.333  G|T: 0.434  \n\tMSL \tT:0.365  G:0.635\tT|T: 0.094  G|G: 0.365  G|T: 0.541
\n\tYRI \tT:0.463  G:0.537\tT|T: 0.204  G|G: 0.278  G|T: 0.519  \n\n AMERICAN \tT:0.582  G:0.418\tT|T: 0.334  G|G: 0.170  G|T:
0.496  \n\tCLM \tT:0.580  G:0.420\tT|T: 0.340  G|G: 0.181  G|T: 0.479  \n\tMXL \tT:0.594  G:0.406\tT|T: 0.328  G|G: 0.141  G|T: 0.531
\n\tPEL \tT:0.641  G:0.359\tT|T: 0.400  G|G: 0.118  G|T: 0.482  \n\tPUR \tT:0.529  G:0.471\tT|T: 0.279  G|G: 0.221  G|T: 0.500  \n\n
EAST ASIAN\tT:0.445  G:0.555\tT|T: 0.218  G|G: 0.327  G|T: 0.454  \n\tCDX \tT:0.570  G:0.430\tT|T: 0.355  G|G: 0.215  G|T: 0.430
\n\tCHB \tT:0.374  G:0.626\tT|T: 0.136  G|G: 0.388  G|T: 0.476  \n\tCHS \tT:0.490  G:0.510\tT|T: 0.238  G|G: 0.257  G|T: 0.505
\n\tJPT \tT:0.269  G:0.731\tT|T: 0.087  G|G: 0.548  G|T: 0.365  \n\tKHV \tT:0.540  G:0.460\tT|T: 0.293  G|G: 0.212  G|T: 0.495  \n\n
EUROPEAN \tT:0.602  G:0.398 \tT|T: 0.378  G|G: 0.173  G|T: 0.449  \n\tCEU \tT:0.652  G:0.348\tT|T: 0.414  G|G: 0.111  G|T: 0.475
\n\tFIN \tT:0.631  G:0.369\tT|T: 0.434  G|G: 0.172  G|T: 0.394  \n\tGBR \tT:0.676  G:0.324\tT|T: 0.418  G|G: 0.066  G|T: 0.516  \n\tIBS
```

```
\tT:0.514  G:0.486\tT|T: 0.271  G|G: 0.243  G|T: 0.486  \n\tTSI \tT:0.556  G:0.444\tT|T: 0.364  G|G: 0.252  G|T: 0.383  \n\n SOUTH
ASIAN\tT:0.459  G:0.541\tT|T: 0.198  G|G: 0.280  G|T: 0.521  \n\tBEB \tT:0.471  G:0.529\tT|T: 0.221  G|G: 0.279  G|T: 0.500  \n\tGIH
\tT:0.427  G:0.573\tT|T: 0.184  G|G: 0.330  G|T: 0.485  \n\tITU \tT:0.495  G:0.505\tT|T: 0.225  G|G: 0.235  G|T: 0.539  \n\tPJL
\tT:0.453  G:0.547\tT|T: 0.219  G|G: 0.312  G|T: 0.469  \n\tSTU \tT:0.451  G:0.549\tT|T: 0.147  G|G: 0.245  G|T: 0.608  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38775850)|| (snp==4274855))
{
        printf(" \n\n Alleles  C/T, Ancestral: C, Ambiguity code: Y, MAF: 0.16 [2]\n Location: 4:38775850 [2] \n SNP ID: rs4274855
[1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: The GWAS-
identified archaic like SNP, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII,
IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL
\tC:0.841  T:0.159\tC|C: 0.723  C|T: 0.235  T|T: 0.042 \n\n AFRICAN  \tC:0.989  T:0.011\tC|C: 0.979  C|T: 0.021  T|T: 0.000  \n\tACB
\tC:0.984  T:0.016\tC|C: 0.969  C|T: 0.031  T|T: 0.000  \n\tASW \tC:0.926  T:0.074\tC|C: 0.852  C|T: 0.148  T|T: 0.000  \n\tESN
\tC:1.000  T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000  \n\tGWD \tC:0.991  T:0.009\tC|C: 0.982  C|T: 0.018  T|T: 0.000  \n\tLWK
\tC:1.000  T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000  \n\tMSL \tC:1.000  T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000  \n\tYRI
\tC:1.000  T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000      \n\n AMERICAN \tC:0.860  T:0.140\tC|C: 0.752  C|T: 0.216  T|T: 0.032
\n\tCLM \tC:0.856  T:0.144\tC|C: 0.734  C|T: 0.245  T|T: 0.021  \n\tMXL \tC:0.914  T:0.086\tC|C: 0.844  C|T: 0.141  T|T: 0.016
\n\tPEL \tC:0.941  T:0.059\tC|C: 0.882  C|T: 0.118  T|T: 0.000  \n\tPUR \tC:0.764  T:0.236\tC|C: 0.606  C|T: 0.317  T|T: 0.077  \n\n
EAST ASIAN\tC:0.676  T:0.324\tC|C: 0.464  C|T: 0.423  T|T: 0.113  \n\tCDX \tC:0.839  T:0.161\tC|C: 0.710  C|T: 0.258  T|T: 0.032
\n\tCHB \tC:0.568  T:0.432\tC|C: 0.301  C|T: 0.534  T|T: 0.165  \n\tCHS \tC:0.695  T:0.305\tC|C: 0.448  C|T: 0.495  T|T: 0.057  \n\tJPT
\tC:0.471  T:0.529\tC|C: 0.212  C|T: 0.519  T|T: 0.269  \n\tKHV \tC:0.828  T:0.172\tC|C: 0.687  C|T: 0.283  T|T: 0.030    \n\n
EUROPEAN \tC:0.793  T:0.207 \tC|C: 0.640  C|T: 0.306  T|T: 0.054  \n\tCEU \tC:0.813  T:0.187\tC|C: 0.667  C|T: 0.293  T|T: 0.040
\n\tFIN \tC:0.914  T:0.086\tC|C: 0.838  C|T: 0.152  T|T: 0.010  \n\tGBR \tC:0.835  T:0.165\tC|C: 0.681  C|T: 0.308  T|T: 0.011  \n\tIBS
\tC:0.724  T:0.276\tC|C: 0.542  C|T: 0.364  T|T: 0.093  \n\tTSI \tC:0.696  T:0.304\tC|C: 0.495  C|T: 0.402  T|T: 0.103  \n\n SOUTH
ASIAN\tC:0.846  T:0.154\tC|C: 0.710  C|T: 0.272  T|T: 0.018  \n\tBEB \tC:0.802  T:0.198\tC|C: 0.628  C|T: 0.349  T|T: 0.023  \n\tGIH
\tC:0.816  T:0.184\tC|C: 0.670  C|T: 0.291  T|T: 0.039  \n\tITU \tC:0.892  T:0.108\tC|C: 0.794  C|T: 0.196  T|T: 0.010  \n\tPJL \tC:0.875
T:0.125\tC|C: 0.760  C|T: 0.229  T|T: 0.010  \n\tSTU \tC:0.838  T:0.162\tC|C: 0.686  C|T: 0.304  T|T: 0.010  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38776582)|| (snp==11466645))
{
        printf(" \n\n Alleles  A/T, Ancestral:A, Ambiguity code: W, MAF: 0.16 [2]\n Location: 4:38776582 [2] \n SNP ID:
rs11466645 [1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: Not
Known\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL
\tA:0.840  T:0.160\tA|A: 0.722  A|T: 0.236  T|T: 0.042 \n\n AFRICAN  \tA:0.989  T:0.011\tA|A: 0.979  A|T: 0.021  T|T: 0.000  \n\tACB
\tA:0.984  T:0.016\tA|A: 0.969  A|T: 0.031  T|T: 0.000  \n\tASW \tA:0.926  T:0.074\tA|A: 0.852  A|T: 0.148  T|T: 0.000  \n\tESN
\tA:1.000  T:0.000\tA|A: 1.000  A|T: 0.000  T|T: 0.000  \n\tGWD \tA:0.991  T:0.009\tA|A: 0.982  A|T: 0.018  T|T: 0.000  \n\tLWK
\tA:1.000  T:0.000\tA|A: 1.000  A|T: 0.000  T|T: 0.000  \n\tMSL \tA:1.000  T:0.000\tA|A: 1.000  A|T: 0.000  T|T: 0.000  \n\tYRI
\tA:1.000  T:0.000\tA|A: 1.000  A|T: 0.000  T|T: 0.000    \n\n AMERICAN \tA:0.860  T:0.140\tA|A: 0.752  A|T: 0.216  T|T: 0.032
\n\tCLM \tA:0.856  T:0.144\tA|A: 0.734  A|T: 0.245  T|T: 0.021  \n\tMXL \tA:0.914  T:0.086\tA|A: 0.844  A|T: 0.141  T|T: 0.016
\n\tPEL \tA:0.941  T:0.059\tA|A: 0.882  A|T: 0.118  T|T: 0.000  \n\tPUR \tA:0.764  T:0.236\tA|A: 0.606  A|T: 0.317  T|T: 0.077  \n\n
EAST ASIAN\tA:0.676  T:0.324\tA|A: 0.464  A|T: 0.423  T|T: 0.113  \n\tCDX \tA:0.839  T:0.161\tA|A: 0.710  A|T: 0.258  T|T: 0.032
\n\tCHB \tA:0.568  T:0.432\tA|A: 0.301  A|T: 0.534  T|T: 0.165  \n\tCHS \tA:0.695  T:0.305\tA|A: 0.448  A|T: 0.495  T|T: 0.057
\n\tJPT \tA:0.471  T:0.529\tA|A: 0.212  A|T: 0.519  T|T: 0.269  \n\tKHV \tA:0.828  T:0.172\tA|A: 0.687  A|T: 0.283  T|T: 0.030  \n\n
```

```
EUROPEAN \tA:0.793  T:0.207 \tA|A: 0.640  A|T: 0.306  T|T: 0.054  \n\tCEU \tA:0.813  T:0.187\tA|A: 0.667  A|T: 0.293  T|T: 0.040
\n\tFIN \tA:0.914  T:0.086\tA|A: 0.838  A|T: 0.152  T|T: 0.010  \n\tGBR \tA:0.835  T:0.165\tA|A: 0.681  A|T: 0.308  T|T: 0.011  \n\tIBS
\tA:0.724  T:0.276\tA|A: 0.542  A|T: 0.364  T|T: 0.093  \n\tTSI \tA:0.696  T:0.304\tA|A: 0.495  A|T: 0.402  T|T: 0.103  \n\n SOUTH
ASIAN\tA:0.844  T:0.156\tA|A: 0.706  A|T: 0.276  T|T: 0.018  \n\tBEB \tA:0.802  T:0.198\tA|A: 0.628  A|T: 0.349  T|T: 0.023  \n\tGIH
\tA:0.816  T:0.184\tA|A: 0.670  A|T: 0.291  T|T: 0.039  \n\tITU \tA:0.887  T:0.113\tA|A: 0.784  A|T: 0.206  T|T: 0.010  \n\tPJL
\tA:0.875  T:0.125\tA|A: 0.760  A|T: 0.229  T|T: 0.010  \n\tSTU \tA:0.833  T:0.167\tA|A: 0.676  A|T: 0.314  T|T: 0.010  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38777282)|| (snp==11466640))
{
            printf(" \n\n Alleles  G/A, Ancestral: G, Ambiguity code: R, MAF: 0.16 [2]\n Location: 4:38777282 [2] \n SNP ID:
rs11466640 [1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: The
GWAS-identified archaic like SNP, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI,
VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL
\tG:0.841  A:0.159\tG|G: 0.723  A|A: 0.042  A|G: 0.235 \n\n AFRICAN  \tG:0.989  A:0.011\tG|G: 0.979  A|A: 0.000  A|G: 0.021
\n\tACB \tG:0.984  A:0.016\tG|G: 0.969  A|A: 0.000  A|G: 0.031  \n\tASW \tG:0.926  A:0.074\tG|G: 0.852  A|A: 0.000  A|G: 0.148
\n\tESN \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000  \n\tGWD \tG:0.991  A:0.009\tG|G: 0.982  A|A: 0.000  A|G: 0.18
\n\tLWK \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000  \n\tMSL \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000
\n\tYRI \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000      \n\n AMERICAN \tG:0.860  A:0.140\tG|G: 0.752  A|A: 0.032  A|G:
0.216  \n\tCLM \tG:0.856  A:0.144\tG|G: 0.734  A|A: 0.021  A|G: 0.245  \n\tMXL \tG:0.914  A:0.086\tG|G: 0.844  A|A: 0.016  A|G:
0.141  \n\tPEL \tG:0.941  A:0.059\tG|G: 0.882  A|A: 0.000  A|G: 0.118  \n\tPUR \tG:0.764  A:0.236\tG|G: 0.606  A|A: 0.077  A|G: 0.317
\n\n EAST ASIAN\tG:0.676  A:0.324\tG|G: 0.464  A|A: 0.113  A|G: 0.423  \n\tCDX \tG:0.839  A:0.161\tG|G: 0.710  A|A: 0.032  A|G:
0.258  \n\tCHB \tG:0.568  A:0.432\tG|G: 0.301  A|A: 0.165  A|G: 0.534  \n\tCHS \tG:0.695  A:0.305\tG|G: 0.448  A|A: 0.057  A|G:
0.495  \n\tJPT \tG:0.471  A:0.529\tG|G: 0.212  A|A: 0.269  A|G: 0.519  \n\tKHV \tG:0.828  A:0.172\tG|G: 0.687  A|A: 0.030  A|G: 0.283
\n\n EUROPEAN \tG:0.793  A:0.207 \tG|G: 0.640  A|A: 0.054  A|G: 0.306  \n\tCEU \tG:0.813  A:0.187\tG|G: 0.667  A|A: 0.040  A|G:
0.293  \n\tFIN \tG:0.914  A:0.086\tG|G: 0.838  A|A: 0.010  A|G: 0.152  \n\tGBR \tG:0.835  A:0.165\tG|G: 0.681  A|A: 0.011  A|G: 0.308
\n\tIBS \tG:0.724  A:0.276\tG|G: 0.542  A|A: 0.093  A|G: 0.364  \n\tTSI \tG:0.696  A:0.304\tG|G: 0.495  A|A: 0.103  A|G: 0.402  \n\n
SOUTH ASIAN\tG:0.846  A:0.154\tG|G: 0.710  A|A: 0.018  A|G: 0.272  \n\tBEB \tG:0.802  A:0.198\tG|G: 0.628  A|A: 0.023  A|G:
0.349  \n\tGIH \tG:0.816  A:0.184\tG|G: 0.670  A|A: 0.039  A|G: 0.291  \n\tITU \tG:0.892  A:0.108\tG|G: 0.794  A|A: 0.010  A|G: 0.196
\n\tPJL \tG:0.875  A:0.125\tG|G: 0.760  A|A: 0.010  A|G: 0.229  \n\tSTU \tG:0.838  A:0.162\tG|G: 0.686  A|A: 0.010  A|G: 0.304
\n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38777473)|| (snp==7694115))
{
            printf(" \n\n Alleles  A/G, Ancestral:G, Ambiguity code: R, MAF: 0.49 [2]\n Location: 4:38777473 [2] \n SNP ID: rs7694115
[1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known
\n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tA:0.512  G:0.488\tA|A: 0.273  A|G: 0.479  G|G: 0.248
\n\n AFRICAN  \tA:0.492  G:0.508\tA|A: 0.248  A|G: 0.489  G|G: 0.263  \n\tACB \tA:0.458  G:0.542\tA|A: 0.219  A|G: 0.479  G|G:
0.302  \n\tASW \tA:0.434  G:0.566\tA|A: 0.180  A|G: 0.508  G|G: 0.311  \n\tESN \tA:0.566  G:0.434\tA|A: 0.313  A|G: 0.505  G|G:
0.182  \n\tGWD \tA:0.531  G:0.469\tA|A: 0.319  A|G: 0.425  G|G: 0.257  \n\tLWK \tA:0.475  G:0.525\tA|A: 0.263  A|G: 0.424  G|G:
0.313  \n\tMSL \tA:0.400  G:0.600\tA|A: 0.129  A|G: 0.541  G|G: 0.329  \n\tYRI \tA:0.537  G:0.463\tA|A: 0.259  A|G: 0.556  G|G:
0.185  \n\n AMERICAN \tA:0.588  G:0.412\tA|A: 0.343  A|G: 0.490  G|G: 0.167  \n\tCLM \tA:0.590  G:0.410\tA|A: 0.362  A|G: 0.457
G|G: 0.181  \n\tMXL \tA:0.594  G:0.406\tA|A: 0.328  A|G: 0.531  G|G: 0.141  \n\tPEL \tA:0.641  G:0.359\tA|A: 0.400  A|G: 0.482  G|G:
0.118  \n\tPUR \tA:0.538  G:0.462\tA|A: 0.288  A|G: 0.500  G|G: 0.212  \n\n EAST ASIAN\tA:0.445  G:0.555\tA|A: 0.218  A|G: 0.454
```

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G|G: 0.327  \n\tCDX \tA:0.570  G:0.430\tA|A: 0.355  A|G: 0.430  G|G: 0.215  \n\tCHB \tA:0.374  G:0.626\tA|A: 0.136  A|G: 0.476
G|G: 0.388  \n\tCHS \tA:0.490  G:0.510\tA|A: 0.238  A|G: 0.505  G|G: 0.257  \n\tJPT \tA:0.269  G:0.731\tA|A: 0.087  A|G: 0.365  G|G:
0.548  \n\tKHV \tA:0.540  G:0.460\tA|A: 0.293  A|G: 0.495  G|G: 0.212  \n\n EUROPEAN \tA:0.605  G:0.395 \tA|A: 0.384  A|G: 0.443
G|G: 0.173  \n\tCEU \tA:0.652  G:0.348\tA|A: 0.414  A|G: 0.475  G|G: 0.111  \n\tFIN \tA:0.646  G:0.354\tA|A: 0.465  A|G: 0.364  G|G:
0.172  \n\tGBR \tA:0.676  G:0.324\tA|A: 0.418  A|G: 0.516  G|G: 0.066  \n\tIBS \tA:0.514  G:0.486\tA|A: 0.271  A|G: 0.486  G|G: 0.243
\n\tTSI \tA:0.556  G:0.444\tA|A: 0.364  A|G: 0.383  G|G: 0.252  \n\n SOUTH ASIAN\tA:0.459  G:0.541\tA|A: 0.198  A|G: 0.521  G|G:
0.280  \n\tBEB \tA:0.471  G:0.529\tA|A: 0.221  A|G: 0.500  G|G: 0.279  \n\tGIH \tA:0.427  G:0.573\tA|A: 0.184  A|G: 0.485  G|G: 0.330
\n\tITU \tA:0.495  G:0.505\tA|A: 0.225  A|G: 0.539  G|G: 0.235  \n\tPJL \tA:0.453  G:0.547\tA|A: 0.219  A|G: 0.469  G|G: 0.312
\n\tSTU \tA:0.451  G:0.549\tA|A: 0.147  A|G: 0.608  G|G: 0.245  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38778850)|| (snp==11466617))
{
        printf(" \n\n Alleles  T/C, Ancestral: T, Ambiguity code: Y, MAF: 0.16 [2]\n Location: 4:38778850 [2] \n SNP ID:
rs11466617 [1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: The
GWAS-identified archaic like SNP, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI,
VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL
\tT:0.840  C:0.160\tT|T: 0.722  C|C: 0.042  C|T: 0.236 \n\n AFRICAN  \tT:0.989  C:0.011\tT|T: 0.979  C|C: 0.000  C|T: 0.021  \n\tACB
\tT:0.984  C:0.016\tT|T: 0.969  C|C: 0.000  C|T: 0.031  \n\tASW \tT:0.926  C:0.074\tT|T: 0.852  C|C: 0.000  C|T: 0.148  \n\tESN
\tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tGWD \tT:0.991  C:0.009\tT|T: 0.982  C|C: 0.000  C|T: 0.018  \n\tLWK
\tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tMSL \tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tYRI
\tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000      \n\n AMERICAN \tT:0.860  C:0.140\tT|T: 0.752  C|C: 0.032  C|T: 0.216
\n\tCLM \tT:0.856  C:0.144\tT|T: 0.734  C|C: 0.021  C|T: 0.245  \n\tMXL \tT:0.914  C:0.086\tT|T: 0.844  C|C: 0.016  C|T: 0.141
\n\tPEL \tT:0.941  C:0.059\tT|T: 0.882  C|C: 0.000  C|T: 0.118  \n\tPUR \tT:0.764  C:0.236\tT|T: 0.606  C|C: 0.077  C|T: 0.317  \n\n
EAST ASIAN\tT:0.676  C:0.324\tT|T: 0.464  C|C: 0.113  C|T: 0.423  \n\tCDX \tT:0.839  C:0.161\tT|T: 0.710  C|C: 0.032  C|T: 0.258
\n\tCHB \tT:0.568  C:0.432\tT|T: 0.301  C|C: 0.165  C|T: 0.534  \n\tCHS \tT:0.695  C:0.305\tT|T: 0.448  C|C: 0.057  C|T: 0.495  \n\tJPT
\tT:0.471  C:0.529\tT|T: 0.212  C|C: 0.269  C|T: 0.519  \n\tKHV \tT:0.828  C:0.172\tT|T: 0.687  C|C: 0.030  C|T: 0.283    \n\n
EUROPEAN \tT:0.793  C:0.207 \tT|T: 0.640  C|C: 0.054  C|T: 0.306  \n\tCEU \tT:0.813  C:0.187\tT|T: 0.667  C|C: 0.040  C|T: 0.293
\n\tFIN \tT:0.914  C:0.086\tT|T: 0.838  C|C: 0.010  C|T: 0.152  \n\tGBR \tT:0.835  C:0.165\tT|T: 0.681  C|C: 0.011  C|T: 0.308  \n\tIBS
\tT:0.724  C:0.276\tT|T: 0.542  C|C: 0.093  C|T: 0.364  \n\tTSI \tT:0.696  C:0.304\tT|T: 0.495  C|C: 0.103  C|T: 0.402  \n\n SOUTH
ASIAN\tT:0.844  C:0.156\tT|T: 0.706  C|C: 0.018  C|T: 0.276  \n\tBEB \tT:0.802  C:0.198\tT|T: 0.628  C|C: 0.023  C|T: 0.349  \n\tGIH
\tT:0.816  C:0.184\tT|T: 0.670  C|C: 0.039  C|T: 0.291  \n\tITU \tT:0.887  C:0.113\tT|T: 0.784  C|C: 0.010  C|T: 0.206  \n\tPJL \tT:0.875
C:0.125\tT|T: 0.760  C|C: 0.010  C|T: 0.229  \n\tSTU \tT:0.833  C:0.167\tT|T: 0.676  C|C: 0.010  C|T: 0.314  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38780600)|| (snp==7653908))
{
        printf(" \n\n Alleles  G/C, Ancestral: G, Ambiguity code: S, MAF: 0.26 [2]\n Location: 4:38780600 [2] \n SNP ID: rs7653908
[1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: The SNP differs
between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not
Known\n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tG:0.743  C:0.257\tG|G: 0.563  C|C: 0.077
C|G: 0.359 \n\n AFRICAN  \tG:0.710  C:0.290\tG|G: 0.507  C|C: 0.086  C|G: 0.407  \n\tACB \tG:0.792  C:0.208\tG|G: 0.625  C|C: 0.042
C|G: 0.333  \n\tASW \tG:0.689  C:0.311\tG|G: 0.459  C|C: 0.082  C|G: 0.459  \n\tESN \tG:0.717  C:0.283\tG|G: 0.515  C|C: 0.081  C|G:
0.404  \n\tGWD \tG:0.735  C:0.265\tG|G: 0.575  C|C: 0.106  C|G: 0.319  \n\tLWK \tG:0.657  C:0.343\tG|G: 0.404  C|C: 0.091  C|G:
0.505  \n\tMSL \tG:0.729  C:0.271\tG|G: 0.541  C|C: 0.082  C|G: 0.376  \n\tYRI \tG:0.653  C:0.347\tG|G: 0.417  C|C: 0.111  C|G: 0.472
```

```
\n\n AMERICAN \tG:0.831  C:0.169\tG|G: 0.712  C|C: 0.049  C|G: 0.239  \n\tCLM \tG:0.840  C:0.160\tG|G: 0.713  C|C: 0.032  C|G:
0.255  \n\tMXL \tG:0.898  C:0.102\tG|G: 0.812  C|C: 0.016  C|G: 0.172  \n\tPEL \tG:0.929  C:0.071\tG|G: 0.871  C|C: 0.012  C|G: 0.118
\n\tPUR \tG:0.702  C:0.298\tG|G: 0.519  C|C: 0.115  C|G: 0.365  \n\n EAST ASIAN\tG:0.652  C:0.348\tG|G: 0.437  C|C: 0.133  C|G:
0.431  \n\tCDX \tG:0.801  C:0.199\tG|G: 0.656  C|C: 0.054  C|G: 0.290  \n\tCHB \tG:0.549  C:0.451\tG|G: 0.291  C|C: 0.194  C|G: 0.515
\n\tCHS \tG:0.690  C:0.310\tG|G: 0.448  C|C: 0.067  C|G: 0.486  \n\tJPT \tG:0.466  C:0.534\tG|G: 0.202  C|C: 0.269  C|G: 0.529
\n\tKHV \tG:0.773  C:0.227\tG|G: 0.616  C|C: 0.071  C|G: 0.313   \n\n EUROPEAN \tG:0.765  C:0.235 \tG|G: 0.596  C|C: 0.066  C|G:
0.338  \n\tCEU \tG:0.798  C:0.202\tG|G: 0.646  C|C: 0.051  C|G: 0.303  \n\tFIN \tG:0.884  C:0.116\tG|G: 0.788  C|C: 0.020  C|G: 0.192
\n\tGBR \tG:0.819  C:0.181\tG|G: 0.648  C|C: 0.011  C|G: 0.341  \n\tIBS \tG:0.664  C:0.336\tG|G: 0.439  C|C: 0.112  C|G: 0.449
\n\tTSI \tG:0.682  C:0.318\tG|G: 0.486  C|C: 0.121  C|G: 0.393  \n\n SOUTH ASIAN\tG:0.797  C:0.203\tG|G: 0.632  C|C: 0.039  C|G:
0.329  \n\tBEB \tG:0.744  C:0.256\tG|G: 0.523  C|C: 0.035  C|G: 0.442  \n\tGIH \tG:0.796  C:0.204\tG|G: 0.641  C|C: 0.049  C|G: 0.311
\n\tITU \tG:0.828  C:0.172\tG|G: 0.696  C|C: 0.039  C|G: 0.265  \n\tPJL \tG:0.828  C:0.172\tG|G: 0.698  C|C: 0.042  C|G: 0.260
\n\tSTU \tG:0.779  C:0.221\tG|G: 0.588  C|C: 0.029  C|G: 0.382  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38780799)|| (snp==7658893))
{
            printf(" \n\n Alleles  G/A, Ancestral:A, Ambiguity code: R, MAF: 0.43 [2]\n Location: 4:38780799 [2] \n SNP ID: rs7658893
[1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]\n Archaic-like haplotype cluster: Not Known\n
Clinical Assertion Description: Not Known \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tG:0.568
A:0.432\tG|G: 0.346  A|A: 0.210  A|G: 0.444 \n\n AFRICAN  \tG:0.466  A:0.534\tG|G: 0.224  A|A: 0.292  A|G: 0.484  \n\tACB
\tG:0.453  A:0.547\tG|G: 0.177  A|A: 0.271  A|G: 0.552  \n\tASW \tG:0.418  A:0.582\tG|G: 0.197  A|A: 0.361  A|G: 0.443  \n\tESN
\tG:0.444  A:0.556\tG|G: 0.202  A|A: 0.313  A|G: 0.485  \n\tGWD \tG:0.509  A:0.491\tG|G: 0.265  A|A: 0.248  A|G: 0.487  \n\tLWK
\tG:0.520  A:0.480\tG|G: 0.253  A|A: 0.212  A|G: 0.535  \n\tMSL \tG:0.435  A:0.565\tG|G: 0.212  A|A: 0.341  A|G: 0.447  \n\tYRI
\tG:0.454  A:0.546\tG|G: 0.241  A|A: 0.333  A|G: 0.426  \n\n AMERICAN \tG:0.648  A:0.352\tG|G: 0.424  A|A: 0.127  A|G: 0.450
\n\tCLM \tG:0.660  A:0.340\tG|G: 0.447  A|A: 0.128  A|G: 0.426  \n\tMXL \tG:0.672  A:0.328\tG|G: 0.422  A|A: 0.078  A|G: 0.500
\n\tPEL \tG:0.682  A:0.318\tG|G: 0.471  A|A: 0.106  A|G: 0.424  \n\tPUR \tG:0.596  A:0.404 \tG|G: 0.365  A|A: 0.173  A|G: 0.462  \n\n
EAST ASIAN\tG:0.476  A:0.524\tG|G: 0.260  A|A: 0.308  A|G: 0.433  \n\tCDX \tG:0.618  A:0.382\tG|G: 0.430  A|A: 0.194  A|G: 0.376
\n\tCHB \tG:0.388  A:0.612\tG|G: 0.155  A|A: 0.379  A|G: 0.466  \n\tCHS \tG:0.495  A:0.505\tG|G: 0.257  A|A: 0.267  A|G: 0.476
\n\tJPT \tG:0.303  A:0.697\tG|G: 0.106  A|A: 0.500  A|G: 0.394  \n\tKHV \tG:0.596  A:0.404\tG|G: 0.374  A|A: 0.182  A|G: 0.444  \n\n
EUROPEAN \tG:0.725  A:0.275 \tG|G: 0.541  A|A: 0.091  A|G: 0.368  \n\tCEU \tG:0.763  A:0.237\tG|G: 0.576  A|A: 0.051  A|G: 0.374
\n\tFIN \tG:0.869  A:0.131\tG|G: 0.758  A|A: 0.020  A|G: 0.222  \n\tGBR \tG:0.780  A:0.220\tG|G: 0.582  A|A: 0.022  A|G: 0.396
\n\tIBS \tG:0.598  A:0.402\tG|G: 0.364  A|A: 0.168  A|G: 0.467  \n\tTSI \tG:0.636  A:0.364\tG|G: 0.449  A|A: 0.178  A|G: 0.374  \n\n
SOUTH ASIAN\tG:0.583  A:0.417\tG|G: 0.346  A|A: 0.180  A|G: 0.474  \n\tBEB \tG:0.570  A:0.430\tG|G: 0.337  A|A: 0.198  A|G:
0.465  \n\tGIH \tG:0.573  A:0.427\tG|G: 0.340  A|A: 0.194  A|G: 0.466  \n\tITU \tG:0.627  A:0.373\tG|G: 0.382  A|A: 0.127  A|G: 0.490
\n\tPJL \tG:0.594  A:0.406\tG|G: 0.396  A|A: 0.208  A|G: 0.396  \n\tSTU \tG:0.549  A:0.451\tG|G: 0.275  A|A: 0.176  A|G: 0.549
\n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38782227)|| (snp==11725309))

{
            printf(" \n\n Alleles  T/C, Ancestral: T, Ambiguity code: Y, MAF: 0.17 [2]\n Location: 4:38782227 [2] \n SNP ID:
rs11725309 [1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: The
GWAS-identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core
haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII,
```

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IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL
\tT:0.826  C:0.174\tT|T: 0.704  C|C: 0.052  C|T: 0.244 \n\n AFRICAN  \tT:0.989  C:0.011\tT|T: 0.977  C|C: 0.000  C|T: 0.023  \n\tACB
\tT:0.979  C:0.021\tT|T: 0.958  C|C: 0.000  C|T: 0.042  \n\tASW \tT:0.926  C:0.074\tT|T: 0.872  C|C: 0.000  C|T: 0.148  \n\tESN
\tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tGWD \tT:0.991  C:0.009\tT|T: 0.982  C|C: 0.000  C|T: 0.018  \n\tLWK
\tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tMSL \tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tYRI
\tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000      \n\n AMERICAN \tT:0.854  C:0.146\tT|T: 0.744  C|C: 0.035  C|T: 0.222
\n\tCLM \tT:0.856  C:0.144\tT|T: 0.734  C|C: 0.021  C|T: 0.245  \n\tMXL \tT:0.891  C:0.109\tT|T: 0.797  C|C: 0.016  C|T: 0.188
\n\tPEL \tT:0.941  C:0.059\tT|T: 0.882  C|C: 0.000  C|T: 0.118  \n\tPUR \tT:0.760  C:0.240\tT|T: 0.606  C|C: 0.087  C|T: 0.308  \n\n
EAST ASIAN\tT:0.626  C:0.374\tT|T: 0.405  C|C: 0.153  C|T: 0.442  \n\tCDX \tT:0.796  C:0.204\tT|T: 0.634  C|C: 0.043  C|T: 0.323
\n\tCHB \tT:0.485  C:0.515\tT|T: 0.233  C|C: 0.262  C|T: 0.505  \n\tCHS \tT:0.633  C:0.367\tT|T: 0.390  C|C: 0.124  C|T: 0.486  \n\tJPT
\tT:0.476  C:0.524\tT|T: 0.221  C|C: 0.269  C|T: 0.510  \n\tKHV \tT:0.763  C:0.237\tT|T: 0.576  C|C: 0.051  C|T: 0.374    \n\n
EUROPEAN \tT:0.786  C:0.214 \tT|T: 0.632  C|C: 0.060  C|T: 0.308  \n\tCEU \tT:0.813  C:0.187\tT|T: 0.667  C|C: 0.040  C|T: 0.293
\n\tFIN \tT:0.909  C:0.091\tT|T: 0.828  C|C: 0.010  C|T: 0.162  \n\tGBR \tT:0.835  C:0.165\tT|T: 0.692  C|C: 0.022  C|T: 0.286  \n\tIBS
\tT:0.701  C:0.299\tT|T: 0.514  C|C: 0.112  C|T: 0.374  \n\tTSI \tT:0.692  C:0.308\tT|T: 0.486  C|C: 0.103  C|T: 0.411  \n\n SOUTH
ASIAN\tT:0.834  C:0.166\tT|T: 0.689  C|C: 0.020  C|T: 0.290  \n\tBEB \tT:0.779  C:0.221\tT|T: 0.593  C|C: 0.035  C|T: 0.372  \n\tGIH
\tT:0.820  C:0.180\tT|T: 0.680  C|C: 0.039  C|T: 0.282  \n\tITU \tT:0.873  C:0.127\tT|T: 0.755  C|C: 0.010  C|T: 0.235  \n\tPJL \tT:0.870
C:0.130\tT|T: 0.750  C|C: 0.010  C|T: 0.240  \n\tSTU \tT:0.824  C:0.176\tT|T: 0.657  C|C: 0.010  C|T: 0.333  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38783057)|| (snp==10034903))
{
            printf(" \n\n Alleles  C/G, Ancestral:G, Ambiguity code: S, MAF: 0.44 [2]\n Location: 4:38783057 [2] \n SNP ID:
rs10034903 [1] \n GWAS Trait: Self-reported allergy [1]\n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description:
Not Known \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tC:0.562  G:0.438\tC|C: 0.343  C|G: 0.437
G|G: 0.220 \n\n AFRICAN  \tC:0.356  G:0.644\tC|C: 0.126  C|G: 0.461  G|G: 0.413  \n\tACB \tC:0.375  G:0.625\tC|C: 0.115  C|G: 0.521
G|G: 0.365  \n\tASW \tC:0.508  G:0.492\tC|C: 0.197  C|G: 0.623  G|G: 0.180  \n\tESN \tC:0.374  G:0.626\tC|C: 0.152  C|G: 0.444  G|G:
0.404  \n\tGWD \tC:0.327  G:0.673\tC|C: 0.133  C|G: 0.389  G|G: 0.478  \n\tLWK \tC:0.343  G:0.657\tC|C: 0.131  C|G: 0.424  G|G:
0.444  \n\tMSL \tC:0.353  G:0.647\tC|C: 0.094  C|G: 0.518  G|G: 0.388  \n\tYRI \tC:0.282  G:0.718\tC|C: 0.083  C|G: 0.398  G|G: 0.519
\n\n AMERICAN \tC:0.749  G:0.251\tC|C: 0.585  C|G: 0.329  G|G: 0.086  \n\tCLM \tC:0.729  G:0.271\tC|C: 0.521  C|G: 0.415  G|G:
0.064  \n\tMXL \tC:0.812  G:0.188\tC|C: 0.656  C|G: 0.312  G|G: 0.031  \n\tPEL \tC:0.882  G:0.118\tC|C: 0.788  C|G: 0.188  G|G: 0.024
\n\tPUR \tC:0.620  G:0.380 \tC|C: 0.433  C|G: 0.375  G|G: 0.192  \n\n EAST ASIAN\tC:0.519  G:0.481\tC|C: 0.278  C|G: 0.482  G|G:
0.240  \n\tCDX \tC:0.634  G:0.366\tC|C: 0.409  C|G: 0.452  G|G: 0.140  \n\tCHB \tC:0.403  G:0.597\tC|C: 0.155  C|G: 0.495  G|G: 0.350
\n\tCHS \tC:0.548  G:0.452\tC|C: 0.286  C|G: 0.524  G|G: 0.190  \n\tJPT \tC:0.399  G:0.601\tC|C: 0.154  C|G: 0.490  G|G: 0.356
\n\tKHV \tC:0.626  G:0.374\tC|C: 0.404  C|G: 0.444  G|G: 0.152  \n\n EUROPEAN \tC:0.722  G:0.278 \tC|C: 0.541  C|G: 0.362  G|G:
0.097  \n\tCEU \tC:0.788  G:0.212\tC|C: 0.626  C|G: 0.323  G|G: 0.051  \n\tFIN \tC:0.854  G:0.146\tC|C: 0.747  C|G: 0.212  G|G: 0.040
\n\tGBR \tC:0.802  G:0.198\tC|C: 0.626  C|G: 0.352  G|G: 0.022  \n\tIBS \tC:0.575  G:0.425\tC|C: 0.336  C|G: 0.477  G|G: 0.187
\n\tTSI \tC:0.617  G:0.383\tC|C: 0.402  C|G: 0.430  G|G: 0.168  \n\n SOUTH ASIAN\tC:0.586  G:0.414\tC|C: 0.329  C|G: 0.513  G|G:
0.157  \n\tBEB \tC:0.564  G:0.436\tC|C: 0.302  C|G: 0.523  G|G: 0.174  \n\tGIH \tC:0.607  G:0.393\tC|C: 0.379  C|G: 0.456  G|G: 0.165
\n\tITU \tC:0.574  G:0.426\tC|C: 0.284  C|G: 0.578  G|G: 0.137  \n\tPJL \tC:0.620  G:0.380\tC|C: 0.375  C|G: 0.490  G|G: 0.135
\n\tSTU \tC:0.564  G:0.436\tC|C: 0.304  C|G: 0.520  G|G: 0.176  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38783103)|| (snp==10004195))
{
```

```
        printf(" \n\n Alleles  T/A, Ancestral:A, Ambiguity code: W, MAF: 0.37 [2]\n Location: 4:38783103 [2] \n SNP ID:
rs10004195 [1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1,2] \n Archaic-like haplotype cluster: Not
Known\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL
\tT:0.626  A:0.374\tT|T: 0.403  A|A: 0.150  A|T: 0.447 \n\n AFRICAN  \tT:0.592  A:0.408\tT|T: 0.340  A|A: 0.156  A|T: 0.504  \n\tACB
\tT:0.604  A:0.396\tT|T: 0.323  A|A: 0.115  A|T: 0.562  \n\tASW \tT:0.689  A:0.311\tT|T: 0.443  A|A: 0.066  A|T: 0.492  \n\tESN
\tT:0.662  A:0.338\tT|T: 0.465  A|A: 0.141  A|T: 0.394  \n\tGWD \tT:0.558  A:0.442\tT|T: 0.310  A|A: 0.195  A|T: 0.496  \n\tLWK
\tT:0.571  A:0.429\tT|T: 0.323  A|A: 0.182  A|T: 0.495  \n\tMSL \tT:0.565  A:0.435\tT|T: 0.247  A|A: 0.118  A|T: 0.635  \n\tYRI
\tT:0.542  A:0.458\tT|T: 0.306  A|A: 0.222  A|T: 0.472  \n\n AMERICAN \tT:0.768  A:0.232\tT|T: 0.611  A|A: 0.075  A|T: 0.314
\n\tCLM \tT:0.734  A:0.266\tT|T: 0.532  A|A: 0.064  A|T: 0.404  \n\tMXL \tT:0.820  A:0.180\tT|T: 0.656  A|A: 0.016  A|T: 0.328
\n\tPEL \tT:0.888  A:0.112\tT|T: 0.800  A|A: 0.024  A|T: 0.176  \n\tPUR \tT:0.668  A:0.332\tT|T: 0.500  A|A: 0.163  A|T: 0.337  \n\n
EAST ASIAN\tT:0.519  A:0.481\tT|T: 0.278  A|A: 0.240  A|T: 0.482  \n\tCDX \tT:0.634  A:0.366\tT|T: 0.409  A|A: 0.140  A|T: 0.452
\n\tCHB \tT:0.403  A:0.597\tT|T: 0.155  A|A: 0.350  A|T: 0.495  \n\tCHS \tT:0.548  A:0.452\tT|T: 0.286  A|A: 0.190  A|T: 0.524
\n\tJPT \tT:0.399  A:0.601\tT|T: 0.154  A|A: 0.356  A|T: 0.490  \n\tKHV \tT:0.626  A:0.374\tT|T: 0.404  A|A: 0.152  A|T: 0.444  \n\n
EUROPEAN \tT:0.721  A:0.279 \tT|T: 0.539  A|A: 0.097  A|T: 0.364  \n\tCEU \tT:0.788  A:0.212\tT|T: 0.626  A|A: 0.051  A|T: 0.323
\n\tFIN \tT:0.848  A:0.152\tT|T: 0.737  A|A: 0.040  A|T: 0.222  \n\tGBR \tT:0.802  A:0.198\tT|T: 0.626  A|A: 0.022  A|T: 0.352  \n\tIBS
\tT:0.575  A:0.425\tT|T: 0.336  A|A: 0.187  A|T: 0.477  \n\tTSI \tT:0.617  A:0.383\tT|T: 0.402  A|A: 0.168  A|T: 0.430  \n\n SOUTH
ASIAN\tT:0.586  A:0.414\tT|T: 0.329  A|A: 0.157  A|T: 0.513  \n\tBEB \tT:0.564  A:0.436\tT|T: 0.302  A|A: 0.174  A|T: 0.523  \n\tGIH
\tT:0.607  A:0.393\tT|T: 0.379  A|A: 0.165  A|T: 0.456  \n\tITU \tT:0.574  A:0.426\tT|T: 0.284  A|A: 0.137  A|T: 0.578  \n\tPJL
\tT:0.620  A:0.380\tT|T: 0.375  A|A: 0.135  A|T: 0.490  \n\tSTU \tT:0.564  A:0.436\tT|T: 0.304  A|A: 0.176  A|T: 0.520  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38785595)|| (snp==12233670))
{
        printf(" \n\n Alleles  C/T, Ancestral:T, Ambiguity code: Y, MAF: 0.41 [2]\n Location: 4:38785595 [2] \n SNP ID:
rs12233670 [1] \n GWAS Trait: Multiple complex diseases, Coronary Artery Disease, Lymphocyte counts, Helicobacter pylori serologic
status, Self-reported allergy [1]\n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known  \n\n\n
Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tC:0.592  T:0.408\tC|C: 0.369  C|T: 0.446  T|T: 0.185 \n\n
AFRICAN  \tC:0.464  T:0.536\tC|C: 0.215  C|T: 0.498  T|T: 0.287  \n\tACB \tC:0.526  T:0.474\tC|C: 0.250  C|T: 0.552  T|T: 0.198
\n\tASW \tC:0.549  T:0.451\tC|C: 0.262  C|T: 0.574  T|T: 0.164  \n\tESN \tC:0.500  T:0.500\tC|C: 0.242  C|T: 0.515  T|T: 0.242
\n\tGWD \tC:0.482  T:0.518\tC|C: 0.239  C|T: 0.487  T|T: 0.274  \n\tLWK \tC:0.384  T:0.616\tC|C: 0.172  C|T: 0.424  T|T: 0.404
\n\tMSL \tC:0.429  T:0.571\tC|C: 0.153  C|T: 0.553  T|T: 0.294  \n\tYRI \tC:0.407  T:0.593\tC|C: 0.194  C|T: 0.426  T|T: 0.380  \n\n
AMERICAN \tC:0.761  T:0.239\tC|C: 0.599  C|T: 0.323  T|T: 0.078  \n\tCLM \tC:0.729  T:0.271\tC|C: 0.521  C|T: 0.415  T|T: 0.064
\n\tMXL \tC:0.820  T:0.180\tC|C: 0.656  C|T: 0.328  T|T: 0.016  \n\tPEL \tC:0.888  T:0.112\tC|C: 0.800  C|T: 0.176  T|T: 0.024  \n\tPUR
\tC:0.649  T:0.351 \tC|C: 0.471  C|T: 0.356  T|T: 0.173  \n\n EAST ASIAN\tC:0.519  T:0.481\tC|C: 0.278  C|T: 0.482  T|T: 0.240
\n\tCDX \tC:0.634  T:0.366\tC|C: 0.409  C|T: 0.452  T|T: 0.140  \n\tCHB \tC:0.403  T:0.597\tC|C: 0.155  C|T: 0.495  T|T: 0.350
\n\tCHS \tC:0.548  T:0.452\tC|C: 0.286  C|T: 0.524  T|T: 0.190  \n\tJPT \tC:0.399  T:0.601\tC|C: 0.154  C|T: 0.490  T|T: 0.356  \n\tKHV
\tC:0.626  T:0.374\tC|C: 0.404  C|T: 0.444  T|T: 0.152  \n\n EUROPEAN \tC:0.722  T:0.278 \tC|C: 0.541  C|T: 0.362  T|T: 0.097
\n\tCEU \tC:0.788  T:0.212\tC|C: 0.626  C|T: 0.323  T|T: 0.051  \n\tFIN \tC:0.854  T:0.146\tC|C: 0.747  C|T: 0.212  T|T: 0.040  \n\tGBR
\tC:0.802  T:0.198\tC|C: 0.626  C|T: 0.352  T|T: 0.022  \n\tIBS \tC:0.575  T:0.425\tC|C: 0.336  C|T: 0.477  T|T: 0.187  \n\tTSI \tC:0.617
T:0.383\tC|C: 0.402  C|T: 0.430  T|T: 0.168  \n\n SOUTH ASIAN\tC:0.586  T:0.414\tC|C: 0.329  C|T: 0.513  T|T: 0.157  \n\tBEB
\tC:0.564  T:0.436\tC|C: 0.302  C|T: 0.523  T|T: 0.174  \n\tGIH \tC:0.607  T:0.393\tC|C: 0.379  C|T: 0.456  T|T: 0.165  \n\tITU \tC:0.574
T:0.426\tC|C: 0.284  C|T: 0.578  T|T: 0.137  \n\tPJL \tC:0.620  T:0.380\tC|C: 0.375  C|T: 0.490  T|T: 0.135  \n\tSTU \tC:0.564
T:0.436\tC|C: 0.304  C|T: 0.520  T|T: 0.176  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
```

```
else if ((chr==38786613)|| (snp==6834581))
{
        printf(" \n\n Alleles  T/C, Ancestral:T, Ambiguity code: Y, MAF: 0.44 [2]\n Location: 4:38786613 [2] \n SNP ID: rs6834581
[1] \n GWAS Trait: Alcohol consumption [1]\n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not
Known \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tT:0.556  C:0.444\tT|T: 0.339  C|C: 0.227  C|T:
0.433 \n\n AFRICAN  \tT:0.337  C:0.663\tT|T: 0.115  C|C: 0.442  C|T: 0.443  \n\tACB \tT:0.344  C:0.656\tT|T: 0.115  C|C: 0.427  C|T:
0.458  \n\tASW \tT:0.467  C:0.533\tT|T: 0.180  C|C: 0.246  C|T: 0.574  \n\tESN \tT:0.359  C:0.641\tT|T: 0.141  C|C: 0.424  C|T: 0.434
\n\tGWD \tT:0.314  C:0.686\tT|T: 0.115  C|C: 0.487  C|T: 0.398  \n\tLWK \tT:0.333  C:0.667\tT|T: 0.131  C|C: 0.465  C|T: 0.404
\n\tMSL \tT:0.324  C:0.676\tT|T: 0.059  C|C: 0.412  C|T: 0.529  \n\tYRI \tT:0.273  C:0.727\tT|T: 0.083  C|C: 0.537  C|T: 0.380  \n\n
AMERICAN \tT:0.746  C:0.254\tT|T: 0.579  C|C: 0.086  C|T: 0.334  \n\tCLM \tT:0.718  C:0.282\tT|T: 0.500  C|C: 0.064  C|T: 0.436
\n\tMXL \tT:0.812  C:0.188\tT|T: 0.656  C|C: 0.031  C|T: 0.312  \n\tPEL \tT:0.882  C:0.118\tT|T: 0.788  C|C: 0.024  C|T: 0.188  \n\tPUR
\tT:0.620  C:0.380 \tT|T: 0.433  C|C: 0.192  C|T: 0.375  \n\n EAST ASIAN\tT:0.519  C:0.481\tT|T: 0.278  C|C: 0.240  C|T: 0.482
\n\tCDX \tT:0.634  C:0.366\tT|T: 0.409  C|C: 0.140  C|T: 0.452  \n\tCHB \tT:0.403  C:0.597\tT|T: 0.155  C|C: 0.350  C|T: 0.495
\n\tCHS \tT:0.548  C:0.452\tT|T: 0.286  C|C: 0.190  C|T: 0.524  \n\tJPT \tT:0.399  C:0.601\tT|T: 0.154  C|C: 0.356  C|T: 0.490  \n\tKHV
\tT:0.626  C:0.374\tT|T: 0.404  C|C: 0.152  C|T: 0.444  \n\n EUROPEAN \tT:0.722  C:0.278 \tT|T: 0.541  C|C: 0.097  C|T: 0.362
\n\tCEU \tT:0.788  C:0.212\tT|T: 0.626  C|C: 0.051  C|T: 0.323  \n\tFIN \tT:0.854  C:0.146\tT|T: 0.747  C|C: 0.040  C|T: 0.212  \n\tGBR
\tT:0.802  C:0.198\tT|T: 0.626  C|C: 0.022  C|T: 0.352  \n\tIBS \tT:0.575  A:0.425\tT|T: 0.336  C|C: 0.187  C|T: 0.477  \n\tTSI \tT:0.617
C:0.383\tT|T: 0.402  C|C: 0.168  C|T: 0.430  \n\n SOUTH ASIAN\tT:0.586  C:0.414\tT|T: 0.329  C|C: 0.157  C|T: 0.513  \n\tBEB
\tT:0.564  C:0.436\tT|T: 0.302  C|C: 0.174  C|T: 0.523  \n\tGIH \tT:0.607  C:0.393\tT|T: 0.379  C|C: 0.165  C|T: 0.456  \n\tITU \tT:0.574
C:0.426\tT|T: 0.284  C|C: 0.137  C|T: 0.578  \n\tPJL \tT:0.620  C:0.380\tT|T: 0.375  C|C: 0.135  C|T: 0.490  \n\tSTU \tT:0.564
C:0.436\tT|T: 0.304  C|C: 0.176  C|T: 0.520  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38788119)|| (snp==4833093))
{
        printf(" \n\n Alleles  G/T, Ancestral:T, Ambiguity code: K, MAF: 0.40 [2]\n Location: 4:38788119 [2] \n SNP ID: rs4833093
[1] \n GWAS Trait: Alcohol consumption [1]\n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not
Known \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tG:0.597  T:0.403\tG|G: 0.373  G|T: 0.446
T|T: 0.180 \n\n AFRICAN  \tG:0.464  T:0.536\tG|G: 0.215  G|T: 0.498  T|T: 0.287  \n\tACB \tG:0.521  T:0.479\tG|G: 0.240  G|T: 0.562
T|T: 0.198  \n\tASW \tG:0.557  T:0.443\tG|G: 0.279  G|T: 0.557  T|T: 0.164  \n\tESN \tG:0.500  T:0.500\tG|G: 0.242  G|T: 0.515  T|T:
0.242  \n\tGWD \tG:0.482  T:0.518\tG|G: 0.239  G|T: 0.487  T|T: 0.274  \n\tLWK \tG:0.389  T:0.611\tG|G: 0.172  G|T: 0.434  T|T:
0.394  \n\tMSL \tG:0.429  T:0.571\tG|G: 0.153  G|T: 0.553  T|T: 0.294  \n\tYRI \tG:0.403  T:0.597\tG|G: 0.194  G|T: 0.417  T|T: 0.389
\n\n AMERICAN \tG:0.765  T:0.235\tG|G: 0.608  G|T: 0.314  T|T: 0.078  \n\tCLM \tG:0.739  T:0.261\tG|G: 0.543  C|T: 0.394  T|T:
0.064  \n\tMXL \tG:0.828  T:0.172\tG|G: 0.672  G|T: 0.312  T|T: 0.016  \n\tPEL \tG:0.888  T:0.112\tG|G: 0.800  G|T: 0.176  T|T: 0.024
\n\tPUR \tG:0.649  T:0.351 \tG|G: 0.471  G|T: 0.356  T|T: 0.173  \n\n EAST ASIAN\tG:0.520  T:0.480\tG|G: 0.278  G|T: 0.484  T|T:
0.238  \n\tCDX \tG:0.640  T:0.360\tG|G: 0.409  G|T: 0.462  T|T: 0.129  \n\tCHB \tG:0.403  T:0.597\tG|G: 0.155  G|T: 0.495  T|T: 0.350
\n\tCHS \tG:0.548  T:0.452\tG|G: 0.286  G|T: 0.524  T|T: 0.190  \n\tJPT \tG:0.399  T:0.601\tG|G: 0.154  G|T: 0.490  T|T: 0.356
\n\tKHV \tG:0.626  T:0.374\tG|G: 0.404  G|T: 0.444  T|T: 0.152  \n\n EUROPEAN \tG:0.721  T:0.279 \tG|G: 0.539  G|T: 0.364  T|T:
0.097  \n\tCEU \tG:0.788  T:0.212\tG|G: 0.626  G|T: 0.323  T|T: 0.051  \n\tFIN \tG:0.854  T:0.146\tG|G: 0.747  G|T: 0.212  T|T: 0.040
\n\tGBR \tG:0.802  T:0.198\tG|G: 0.626  G|T: 0.352  T|T: 0.022  \n\tIBS \tG:0.575  T:0.425\tG|G: 0.336  G|T: 0.477  T|T: 0.187  \n\tTSI
\tG:0.612  T:0.388\tG|G: 0.393  G|T: 0.439  T|T: 0.168  \n\n SOUTH ASIAN\tG:0.608  T:0.392\tG|G: 0.350  G|T: 0.517  T|T: 0.133
\n\tBEB \tG:0.576  T:0.424\tG|G: 0.326  G|T: 0.500  T|T: 0.174  \n\tGIH \tG:0.665  T:0.335\tG|G: 0.447  G|T: 0.437  T|T: 0.117  \n\tITU
\tG:0.593  T:0.407\tG|G: 0.284  G|T: 0.618  T|T: 0.098  \n\tPJL \tG:0.630  T:0.370\tG|G: 0.375  G|T: 0.510  T|T: 0.115  \n\tSTU
\tG:0.574  T:0.426\tG|G: 0.314  G|T: 0.520  T|T: 0.167  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
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}
else if ((chr==38790719)|| (snp==6531663))
{
        printf(" \n\n Alleles  T/C, Ancestral:C, Ambiguity code: Y, MAF: 0.45 [2]\n Location: 4:38790719 [2] \n SNP ID: rs6531663 [1] \n GWAS Trait: Alcohol consumption [1]\n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tT:0.548  C:0.452\tT|T: 0.334  C|C: 0.239  C|T: 0.427 \n\n AFRICAN  \tT:0.304  C:0.696\tT|T: 0.094  C|C: 0.486  C|T: 0.421  \n\tACB \tT:0.323  C:0.677\tT|T: 0.094  C|C: 0.448  C|T: 0.458  \n\tASW \tT:0.410  C:0.590\tT|T: 0.148  C|C: 0.328  C|T: 0.525  \n\tESN \tT:0.348  C:0.652\tT|T: 0.141  C|C: 0.444  C|T: 0.414  \n\tGWD \tT:0.288  C:0.712\tT|T: 0.097  C|C: 0.522  C|T: 0.381  \n\tLWK \tT:0.283  C:0.717\tT|T: 0.061  C|C: 0.495  C|T: 0.444  \n\tMSL \tT:0.271  C:0.729\tT|T: 0.059  C|C: 0.518  C|T: 0.424  \n\tYRI \tT:0.250  C:0.750\tT|T: 0.074  C|C: 0.574  C|T: 0.352  \n\n AMERICAN \tT:0.748  C:0.252\tT|T: 0.582  C|C: 0.086  C|T: 0.331  \n\tCLM \tT:0.729  C:0.271\tT|T: 0.521  C|C: 0.064  C|T: 0.415  \n\tMXL \tT:0.820  C:0.180\tT|T: 0.672  C|C: 0.031  C|T: 0.297  \n\tPEL \tT:0.882  C:0.118\tT|T: 0.788  C|C: 0.024  C|T: 0.188  \n\tPUR \tT:0.611  C:0.389 \tT|T: 0.413  C|C: 0.192  C|T: 0.394  \n\n EAST ASIAN\tT:0.520  C:0.480\tT|T: 0.280  C|C: 0.240  C|T: 0.480  \n\tCDX \tT:0.640  C:0.360\tT|T: 0.419  C|C: 0.140  C|T: 0.441  \n\tCHB \tT:0.408  C:0.592\tT|T: 0.155  C|C: 0.340  C|T: 0.505  \n\tCHS \tT:0.543  C:0.457\tT|T: 0.286  C|C: 0.200  C|T: 0.514  \n\tJPT \tT:0.399  C:0.601\tT|T: 0.154  C|C: 0.356  C|T: 0.490  \n\tKHV \tT:0.626  C:0.374\tT|T: 0.404  C|C: 0.152  C|T: 0.444  \n\n EUROPEAN \tT:0.721  C:0.279 \tT|T: 0.539  C|C: 0.097  C|T: 0.364  \n\tCEU \tT:0.788  C:0.212\tT|T: 0.626  C|C: 0.051  C|T: 0.323  \n\tFIN \tT:0.854  C:0.146\tT|T: 0.747  C|C: 0.040  C|T: 0.212  \n\tGBR \tT:0.802  C:0.198\tT|T: 0.626  C|C: 0.022  C|T: 0.352  \n\tIBS \tT:0.575  C:0.425\tT|T: 0.336  C|C: 0.187  C|T: 0.477  \n\tTSI \tT:0.612  C:0.388\tT|T: 0.393  C|C: 0.168  C|T: 0.439  \n\n SOUTH ASIAN\tT:0.586  C:0.414\tT|T: 0.329  C|C: 0.157  C|T: 0.513  \n\tBEB \tT:0.564  C:0.436\tT|T: 0.302  C|C: 0.174  C|T: 0.523  \n\tGIH \tT:0.607  C:0.393\tT|T: 0.379  C|C: 0.165  C|T: 0.456  \n\tITU \tT:0.574  C:0.426\tT|T: 0.284  C|C: 0.137  C|T: 0.578  \n\tPJL \tT:0.620  C:0.380\tT|T: 0.375  C|C: 0.135  C|T: 0.490  \n\tSTU \tT:0.564  C:0.436\tT|T: 0.304  C|C: 0.176  C|T: 0.520  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38790903)|| (snp==4543123))
{
        printf(" \n\n Alleles  A/G, Ancestral:G, Ambiguity code: R, MAF: 0.37 [2]\n Location: 4:38790903 [2] \n SNP ID: rs4543123 [1] \n GWAS Trait: Amyotrophic lateral sclerosis, PAget's disease, Helicobacter pylori serologic status, Alcohol consumption, Self-reported allergy [1,2] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tA:0.632  G:0.368\tA|A: 0.416  A|G: 0.433  G|G: 0.151 \n\n AFRICAN  \tA:0.467  G:0.533\tA|A: 0.201  A|G: 0.533  G|G: 0.266  \n\tACB \tA:0.458  G:0.542\tA|A: 0.167  A|G: 0.583  G|G: 0.250  \n\tASW \tA:0.566  G:0.434\tA|A: 0.262  A|G: 0.607  G|G: 0.131  \n\tESN \tA:0.455  G:0.545\tA|A: 0.192  A|G: 0.525  G|G: 0.283  \n\tGWD \tA:0.429  G:0.571\tA|A: 0.159  A|G: 0.540  G|G: 0.301  \n\tLWK \tA:0.515  G:0.485\tA|A: 0.273  A|G: 0.485  G|G: 0.242  \n\tMSL \tA:0.447  G:0.553\tA|A: 0.176  A|G: 0.541  G|G: 0.282  \n\tYRI \tA:0.444  G:0.556\tA|A: 0.204  A|G: 0.481  G|G: 0.315  \n\n AMERICAN \tA:0.775  G:0.225\tA|A: 0.631  A|G: 0.288  G|G: 0.081  \n\tCLM \tA:0.771  G:0.229\tA|A: 0.606  A|G: 0.330  G|G: 0.064  \n\tMXL \tA:0.836  G:0.164\tA|A: 0.703  A|G: 0.266  G|G: 0.031  \n\tPEL \tA:0.906  G:0.094\tA|A: 0.824  A|G: 0.165  G|G: 0.012  \n\tPUR \tA:0.635  G:0.365\tA|A: 0.452  A|G: 0.365  G|G: 0.183  \n\n EAST ASIAN\tA:0.591  G:0.409\tA|A: 0.353  A|G: 0.476  G|G: 0.171  \n\tCDX \tA:0.720  G:0.280\tA|A: 0.505  A|G: 0.430  G|G: 0.065  \n\tCHB \tA:0.466  G:0.534\tA|A: 0.214  A|G: 0.505  G|G: 0.282  \n\tCHS \tA:0.629  G:0.371\tA|A: 0.390  A|G: 0.476  G|G: 0.133  \n\tJPT \tA:0.462  G:0.538\tA|A: 0.202  A|G: 0.519  G|G: 0.279  \n\tKHV \tA:0.697  G:0.303\tA|A: 0.475  A|G: 0.444  G|G: 0.081  \n\n EUROPEAN \tA:0.733  G:0.267 \tA|A: 0.555  A|G: 0.356  G|G: 0.089  \n\tCEU \tA:0.788  G:0.212\tA|A: 0.626  A|G: 0.323  G|G: 0.051  \n\tFIN \tA:0.854  G:0.146\tA|A: 0.747  A|G: 0.212  G|G: 0.040  \n\tGBR \tA:0.808  G:0.192\tA|A: 0.637  A|G: 0.341  G|G: 0.022  \n\tIBS \tA:0.603  G:0.397\tA|A: 0.383  A|G: 0.439  G|G: 0.178  \n\tTSI \tA:0.636  G:0.364\tA|A: 0.411  A|G: 0.449  G|G: 0.140  \n\n SOUTH ASIAN\tA:0.692  G:0.308\tA|A: 0.474  A|G: 0.436  G|G: 0.090  \n\tBEB \tA:0.640  G:0.360\tA|A: 0.419  A|G: 0.442  G|G: 0.140  \n\tGIH \tA:0.699  G:0.301\tA|A: 0.505  A|G: 0.388  G|G: 0.107  \n\tITU \tA:0.706  G:0.294\tA|A: 0.471  A|G: 0.471  G|G: 0.059  \n\tPJL \tA:0.719  G:0.281\tA|A: 0.521  A|G: 0.396  G|G: 0.083  \n\tSTU \tA:0.691  G:0.309\tA|A: 0.451  A|G: 0.480  G|G: 0.069  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
```

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printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38796255)|| (snp==4624663))
{
        printf(" \n\n Alleles  T/C, Ancestral: T, Ambiguity code: Y, MAF: 0.03 [2]\n Location: 4:38796255 [2] \n SNP ID: rs4624663 [1] \n GWAS Trait: Panic disorder [1] \n Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tT:0.970  C:0.030\tT|T: 0.943  C|C: 0.003  C|T: 0.054 \n\n AFRICAN  \tT:0.921  C:0.079\tT|T: 0.849  C|C: 0.006  C|T: 0.145  \n\tACB \tT:0.917  C:0.083\tT|T: 0.844  C|C: 0.010  C|T: 0.146  \n\tASW \tT:0.918  C:0.082\tT|T: 0.836  C|C: 0.000  C|T: 0.164  \n\tESN \tT:0.924  C:0.076\tT|T: 0.848  C|C: 0.000  C|T: 0.152  \n\tGWD \tT:0.920  C:0.080\tT|T: 0.850  C|C: 0.009  C|T: 0.142  \n\tLWK \tT:0.934  C:0.066\tT|T: 0.879  C|C: 0.010  C|T: 0.111  \n\tMSL \tT:0.924  C:0.076\tT|T: 0.859  C|C: 0.012  C|T: 0.129  \n\tYRI \tT:0.912  C:0.088\tT|T: 0.824  C|C: 0.000  C|T: 0.176    \n\n AMERICAN \tT:0.980  C:0.020\tT|T: 0.960  C|C: 0.000  C|T: 0.040  \n\tCLM \tT:0.968  C:0.032\tT|T: 0.936  C|C: 0.000  C|T: 0.064  \n\tMXL \tT:0.984  C:0.016\tT|T: 0.969  C|C: 0.000  C|T: 0.031  \n\tPEL \tT:0.994  C:0.006\tT|T: 0.988  C|C: 0.000  C|T: 0.012  \n\tPUR \tT:0.976  C:0.024\tT|T: 0.952  C|C: 0.000  C|T: 0.048  \n\n EAST ASIAN\tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tCDX \tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tCHB \tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tCHS \tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tJPT \tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tKHV \tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\n EUROPEAN \tT:0.975  C:0.025 \tT|T: 0.954  C|C: 0.004  C|T: 0.042  \n\tCEU \tT:0.990  C:0.010\tT|T: 0.980  C|C: 0.000  C|T: 0.020  \n\tFIN \tT:0.970  C:0.030\tT|T: 0.949  C|C: 0.010  C|T: 0.040  \n\tGBR \tT:0.978  C:0.022\tT|T: 0.956  C|C: 0.000  C|T: 0.044  \n\tIBS \tT:0.949  C:0.051\tT|T: 0.907  C|C: 0.009  C|T: 0.084  \n\tTSI \tT:0.991  C:0.009\tT|T: 0.981  C|C: 0.000  C|T: 0.019  \n\n SOUTH ASIAN\tT:0.993  C:0.007\tT|T: 0.988  C|C: 0.002  C|T: 0.010  \n\tBEB \tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tGIH \tT:0.990  C:0.010\tT|T: 0.981  C|C: 0.000  C|T: 0.019  \n\tITU \tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tPJL \tT:0.979  C:0.021\tT|T: 0.969  C|C: 0.010  C|T: 0.021  \n\tSTU \tT:0.995  C:0.005\tT|T: 0.990  C|C: 0.000  C|T: 0.010  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
 else if ((chr==38798089)|| (snp==4833095))
{
        printf(" \n\n Alleles  T/C, Ancestral:C, Ambiguity code: Y, MAF: 0.43 [2]\n Location: 4:38798089 [2] \n SNP ID: rs4833095 [1] \n GWAS Trait: Amyotrophic lateral sclerosis, Paget's disease, Helicobacter pylori serologic status, Alcohol consumption, Self-reported allergy, Leprosy, Asthma and Seasonal allergic rhinitis, Hay fever [1,2]\n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Schuring et al. (2009) studied association of an asn248-to-ser (N248S) SNP in the TLR1 gene and leprosy (LPRS5; 613223) in a Bangladeshi population consisting of 842 patients and 543 controls. They found that the S allele was slightly more frequent among patients than controls (54% vs 51%; OR = 1.12). Homozygosity for S248 was significantly associated with leprosy per se (OR = 1.34), whereas heterozygosity was found to be protective against leprosy (OR = 0.78). In contrast, the homozygous N248 genotype was equally distributed among patients and controls. No difference in allele frequency or genotype was associated with leprosy classification or serologic status. However, patients who experienced erythema nodosum leprosum reactions were more likely to have the N248 allele (68%) than were patients who had no reactions (46%). Schuring et al. (2009) noted that amino acid 248 of TLR1 is located in the external ligand-binding site of the receptor, and that Omueti et al. (2007) had shown that the S248 variant enabled normal function, whereas the N248 variant diminished the response of TLR1 to bacterial agonists. [3] \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tT:0.425  C:0.575\tT|T: 0.232  C|C: 0.382  C|T: 0.386 \n\n AFRICAN  \tT:0.120  C:0.880\tT|T: 0.015  C|C: 0.775  C|T: 0.210  \n\tACB \tT:0.161  C:0.839\tT|T: 0.021  C|C: 0.698  C|T: 0.281  \n\tASW \tT:0.230  C:0.770\tT|T: 0.049  C|C: 0.590  C|T: 0.361  \n\tESN \tT:0.106  C:0.894\tT|T: 0.010  C|C: 0.798  C|T: 0.192  \n\tGWD \tT:0.142  C:0.858\tT|T: 0.018  C|C: 0.735  C|T: 0.248  \n\tLWK \tT:0.076  C:0.924\tT|T: 0.000  C|C: 0.848  C|T: 0.152  \n\tMSL \tT:0.071  C:0.929\tT|T: 0.000  C|C: 0.859  C|T: 0.141  \n\tYRI \tT:0.093  C:0.907\tT|T: 0.019  C|C: 0.833  C|T: 0.148  \n\n AMERICAN \tT:0.527  C:0.473\tT|T: 0.291  C|C: 0.236  C|T: 0.473  \n\tCLM \tT:0.553  C:0.447\tT|T: 0.309  C|C: 0.202  C|T: 0.489  \n\tMXL \tT:0.508  C:0.492\tT|T: 0.250  C|C: 0.234  C|T: 0.516  \n\tPEL \tT:0.494  C:0.506\tT|T: 0.271  C|C: 0.282  C|T: 0.447  \n\tPUR \tT:0.543  C:0.457 \tT|T: 0.317  C|C: 0.231  C|T: 0.452  \n\n EAST ASIAN\tT:0.401  C:0.599\tT|T: 0.165  C|C: 0.363  C|T: 0.472  \n\tCDX \tT:0.484  C:0.516\tT|T: 0.247  C|C: 0.280  C|T: 0.473  \n\tCHB \tT:0.320  C:0.680\tT|T: 0.087  C|C: 0.447  C|T: 0.466  \n\tCHS \tT:0.395  C:0.605\tT|T: 0.152  C|C: 0.362  C|T: 0.486  \n\tJPT \tT:0.303  C:0.697\tT|T: 0.087  C|C: 0.481  C|T: 0.433  \n\tKHV \tT:0.515  C:0.485\tT|T: 0.263  C|C: 0.232  C|T: 0.505  \n\n EUROPEAN \tT:0.720  C:0.280 \tT|T: 0.537  C|C: 0.097  C|T: 0.366  \n\tCEU \tT:0.793  C:0.207\tT|T: 0.636  C|C: 0.051  C|T: 0.313  \n\tFIN \tT:0.848  C:0.152\tT|T: 0.737  C|C: 0.040  C|T: 0.222  \n\tGBR \tT:0.802  C:0.198\tT|T: 0.626  C|C: 0.022  C|T: 0.352  \n\tIBS \tT:0.575  A:0.425\tT|T: 0.336  C|C: 0.187  C|T: 0.477  \n\tTSI \tT:0.607  C:0.393\tT|T: 0.383  C|C: 0.168  C|T: 0.449  \n\n SOUTH ASIAN\tT:0.488  C:0.512\tT|T: 0.241  C|C: 0.266  C|T: 0.493  \n\tBEB \tT:0.477  C:0.523\tT|T: 0.209  C|C: 0.256  C|T: 0.535  \n\tGIH \tT:0.529  C:0.471\tT|T: 0.262  C|C: 0.204  C|T: 0.534  \n\tITU \tT:0.446  C:0.554\tT|T: 0.176  C|C: 0.284  C|T: 0.539  \n\tPJL \tT:0.531  C:0.469\tT|T: 0.333  C|C: 0.271  C|T: 0.396  \n\tSTU \tT:0.456  C:0.544\tT|T: 0.225  C|C: 0.314  C|T: 0.461  \n\n");
```

```
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J.(2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.ExAC Browser. (2016). Exome Aggregation Consortium. Retrieved March 12, 2017 from http://exac.broadinstitute.org/\n3.Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38799664)|| (snp==5743604))
{
        printf(" \n\n Alleles  A/G, Ancestral:G, Ambiguity code: R, MAF: 0.47 [2]\n Location: 4:38799664 [2] \n SNP ID: rs5743604 [1] \n GWAS Trait: Helicobacter pylori serologic status, Alcohol consumption, Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tA:0.532  G:0.468\tA|A: 0.306  A|G: 0.451  G|G: 0.243 \n\n AFRICAN  \tA:0.377  G:0.623\tA|A: 0.142  A|G: 0.469  G|G: 0.389  \n\tACB \tA:0.438  G:0.562\tA|A: 0.177  A|G: 0.521  G|G: 0.302  \n\tASW \tA:0.393  G:0.607\tA|A: 0.148  A|G: 0.492  G|G: 0.361  \n\tESN \tA:0.318  G:0.682\tA|A: 0.081  A|G: 0.475  G|G: 0.444  \n\tGWD \tA:0.482  G:0.518\tA|A: 0.230  A|G: 0.504  G|G: 0.265  \n\tLWK \tA:0.283  G:0.717\tA|A: 0.051  A|G: 0.465  G|G: 0.485  \n\tMSL \tA:0.324  G:0.676\tA|A: 0.106  A|G: 0.435  G|G: 0.459  \n\tYRI \tA:0.384  G:0.616\tA|A: 0.185  A|G: 0.398  G|G: 0.417  \n\n AMERICAN \tA:0.563  G:0.437\tA|A: 0.326  A|G: 0.476  G|G: 0.199  \n\tCLM \tA:0.596  G:0.404\tA|A: 0.362  A|G: 0.468  G|G: 0.170  \n\tMXL \tA:0.523  G:0.477\tA|A: 0.266  A|G: 0.516  G|G: 0.219  \n\tPEL \tA:0.524  G:0.476\tA|A: 0.282  A|G: 0.482  G|G: 0.235  \n\tPUR \tA:0.591  G:0.409\tA|A: 0.365  A|G: 0.452  G|G: 0.183  \n\n EAST ASIAN\tA:0.472  G:0.528\tA|A: 0.224  A|G: 0.496  G|G: 0.280  \n\tCDX \tA:0.565  G:0.435\tA|A: 0.323  A|G: 0.484  G|G: 0.194  \n\tCHB \tA:0.374  G:0.626\tA|A: 0.136  A|G: 0.476  G|G: 0.388  \n\tCHS \tA:0.486  G:0.514\tA|A: 0.219  A|G: 0.533  G|G: 0.248  \n\tJPT \tA:0.365  G:0.635\tA|A: 0.125  A|G: 0.481  G|G: 0.394  \n\tKHV \tA:0.586  G:0.414\tA|A: 0.333  A|G: 0.505  G|G: 0.162  \n\n EUROPEAN \tA:0.726  G:0.274 \tA|A: 0.545  A|G: 0.362  G|G: 0.093  \n\tCEU \tA:0.788  G:0.212\tA|A: 0.636  A|G: 0.303  G|G: 0.061  \n\tFIN \tA:0.854  G:0.146\tA|A: 0.747  A|G: 0.212  G|G: 0.040  \n\tGBR \tA:0.808  G:0.192\tA|A: 0.637  A|G: 0.341  G|G: 0.022  \n\tIBS \tA:0.579  G:0.421\tA|A: 0.346  A|G: 0.467  G|G: 0.187  \n\tTSI \tA:0.626  G:0.374\tA|A: 0.393  A|G: 0.467  G|G: 0.140  \n\n SOUTH ASIAN\tA:0.580  G:0.420\tA|A: 0.352  A|G: 0.456  G|G: 0.192  \n\tBEB \tA:0.552  G:0.448\tA|A: 0.314  A|G: 0.477  G|G: 0.209  \n\tGIH \tA:0.621  G:0.379\tA|A: 0.379  A|G: 0.485  G|G: 0.136  \n\tITU \tA:0.539  G:0.461\tA|A: 0.294  A|G: 0.490  G|G: 0.216  \n\tPJL \tA:0.620  G:0.380\tA|A: 0.448  A|G: 0.344  G|G: 0.208  \n\tSTU \tA:0.564  G:0.436\tA|A: 0.324  A|G: 0.480  G|G: 0.196  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
 }
else if ((chr==38800907)|| (snp==5743596))
{
        printf(" \n\n Alleles  G/A, Ancestral: G, Ambiguity code: R, MAF: 0.14 [2]\n Location: 4:38800907 [2] \n SNP ID: rs5743596 [1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL  \tG:0.861  A:0.139\tG|G: 0.760  A|A: 0.038  A|G: 0.202 \n\n AFRICAN  \tG:0.990  A:0.010\tG|G: 0.980  A|A: 0.000  A|G: 0.020  \n\tACB \tG:0.984  A:0.016\tG|G: 0.969  A|A: 0.000  A|G: 0.031  \n\tASW \tG:0.934  A:0.066\tG|G: 0.869  A|A: 0.000  A|G: 0.131  \n\tESN \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000  \n\tGWD \tG:0.991  A:0.009\tG|G: 0.982  A|A: 0.000  A|G: 0.018  \n\tLWK \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000  \n\tMSL \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000  \n\tYRI \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000      \n\n AMERICAN \tG:0.879  A:0.121\tG|G: 0.790  A|A: 0.032  A|G: 0.179  \n\tCLM \tG:0.878  A:0.122\tG|G: 0.766  A|A: 0.011  A|G: 0.223  \n\tMXL \tG:0.930  A:0.070\tG|G: 0.875  A|A: 0.016  A|G: 0.109  \n\tPEL \tG:0.947  A:0.053\tG|G: 0.894  A|A: 0.000  A|G: 0.106  \n\tPUR \tG:0.793  A:0.207\tG|G: 0.673  A|A: 0.087  A|G: 0.240  \n\n EAST ASIAN\tG:0.723  A:0.277\tG|G: 0.550  A|A: 0.103  A|G: 0.347  \n\tCDX \tG:0.898  A:0.102\tG|G: 0.817  A|A: 0.022  A|G: 0.161  \n\tCHB \tG:0.612  A:0.388\tG|G: 0.379  A|A: 0.155  A|G: 0.466  \n\tCHS \tG:0.724  A:0.276\tG|G: 0.524  A|A: 0.076  A|G: 0.400  \n\tJPT \tG:0.514  A:0.486\tG|G: 0.269  A|A: 0.240  A|G: 0.490  \n\tKHV \tG:0.894  A:0.106\tG|G: 0.798  A|A: 0.010  A|G: 0.192  \n\n EUROPEAN \tG:0.824  A:0.176 \tG|G: 0.694  A|A: 0.046  A|G: 0.260  \n\tCEU \tG:0.828  A:0.172\tG|G: 0.697  A|A: 0.040  A|G: 0.263  \n\tFIN \tG:0.944  A:0.056\tG|G: 0.899  A|A: 0.010  A|G: 0.091  \n\tGBR \tG:0.868  A:0.132\tG|G: 0.747  A|A: 0.011  A|G: 0.242
```

```
\n\tIBS \tG:0.748  A:0.252\tG|G: 0.570  A|A: 0.075  A|G: 0.355  \n\tTSI \tG:0.748  A:0.252\tG|G: 0.579  A|A: 0.084  A|G: 0.336  \n\n
SOUTH ASIAN\tG:0.855  A:0.145\tG|G: 0.728  A|A: 0.018  A|G: 0.254  \n\tBEB \tG:0.808  A:0.192\tG|G: 0.640  A|A: 0.023  A|G:
0.337  \n\tGIH \tG:0.820  A:0.180\tG|G: 0.680  A|A: 0.039  A|G: 0.282  \n\tITU \tG:0.902  A:0.098\tG|G: 0.814  A|A: 0.010  A|G: 0.176
\n\tPJL \tG:0.885  A:0.115\tG|G: 0.781  A|A: 0.010  A|G: 0.208  \n\tSTU \tG:0.853  A:0.147\tG|G: 0.716  A|A: 0.010  A|G: 0.275
\n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38801023)|| (snp==5743595))
{
        printf(" \n\n Alleles  A/G, Ancestral:A, Ambiguity code: R, MAF: 0.18 [2]\n Location: 4:38801023 [2] \n SNP ID: rs5743595
[1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n
Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tA:0.821
G:0.179\tA|A: 0.698  A|G: 0.246  G|G: 0.056 \n\n AFRICAN  \tA:0.988  G:0.012\tA|A: 0.976  A|G: 0.024  G|G: 0.000  \n\tACB
\tA:0.974  G:0.026\tA|A: 0.948  A|G: 0.052  G|G: 0.000  \n\tASW \tA:0.926  G:0.074\tA|A: 0.852  A|G: 0.148  G|G: 0.000  \n\tESN
\tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\tGWD \tA:0.991  G:0.009\tA|A: 0.982  A|G: 0.018  G|G: 0.000  \n\tLWK
\tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\tMSL \tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\tYRI
\tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000   \n\n AMERICAN \tA:0.854  G:0.146\tA|A: 0.744  A|G: 0.222  G|G: 0.035
\n\tCLM \tA:0.856  G:0.144\tA|A: 0.734  A|G: 0.245  G|G: 0.021  \n\tMXL \tA:0.891  G:0.109\tA|A: 0.797  A|G: 0.188  G|G: 0.016
\n\tPEL \tA:0.941  G:0.059\tA|A: 0.882  A|G: 0.118  G|G: 0.000  \n\tPUR \tA:0.760  G:0.240\tA|A: 0.606  A|G: 0.308  G|G: 0.087  \n\n
EAST ASIAN\tA:0.606  G:0.394\tA|A: 0.385  A|G: 0.442  G|G: 0.173  \n\tCDX \tA:0.796  G:0.204\tA|A: 0.634  A|G: 0.323  G|G: 0.043
\n\tCHB \tA:0.461  G:0.539\tA|A: 0.223  A|G: 0.476  G|G: 0.301  \n\tCHS \tA:0.605  G:0.395\tA|A: 0.352  A|G: 0.505  G|G: 0.143
\n\tJPT \tA:0.442  G:0.558\tA|A: 0.183  A|G: 0.519  G|G: 0.298  \n\tKHV \tA:0.753  G:0.247\tA|A: 0.566  A|G: 0.374  G|G: 0.061  \n\n
EUROPEAN \tA:0.781  G:0.219 \tA|A: 0.626  A|G: 0.310  G|G: 0.064  \n\tCEU \tA:0.813  G:0.187\tA|A: 0.667  A|G: 0.293  G|G: 0.040
\n\tFIN \tA:0.909  G:0.091\tA|A: 0.828  A|G: 0.162  G|G: 0.010  \n\tGBR \tA:0.830  G:0.170\tA|A: 0.681  A|G: 0.297  G|G: 0.022
\n\tIBS \tA:0.696  G:0.304\tA|A: 0.505  A|G: 0.383  G|G: 0.112  \n\tTSI \tA:0.678  G:0.322\tA|A: 0.477  A|G: 0.402  G|G: 0.121  \n\n
SOUTH ASIAN\tA:0.835  G:0.165\tA|A: 0.689  A|G: 0.292  G|G: 0.018  \n\tBEB \tA:0.785  G:0.215\tA|A: 0.593  A|G: 0.384  G|G:
0.023  \n\tGIH \tA:0.811  G:0.189\tA|A: 0.660  A|G: 0.301  G|G: 0.039  \n\tITU \tA:0.882  G:0.118\tA|A: 0.775  A|G: 0.216  G|G: 0.010
\n\tPJL \tA:0.865  G:0.135\tA|A: 0.740  A|G: 0.250  G|G: 0.010  \n\tSTU \tA:0.828  G:0.172\tA|A: 0.667  A|G: 0.324  G|G: 0.010
\n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38801130)|| (snp==5743594))
{
        printf(" \n\n Alleles  G/A, Ancestral: G, Ambiguity code: R, MAF: 0.05 [2]\n Location: 4:38801130 [2] \n SNP ID:
rs5743594 [1] \n GWAS Trait: Height [1,2] \n Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs
from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern
human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2]
\tGenotype Frequency [2] \n\n ALL      \tG:0.949  A:0.051\tG|G: 0.903  A|A: 0.005  A|G: 0.092 \n\n AFRICAN  \tG:0.995
A:0.005\tG|G: 0.992  A|A: 0.002  A|G: 0.006  \n\tACB \tG:0.969  A:0.031\tG|G: 0.948  A|A: 0.010  A|G: 0.042  \n\tASW \tG:1.000
A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000  \n\tESN \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000  \n\tGWD \tG:1.000
A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000  \n\tLWK \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000  \n\tMSL \tG:1.000
A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000  \n\tYRI \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000      \n\n AMERICAN
\tG:0.929  A:0.071\tG|G: 0.862  A|A: 0.003  A|G: 0.135  \n\tCLM \tG:0.904  A:0.096\tG|G: 0.809  A|A: 0.000  A|G: 0.191  \n\tMXL
\tG:0.992  A:0.008\tG|G: 0.984  A|A: 0.000  A|G: 0.016  \n\tPEL \tG:0.971  A:0.029\tG|G: 0.941  A|A: 0.000  A|G: 0.059  \n\tPUR
\tG:0.880  A:0.120\tG|G: 0.769  A|A: 0.010  A|G: 0.221  \n\n EAST ASIAN\tG:0.999  A:0.001\tG|G: 0.998  A|A: 0.000  A|G: 0.002
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\n\tCDX \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000  \n\tCHB \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000
\n\tCHS \tG:0.995  A:0.005\tG|G: 0.990  A|A: 0.000  A|G: 0.010  \n\tJPT \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000
\n\tKHV \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000   \n\n EUROPEAN \tG:0.843  A:0.157 \tG|G: 0.702  A|A: 0.016  A|G:
0.282  \n\tCEU \tG:0.833  A:0.167\tG|G: 0.687  A|A: 0.020  A|G: 0.293  \n\tFIN \tG:0.828  A:0.172\tG|G: 0.667  A|A: 0.010  A|G: 0.323
\n\tGBR \tG:0.797  A:0.203\tG|G: 0.626  A|A: 0.033  A|G: 0.341  \n\tIBS \tG:0.902  A:0.098\tG|G: 0.804  A|A: 0.000  A|G: 0.196
\n\tTSI \tG:0.846  A:0.154\tG|G: 0.710  A|A: 0.019  A|G: 0.271  \n\n SOUTH ASIAN\tG:0.958  A:0.042\tG|G: 0.920  A|A: 0.004  A|G:
0.076  \n\tBEB \tG:0.965  A:0.035\tG|G: 0.930  A|A: 0.000  A|G: 0.070  \n\tGIH \tG:0.961  A:0.039\tG|G: 0.922  A|A: 0.000  A|G: 0.078
\n\tITU \tG:0.956  A:0.044\tG|G: 0.922  A|A: 0.010  A|G: 0.069  \n\tPJL \tG:0.938  A:0.062\tG|G: 0.885  A|A: 0.010  A|G: 0.104
\n\tSTU \tG:0.971  A:0.029\tG|G: 0.941  A|A: 0.000  A|G: 0.059  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38801442)|| (snp==5743592))
{
        printf(" \n\n Alleles  A/G, Ancestral:G, Ambiguity code: R, MAF: 0.18 [2]\n Location: 4:38801442 [2] \n SNP ID: rs5743592
[1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: The GWAS-
identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II,
V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n
Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tA:0.818
G:0.182\tA|A: 0.694  A|G: 0.249  G|G: 0.058 \n\n AFRICAN  \tA:0.988  G:0.012\tA|A: 0.976  A|G: 0.024  G|G: 0.000  \n\tACB
\tA:0.974  G:0.026\tA|A: 0.948  A|G: 0.052  G|G: 0.000  \n\tASW \tA:0.926  G:0.074\tA|A: 0.852  A|G: 0.148  G|G: 0.000  \n\tESN
\tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\tGWD \tA:0.991  G:0.009\tA|A: 0.982  A|G: 0.018  G|G: 0.000  \n\tLWK
\tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\tMSL \tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\tYRI
\tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000   \n\n AMERICAN \tA:0.850  G:0.150\tA|A: 0.738  A|G: 0.225  G|G: 0.037
\n\tCLM \tA:0.840  G:0.160\tA|A: 0.713  A|G: 0.255  G|G: 0.032  \n\tMXL \tA:0.891  G:0.109\tA|A: 0.797  A|G: 0.188  G|G: 0.016
\n\tPEL \tA:0.941  G:0.059\tA|A: 0.882  A|G: 0.118  G|G: 0.000  \n\tPUR \tA:0.760  G:0.240\tA|A: 0.606  A|G: 0.308  G|G: 0.087  \n\n
EAST ASIAN\tA:0.595  G:0.405\tA|A: 0.369  A|G: 0.452  G|G: 0.179  \n\tCDX \tA:0.790  G:0.210\tA|A: 0.624  A|G: 0.333  G|G: 0.043
\n\tCHB \tA:0.442  G:0.558\tA|A: 0.194  A|G: 0.495  G|G: 0.311  \n\tCHS \tA:0.576  G:0.424\tA|A: 0.314  A|G: 0.524  G|G: 0.162
\n\tJPT \tA:0.438  G:0.562\tA|A: 0.183  A|G: 0.510  G|G: 0.308  \n\tKHV \tA:0.758  G:0.242\tA|A: 0.566  A|G: 0.384  G|G: 0.051  \n\n
EUROPEAN \tA:0.779  G:0.221 \tA|A: 0.622  A|G: 0.314  G|G: 0.064  \n\tCEU \tA:0.813  G:0.187\tA|A: 0.667  A|G: 0.293  G|G: 0.040
\n\tFIN \tA:0.909  G:0.091\tA|A: 0.828  A|G: 0.162  G|G: 0.010  \n\tGBR \tA:0.830  G:0.170\tA|A: 0.681  A|G: 0.297  G|G: 0.022
\n\tIBS \tA:0.692  G:0.308\tA|A: 0.495  A|G: 0.393  G|G: 0.112  \n\tTSI \tA:0.673  G:0.327\tA|A: 0.467  A|G: 0.411  G|G: 0.121  \n\n
SOUTH ASIAN\tA:0.835  G:0.165\tA|A: 0.689  A|G: 0.292  G|G: 0.018  \n\tBEB \tA:0.779  G:0.221\tA|A: 0.581  A|G: 0.395  G|G:
0.023  \n\tGIH \tA:0.806  G:0.194\tA|A: 0.650  A|G: 0.311  G|G: 0.039  \n\tITU \tA:0.877  G:0.123\tA|A: 0.765  A|G: 0.225  G|G: 0.010
\n\tPJL \tA:0.865  G:0.135\tA|A: 0.740  A|G: 0.250  G|G: 0.010  \n\tSTU \tA:0.843  G:0.157\tA|A: 0.696  A|G: 0.294  G|G: 0.010
\n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38803868)|| (snp==5743571))
{
        printf(" \n\n Alleles  C/T, Ancestral: C, Ambiguity code: Y, MAF: 0.18 [2]\n Location: 4:38803868 [2] \n SNP ID: rs5743571
[1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: The GWAS-
identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II,
V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n
Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tC:0.821
T:0.179\tC|C: 0.698  C|T: 0.246  T|T: 0.056 \n\n AFRICAN  \tC:0.988  T:0.012\tC|C: 0.976  C|T: 0.024  T|T: 0.000  \n\tACB \tC:0.974
```

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T:0.026\tC|C: 0.948  C|T: 0.052  T|T: 0.000  \n\tASW \tC:0.926  T:0.074\tC|C: 0.852  C|T: 0.148  T|T: 0.000  \n\tESN \tC:1.000
T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000  \n\tGWD \tC:0.991  T:0.009\tC|C: 0.982  C|T: 0.018  T|T: 0.000  \n\tLWK \tC:1.000
T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000  \n\tMSL \tC:1.000  T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000  \n\tYRI \tC:1.000
T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000      \n\n AMERICAN \tC:0.850  T:0.150\tC|C: 0.738  C|T: 0.225  T|T: 0.037  \n\tCLM
\tC:0.840  T:0.160\tC|C: 0.713  C|T: 0.255  T|T: 0.032  \n\tMXL \tC:0.891  T:0.109\tC|C: 0.797  C|T: 0.188  T|T: 0.016  \n\tPEL
\tC:0.941  T:0.059\tC|C: 0.882  C|T: 0.118  T|T: 0.000  \n\tPUR \tC:0.760  T:0.240\tC|C: 0.606  C|T: 0.308  T|T: 0.087  \n\n EAST
ASIAN\tC:0.606  T:0.394\tC|C: 0.385  C|T: 0.442  T|T: 0.173  \n\tCDX \tC:0.796  T:0.204\tC|C: 0.634  C|T: 0.323  T|T: 0.043  \n\tCHB
\tC:0.461  T:0.539\tC|C: 0.223  C|T: 0.476  T|T: 0.301  \n\tCHS \tC:0.600  T:0.400\tC|C: 0.352  C|T: 0.495  T|T: 0.152  \n\tJPT \tC:0.442
T:0.558\tC|C: 0.183  C|T: 0.519  T|T: 0.298  \n\tKHV \tC:0.758  T:0.242\tC|C: 0.566  C|T: 0.384  T|T: 0.051    \n\n EUROPEAN
\tC:0.780  T:0.220 \tC|C: 0.624  C|T: 0.312  T|T: 0.064  \n\tCEU \tC:0.813  T:0.187\tC|C: 0.667  C|T: 0.293  T|T: 0.040  \n\tFIN
\tC:0.909  T:0.091\tC|C: 0.828  C|T: 0.162  T|T: 0.010  \n\tGBR \tC:0.830  T:0.170\tC|C: 0.681  C|T: 0.297  T|T: 0.022  \n\tIBS
\tC:0.692  T:0.308\tC|C: 0.495  C|T: 0.393  T|T: 0.112  \n\tTSI \tC:0.678  T:0.322\tC|C: 0.477  C|T: 0.402  T|T: 0.121  \n\n SOUTH
ASIAN\tC:0.836  T:0.164\tC|C: 0.691  C|T: 0.290  T|T: 0.018  \n\tBEB \tC:0.779  T:0.221\tC|C: 0.581  C|T: 0.395  T|T: 0.023  \n\tGIH
\tC:0.811  T:0.189\tC|C: 0.660  C|T: 0.301  T|T: 0.039  \n\tITU \tC:0.877  T:0.123\tC|C: 0.765  C|T: 0.225  T|T: 0.010  \n\tPJL \tC:0.865
T:0.135\tC|C: 0.740  C|T: 0.250  T|T: 0.010  \n\tSTU \tC:0.843  T:0.157\tC|C: 0.696  C|T: 0.294  T|T: 0.010  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38804362)|| (snp==5743565))
{
            printf(" \n\n Alleles  T/C, Ancestral: T, Ambiguity code: Y, MAF: 0.18 [2]\n Location: 4:38804362 [2] \n SNP ID: rs5743565
[1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: The GWAS-
identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II,
V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n
Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tT:0.820
C:0.180\tT|T: 0.697  C|C: 0.057  C|T: 0.246 \n\n AFRICAN  \tT:0.988  C:0.012\tT|T: 0.976  C|C: 0.000  C|T: 0.024  \n\tACB \tT:0.974
C:0.026\tT|T: 0.948  C|C: 0.000  C|T: 0.052  \n\tASW \tT:0.926  C:0.074\tT|T: 0.852  C|C: 0.000  C|T: 0.148  \n\tESN \tT:1.000
C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000   \n\tGWD \tT:0.991  C:0.009\tT|T: 0.982  C|C: 0.000  C|T: 0.018  \n\tLWK \tT:1.000
C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000   \n\tMSL \tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000   \n\tYRI \tT:1.000
C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000      \n\n AMERICAN \tT:0.850  C:0.150\tT|T: 0.738  C|C: 0.037  C|T: 0.225  \n\tCLM
\tT:0.840  C:0.160\tT|T: 0.713  C|C: 0.032  C|T: 0.255  \n\tMXL \tT:0.891  C:0.109\tT|T: 0.797  C|C: 0.016  C|T: 0.188  \n\tPEL
\tT:0.941  C:0.059\tT|T: 0.882  C|C: 0.000  C|T: 0.118  \n\tPUR \tT:0.760  C:0.240\tT|T: 0.606  C|C: 0.087  C|T: 0.308  \n\n EAST
ASIAN\tT:0.605  C:0.395\tT|T: 0.385  C|C: 0.175  C|T: 0.440  \n\tCDX \tT:0.796  C:0.204\tT|T: 0.634  C|C: 0.043  C|T: 0.323  \n\tCHB
\tT:0.461  C:0.539\tT|T: 0.223  C|C: 0.301  C|T: 0.476  \n\tCHS \tT:0.600  C:0.400\tT|T: 0.352  C|C: 0.152  C|T: 0.495  \n\tJPT \tT:0.442
C:0.558\tT|T: 0.183  C|C: 0.298  C|T: 0.519  \n\tKHV \tT:0.753  C:0.247\tT|T: 0.566  C|C: 0.061  C|T: 0.374    \n\n EUROPEAN
\tT:0.779  C:0.221 \tT|T: 0.622  C|C: 0.064  C|T: 0.314  \n\tCEU \tT:0.813  C:0.187\tT|T: 0.667  C|C: 0.040  C|T: 0.293  \n\tFIN
\tT:0.904  C:0.096\tT|T: 0.818  C|C: 0.010  C|T: 0.172  \n\tGBR \tT:0.830  C:0.170\tT|T: 0.681  C|C: 0.022  C|T: 0.297  \n\tIBS \tT:0.692
C:0.308\tT|T: 0.495  C|C: 0.112  C|T: 0.393  \n\tTSI \tT:0.678  C:0.322\tT|T: 0.477  C|C: 0.121  C|T: 0.402  \n\n SOUTH
ASIAN\tT:0.835  C:0.165\tT|T: 0.691  C|C: 0.020  C|T: 0.288  \n\tBEB \tT:0.779  C:0.221\tT|T: 0.581  C|C: 0.023  C|T: 0.395  \n\tGIH
\tT:0.811  C:0.189\tT|T: 0.660  C|C: 0.039  C|T: 0.301  \n\tITU \tT:0.877  C:0.123\tT|T: 0.765  C|C: 0.010  C|T: 0.225  \n\tPJL \tT:0.859
C:0.141\tT|T: 0.740  C|C: 0.021  C|T: 0.240  \n\tSTU \tT:0.843  C:0.157\tT|T: 0.696  C|C: 0.010  C|T: 0.294  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38804398)|| (snp==5743563))
{
```

```
        printf(" \n\n Alleles  A/G, Ancestral:G, Ambiguity code: R, MAF: 0.18 [2]\n Location: 4:38804398 [2] \n SNP ID: rs5743563
[1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: The GWAS-
identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II,
V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n
Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tA:0.820
G:0.180\tA|A: 0.697  A|G: 0.246  G|G: 0.057 \n\n AFRICAN  \tA:0.988  G:0.012\tA|A: 0.976  A|G: 0.024  G|G: 0.000      \n\tACB
\tA:0.974  G:0.026\tA|A: 0.948  A|G: 0.052  G|G: 0.000  \n\tASW \tA:0.926  G:0.074\tA|A: 0.852  A|G: 0.148  G|G: 0.000  \n\tESN
\tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\tGWD \tA:0.991  G:0.009\tA|A: 0.982  A|G: 0.018  G|G: 0.000  \n\tLWK
\tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\tMSL \tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000  \n\tYRI
\tA:1.000  G:0.000\tA|A: 1.000  A|G: 0.000  G|G: 0.000    \n\n AMERICAN \tA:0.850  G:0.150\tA|A: 0.738  A|G: 0.225  G|G: 0.037
\n\tCLM \tA:0.840  G:0.160\tA|A: 0.713  A|G: 0.255  G|G: 0.032  \n\tMXL \tA:0.891  G:0.109\tA|A: 0.797  A|G: 0.188  G|G: 0.016
\n\tPEL \tA:0.941  G:0.059\tA|A: 0.882  A|G: 0.118  G|G: 0.000  \n\tPUR \tA:0.760  G:0.240\tA|A: 0.606  A|G: 0.308  G|G: 0.087  \n\n
EAST ASIAN\tA:0.605  G:0.395\tA|A: 0.385  A|G: 0.440  G|G: 0.175  \n\tCDX \tA:0.796  G:0.204\tA|A: 0.634  A|G: 0.323  G|G: 0.043
\n\tCHB \tA:0.461  G:0.539\tA|A: 0.223  A|G: 0.476  G|G: 0.301  \n\tCHS \tA:0.600  G:0.400\tA|A: 0.352  A|G: 0.495  G|G: 0.152
\n\tJPT \tA:0.442  G:0.558\tA|A: 0.183  A|G: 0.519  G|G: 0.298  \n\tKHV \tA:0.753  G:0.247\tA|A: 0.566  A|G: 0.374  G|G: 0.061  \n\n
EUROPEAN \tA:0.779  G:0.221 \tA|A: 0.622  A|G: 0.314  G|G: 0.064  \n\tCEU \tA:0.813  G:0.187\tA|A: 0.667  A|G: 0.293  G|G: 0.040
\n\tFIN \tA:0.904  G:0.096\tA|A: 0.818  A|G: 0.172  G|G: 0.010  \n\tGBR \tA:0.830  G:0.170\tA|A: 0.681  A|G: 0.297  G|G: 0.022
\n\tIBS \tA:0.692  G:0.308\tA|A: 0.495  A|G: 0.393  G|G: 0.112  \n\tTSI \tA:0.678  G:0.322\tA|A: 0.477  A|G: 0.402  G|G: 0.121  \n\n
SOUTH ASIAN\tA:0.835  G:0.165\tA|A: 0.691  A|G: 0.288  G|G: 0.020  \n\tBEB \tA:0.779  G:0.221\tA|A: 0.581  A|G: 0.395  G|G:
0.023  \n\tGIH \tA:0.811  G:0.189\tA|A: 0.660  A|G: 0.301  G|G: 0.039  \n\tITU \tA:0.877  G:0.123\tA|A: 0.765  A|G: 0.225  G|G: 0.010
\n\tPJL \tA:0.859  G:0.141\tA|A: 0.740  A|G: 0.240  G|G: 0.021  \n\tSTU \tA:0.843  G:0.157\tA|A: 0.696  A|G: 0.294  G|G: 0.010
\n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38804475)|| (snp==5743562))
{
        printf(" \n\n Alleles  T/C, Ancestral: T, Ambiguity code: Y, MAF: 0.18 [2]\n Location: 4:38804475 [2] \n SNP ID: rs5743562
[1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: The GWAS-
identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II,
V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n
Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tT:0.820
C:0.180\tT|T: 0.697  C|C: 0.056  C|T: 0.246 \n\n AFRICAN  \tT:0.988  C:0.012\tT|T: 0.976  C|C: 0.000  C|T: 0.024  \n\tACB \tT:0.974
C:0.026\tT|T: 0.948  C|C: 0.000  C|T: 0.052  \n\tASW \tT:0.926  C:0.074\tT|T: 0.852  C|C: 0.000  C|T: 0.148  \n\tESN \tT:1.000
C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tGWD \tT:0.991  C:0.009\tT|T: 0.982  C|C: 0.000  C|T: 0.018  \n\tLWK \tT:1.000
C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tMSL \tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000  \n\tYRI \tT:1.000
C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000      \n\n AMERICAN \tT:0.850  C:0.150\tT|T: 0.738  C|C: 0.037  C|T: 0.225  \n\tCLM
\tT:0.840  C:0.160\tT|T: 0.713  C|C: 0.032  C|T: 0.255  \n\tMXL \tT:0.891  C:0.109\tT|T: 0.797  C|C: 0.016  C|T: 0.188  \n\tPEL
\tT:0.941  C:0.059\tT|T: 0.882  C|C: 0.000  C|T: 0.118  \n\tPUR \tT:0.760  C:0.240\tT|T: 0.606  C|C: 0.087  C|T: 0.308  \n\n EAST
ASIAN\tT:0.606  C:0.394\tT|T: 0.385  C|C: 0.173  C|T: 0.442  \n\tCDX \tT:0.796  C:0.204\tT|T: 0.634  C|C: 0.043  C|T: 0.323  \n\tCHB
\tT:0.461  C:0.539\tT|T: 0.223  C|C: 0.301  C|T: 0.476  \n\tCHS \tT:0.600  C:0.400\tT|T: 0.352  C|C: 0.152  C|T: 0.495  \n\tJPT \tT:0.442
C:0.558\tT|T: 0.183  C|C: 0.298  C|T: 0.519  \n\tKHV \tT:0.758  C:0.242\tT|T: 0.566  C|C: 0.051  C|T: 0.384    \n\n EUROPEAN
\tT:0.779  C:0.221 \tT|T: 0.622  C|C: 0.064  C|T: 0.314  \n\tCEU \tT:0.813  C:0.187\tT|T: 0.667  C|C: 0.040  C|T: 0.293  \n\tFIN
\tT:0.904  C:0.096\tT|T: 0.818  C|C: 0.010  C|T: 0.172  \n\tGBR \tT:0.830  C:0.170\tT|T: 0.681  C|C: 0.022  C|T: 0.297  \n\tIBS \tT:0.692
C:0.308\tT|T: 0.495  C|C: 0.112  C|T: 0.393  \n\tTSI \tT:0.678  C:0.322\tT|T: 0.477  C|C: 0.121  C|T: 0.402  \n\n SOUTH
ASIAN\tT:0.836  C:0.164\tT|T: 0.691  C|C: 0.018  C|T: 0.290  \n\tBEB \tT:0.779  C:0.221\tT|T: 0.581  C|C: 0.023  C|T: 0.395  \n\tGIH
\tT:0.811  C:0.189\tT|T: 0.660  C|C: 0.039  C|T: 0.301  \n\tITU \tT:0.877  C:0.123\tT|T: 0.765  C|C: 0.010  C|T: 0.225  \n\tPJL \tT:0.865
C:0.135\tT|T: 0.740  C|C: 0.010  C|T: 0.250  \n\tSTU \tT:0.843  C:0.157\tT|T: 0.696  C|C: 0.010  C|T: 0.294  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
```

```
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38805206)|| (snp==5743557))
{
            printf(" \n\n Alleles  G/A, Ancestral: G, Ambiguity code: R, MAF: 0.18 [2]\n Location: 4:38805206 [2] \n SNP ID: rs5743557 [1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: The GWAS-identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL \tG:0.821  A:0.179\tG|G: 0.698  A|A: 0.056  A|G: 0.246 \n\n AFRICAN  \tG:0.988  A:0.012\tG|G: 0.976  A|A: 0.000  A|G: 0.024 \n\tACB \tG:0.974  A:0.026\tG|G: 0.948  A|A: 0.000  A|G: 0.052  \n\tASW \tG:0.926  A:0.074\tG|G: 0.852  A|A: 0.000  A|G: 0.148 \n\tESN \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000  \n\tGWD \tG:0.991  A:0.009\tG|G: 0.982  A|A: 0.000  A|G: 0.018 \n\tLWK \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000  \n\tMSL \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000 \n\tYRI \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000      \n\n AMERICAN \tG:0.852  A:0.148\tG|G: 0.741  A|A: 0.037  A|G: 0.222  \n\tCLM \tG:0.840  A:0.160\tG|G: 0.713  A|A: 0.032  A|G: 0.255  \n\tMXL \tG:0.891  A:0.109\tG|G: 0.797  A|A: 0.016  A|G: 0.188  \n\tPEL \tG:0.941  A:0.059\tG|G: 0.882  A|A: 0.000  A|G: 0.118  \n\tPUR \tG:0.764  A:0.236\tG|G: 0.615  A|A: 0.087  A|G: 0.298 \n\n EAST ASIAN\tG:0.607  A:0.393\tG|G: 0.385  A|A: 0.171  A|G: 0.444  \n\tCDX \tG:0.796  A:0.204\tG|G: 0.634  A|A: 0.043  A|G: 0.323  \n\tCHB \tG:0.466  A:0.534\tG|G: 0.223  A|A: 0.291  A|G: 0.485  \n\tCHS \tG:0.600  A:0.400\tG|G: 0.352  A|A: 0.152  A|G: 0.495  \n\tJPT \tG:0.442  A:0.558\tG|G: 0.183  A|A: 0.298  A|G: 0.519  \n\tKHV \tG:0.758  A:0.242\tG|G: 0.566  A|A: 0.051  A|G: 0.384 \n\n EUROPEAN \tG:0.779  A:0.221 \tG|G: 0.622  A|A: 0.064  A|G: 0.314  \n\tCEU \tG:0.813  A:0.187\tG|G: 0.667  A|A: 0.040  A|G: 0.293  \n\tFIN \tG:0.904  A:0.096\tG|G: 0.818  A|A: 0.010  A|G: 0.172  \n\tGBR \tG:0.830  A:0.170\tG|G: 0.681  A|A: 0.022  A|G: 0.297 \n\tIBS \tG:0.692  A:0.308\tG|G: 0.495  A|A: 0.112  A|G: 0.393  \n\tTSI \tG:0.678  A:0.322\tG|G: 0.477  A|A: 0.121  A|G: 0.402  \n\n SOUTH ASIAN\tG:0.837  A:0.163\tG|G: 0.693  A|A: 0.018  A|G: 0.288  \n\tBEB \tG:0.779  A:0.221\tG|G: 0.581  A|A: 0.023  A|G: 0.395  \n\tGIH \tG:0.811  A:0.189\tG|G: 0.660  A|A: 0.039  A|G: 0.301  \n\tITU \tG:0.882  A:0.118\tG|G: 0.775  A|A: 0.010  A|G: 0.216 \n\tPJL \tG:0.865  A:0.135\tG|G: 0.740  A|A: 0.010  A|G: 0.250  \n\tSTU \tG:0.843  A:0.157\tG|G: 0.696  A|A: 0.010  A|G: 0.294 \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38809148)|| (snp==11722813))
{
            printf(" \n\n Alleles  C/T, Ancestral: T, Ambiguity code: Y, MAF: 0.18 [2]\n Location: 4:38809148 [2] \n SNP ID: rs11722813 [1] \n GWAS Trait: Helicobacter pylori serologic status [1] \n Archaic-like haplotype cluster: The GWAS-identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tC:0.821  T:0.179\tC|C: 0.697  C|T: 0.247  T|T: 0.056 \n\n AFRICAN  \tC:0.988  T:0.012\tC|C: 0.976  C|T: 0.024  T|T: 0.000  \n\tACB \tC:0.974  T:0.026\tC|C: 0.948  C|T: 0.052  T|T: 0.000  \n\tASW \tC:0.926  T:0.074\tC|C: 0.852  C|T: 0.148  T|T: 0.000  \n\tESN \tC:1.000  T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000  \n\tGWD \tC:0.991  T:0.009\tC|C: 0.982  C|T: 0.018  T|T: 0.000  \n\tLWK \tC:1.000  T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000  \n\tMSL \tC:1.000  T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000  \n\tYRI \tC:1.000  T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000      \n\n AMERICAN \tC:0.850  T:0.150\tC|C: 0.738  C|T: 0.225  T|T: 0.037  \n\tCLM \tC:0.840  T:0.160\tC|C: 0.713  C|T: 0.255  T|T: 0.032  \n\tMXL \tC:0.891  T:0.109\tC|C: 0.797  C|T: 0.188  T|T: 0.016  \n\tPEL \tC:0.941  T:0.059\tC|C: 0.882  C|T: 0.118  T|T: 0.000  \n\tPUR \tC:0.760  T:0.240\tC|C: 0.606  C|T: 0.308  T|T: 0.087  \n\n EAST ASIAN\tC:0.605  T:0.395\tC|C: 0.383  C|T: 0.444  T|T: 0.173  \n\tCDX \tC:0.796  T:0.204\tC|C: 0.634  C|T: 0.323  T|T: 0.043  \n\tCHB \tC:0.461  T:0.539\tC|C: 0.223  C|T: 0.476  T|T: 0.301  \n\tCHS \tC:0.600  T:0.400\tC|C: 0.352  C|T: 0.495  T|T: 0.152  \n\tJPT \tC:0.438  T:0.562\tC|C: 0.173  C|T: 0.529  T|T: 0.298  \n\tKHV \tC:0.758  T:0.242\tC|C: 0.566  C|T: 0.384  T|T: 0.051     \n\n EUROPEAN \tC:0.782  T:0.218 \tC|C: 0.626  C|T: 0.312  T|T: 0.062  \n\tCEU \tC:0.813  T:0.187\tC|C: 0.667  C|T: 0.293  T|T: 0.040  \n\tFIN \tC:0.904  T:0.096\tC|C: 0.818  C|T: 0.172  T|T: 0.010  \n\tGBR \tC:0.835  T:0.165\tC|C: 0.692  C|T: 0.286  T|T: 0.022  \n\tIBS \tC:0.692  T:0.308\tC|C: 0.495  C|T: 0.393  T|T: 0.112  \n\tTSI \tC:0.687  T:0.313\tC|C: 0.486  C|T: 0.402  T|T: 0.112  \n\n SOUTH ASIAN\tC:0.835  T:0.165\tC|C: 0.689  C|T: 0.292  T|T: 0.018  \n\tBEB \tC:0.779  T:0.221\tC|C: 0.581  C|T: 0.395  T|T: 0.023  \n\tGIH \tC:0.811  T:0.189\tC|C: 0.660  C|T: 0.301  T|T: 0.039  \n\tITU \tC:0.873  T:0.127\tC|C: 0.755  C|T: 0.235  T|T: 0.010  \n\tPJL \tC:0.865  T:0.135\tC|C: 0.740  C|T: 0.250  T|T: 0.010  \n\tSTU \tC:0.843  T:0.157\tC|C: 0.696  C|T: 0.294  T|T: 0.010  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
```

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printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38809930)|| (snp==2101521))
{
            printf(" \n\n Alleles  G/A, Ancestral:A, Ambiguity code: R, MAF: 0.48 [2]\n Location: 4:38809930 [2] \n SNP ID: rs2101521
[1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1,2]\n Archaic-like haplotype cluster: Not Known\n
Clinical Assertion Description: Not Known \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tG:0.525
A:0.475\tG|G: 0.306  A|A: 0.256  A|G: 0.438 \n\n AFRICAN  \tG:0.336  A:0.664\tG|G: 0.113  A|A: 0.442  A|G: 0.445  \n\tACB
\tG:0.385  A:0.615\tG|G: 0.135  A|A: 0.365  A|G: 0.500  \n\tASW \tG:0.410  A:0.590\tG|G: 0.180  A|A: 0.361  A|G: 0.459  \n\tESN
\tG:0.348  A:0.652\tG|G: 0.131  A|A: 0.434  A|G: 0.434  \n\tGWD \tG:0.420  A:0.580\tG|G: 0.168  A|A: 0.327  A|G: 0.504  \n\tLWK
\tG:0.232  A:0.768\tG|G: 0.030  A|A: 0.566  A|G: 0.404  \n\tMSL \tG:0.253  A:0.747\tG|G: 0.094  A|A: 0.588  A|G: 0.318  \n\tYRI
\tG:0.310  A:0.690\tG|G: 0.074  A|A: 0.454  A|G: 0.472  \n\n AMERICAN \tG:0.581  A:0.419\tG|G: 0.346  A|A: 0.184  A|G: 0.470
\n\tCLM \tG:0.612  A:0.388\tG|G: 0.372  A|A: 0.149  A|G: 0.479  \n\tMXL \tG:0.531  A:0.469\tG|G: 0.266  A|A: 0.203  A|G: 0.531
\n\tPEL \tG:0.524  A:0.476\tG|G: 0.294  A|A: 0.247  A|G: 0.459  \n\tPUR \tG:0.630  A:0.370 \tG|G: 0.413  A|A: 0.154  A|G: 0.433  \n\n
EAST ASIAN\tG:0.421  A:0.579\tG|G: 0.183  A|A: 0.341  A|G: 0.476  \n\tCDX \tG:0.565  A:0.435\tG|G: 0.301  A|A: 0.172  A|G: 0.527
\n\tCHB \tG:0.320  A:0.680\tG|G: 0.087  A|A: 0.447  A|G: 0.466  \n\tCHS \tG:0.386  A:0.614\tG|G: 0.152  A|A: 0.381  A|G: 0.467
\n\tJPT \tG:0.284  A:0.716\tG|G: 0.048  A|A: 0.481  A|G: 0.471  \n\tKHV \tG:0.571  A:0.429\tG|G: 0.343  A|A: 0.202  A|G: 0.455  \n\n
EUROPEAN \tG:0.741  A:0.259 \tG|G: 0.565  A|A: 0.083  A|G: 0.352  \n\tCEU \tG:0.803  A:0.197\tG|G: 0.657  A|A: 0.051  A|G: 0.293
\n\tFIN \tG:0.859  A:0.141\tG|G: 0.747  A|A: 0.030  A|G: 0.222  \n\tGBR \tG:0.808  A:0.192\tG|G: 0.637  A|A: 0.022  A|G: 0.341
\n\tIBS \tG:0.617  A:0.383\tG|G: 0.393  A|A: 0.159  A|G: 0.449  \n\tTSI \tG:0.640  A:0.360\tG|G: 0.421  A|A: 0.140  A|G: 0.439  \n\n
SOUTH ASIAN\tG:0.626  A:0.374\tG|G: 0.397  A|A: 0.145  A|G: 0.458  \n\tBEB \tG:0.622  A:0.378\tG|G: 0.360  A|A: 0.116  A|G:
0.523  \n\tGIH \tG:0.626  A:0.374\tG|G: 0.398  A|A: 0.146  A|G: 0.456  \n\tITU \tG:0.618  A:0.382\tG|G: 0.373  A|A: 0.137  A|G: 0.490
\n\tPJL \tG:0.672  A:0.328\tG|G: 0.500  A|A: 0.156  A|G: 0.344  \n\tSTU \tG:0.593  A:0.407\tG|G: 0.353  A|A: 0.167  A|G: 0.480
\n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38811255)|| (snp==17616434))
{
            printf(" \n\n Alleles  T/C, Ancestral:C, Ambiguity code: Y, MAF: 0.43 [2]\n Location: 4:38811255 [2] \n SNP ID:
rs17616434 [1] \n GWAS Trait: Helicobacter pylori serologic status, Alcohol consumption, Self-reported allergy, Allergic sensitization
[1,2]\n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known \n\n\n Population  \tAllele Frequency
[2] \tGenotype Frequency [2] \n\n ALL      \tT:0.427  C:0.573\tT|T: 0.238  C|C: 0.385  C|T: 0.376 \n\n AFRICAN  \tT:0.103
C:0.897\tT|T: 0.017  C|C: 0.811  C|T: 0.172  \n\tACB \tT:0.167  C:0.833\tT|T: 0.010  C|C: 0.677  C|T: 0.312  \n\tASW \tT:0.254
C:0.746\tT|T: 0.098  C|C: 0.590  C|T: 0.311  \n\tESN \tT:0.106  C:0.894\tT|T: 0.020  C|C: 0.808  C|T: 0.172  \n\tGWD \tT:0.044
C:0.956\tT|T: 0.009  C|C: 0.920  C|T: 0.071  \n\tLWK \tT:0.076  C:0.924\tT|T: 0.010  C|C: 0.859  C|T: 0.131  \n\tMSL \tT:0.035
C:0.965\tT|T: 0.000  C|C: 0.929  C|T: 0.071  \n\tYRI \tT:0.097  C:0.903\tT|T: 0.000  C|C: 0.806  C|T: 0.194  \n\n AMERICAN \tT:0.530
C:0.470\tT|T: 0.297  C|C: 0.236  C|T: 0.467  \n\tCLM \tT:0.574  C:0.426\tT|T: 0.340  C|C: 0.191  C|T: 0.468  \n\tMXL \tT:0.500
C:0.500\tT|T: 0.234  C|C: 0.234  C|T: 0.531  \n\tPEL \tT:0.494  C:0.506\tT|T: 0.271  C|C: 0.282  C|T: 0.447  \n\tPUR \tT:0.538  C:0.462
\tT|T: 0.317  C|C: 0.240  C|T: 0.442  \n\n EAST ASIAN\tT:0.396  C:0.604\tT|T: 0.155  C|C: 0.363  C|T: 0.482  \n\tCDX \tT:0.516
C:0.484\tT|T: 0.237  C|C: 0.204  C|T: 0.559  \n\tCHB \tT:0.306  C:0.694\tT|T: 0.078  C|C: 0.466  C|T: 0.456  \n\tCHS \tT:0.381
C:0.619\tT|T: 0.162  C|C: 0.400  C|T: 0.438  \n\tJPT \tT:0.274  C:0.726\tT|T: 0.048  C|C: 0.500  C|T: 0.452  \n\tKHV \tT:0.520
C:0.480\tT|T: 0.263  C|C: 0.222  C|T: 0.515  \n\n EUROPEAN \tT:0.716  C:0.284 \tT|T: 0.533  C|C: 0.101  C|T: 0.366  \n\tCEU
\tT:0.788  C:0.212\tT|T: 0.626  C|C: 0.051  C|T: 0.323  \n\tFIN \tT:0.843  C:0.157\tT|T: 0.727  C|C: 0.040  C|T: 0.232  \n\tGBR
\tT:0.802  C:0.198\tT|T: 0.626  C|C: 0.022  C|T: 0.352  \n\tIBS \tT:0.575  A:0.425\tT|T: 0.346  C|C: 0.196  C|T: 0.458  \n\tTSI \tT:0.598
C:0.402\tT|T: 0.374  C|C: 0.178  C|T: 0.449  \n\n SOUTH ASIAN\tT:0.525  C:0.475\tT|T: 0.280  C|C: 0.231  C|T: 0.489  \n\tBEB
\tT:0.529  C:0.471\tT|T: 0.279  C|C: 0.221  C|T: 0.500  \n\tGIH \tT:0.539  C:0.461\tT|T: 0.262  C|C: 0.184  C|T: 0.553  \n\tITU \tT:0.475
C:0.525\tT|T: 0.186  C|C: 0.235  C|T: 0.578  \n\tPJL \tT:0.573  C:0.427\tT|T: 0.396  C|C: 0.250  C|T: 0.354  \n\tSTU \tT:0.510
C:0.490\tT|T: 0.284  C|C: 0.265  C|T: 0.451  \n\n");
```

```
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38813881)|| (snp==4833103))
{
        printf(" \n\n Alleles  A/C, Ancestral: C, Ambiguity code: M, MAF: 0.14 [2]\n Location: 4:38813881 [2] \n SNP ID: rs4833103 [1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tA:0.138  C:0.862\tA|A: 0.062  A|C: 0.153  C|C: 0.786 \n\n AFRICAN  \tA:0.018  C:0.982\tA|A: 0.003  A|C: 0.030  C|C: 0.967  \n\tACB \tA:0.042  C:0.958\tA|A: 0.000  A|C: 0.083  C|C: 0.917  \n\tASW \tA:0.131  C:0.869\tA|A: 0.033  A|C: 0.197  C|C: 0.770  \n\tESN \tA:0.000  C:1.000\tA|A: 0.000  A|C: 0.000  C|C: 1.000  \n\tGWD \tA:0.000  C:1.000\tA|A: 0.000  A|C: 0.000  C|C: 1.000  \n\tLWK \tA:0.000  C:1.000\tA|A: 0.000  A|C: 0.000  C|C: 1.000  \n\tMSL \tA:0.000  C:1.000\tA|A: 0.000  A|C: 0.000  C|C: 1.000  \n\tYRI \tA:0.000  C:1.000\tA|A: 0.000  A|C: 0.000  C|C: 1.000  \n\n AMERICAN \tA:0.207  T:0.793\tA|A: 0.058  A|C: 0.300  C|C: 0.643  \n\tCLM \tA:0.266  C:0.734\tA|A: 0.106  A|C: 0.319  C|C: 0.574  \n\tMXL \tA:0.164  C:0.836\tA|A: 0.031  A|C: 0.266  C|C: 0.703  \n\tPEL \tA:0.094  C:0.906\tA|A: 0.000  A|C: 0.188  C|C: 0.812  \n\tPUR \tA:0.274  C:0.726\tA|A: 0.077  A|C: 0.394  C|C: 0.529  \n\n EAST ASIAN\tA:0.000  C:1.000\tA|A: 0.000  A|C: 0.000  C|C: 1.000 \n\n\tCDX \tA:0.000  C:1.000\tA|A: 0.000  A|C: 0.000  C|C: 1.000  \n\tCHB \tA:0.000  C:1.000\tA|A: 0.000  A|C: 0.000  C|C: 1.000  \n\tCHS \tA:0.000  C:1.000\tA|A: 0.000  A|C: 0.000  C|C: 1.000  \n\tJPT \tA:0.000  C:1.000\tA|A: 0.000  A|C: 0.000  C|C: 1.000  \n\tKHV \tA:0.000  C:1.000\tA|A: 0.000  A|C: 0.000  C|C: 1.000      \n\n EUROPEAN \tA:0.505  C:0.495 \tA|A: 0.262  A|C: 0.485  C|C: 0.252  \n\tCEU \tA:0.586  C:0.414\tA|A: 0.333  A|C: 0.505  C|C: 0.162  \n\tFIN \tA:0.657  C:0.343\tA|A: 0.444  A|C: 0.424  C|C: 0.131  \n\tGBR \tA:0.549  C:0.451\tA|A: 0.253  A|C: 0.593  C|C: 0.154  \n\tIBS \tA:0.383  C:0.617\tA|A: 0.140  A|C: 0.486  C|C: 0.374  \n\tTSI \tA:0.374  C:0.626\tA|A: 0.159  A|C: 0.430  C|C: 0.411  \n\n SOUTH ASIAN\tA:0.014  C:0.986\tA|A: 0.000  A|C: 0.029  C|C: 0.971  \n\tBEB \tA:0.012  C:0.988\tA|A: 0.000  A|C: 0.023  C|C: 0.977  \n\tGIH \tA:0.024  C:0.976\tA|A: 0.000  A|C: 0.049  C|C: 0.951  \n\tITU \tA:0.005  C:0.995\tA|A: 0.000  A|C: 0.010  C|C: 0.990  \n\tPJL \tA:0.021  C:0.979\tA|A: 0.000  A|C: 0.042  C|C: 0.958  \n\tSTU \tA:0.010  C:0.990\tA|A: 0.000  A|C: 0.020  C|C: 0.980  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38814717)|| (snp==6815814))
{
        printf(" \n\n Alleles  A/C, Ancestral: C, Ambiguity code: M, MAF: 0.44 [2]\n Location: 4:38814717 [2] \n SNP ID: rs6815814 [1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL  \tA:0.436  C:0.564\tA|A: 0.250  A|C: 0.371  C|C: 0.378 \n\n AFRICAN  \tA:0.103  C:0.897\tA|A: 0.017  A|C: 0.172  C|C: 0.811  \n\tACB \tA:0.161  C:0.839\tA|A: 0.010  A|C: 0.302  C|C: 0.688  \n\tASW \tA:0.262  C:0.738\tA|A: 0.098  A|C: 0.328  C|C: 0.574  \n\tESN \tA:0.106  C:0.894\tA|A: 0.020  A|C: 0.172  C|C: 0.808  \n\tGWD \tA:0.044  C:0.956\tA|A: 0.009  A|C: 0.071  C|C: 0.920  \n\tLWK \tA:0.076  C:0.924\tA|A: 0.010  A|C: 0.131  C|C: 0.859  \n\tMSL \tA:0.035  C:0.965\tA|A: 0.000  A|C: 0.071  C|C: 0.929  \n\tYRI \tA:0.097  C:0.903\tA|A: 0.000  A|C: 0.194  C|C: 0.806      \n\n AMERICAN \tA:0.612  T:0.388\tA|A: 0.398  A|C: 0.429  C|C: 0.173  \n\tCLM \tA:0.649  C:0.351\tA|A: 0.447  A|C: 0.404  C|C: 0.149  \n\tMXL \tA:0.656  C:0.344\tA|A: 0.406  A|C: 0.500  C|C: 0.094  \n\tPEL \tA:0.629  C:0.371\tA|A: 0.435  A|C: 0.388  C|C: 0.176  \n\tPUR \tA:0.538  C:0.462\tA|A: 0.317  A|C: 0.442  C|C: 0.240  \n\n EAST ASIAN\tA:0.416  C:0.584\tA|A: 0.177  A|C: 0.478  C|C: 0.345 \n\n\tCDX \tA:0.548  C:0.452\tA|A: 0.280  A|C: 0.538  C|C: 0.183  \n\tCHB \tA:0.320  C:0.680\tA|A: 0.087  A|C: 0.466  C|C: 0.447  \n\tCHS \tA:0.400  C:0.600\tA|A: 0.171  A|C: 0.457  C|C: 0.371  \n\tJPT \tA:0.288  C:0.712\tA|A: 0.067  A|C: 0.442  C|C: 0.490  \n\tKHV \tA:0.540  C:0.460\tA|A: 0.293  A|C: 0.495  C|C: 0.212      \n\n EUROPEAN \tA:0.710  C:0.290 \tA|A: 0.529  A|C: 0.362  C|C: 0.109  \n\tCEU \tA:0.793  C:0.207\tA|A: 0.636  A|C: 0.313  C|C: 0.051  \n\tFIN \tA:0.843  C:0.157\tA|A: 0.727  A|C: 0.232  C|C: 0.040  \n\tGBR \tA:0.802  C:0.198\tA|A: 0.626  A|C: 0.352  C|C: 0.022  \n\tIBS \tA:0.556  C:0.444\tA|A: 0.327  A|C: 0.458  C|C: 0.215  \n\tTSI \tA:0.584  C:0.416\tA|A: 0.364  A|C: 0.439  C|C: 0.196  \n\n
```

```
SOUTH ASIAN\tA:0.501  C:0.499\tA|A: 0.252  A|C: 0.499  C|C: 0.249  \n\tBEB \tA:0.517  C:0.483\tA|A: 0.279  A|C: 0.477  C|C:
0.244  \n\tGIH \tA:0.500  C:0.500\tA|A: 0.204  A|C: 0.592  C|C: 0.204  \n\tITU \tA:0.451  C:0.549\tA|A: 0.176  A|C: 0.549  C|C: 0.275
\n\tPJL \tA:0.552  C:0.448\tA|A: 0.354  A|C: 0.396  C|C: 0.250  \n\tSTU \tA:0.490  C:0.510\tA|A: 0.255  A|C: 0.471  C|C: 0.275  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38819365)|| (snp==7696175))
{
        printf(" \n\n Alleles  T/C, Ancestral: C, Ambiguity code: Y, MAF: 0.22 [2]\n Location: 4:38819365 [2] \n SNP ID: rs7696175
[1] \n GWAS Trait: Breast cancer, Multiple complex diseases, Self-reported allergy, Breast Neoplasms [1,2] \n Archaic-like haplotype
cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX,
And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion
Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tT:0.217  C:0.783\tT|T: 0.075
C|C: 0.641  C|T: 0.284 \n\n AFRICAN  \tT:0.018  C:0.982\tT|T: 0.002  C|C: 0.965  C|T: 0.033  \n\tACB \tT:0.036  C:0.964\tT|T: 0.000
C|C: 0.927  C|T: 0.073  \n\tASW \tT:0.098  C:0.902\tT|T: 0.016  C|C: 0.820  C|T: 0.164  \n\tESN \tT:0.000  C:1.000\tT|T: 0.000  C|C:
1.000  C|T: 0.000  \n\tGWD \tT:0.013  C:0.987\tT|T: 0.973  C|C: 0.000  C|T: 0.027  \n\tLWK \tT:0.010  C:0.990\tT|T: 0.980  C|C: 0.000
C|T: 0.020  \n\tMSL \tT:0.000  C:1.000\tT|T: 0.000  C|C: 1.000  C|T: 0.000  \n\tYRI \tT:0.000  C:1.000\tT|T: 0.000  C|C: 1.000  C|T:
0.000      \n\n AMERICAN \tT:0.343  C:0.657\tT|T: 0.133  C|C: 0.447  C|T: 0.421  \n\tCLM \tT:0.388  C:0.612\tT|T: 0.213  C|C: 0.436
C|T: 0.351  \n\tMXL \tT:0.406  C:0.594\tT|T: 0.141  C|C: 0.328  C|T: 0.531  \n\tPEL \tT:0.282  C:0.718\tT|T: 0.071  C|C: 0.506  C|T:
0.424  \n\tPUR \tT:0.312  C:0.688\tT|T: 0.106  C|C: 0.481  C|T: 0.413  \n\n EAST ASIAN\tT:0.152  C:0.848\tT|T: 0.024  C|C: 0.720
C|T: 0.256  \n\tCDX \tT:0.177  C:0.823\tT|T: 0.043  C|C: 0.688  C|T: 0.269  \n\tCHB \tT:0.117  C:0.883\tT|T: 0.000  C|C: 0.767  C|T:
0.233  \n\tCHS \tT:0.186  C:0.814\tT|T: 0.048  C|C: 0.676  C|T: 0.276  \n\tJPT \tT:0.087  C:0.913\tT|T: 0.000  C|C: 0.827  C|T: 0.173
\n\tKHV \tT:0.197  C:0.803\tT|T: 0.030  C|C: 0.636  C|T: 0.333   \n\n EUROPEAN \tT:0.427  C:0.573 \tT|T: 0.197  C|C: 0.342  C|T:
0.461  \n\tCEU \tT:0.490  C:0.510\tT|T: 0.253  C|C: 0.273  C|T: 0.475  \n\tFIN \tT:0.434  C:0.566\tT|T: 0.222  C|C: 0.354  C|T: 0.424
\n\tGBR \tT:0.467  C:0.533\tT|T: 0.154  C|C: 0.220  C|T: 0.626  \n\tIBS \tT:0.402  C:0.598\tT|T: 0.168  C|C: 0.364  C|T: 0.467  \n\tTSI
\tT:0.355  C:0.645\tT|T: 0.187  C|C: 0.477  C|T: 0.336  \n\n SOUTH ASIAN\tT:0.247  C:0.753\tT|T: 0.061  C|C: 0.566  C|T: 0.372
\n\tBEB \tT:0.279  C:0.721\tT|T: 0.093  C|C: 0.535  C|T: 0.372  \n\tGIH \tT:0.248  C:0.752\tT|T: 0.049  C|C: 0.553  C|T: 0.398  \n\tITU
\tT:0.211  C:0.789\tT|T: 0.049  C|C: 0.627  C|T: 0.324  \n\tPJL \tT:0.276  C:0.724\tT|T: 0.062  C|C: 0.510  C|T: 0.427  \n\tSTU \tT:0.230
C:0.770\tT|T: 0.059  C|C: 0.598  C|T: 0.343  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38828729)|| (snp==5743810))
{
        printf(" \n\n Alleles  A/G, Ancestral:G, Ambiguity code: R, MAF: 0.12 [2]\n Location: 4:38828729 [2] \n SNP ID: rs5743810
[1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and
differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other
modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele
Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tA:0.115  G:0.885\tA|A: 0.042  A|G: 0.146  G|G: 0.812 \n\n AFRICAN  \tA:0.017
G:0.983\tA|A: 0.002  A|G: 0.030  G|G: 0.968  \n\tACB \tA:0.036  G:0.964\tA|A: 0.010  A|G: 0.052  G|G: 0.938  \n\tASW \tA:0.074
G:0.926\tA|A: 0.000  A|G: 0.148  G|G: 0.852  \n\tESN \tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000  \n\tGWD \tA:0.013
G:0.987\tA|A: 0.000  A|G: 0.027  G|G: 0.973  \n\tLWK \tA:0.015  G:0.985\tA|A: 0.000  A|G: 0.030  G|G: 0.970  \n\tMSL \tA:0.000
G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000  \n\tYRI \tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000  \n\n AMERICAN
\tA:0.183  G:0.817\tA|A: 0.049  A|G: 0.268  G|G: 0.683  \n\tCLM \tA:0.255  G:0.745\tA|A: 0.096  A|G: 0.319  G|G: 0.585  \n\tMXL
\tA:0.141  G:0.859\tA|A: 0.031  A|G: 0.219  G|G: 0.750  \n\tPEL \tA:0.082  G:0.918\tA|A: 0.000  A|G: 0.165  G|G: 0.835  \n\tPUR
\tA:0.226  G:0.774\tA|A: 0.058  A|G: 0.337  G|G: 0.606  \n\n EAST ASIAN\tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000
\n\tCDX \tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000  \n\tCHB \tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000
```

```
\n\tCHS \tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000  \n\tJPT \tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000
\n\tKHV \tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000   \n\n EUROPEAN \tA:0.409  G:0.591 \tA|A: 0.175  A|G: 0.467  G|G:
0.358  \n\tCEU \tA:0.485  G:0.515\tA|A: 0.242  A|G: 0.485  G|G: 0.273  \n\tFIN \tA:0.424  G:0.576\tA|A: 0.222  A|G: 0.404  G|G: 0.374
\n\tGBR \tA:0.451  G:0.549\tA|A: 0.143  A|G: 0.615  G|G: 0.242  \n\tIBS \tA:0.355  G:0.645\tA|A: 0.121  A|G: 0.467  G|G: 0.411
\n\tTSI \tA:0.341  G:0.659\tA|A: 0.150  A|G: 0.383  G|G: 0.467  \n\n SOUTH ASIAN\tA:0.017  G:0.983\tA|A: 0.000  A|G: 0.035  G|G:
0.965  \n\tBEB \tA:0.017  G:0.983\tA|A: 0.000  A|G: 0.035  G|G: 0.965  \n\tGIH \tA:0.029  G:0.971\tA|A: 0.000  A|G: 0.058  G|G: 0.942
\n\tITU \tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000  \n\tPJL \tA:0.036  G:0.964\tA|A: 0.000  A|G: 0.073  G|G: 0.927
\n\tSTU \tA:0.005  G:0.995\tA|A: 0.000  A|G: 0.010  G|G: 0.990  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38829975)|| (snp==1039559))
{
        printf(" \n\n Alleles  G/A, Ancestral:A, Ambiguity code: R, MAF: 0.33 [2]\n Location: 4:38829975 [2] \n SNP ID: rs1039559
[1] \n GWAS Trait: Self-reported allergy [1]\n Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs
from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern
human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known \n\n\n Population  \tAllele Frequency [2]
\tGenotype Frequency [2] \n\n ALL      \tG:0.332  A:0.668\tG|G: 0.140  A|A: 0.475  A|G: 0.385 \n\n AFRICAN  \tG:0.120
A:0.880\tG|G: 0.012  A|A: 0.772  A|G: 0.216  \n\tACB \tG:0.135  A:0.865\tG|G: 0.021  A|A: 0.750  A|G: 0.229  \n\tASW \tG:0.172
A:0.828\tG|G: 0.016  A|A: 0.672  A|G: 0.311  \n\tESN \tG:0.131  A:0.869\tG|G: 0.010  A|A: 0.747  A|G: 0.242  \n\tGWD \tG:0.124
A:0.876\tG|G: 0.009  A|A: 0.761  A|G: 0.230  \n\tLWK \tG:0.061  A:0.939\tG|G: 0.000  A|A: 0.879  A|G: 0.121  \n\tMSL \tG:0.124
A:0.876\tG|G: 0.012  A|A: 0.765  A|G: 0.224  \n\tYRI \tG:0.116  A:0.884\tG|G: 0.019  A|A: 0.787  A|G: 0.194  \n\n AMERICAN
\tG:0.513  A:0.487\tG|G: 0.282  A|A: 0.256  A|G: 0.461  \n\tCLM \tG:0.495  A:0.505\tG|G: 0.298  A|A: 0.309  A|G: 0.394  \n\tMXL
\tG:0.602  A:0.398\tG|G: 0.328  A|A: 0.125  A|G: 0.547  \n\tPEL \tG:0.594  A:0.406\tG|G: 0.376  A|A: 0.188  A|G: 0.435  \n\tPUR
\tG:0.409  A:0.591 \tG|G: 0.163  A|A: 0.346  A|G: 0.490  \n\n EAST ASIAN\tG:0.272  A:0.728\tG|G: 0.085  A|A: 0.542  A|G: 0.373
\n\tCDX \tG:0.323  A:0.677\tG|G: 0.097  A|A: 0.452  A|G: 0.452  \n\tCHB \tG:0.189  A:0.811\tG|G: 0.029  A|A: 0.650  A|G: 0.320
\n\tCHS \tG:0.281  A:0.719\tG|G: 0.124  A|A: 0.562  A|G: 0.314  \n\tJPT \tG:0.245  A:0.755\tG|G: 0.067  A|A: 0.577  A|G: 0.356
\n\tKHV \tG:0.328  A:0.672\tG|G: 0.111  A|A: 0.455  A|G: 0.434  \n\n EUROPEAN \tG:0.456  A:0.544 \tG|G: 0.219  A|A: 0.306  A|G:
0.475  \n\tCEU \tG:0.530  A:0.470\tG|G: 0.273  A|A: 0.212  A|G: 0.515  \n\tFIN \tG:0.455  A:0.545\tG|G: 0.242  A|A: 0.333  A|G: 0.424
\n\tGBR \tG:0.511  A:0.489\tG|G: 0.220  A|A: 0.198  A|G: 0.582  \n\tIBS \tG:0.416  A:0.584\tG|G: 0.168  A|A: 0.336  A|G: 0.495
\n\tTSI \tG:0.383  A:0.617\tG|G: 0.196  A|A: 0.430  A|G: 0.374  \n\n SOUTH ASIAN\tG:0.425  A:0.575\tG|G: 0.186  A|A: 0.335  A|G:
0.479  \n\tBEB \tG:0.442  A:0.558\tG|G: 0.209  A|A: 0.326  A|G: 0.465  \n\tGIH \tG:0.471  A:0.529\tG|G: 0.175  A|A: 0.233  A|G: 0.592
\n\tITU \tG:0.353  A:0.647\tG|G: 0.098  A|A: 0.392  A|G: 0.510  \n\tPJL \tG:0.427  A:0.573\tG|G: 0.240  A|A: 0.385  A|G: 0.375
\n\tSTU \tG:0.436  A:0.564\tG|G: 0.216  A|A: 0.343  A|G: 0.441  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38831106)|| (snp==5743794))
{
        printf(" \n\n Alleles  C/T, Ancestral: C, Ambiguity code: Y, MAF: 0.18 [2]\n Location: 4:38831106 [2] \n SNP ID: rs5743794
[1] \n GWAS Trait: Suicide attempts in bipolar disorder, Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like
haplotype cluster: The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n
Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tC:0.824
T:0.176\tC|C: 0.696  C|T: 0.256  T|T: 0.048 \n\n AFRICAN  \tC:0.986  T:0.014\tC|C: 0.971  C|T: 0.029  T|T: 0.000  \n\tACB \tC:0.969
T:0.031\tC|C: 0.938  C|T: 0.062  T|T: 0.000  \n\tASW \tC:0.926  T:0.074\tC|C: 0.852  C|T: 0.148  T|T: 0.000  \n\tESN \tC:1.000
T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000  \n\tGWD \tC:0.991  T:0.009\tC|C: 0.982  C|T: 0.018  T|T: 0.000  \n\tLWK \tC:1.000
T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000  \n\tMSL \tC:0.994  T:0.006\tC|C: 0.988  C|T: 0.012  T|T: 0.000  \n\tYRI \tC:0.995
```

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T:0.005\tC|C: 0.991  C|T: 0.009  T|T: 0.000      \n\n AMERICAN \tC:0.840  T:0.160\tC|C: 0.715  C|T: 0.251  T|T: 0.035  \n\tCLM
\tC:0.819  T:0.181\tC|C: 0.670  C|T: 0.298  T|T: 0.032  \n\tMXL \tC:0.891  T:0.109\tC|C: 0.797  C|T: 0.188  T|T: 0.016  \n\tPEL
\tC:0.929  T:0.071\tC|C: 0.859  C|T: 0.141  T|T: 0.000  \n\tPUR \tC:0.755  T:0.245\tC|C: 0.587  C|T: 0.337  T|T: 0.077  \n\n EAST
ASIAN\tC:0.667  T:0.333\tC|C: 0.454  C|T: 0.425  T|T: 0.121  \n\tCDX \tC:0.833  T:0.167\tC|C: 0.699  C|T: 0.269  T|T: 0.032  \n\tCHB
\tC:0.534  T:0.466\tC|C: 0.282  C|T: 0.505  T|T: 0.214  \n\tCHS \tC:0.676  T:0.324\tC|C: 0.429  C|T: 0.495  T|T: 0.076  \n\tJPT \tC:0.505
T:0.495\tC|C: 0.260  C|T: 0.490  T|T: 0.250  \n\tKHV \tC:0.808  T:0.192\tC|C: 0.636  C|T: 0.343  T|T: 0.020    \n\n EUROPEAN
\tC:0.771  T:0.229 \tC|C: 0.606  C|T: 0.330  T|T: 0.064  \n\tCEU \tC:0.808  T:0.192\tC|C: 0.657  C|T: 0.303  T|T: 0.040  \n\tFIN
\tC:0.909  T:0.091\tC|C: 0.828  C|T: 0.162  T|T: 0.010  \n\tGBR \tC:0.830  T:0.170\tC|C: 0.670  C|T: 0.319  T|T: 0.011  \n\tIBS
\tC:0.673  T:0.327\tC|C: 0.458  C|T: 0.430  T|T: 0.112  \n\tTSI \tC:0.659  T:0.341\tC|C: 0.449  C|T: 0.421  T|T: 0.131  \n\n SOUTH
ASIAN\tC:0.813  T:0.187\tC|C: 0.654  C|T: 0.317  T|T: 0.029  \n\tBEB \tC:0.767  T:0.233\tC|C: 0.558  C|T: 0.419  T|T: 0.023  \n\tGIH
\tC:0.791  T:0.209\tC|C: 0.631  C|T: 0.320  T|T: 0.049  \n\tITU \tC:0.843  T:0.157\tC|C: 0.706  C|T: 0.275  T|T: 0.020  \n\tPJL \tC:0.828
T:0.172\tC|C: 0.688  C|T: 0.281  T|T: 0.031  \n\tSTU \tC:0.828  T:0.172\tC|C: 0.676  C|T: 0.304  T|T: 0.020  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38831586)|| (snp==5743788))
{
            printf(" \n\n Alleles  C/G, Ancestral:G, Ambiguity code: S, MAF: 0.39 [2]\n Location: 4:38831586 [2] \n SNP ID: rs5743788
[1] \n GWAS Trait: Self-reported allergy [1]\n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known
\n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tC:0.388  G:0.612\tC|C: 0.165  C|G: 0.446  G|G: 0.389
\n\n AFRICAN  \tC:0.286  G:0.714\tC|C: 0.071  C|G: 0.430  G|G: 0.499  \n\tACB \tC:0.271  G:0.729\tC|C: 0.073  C|G: 0.396  G|G:
0.531  \n\tASW \tC:0.287  G:0.713\tC|C: 0.049  C|G: 0.475  G|G: 0.475  \n\tESN \tC:0.273  G:0.727\tC|C: 0.040  C|G: 0.465  G|G: 0.495
\n\tGWD \tC:0.367  G:0.633\tC|C: 0.115  C|G: 0.504  G|G: 0.381  \n\tLWK \tC:0.202  G:0.798\tC|C: 0.040  C|G: 0.323  G|G: 0.636
\n\tMSL \tC:0.276  G:0.724\tC|C: 0.059  C|G: 0.435  G|G: 0.506  \n\tYRI \tC:0.310  G:0.690\tC|C: 0.102  C|G: 0.417  G|G: 0.481  \n\n
AMERICAN \tC:0.539  G:0.461\tC|C: 0.300  C|G: 0.478  G|G: 0.222  \n\tCLM \tC:0.521  G:0.479\tC|C: 0.330  C|G: 0.383  G|G: 0.287
\n\tMXL \tC:0.602  G:0.398\tC|C: 0.328  C|G: 0.547  G|G: 0.125  \n\tPEL \tC:0.612  G:0.388\tC|C: 0.400  C|G: 0.424  G|G: 0.176
\n\tPUR \tC:0.457  G:0.543 \tC|C: 0.173  C|G: 0.567  G|G: 0.260  \n\n EAST ASIAN\tC:0.272  G:0.728\tC|C: 0.085  C|G: 0.373  G|G:
0.542  \n\tCDX \tC:0.323  G:0.677\tC|C: 0.097  C|G: 0.452  G|G: 0.452  \n\tCHB \tC:0.194  G:0.806\tC|C: 0.029  C|G: 0.330  G|G: 0.641
\n\tCHS \tC:0.281  G:0.719\tC|C: 0.124  C|G: 0.314  G|G: 0.562  \n\tJPT \tC:0.240  G:0.760\tC|C: 0.067  C|G: 0.346  G|G: 0.587
\n\tKHV \tC:0.328  G:0.672\tC|C: 0.111  C|G: 0.434  G|G: 0.455  \n\n EUROPEAN \tC:0.487  G:0.513 \tC|C: 0.250  C|G: 0.473  G|G:
0.276  \n\tCEU \tC:0.540  G:0.460\tC|C: 0.273  C|G: 0.535  G|G: 0.192  \n\tFIN \tC:0.505  G:0.495\tC|C: 0.303  C|G: 0.404  G|G: 0.293
\n\tGBR \tC:0.533  G:0.467\tC|C: 0.264  C|G: 0.538  G|G: 0.198  \n\tIBS \tC:0.463  G:0.537\tC|C: 0.215  C|G: 0.495  G|G: 0.290
\n\tTSI \tC:0.407  G:0.593\tC|C: 0.206  C|G: 0.402  G|G: 0.393  \n\n SOUTH ASIAN\tC:0.437  G:0.563\tC|C: 0.190  C|G: 0.493  G|G:
0.317  \n\tBEB \tC:0.453  G:0.547\tC|C: 0.209  C|G: 0.488  G|G: 0.302  \n\tGIH \tC:0.476  G:0.524\tC|C: 0.175  C|G: 0.602  G|G: 0.223
\n\tITU \tC:0.353  G:0.647\tC|C: 0.098  C|G: 0.510  G|G: 0.392  \n\tPJL \tC:0.464  G:0.536\tC|C: 0.260  C|G: 0.406  G|G: 0.333
\n\tSTU \tC:0.441  G:0.559\tC|C: 0.216  C|G: 0.451  G|G: 0.333  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38842128)|| (snp==7665774))
{
            printf(" \n\n Alleles  G/C, Ancestral: C, Ambiguity code: S, MAF: 0.34 [2]\n Location: 4:38842128 [2] \n SNP ID: rs7665774
[1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and
differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other
modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele
Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tG:0.344  C:0.656\tG|G: 0.144  C|C: 0.455  C|G: 0.401 \n\n AFRICAN  \tG:0.130
C:0.870\tG|G: 0.017  C|C: 0.756  C|G: 0.227  \n\tACB \tG:0.146  C:0.854\tG|G: 0.021  C|C: 0.729  C|G: 0.250  \n\tASW \tG:0.164
```

```
C:0.836\tG|G: 0.016  C|C: 0.689  C|G: 0.295  \n\tESN \tG:0.146  C:0.854\tG|G: 0.030  C|C: 0.737  C|G: 0.232  \n\tGWD \tG:0.142
C:0.858\tG|G: 0.018  C|C: 0.735  C|G: 0.248  \n\tLWK \tG:0.061  C:0.939\tG|G: 0.000  C|C: 0.879  C|G: 0.121  \n\tMSL \tG:0.135
C:0.865\tG|G: 0.012  C|C: 0.741  C|G: 0.247  \n\tYRI \tG:0.130  C:0.870\tG|G: 0.019  C|C: 0.759  C|G: 0.222    \n\n AMERICAN
\tG:0.468  C:0.532\tG|G: 0.219  C|C: 0.282  C|G: 0.499  \n\tCLM \tG:0.468  C:0.532\tG|G: 0.266  C|C: 0.330  C|G: 0.404  \n\tMXL
\tG:0.555  C:0.445\tG|G: 0.281  C|C: 0.172  C|G: 0.547  \n\tPEL \tG:0.518  C:0.482\tG|G: 0.235  C|C: 0.200  C|G: 0.565  \n\tPUR
\tG:0.375  C:0.625\tG|G: 0.125  C|C: 0.375  C|G: 0.500  \n\n EAST ASIAN\tG:0.287  C:0.713\tG|G: 0.093  C|C: 0.520  C|G: 0.387
\n\tCDX \tG:0.371  C:0.629\tG|G: 0.129  C|C: 0.387  C|G: 0.484  \n\tCHB \tG:0.189  C:0.811\tG|G: 0.029  C|C: 0.650  C|G: 0.320
\n\tCHS \tG:0.267  C:0.733\tG|G: 0.105  C|C: 0.571  C|G: 0.324  \n\tJPT \tG:0.255  C:0.745\tG|G: 0.067  C|C: 0.558  C|G: 0.375
\n\tKHV \tG:0.364  C:0.636\tG|G: 0.141  C|C: 0.414  C|G: 0.444    \n\n EUROPEAN \tG:0.461  C:0.539 \tG|G: 0.221  C|C: 0.298  C|G:
0.481  \n\tCEU \tG:0.535  C:0.465\tG|G: 0.283  C|C: 0.212  C|G: 0.505  \n\tFIN \tG:0.460  C:0.540\tG|G: 0.242  C|C: 0.323  C|G: 0.434
\n\tGBR \tG:0.522  C:0.478\tG|G: 0.220  C|C: 0.176  C|G: 0.604  \n\tIBS \tG:0.421  C:0.579\tG|G: 0.168  C|C: 0.327  C|G: 0.505
\n\tTSI \tG:0.383  C:0.617\tG|G: 0.196  C|C: 0.430  C|G: 0.374  \n\n SOUTH ASIAN\tG:0.486  C:0.514\tG|G: 0.237  C|C: 0.266  C|G:
0.497  \n\tBEB \tG:0.494  C:0.506\tG|G: 0.221  C|C: 0.233  C|G: 0.547  \n\tGIH \tG:0.563  C:0.437\tG|G: 0.272  C|C: 0.146  C|G: 0.583
\n\tITU \tG:0.431  C:0.569\tG|G: 0.206  C|C: 0.343  C|G: 0.451  \n\tPJL \tG:0.464  C:0.536\tG|G: 0.260  C|C: 0.333  C|G: 0.406
\n\tSTU \tG:0.475  C:0.525\tG|G: 0.225  C|C: 0.275  C|G: 0.500  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38843577)|| (snp==7673348))
{
        printf(" \n\n Alleles  G/A, Ancestral:A, Ambiguity code: R, MAF: 0.46 [2]\n Location: 4:38843577 [2] \n SNP ID: rs7673348
[1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]\n Archaic-like haplotype cluster: Not Known\n
Clinical Assertion Description: Not Known \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tG:0.456
A:0.544\tG|G: 0.252  A|A: 0.340  A|G: 0.408 \n\n AFRICAN  \tG:0.200  A:0.800\tG|G: 0.035  A|A: 0.634  A|G: 0.331  \n\tACB
\tG:0.219  A:0.781\tG|G: 0.031  A|A: 0.594  A|G: 0.375  \n\tASW \tG:0.238  A:0.762\tG|G: 0.115  A|A: 0.639  A|G: 0.246  \n\tESN
\tG:0.207  A:0.793\tG|G: 0.040  A|A: 0.626  A|G: 0.333  \n\tGWD \tG:0.208  A:0.792\tG|G: 0.027  A|A: 0.611  A|G: 0.363  \n\tLWK
\tG:0.136  A:0.864\tG|G: 0.010  A|A: 0.737  A|G: 0.253  \n\tMSL \tG:0.182  A:0.818\tG|G: 0.012  A|A: 0.647  A|G: 0.341  \n\tYRI
\tG:0.222  A:0.778\tG|G: 0.037  A|A: 0.593  A|G: 0.370  \n\n AMERICAN \tG:0.572  A:0.428\tG|G: 0.331  A|A: 0.187  A|G: 0.481
\n\tCLM \tG:0.606  A:0.394\tG|G: 0.415  A|A: 0.202  A|G: 0.383  \n\tMXL \tG:0.594  A:0.406\tG|G: 0.344  A|A: 0.156  A|G: 0.500
\n\tPEL \tG:0.559  A:0.441\tG|G: 0.282  A|A: 0.165  A|G: 0.553  \n\tPUR \tG:0.538  A:0.462 \tG|G: 0.288  A|A: 0.212  A|G: 0.500  \n\n
EAST ASIAN\tG:0.312  A:0.688\tG|G: 0.099  A|A: 0.474  A|G: 0.427  \n\tCDX \tG:0.398  A:0.602\tG|G: 0.140  A|A: 0.344  A|G: 0.516
\n\tCHB \tG:0.252  A:0.748\tG|G: 0.049  A|A: 0.544  A|G: 0.408  \n\tCHS \tG:0.300  A:0.700\tG|G: 0.105  A|A: 0.505  A|G: 0.390
\n\tJPT \tG:0.260  A:0.740\tG|G: 0.067  A|A: 0.548  A|G: 0.385  \n\tKHV \tG:0.364  A:0.636\tG|G: 0.141  A|A: 0.414  A|G: 0.444  \n\n
EUROPEAN \tG:0.735  A:0.265 \tG|G: 0.559  A|A: 0.089  A|G: 0.352  \n\tCEU \tG:0.798  A:0.202\tG|G: 0.636  A|A: 0.040  A|G: 0.323
\n\tFIN \tG:0.884  A:0.116\tG|G: 0.788  A|A: 0.020  A|G: 0.192  \n\tGBR \tG:0.824  A:0.176\tG|G: 0.659  A|A: 0.011  A|G: 0.330
\n\tIBS \tG:0.593  A:0.407\tG|G: 0.355  A|A: 0.168  A|G: 0.477  \n\tTSI \tG:0.603  A:0.397\tG|G: 0.393  A|A: 0.187  A|G: 0.421  \n\n
SOUTH ASIAN\tG:0.579  A:0.421\tG|G: 0.329  A|A: 0.172  A|G: 0.499  \n\tBEB \tG:0.570  A:0.430\tG|G: 0.279  A|A: 0.140  A|G:
0.581  \n\tGIH \tG:0.626  A:0.374\tG|G: 0.350  A|A: 0.097  A|G: 0.553  \n\tITU \tG:0.544  A:0.456\tG|G: 0.314  A|A: 0.225  A|G: 0.461
\n\tPJL \tG:0.604  A:0.396\tG|G: 0.396  A|A: 0.188  A|G: 0.417  \n\tSTU \tG:0.549  A:0.451\tG|G: 0.304  A|A: 0.206  A|G: 0.490
\n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38845358)|| (snp==7687447))
{
        printf(" \n\n Alleles  C/G, Ancestral:G, Ambiguity code: S, MAF: 0.49 [2]\n Location: 4:38845358 [2] \n SNP ID: rs7687447
[1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]\n Archaic-like haplotype cluster: Not Known\n
```

```
Clinical Assertion Description: Not Known \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tC:0.489
G:0.511\tC|C: 0.274  C|G: 0.430  G|G: 0.296 \n\n AFRICAN  \tC:0.272  G:0.728\tC|C: 0.071  C|G: 0.402  G|G: 0.526  \n\tACB \tC:0.318
G:0.682\tC|C: 0.094  C|G: 0.448  G|G: 0.458  \n\tASW \tC:0.295  G:0.705\tC|C: 0.131  C|G: 0.328  G|G: 0.541  \n\tESN \tC:0.268
G:0.732\tC|C: 0.081  C|G: 0.374  G|G: 0.545  \n\tGWD \tC:0.265  G:0.735\tC|C: 0.053  C|G: 0.425  G|G: 0.522  \n\tLWK \tC:0.232
G:0.768\tC|C: 0.061  C|G: 0.343  G|G: 0.596  \n\tMSL \tC:0.259  G:0.741\tC|C: 0.035  C|G: 0.447  G|G: 0.518  \n\tYRI \tC:0.278
G:0.722\tC|C: 0.065  C|G: 0.426  G|G: 0.509  \n\n AMERICAN \tC:0.575  G:0.425\tC|C: 0.334  C|G: 0.481  G|G: 0.184  \n\tCLM
\tC:0.612  G:0.388\tC|C: 0.415  C|G: 0.394  G|G: 0.191  \n\tMXL \tC:0.594  G:0.406\tC|C: 0.344  C|G: 0.500  G|G: 0.156  \n\tPEL
\tC:0.559  G:0.441\tC|C: 0.282  C|G: 0.553  G|G: 0.165  \n\tPUR \tC:0.543  G:0.457 \tC|C: 0.298  C|G: 0.490  G|G: 0.212  \n\n EAST
ASIAN\tC:0.367  G:0.633\tC|C: 0.141  C|G: 0.452  G|G: 0.407  \n\tCDX \tC:0.462  G:0.538\tC|C: 0.204  C|G: 0.516  G|G: 0.280
\n\tCHB \tC:0.335  G:0.665\tC|C: 0.107  C|G: 0.456  G|G: 0.437  \n\tCHS \tC:0.333  G:0.667\tC|C: 0.124  C|G: 0.419  G|G: 0.457
\n\tJPT \tC:0.279  G:0.721\tC|C: 0.087  C|G: 0.385  G|G: 0.529  \n\tKHV \tC:0.439  G:0.561\tC|C: 0.192  C|G: 0.495  G|G: 0.313  \n\n
EUROPEAN \tC:0.736  G:0.264 \tC|C: 0.561  C|G: 0.350  G|G: 0.089  \n\tCEU \tC:0.798  G:0.202\tC|C: 0.636  C|G: 0.323  G|G: 0.040
\n\tFIN \tC:0.884  G:0.116\tC|C: 0.788  C|G: 0.192  G|G: 0.020  \n\tGBR \tC:0.824  G:0.176\tC|C: 0.659  C|G: 0.330  G|G: 0.011
\n\tIBS \tC:0.598  G:0.402\tC|C: 0.364  C|G: 0.467  G|G: 0.168  \n\tTSI \tC:0.603  G:0.397\tC|C: 0.393  C|G: 0.421  G|G: 0.187  \n\n
SOUTH ASIAN\tC:0.592  G:0.408\tC|C: 0.348  C|G: 0.489  G|G: 0.164  \n\tBEB \tC:0.587  G:0.413\tC|C: 0.302  C|G: 0.570  G|G:
0.128  \n\tGIH \tC:0.631  G:0.369\tC|C: 0.359  C|G: 0.544  G|G: 0.097  \n\tITU \tC:0.564  G:0.436\tC|C: 0.333  C|G: 0.461  G|G: 0.206
\n\tPJL \tC:0.615  G:0.385\tC|C: 0.417  C|G: 0.396  G|G: 0.188  \n\tSTU \tC:0.564  G:0.436\tC|C: 0.324  C|G: 0.480  G|G: 0.196  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38845390)|| (snp==6531672 ))
{
            printf(" \n\n Alleles  T/C, Ancestral: C, Ambiguity code: Y, MAF: 0.33 [2]\n Location: 4:38845390 [2] \n SNP ID: rs6531672
[1]  \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and
differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other
modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele
Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tT:0.331  C:0.669\tT|T: 0.133  C|C: 0.470  C|T: 0.397 \n\n AFRICAN  \tT:0.120
C:0.880\tT|T: 0.012  C|C: 0.772  C|T: 0.216  \n\tACB \tT:0.135  C:0.865\tT|T: 0.021  C|C: 0.750  C|T: 0.229  \n\tASW \tT:0.164
C:0.836\tT|T: 0.016  C|C: 0.689  C|T: 0.295  \n\tESN \tT:0.136  C:0.864\tT|T: 0.010  C|C: 0.737  C|T: 0.253  \n\tGWD \tT:0.124
C:0.876\tT|T: 0.009  C|C: 0.761  C|T: 0.230  \n\tLWK \tT:0.061  C:0.939\tT|T: 0.000  C|C: 0.879  C|T: 0.121  \n\tMSL \tT:0.124
C:0.876\tT|T: 0.012  C|C: 0.765  C|T: 0.224  \n\tYRI \tT:0.116  C:0.884\tT|T: 0.019  C|C: 0.787  C|T: 0.194    \n\n AMERICAN
\tT:0.463  C:0.537\tT|T: 0.210  C|C: 0.285  C|T: 0.504  \n\tCLM \tT:0.463  C:0.537\tT|T: 0.255  C|C: 0.330  C|T: 0.415  \n\tMXL
\tT:0.539  C:0.461\tT|T: 0.266  C|C: 0.188  C|T: 0.547  \n\tPEL \tT:0.512  C:0.488\tT|T: 0.224  C|C: 0.200  C|T: 0.576  \n\tPUR
\tT:0.375  C:0.625\tT|T: 0.125  C|C: 0.375  C|T: 0.500  \n\n EAST ASIAN\tT:0.287  C:0.713\tT|T: 0.091  C|C: 0.518  C|T: 0.391
\n\tCDX \tT:0.366  C:0.634\tT|T: 0.129  C|C: 0.398  C|T: 0.473  \n\tCHB \tT:0.209  C:0.791\tT|T: 0.039  C|C: 0.621  C|T: 0.340
\n\tCHS \tT:0.281  C:0.719\tT|T: 0.105  C|C: 0.543  C|T: 0.352  \n\tJPT \tT:0.240  C:0.760\tT|T: 0.058  C|C: 0.577  C|T: 0.365  \n\tKHV
\tT:0.348  C:0.652\tT|T: 0.131  C|C: 0.434  C|T: 0.434    \n\n EUROPEAN \tT:0.458  C:0.542 \tT|T: 0.221  C|C: 0.304  C|T: 0.475
\n\tCEU \tT:0.535  C:0.465\tT|T: 0.283  C|C: 0.212  C|T: 0.505  \n\tFIN \tT:0.460  C:0.540\tT|T: 0.242  C|C: 0.323  C|T: 0.434  \n\tGBR
\tT:0.511  C:0.489\tT|T: 0.220  C|C: 0.198  C|T: 0.582  \n\tIBS \tT:0.421  C:0.579\tT|T: 0.168  C|C: 0.327  C|T: 0.505  \n\tTSI \tT:0.379
C:0.621\tT|T: 0.196  C|C: 0.439  C|T: 0.364  \n\n SOUTH ASIAN\tT:0.439  C:0.561\tT|T: 0.194  C|C: 0.317  C|T: 0.489  \n\tBEB
\tT:0.436  C:0.564\tT|T: 0.198  C|C: 0.326  C|T: 0.477  \n\tGIH \tT:0.515  C:0.485\tT|T: 0.214  C|C: 0.184  C|T: 0.602  \n\tITU \tT:0.363
C:0.637\tT|T: 0.118  C|C: 0.392  C|T: 0.490  \n\tPJL \tT:0.432  C:0.568\tT|T: 0.229  C|C: 0.365  C|T: 0.406  \n\tSTU \tT:0.446
C:0.554\tT|T: 0.216  C|C: 0.324  C|T: 0.461  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38846296)|| (snp==6531673 ))
```

```
{
        printf(" \n\n Alleles  T/C, Ancestral: C, Ambiguity code: Y, MAF: 0.36 [2]\n Location: 4:38846296 [2] \n SNP ID: rs6531673
[1]  \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and
differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other
modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele
Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tT:0.359  C:0.641\tT|T: 0.153  C|C: 0.434  C|T: 0.413 \n\n AFRICAN  \tT:0.139
C:0.861\tT|T: 0.017  C|C: 0.738  C|T: 0.245  \n\tACB \tT:0.156  C:0.844\tT|T: 0.021  C|C: 0.708  C|T: 0.271  \n\tASW \tT:0.164
C:0.836\tT|T: 0.016  C|C: 0.689  C|T: 0.295  \n\tESN \tT:0.157  C:0.843\tT|T: 0.030  C|C: 0.717  C|T: 0.253  \n\tGWD \tT:0.142
C:0.858\tT|T: 0.018  C|C: 0.735  C|T: 0.248  \n\tLWK \tT:0.091  C:0.909\tT|T: 0.000  C|C: 0.818  C|T: 0.182  \n\tMSL \tT:0.135
C:0.865\tT|T: 0.012  C|C: 0.741  C|T: 0.247  \n\tYRI \tT:0.139  C:0.861\tT|T: 0.019  C|C: 0.741  C|T: 0.241    \n\n AMERICAN
\tT:0.480  C:0.520\tT|T: 0.225  C|C: 0.265  C|T: 0.510  \n\tCLM \tT:0.484  C:0.516\tT|T: 0.287  C|C: 0.319  C|T: 0.394  \n\tMXL
\tT:0.555  C:0.445\tT|T: 0.281  C|C: 0.172  C|T: 0.547  \n\tPEL \tT:0.524  C:0.476\tT|T: 0.235  C|C: 0.188  C|T: 0.576  \n\tPUR
\tT:0.394  C:0.606\tT|T: 0.125  C|C: 0.337  C|T: 0.538  \n\n EAST ASIAN\tT:0.303  C:0.697\tT|T: 0.099  C|C: 0.494  C|T: 0.407
\n\tCDX \tT:0.398  C:0.602\tT|T: 0.140  C|C: 0.344  C|T: 0.516  \n\tCHB \tT:0.223  C:0.777\tT|T: 0.049  C|C: 0.602  C|T: 0.350
\n\tCHS \tT:0.286  C:0.714\tT|T: 0.105  C|C: 0.533  C|T: 0.362  \n\tJPT \tT:0.255  C:0.745\tT|T: 0.067  C|C: 0.558  C|T: 0.375  \n\tKHV
\tT:0.364  C:0.636\tT|T: 0.141  C|C: 0.414  C|T: 0.444    \n\n EUROPEAN \tT:0.490  C:0.510 \tT|T: 0.252  C|C: 0.272  C|T: 0.475
\n\tCEU \tT:0.545  C:0.455\tT|T: 0.283  C|C: 0.192  C|T: 0.525  \n\tFIN \tT:0.510  C:0.490\tT|T: 0.303  C|C: 0.283  C|T: 0.414  \n\tGBR
\tT:0.544  C:0.456\tT|T: 0.264  C|C: 0.176  C|T: 0.560  \n\tIBS \tT:0.463  C:0.537\tT|T: 0.215  C|C: 0.290  C|T: 0.495  \n\tTSI \tT:0.402
C:0.598\tT|T: 0.206  C|C: 0.402  C|T: 0.393  \n\n SOUTH ASIAN\tT:0.496  C:0.504\tT|T: 0.239  C|C: 0.247  C|T: 0.513  \n\tBEB
\tT:0.506  C:0.494\tT|T: 0.221  C|C: 0.209  C|T: 0.570  \n\tGIH \tT:0.563  C:0.437\tT|T: 0.262  C|C: 0.136  C|T: 0.602  \n\tITU \tT:0.431
C:0.569\tT|T: 0.206  C|C: 0.343  C|T: 0.451  \n\tPJL \tT:0.500  C:0.500\tT|T: 0.281  C|C: 0.281  C|T: 0.438  \n\tSTU \tT:0.480
C:0.520\tT|T: 0.225  C|C: 0.265  C|T: 0.510  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38854763)|| (snp==7681628))
{
        printf(" \n\n Alleles  G/A, Ancestral:A, Ambiguity code: R, MAF: 0.36 [2]\n Location: 4:38854763 [2] \n SNP ID: rs7681628
[1] \n GWAS Trait: Self-reported allergy [1]\n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known
\n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tG:0.362  A:0.638\tG|G: 0.154  A|A: 0.431  A|G: 0.415
\n\n AFRICAN  \tG:0.150  A:0.850\tG|G: 0.020  A|A: 0.720  A|G: 0.260  \n\tACB \tG:0.172  A:0.828\tG|G: 0.021  A|A: 0.677  A|G:
0.302  \n\tASW \tG:0.164  A:0.836\tG|G: 0.016  A|A: 0.689  A|G: 0.295  \n\tESN \tG:0.167  A:0.833\tG|G: 0.030  A|A: 0.697  A|G:
0.273  \n\tGWD \tG:0.146  A:0.854\tG|G: 0.018  A|A: 0.726  A|G: 0.257  \n\tLWK \tG:0.096  A:0.904\tG|G: 0.000  A|A: 0.808  A|G:
0.192  \n\tMSL \tG:0.159  A:0.841\tG|G: 0.024  A|A: 0.706  A|G: 0.271  \n\tYRI \tG:0.153  A:0.847\tG|G: 0.028  A|A: 0.722  A|G:
0.250  \n\n AMERICAN \tG:0.480  A:0.520\tG|G: 0.225  A|A: 0.265  A|G: 0.510  \n\tCLM \tG:0.484  A:0.516\tG|G: 0.287  A|A: 0.319
A|G: 0.394  \n\tMXL \tG:0.555  A:0.445\tG|G: 0.281  A|A: 0.172  A|G: 0.547  \n\tPEL \tG:0.524  A:0.476\tG|G: 0.235  A|A: 0.188  A|G:
0.576  \n\tPUR \tG:0.394  A:0.606 \tG|G: 0.125  A|A: 0.337  A|G: 0.538  \n\n EAST ASIAN\tG:0.303  A:0.697\tG|G: 0.099  A|A: 0.494
A|G: 0.407  \n\tCDX \tG:0.398  A:0.602\tG|G: 0.140  A|A: 0.344  A|G: 0.516  \n\tCHB \tG:0.223  A:0.777\tG|G: 0.049  A|A: 0.602
A|G: 0.350  \n\tCHS \tG:0.286  A:0.714\tG|G: 0.105  A|A: 0.533  A|G: 0.362  \n\tJPT \tG:0.255  A:0.745\tG|G: 0.067  A|A: 0.558  A|G:
0.375  \n\tKHV \tG:0.364  A:0.636\tG|G: 0.141  A|A: 0.414  A|G: 0.444  \n\n EUROPEAN \tG:0.489  A:0.511 \tG|G: 0.254  A|A: 0.276
A|G: 0.469  \n\tCEU \tG:0.545  A:0.455\tG|G: 0.283  A|A: 0.192  A|G: 0.525  \n\tFIN \tG:0.505  A:0.495\tG|G: 0.303  A|A: 0.293  A|G:
0.404  \n\tGBR \tG:0.544  A:0.456\tG|G: 0.264  A|A: 0.176  A|G: 0.560  \n\tIBS \tG:0.467  A:0.533\tG|G: 0.224  A|A: 0.290  A|G: 0.486
\n\tTSI \tG:0.397  A:0.603\tG|G: 0.206  A|A: 0.411  A|G: 0.383  \n\n SOUTH ASIAN\tG:0.494  A:0.506\tG|G: 0.239  A|A: 0.252  A|G:
0.509  \n\tBEB \tG:0.494  A:0.506\tG|G: 0.221  A|A: 0.233  A|G: 0.547  \n\tGIH \tG:0.563  A:0.437\tG|G: 0.262  A|A: 0.136  A|G: 0.602
\n\tITU \tG:0.431  A:0.569\tG|G: 0.206  A|A: 0.343  A|G: 0.451  \n\tPJL \tG:0.500  A:0.500\tG|G: 0.281  A|A: 0.281  A|G: 0.438
\n\tSTU \tG:0.480  A:0.520\tG|G: 0.225  A|A: 0.265  A|G: 0.510  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
```

```
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38857718)|| (snp==2174284))
{
        printf(" \n\n Alleles  C/T, Ancestral: G, Ambiguity code: Y, MAF: 0.16 [2]\n Location: 4:38857718 [2] \n SNP ID: rs2174284 [1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tC:0.839  T:0.161\tC|C: 0.720  C|T: 0.238  T|T: 0.042 \n\n AFRICAN  \tC:0.989  T:0.011\tC|C: 0.977  C|T: 0.023  T|T: 0.000  \n\tACB \tC:0.974  T:0.026\tC|C: 0.948  C|T: 0.052  T|T: 0.000  \n\tASW \tC:0.934  T:0.066\tC|C: 0.869  C|T: 0.131  T|T: 0.000  \n\tESN \tC:1.000  T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000  \n\tGWD \tC:0.991  T:0.009\tC|C: 0.982  C|T: 0.018  T|T: 0.000  \n\tLWK \tC:1.000  T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000  \n\tMSL \tC:1.000  T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000  \n\tYRI \tC:1.000  T:0.000\tC|C: 1.000  C|T: 0.000  T|T: 0.000      \n\n AMERICAN \tC:0.840  T:0.160\tC|C: 0.718  C|T: 0.245  T|T: 0.037  \n\tCLM \tC:0.824  T:0.176\tC|C: 0.681  C|T: 0.287  T|T: 0.032  \n\tMXL \tC:0.891  T:0.109\tC|C: 0.797  C|T: 0.188  T|T: 0.016  \n\tPEL \tC:0.929  T:0.071\tC|C: 0.859  C|T: 0.141  T|T: 0.000  \n\tPUR \tC:0.750  T:0.250\tC|C: 0.587  C|T: 0.327  T|T: 0.087  \n\n EAST ASIAN\tC:0.728  T:0.272\tC|C: 0.546  C|T: 0.365  T|T: 0.089  \n\tCDX \tC:0.892  T:0.108\tC|C: 0.796  C|T: 0.194  T|T: 0.011  \n\tCHB \tC:0.621  T:0.379\tC|C: 0.379  C|T: 0.485  T|T: 0.136  \n\tCHS \tC:0.724  T:0.276\tC|C: 0.505  C|T: 0.438  T|T: 0.057  \n\tJPT \tC:0.538  T:0.462\tC|C: 0.298  C|T: 0.481  T|T: 0.221  \n\tKHV \tC:0.889  T:0.111\tC|C: 0.788  C|T: 0.202  T|T: 0.010    \n\n EUROPEAN \tC:0.770  T:0.230 \tC|C: 0.606  C|T: 0.328  T|T: 0.066  \n\tCEU \tC:0.813  T:0.187\tC|C: 0.667  C|T: 0.293  T|T: 0.040  \n\tFIN \tC:0.909  T:0.091\tC|C: 0.828  C|T: 0.162  T|T: 0.010  \n\tGBR \tC:0.830  T:0.170\tC|C: 0.670  C|T: 0.319  T|T: 0.011  \n\tIBS \tC:0.678  T:0.322\tC|C: 0.458  C|T: 0.439  T|T: 0.103  \n\tTSI \tC:0.645  T:0.355\tC|C: 0.439  C|T: 0.411  T|T: 0.150  \n\n SOUTH ASIAN\tC:0.822  T:0.178\tC|C: 0.671  C|T: 0.303  T|T: 0.027  \n\tBEB \tC:0.779  T:0.221\tC|C: 0.581  C|T: 0.395  T|T: 0.023  \n\tGIH \tC:0.796  T:0.204\tC|C: 0.641  C|T: 0.311  T|T: 0.049  \n\tITU \tC:0.858  T:0.142\tC|C: 0.735  C|T: 0.245  T|T: 0.020  \n\tPJL \tC:0.833  T:0.167\tC|C: 0.698  C|T: 0.271  T|T: 0.031  \n\tSTU \tC:0.838  T:0.162\tC|C: 0.686  C|T: 0.304  T|T: 0.010  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n   JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38860500)|| (snp==3860069))
{
        printf(" \n\n Alleles  A/C, Ancestral: A, Ambiguity code: M, MAF: 0.46 [2]\n Location: 4:38860500 [2] \n SNP ID: rs3860069 [1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tA:0.543  C:0.457\tA|A: 0.313  A|C: 0.458  C|C: 0.228 \n\n AFRICAN  \tA:0.393  C:0.607\tA|A: 0.151  A|C: 0.483  C|C: 0.366  \n\tACB \tA:0.422  C:0.578\tA|A: 0.188  A|C: 0.469  C|C: 0.344  \n\tASW \tA:0.467  C:0.533\tA|A: 0.246  A|C: 0.443  C|C: 0.311  \n\tESN \tA:0.379  C:0.621\tA|A: 0.141  A|C: 0.475  C|C: 0.384  \n\tGWD \tA:0.354  C:0.646\tA|A: 0.124  A|C: 0.460  C|C: 0.416  \n\tLWK \tA:0.414  C:0.586\tA|A: 0.162  A|C: 0.505  C|C: 0.333  \n\tMSL \tA:0.394  C:0.606\tA|A: 0.165  A|C: 0.459  C|C: 0.376  \n\tYRI \tA:0.356  C:0.644\tA|A: 0.083  A|C: 0.546  C|C: 0.370  \n\n AMERICAN \tA:0.588  T:0.412\tA|A: 0.354  A|C: 0.467  C|C: 0.179  \n\tCLM \tA:0.617  C:0.383\tA|A: 0.426  A|C: 0.383  C|C: 0.191  \n\tMXL \tA:0.602  C:0.398\tA|A: 0.359  A|C: 0.484  C|C: 0.156  \n\tPEL \tA:0.571  C:0.429\tA|A: 0.294  A|C: 0.553  C|C: 0.153  \n\tPUR \tA:0.567  C:0.433\tA|A: 0.337  A|C: 0.462  C|C: 0.202  \n\n EAST ASIAN\tA:0.446  C:0.554\tA|A: 0.196  A|C: 0.500  C|C: 0.304 \n\n\tCDX \tA:0.548  C:0.452\tA|A: 0.280  A|C: 0.538  C|C: 0.183  \n\tCHB \tA:0.379  C:0.621\tA|A: 0.136  A|C: 0.485  C|C: 0.379  \n\tCHS \tA:0.433  C:0.567\tA|A: 0.190  A|C: 0.486  C|C: 0.324  \n\tJPT \tA:0.346  C:0.654\tA|A: 0.135  A|C: 0.423  C|C: 0.442  \n\tKHV \tA:0.540  C:0.460\tA|A: 0.253  A|C: 0.576  C|C: 0.172      \n\n EUROPEAN \tA:0.736  C:0.264 \tA|A: 0.563  A|C: 0.346  C|C: 0.091  \n\tCEU \tA:0.798  C:0.202\tA|A: 0.636  A|C: 0.323  C|C: 0.040  \n\tFIN \tA:0.884  C:0.116\tA|A: 0.788  A|C: 0.192  C|C: 0.020  \n\tGBR \tA:0.830  C:0.170\tA|A: 0.670  A|C: 0.319  C|C: 0.011  \n\tIBS \tA:0.593  C:0.407\tA|A: 0.364  A|C: 0.458  C|C: 0.178  \n\tTSI \tA:0.603  C:0.397\tA|A: 0.393  A|C: 0.421  C|C: 0.187  \n\n SOUTH ASIAN\tA:0.615  C:0.385\tA|A: 0.368  A|C: 0.493  C|C: 0.139  \n\tBEB \tA:0.593  C:0.407\tA|A: 0.314  A|C: 0.558  C|C: 0.128  \n\tGIH \tA:0.646  C:0.354\tA|A: 0.388  A|C: 0.515  C|C: 0.097  \n\tITU \tA:0.593  C:0.407\tA|A: 0.333  A|C: 0.520  C|C: 0.147  \n\tPJL \tA:0.646  C:0.354\tA|A: 0.438  A|C: 0.417  C|C: 0.146  \n\tSTU \tA:0.593  C:0.407\tA|A: 0.363  A|C: 0.461  C|C: 0.176  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n   JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
```

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printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38865806)|| (snp==17582830))
{
        printf(" \n\n Alleles  A/G, Ancestral:A, Ambiguity code: R, MAF: 0.21 [2]\n Location: 4:38865806 [2] \n SNP ID: rs17582830 [1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known   \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tA:0.794  G:0.206\tA|A: 0.645  A|G: 0.300  G|G: 0.056 \n\n AFRICAN  \tA:0.923  G:0.077\tA|A: 0.850  A|G: 0.145  G|G: 0.005  \n\tACB \tA:0.880  G:0.120\tA|A: 0.781  A|G: 0.198  G|G: 0.021  \n\tASW \tA:0.885  G:0.115\tA|A: 0.770  A|G: 0.230  G|G: 0.000  \n\tESN \tA:0.934  G:0.066\tA|A: 0.869  A|G: 0.131  G|G: 0.000  \n\tGWD \tA:0.960  G:0.040\tA|A: 0.920  A|G: 0.080  G|G: 0.000  \n\tLWK \tA:0.874  G:0.126\tA|A: 0.747  A|G: 0.253  G|G: 0.000  \n\tMSL \tA:0.947  G:0.053\tA|A: 0.894  A|G: 0.106  G|G: 0.000  \n\tYRI \tA:0.958  G:0.042\tA|A: 0.926  A|G: 0.065  G|G: 0.009   \n\n AMERICAN \tA:0.820  G:0.180\tA|A: 0.686  A|G: 0.268  G|G: 0.046  \n\tCLM \tA:0.798  G:0.202\tA|A: 0.638  A|G: 0.319  G|G: 0.043  \n\tMXL \tA:0.875  G:0.125\tA|A: 0.766  A|G: 0.219  G|G: 0.016  \n\tPEL \tA:0.912  G:0.088\tA|A: 0.824  A|G: 0.176  G|G: 0.000  \n\tPUR \tA:0.731  G:0.269\tA|A: 0.567  A|G: 0.327  G|G: 0.106  \n\n EAST ASIAN\tA:0.661  G:0.339\tA|A: 0.437  A|G: 0.448  G|G: 0.115  \n\tCDX \tA:0.801  G:0.199\tA|A: 0.634  A|G: 0.333  G|G: 0.032  \n\tCHB \tA:0.534  G:0.466\tA|A: 0.272  A|G: 0.524  G|G: 0.204  \n\tCHS \tA:0.681  G:0.319\tA|A: 0.438  A|G: 0.486  G|G: 0.076  \n\tJPT \tA:0.510  G:0.490\tA|A: 0.250  A|G: 0.519  G|G: 0.231  \n\tKHV \tA:0.798  G:0.202\tA|A: 0.616  A|G: 0.364  G|G: 0.020  \n\n EUROPEAN \tA:0.766  G:0.234 \tA|A: 0.604  A|G: 0.324  G|G: 0.072  \n\tCEU \tA:0.813  G:0.187\tA|A: 0.667  A|G: 0.293  G|G: 0.040  \n\tFIN \tA:0.909  G:0.091\tA|A: 0.828  A|G: 0.162  G|G: 0.010  \n\tGBR \tA:0.813  G:0.187\tA|A: 0.648  A|G: 0.330  G|G: 0.022  \n\tIBS \tA:0.678  G:0.322\tA|A: 0.458  A|G: 0.439  G|G: 0.103  \n\tTSI \tA:0.640  G:0.360\tA|A: 0.449  A|G: 0.383  G|G: 0.168  \n\n SOUTH ASIAN\tA:0.769  G:0.231\tA|A: 0.593  A|G: 0.352  G|G: 0.055  \n\tBEB \tA:0.709  G:0.291\tA|A: 0.500  A|G: 0.419  G|G: 0.081  \n\tGIH \tA:0.752  G:0.248\tA|A: 0.573  A|G: 0.359  G|G: 0.068  \n\tITU \tA:0.775  G:0.225\tA|A: 0.598  A|G: 0.353  G|G: 0.049  \n\tPJL \tA:0.807  G:0.193\tA|A: 0.656  A|G: 0.302  G|G: 0.042  \n\tSTU \tA:0.794  G:0.206\tA|A: 0.627  A|G: 0.333  G|G: 0.039  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38873181)|| (snp==2130296))
{
        printf(" \n\n Alleles  A/G, Ancestral:G, Ambiguity code: R, MAF: 0.20 [2]\n Location: 4:38873181 [2] \n SNP ID: rs2130296 [1] \n GWAS Trait: Multiple complex diseases [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tA:0.796  G:0.204\tA|A: 0.658  A|G: 0.275  G|G: 0.067 \n\n AFRICAN  \tA:0.603  G:0.397\tA|A: 0.366  A|G: 0.474  G|G: 0.160  \n\tACB \tA:0.583  G:0.417\tA|A: 0.375  A|G: 0.417  G|G: 0.208  \n\tASW \tA:0.615  G:0.385\tA|A: 0.361  A|G: 0.508  G|G: 0.131  \n\tESN \tA:0.646  G:0.354\tA|A: 0.374  A|G: 0.545  G|G: 0.081  \n\tGWD \tA:0.575  G:0.425\tA|A: 0.336  A|G: 0.478  G|G: 0.186  \n\tLWK \tA:0.616  G:0.384\tA|A: 0.394  A|G: 0.444  G|G: 0.162  \n\tMSL \tA:0.629  G:0.371\tA|A: 0.400  A|G: 0.459  G|G: 0.141  \n\tYRI \tA:0.569  G:0.431\tA|A: 0.333  A|G: 0.472  G|G: 0.194   \n\n AMERICAN \tA:0.862  G:0.138\tA|A: 0.744  A|G: 0.236  G|G: 0.020  \n\tCLM \tA:0.819  G:0.181\tA|A: 0.660  A|G: 0.319  G|G: 0.021  \n\tMXL \tA:0.945  G:0.055\tA|A: 0.891  A|G: 0.109  G|G: 0.000  \n\tPEL \tA:0.935  G:0.065\tA|A: 0.871  A|G: 0.129  G|G: 0.00  \n\tPUR \tA:0.788  G:0.212\tA|A: 0.625  A|G: 0.327  G|G: 0.048  \n\n EAST ASIAN\tA:0.986  G:0.014\tA|A: 0.972  A|G: 0.028  G|G: 0.000  \n\tCDX \tA:0.995  G:0.005\tA|A: 0.989  A|G: 0.011  G|G: 0.000  \n\tCHB \tA:0.966  G:0.034\tA|A: 0.932  A|G: 0.068  G|G: 0.000  \n\tCHS \tA:0.990  G:0.010\tA|A: 0.981  A|G: 0.019  G|G: 0.000  \n\tJPT \tA:0.995  G:0.005\tA|A: 0.990  A|G: 0.010  G|G: 0.000  \n\tKHV \tA:0.985  G:0.015\tA|A: 0.970  A|G: 0.030  G|G: 0.000  \n\n EUROPEAN \tA:0.726  G:0.274 \tA|A: 0.545  A|G: 0.362  G|G: 0.093  \n\tCEU \tA:0.737  G:0.263\tA|A: 0.545  A|G: 0.384  G|G: 0.071  \n\tFIN \tA:0.581  G:0.419\tA|A: 0.354  A|G: 0.455  G|G: 0.192  \n\tGBR \tA:0.698  G:0.302\tA|A: 0.495  A|G: 0.407  G|G: 0.099  \n\tIBS \tA:0.827  G:0.173\tA|A: 0.692  A|G: 0.271  G|G: 0.037  \n\tTSI \tA:0.771  G:0.229\tA|A: 0.617  A|G: 0.308  G|G: 0.075  \n\n SOUTH ASIAN\tA:0.885  G:0.115\tA|A: 0.785  A|G: 0.200  G|G: 0.014  \n\tBEB \tA:0.907  G:0.093\tA|A: 0.814  A|G: 0.186  G|G: 0.000  \n\tGIH \tA:0.913  G:0.087\tA|A: 0.825  A|G: 0.175  G|G: 0.000  \n\tITU \tA:0.858  G:0.142\tA|A: 0.735  A|G: 0.245  G|G: 0.020  \n\tPJL \tA:0.849  G:0.151\tA|A: 0.750  A|G: 0.198  G|G: 0.052  \n\tSTU \tA:0.902  G:0.098\tA|A: 0.804  A|G: 0.196  G|G: 0.000  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
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printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38876573)|| (snp==721653))
{
        printf(" \n\n Alleles  T/C, Ancestral:C, Ambiguity code: Y, MAF: 0.45 [2]\n Location: 4:38876573 [2] \n SNP ID: rs721653 [1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tT:0.552  C:0.448\tT|T: 0.313  C|C: 0.209  C|T: 0.478 \n\n AFRICAN  \tT:0.491  C:0.509\tT|T: 0.238  C|C: 0.256  C|T: 0.507  \n\tACB \tT:0.464  C:0.536\tT|T: 0.250  C|C: 0.323  C|T: 0.427 \n\tASW \tT:0.410  C:0.590\tT|T: 0.115  C|C: 0.295  C|T: 0.590  \n\tESN \tT:0.566  C:0.434\tT|T: 0.313  C|C: 0.182  C|T: 0.505 \n\tGWD \tT:0.518  C:0.482\tT|T: 0.248  C|C: 0.212  C|T: 0.540  \n\tLWK \tT:0.424  C:0.576\tT|T: 0.152  C|C: 0.303  C|T: 0.545 \n\tMSL \tT:0.524  C:0.476\tT|T: 0.306  C|C: 0.259  C|T: 0.435  \n\tYRI \tT:0.500  C:0.500\tT|T: 0.241  C|C: 0.241  C|T: 0.519  \n\n AMERICAN \tT:0.599  C:0.401\tT|T: 0.378  C|C: 0.179  C|T: 0.444  \n\tCLM \tT:0.569  C:0.431\tT|T: 0.287  C|C: 0.149  C|T: 0.564 \n\tMXL \tT:0.641  C:0.359\tT|T: 0.438  C|C: 0.156  C|T: 0.406  \n\tPEL \tT:0.700  C:0.300\tT|T: 0.529  C|C: 0.129  C|T: 0.341  \n\tPUR \tT:0.519  C:0.481 \tT|T: 0.298  C|C: 0.260  C|T: 0.442  \n\n EAST ASIAN\tT:0.574  C:0.426\tT|T: 0.345  C|C: 0.196  C|T: 0.458 \n\tCDX \tT:0.710  C:0.290\tT|T: 0.484  C|C: 0.065  C|T: 0.452  \n\tCHB \tT:0.456  C:0.544\tT|T: 0.204  C|C: 0.291  C|T: 0.505 \n\tCHS \tT:0.581  C:0.419\tT|T: 0.362  C|C: 0.200  C|T: 0.438  \n\tJPT \tT:0.447  C:0.553\tT|T: 0.212  C|C: 0.317  C|T: 0.471  \n\tKHV \tT:0.697  C:0.303\tT|T: 0.485  C|C: 0.091  C|T: 0.424  \n\n EUROPEAN \tT:0.490  C:0.510 \tT|T: 0.249  C|C: 0.268  C|T: 0.483 \n\tCEU \tT:0.551  C:0.449\tT|T: 0.303  C|C: 0.202  C|T: 0.495  \n\tFIN \tT:0.485  C:0.515\tT|T: 0.253  C|C: 0.283  C|T: 0.465  \n\tGBR \tT:0.511  C:0.489\tT|T: 0.220  C|C: 0.198  C|T: 0.582  \n\tIBS \tT:0.505  C:0.495\tT|T: 0.234  C|C: 0.224  C|T: 0.542  \n\tTSI \tT:0.407 C:0.593\tT|T: 0.234  C|C: 0.421  C|T: 0.346  \n\n SOUTH ASIAN\tT:0.642  C:0.358\tT|T: 0.403  C|C: 0.119  C|T: 0.479  \n\tBEB \tT:0.605  C:0.395\tT|T: 0.360  C|C: 0.151  C|T: 0.488  \n\tGIH \tT:0.660  C:0.340\tT|T: 0.437  C|C: 0.117  C|T: 0.447  \n\tITU \tT:0.632 C:0.368\tT|T: 0.392  C|C: 0.127  C|T: 0.480  \n\tPJL \tT:0.620  C:0.380\tT|T: 0.375  C|C: 0.135  C|T: 0.490  \n\tSTU \tT:0.686 C:0.314\tT|T: 0.441  C|C: 0.069  C|T: 0.490  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD: Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima, Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38878692)|| (snp==902136))
{
        printf(" \n\n Alleles  C/A/G, Ancestral:A, Ambiguity code: V, MAF: 0.45 [2]\n Location: 4:38878692 [2] \n SNP ID: rs902136 [1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tC:0.555  A:0.445\tC|C: 0.314  A|A: 0.204 A|C: 0.482 \n\n AFRICAN  \tC:0.467  A:0.533\tC|C: 0.209  A|A: 0.275  A|C: 0.516  \n\tACB \tC:0.458  A:0.542\tC|C: 0.229  A|A: 0.312 A|C: 0.458  \n\tASW \tC:0.402  A:0.598\tC|C: 0.115  A|A: 0.311  A|C: 0.574  \n\tESN \tC:0.551  A:0.449\tC|C: 0.293  A|A: 0.192  A|C: 0.515  \n\tGWD \tC:0.509  A:0.491\tC|C: 0.239  A|A: 0.221  A|C: 0.540  \n\tLWK \tC:0.343  A:0.657\tC|C: 0.081  A|A: 0.394  A|C: 0.525  \n\tMSL \tC:0.482  A:0.518\tC|C: 0.235  A|A: 0.271  A|C: 0.494  \n\tYRI \tC:0.491  A:0.509\tC|C: 0.231  A|A: 0.250  A|C: 0.519 \n\n AMERICAN \tC:0.607  A:0.393\tC|C: 0.372  A|A: 0.159  A|C: 0.470  \n\tCLM \tC:0.585  A:0.415\tC|C: 0.309  A|A: 0.138  A|C: 0.553  \n\tMXL \tC:0.656  A:0.344\tC|C: 0.438  A|A: 0.125  A|C: 0.438  \n\tPEL \tC:0.712  A:0.288\tC|C: 0.541  A|A: 0.118  A|C: 0.341 \n\tPUR \tC:0.510  A:0.490\tC|C: 0.250  A|A: 0.231  A|C: 0.519  \n\n EAST ASIAN\tC:0.573  A:0.427\tC|C: 0.343  A|A: 0.196  A|C: 0.460  \n\tCDX \tC:0.710  A:0.290\tC|C: 0.484  A|A: 0.065  A|C: 0.452  \n\tCHB \tC:0.456  A:0.544\tC|C: 0.204  A|A: 0.291  A|C: 0.505 \n\tCHS \tC:0.581  A:0.419\tC|C: 0.362  A|A: 0.200  A|C: 0.438  \n\tJPT \tC:0.447  A:0.553\tC|C: 0.212  A|A: 0.317  A|C: 0.471 \n\tKHV \tC:0.692  A:0.308\tC|C: 0.475  A|A: 0.091  A|C: 0.434  \n\n EUROPEAN \tC:0.516  A:0.484 \tC|C: 0.276  A|A: 0.245  A|C: 0.479  \n\tCEU \tC:0.561  A:0.439\tC|C: 0.303  A|A: 0.182  A|C: 0.515  \n\tFIN \tC:0.515  A:0.485\tC|C: 0.303  A|A: 0.273  A|C: 0.424 \n\tGBR \tC:0.544  A:0.456\tC|C: 0.264  A|A: 0.176  A|C: 0.560  \n\tIBS \tC:0.547  A:0.453\tC|C: 0.280  A|A: 0.187  A|C: 0.533 \n\tTSI \tC:0.421  A:0.579\tC|C: 0.234  A|A: 0.393  A|C: 0.374  \n\n SOUTH ASIAN\tC:0.658  A:0.342\tC|C: 0.423  A|A: 0.106  A|C: 0.470  \n\tBEB \tC:0.605  A:0.395\tC|C: 0.360  A|A: 0.151  A|C: 0.488  \n\tGIH \tC:0.684  A:0.316\tC|C: 0.456  A|A: 0.087  A|C: 0.456 \n\tITU \tC:0.647  A:0.353\tC|C: 0.412  A|A: 0.118  A|C: 0.471  \n\tPJL \tC:0.646  A:0.354\tC|C: 0.417  A|A: 0.125  A|C: 0.458 \n\tSTU \tC:0.701  A:0.299\tC|C: 0.461  A|A: 0.059  A|C: 0.480  \n\n");
```

```
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
 else if ((chr==38880267)|| (snp==11943027))
{
            printf(" \n\n Alleles  G/C, Ancestral:C, Ambiguity code: S, MAF: 0.12 [2]\n Location: 4:38880267 [2] \n SNP ID:
rs11943027 [1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV,
VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and
other modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele
Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tG:0.118  C:0.882\tG|G: 0.044  C|C: 0.808  C|G: 0.148 \n\n AFRICAN  \tG:0.018
C:0.982\tG|G: 0.003  C|C: 0.967  C|G: 0.030  \n\tACB \tG:0.042  C:0.958\tG|G: 0.010  C|C: 0.927  C|G: 0.062  \n\tASW \tG:0.074
C:0.926\tG|G: 0.016  C|C: 0.869  C|G: 0.115  \n\tESN \tG:0.000  C:1.000\tG|G: 0.000  C|C: 1.000  C|G: 0.000  \n\tGWD \tG:0.018
C:0.982\tG|G: 0.000  C|C: 0.965  C|G: 0.035  \n\tLWK \tG:0.015  C:0.985\tG|G: 0.000  C|C: 0.970  C|G: 0.030  \n\tMSL \tG:0.000
C:1.000\tG|G: 0.000  C|C: 1.000  C|G: 0.000  \n\tYRI \tG:0.000  C:1.000\tG|G: 0.000  C|C: 1.000  C|G: 0.000     \n\n AMERICAN
\tG:0.189  C:0.811\tG|G: 0.052  C|C: 0.674  C|G: 0.274  \n\tCLM \tG:0.261  C:0.739\tG|G: 0.096  C|C: 0.574  C|G: 0.330  \n\tMXL
\tG:0.133  C:0.867\tG|G: 0.031  C|C: 0.766  C|G: 0.203  \n\tPEL \tG:0.082  C:0.918\tG|G: 0.000  C|C: 0.835  C|G: 0.165  \n\tPUR
\tG:0.245  C:0.755\tG|G: 0.067  C|C: 0.577  C|G: 0.356  \n\n EAST ASIAN\tG:0.000  C:1.000\tG|G: 0.000  C|C: 1.000  C|G: 0.000
\n\tCDX \tG:0.000  C:1.000\tG|G: 0.000  C|C: 1.000  C|G: 0.000  \n\tCHB \tG:0.000  C:1.000\tG|G: 0.000  C|C: 1.000  C|G: 0.000
\n\tCHS \tG:0.000  C:1.000\tG|G: 0.000  C|C: 1.000  C|G: 0.000  \n\tJPT \tG:0.000  C:1.000\tG|G: 0.000  C|C: 1.000  C|G: 0.000
\n\tKHV \tG:0.000  C:1.000\tG|G: 0.000  C|C: 1.000  C|G: 0.000     \n\n EUROPEAN \tG:0.408  C:0.592 \tG|G: 0.179  C|C: 0.364  C|G:
0.457  \n\tCEU \tG:0.490  C:0.510\tG|G: 0.242  C|C: 0.263  C|G: 0.495  \n\tFIN \tG:0.429  C:0.571\tG|G: 0.222  C|C: 0.364  C|G: 0.414
\n\tGBR \tG:0.445  C:0.555\tG|G: 0.143  C|C: 0.253  C|G: 0.604  \n\tIBS \tG:0.360  C:0.640\tG|G: 0.131  C|C: 0.411  C|G: 0.458
\n\tTSI \tG:0.327  C:0.673\tG|G: 0.159  C|C: 0.505  C|G: 0.336  \n\n SOUTH ASIAN\tG:0.027  C:0.973\tG|G: 0.000  C|C: 0.947  C|G:
0.053  \n\tBEB \tG:0.041  C:0.959\tG|G: 0.000  C|C: 0.919  C|G: 0.081  \n\tGIH \tG:0.029  C:0.971\tG|G: 0.000  C|C: 0.942  C|G: 0.058
\n\tITU \tG:0.000  C:1.000\tG|G: 0.000  C|C: 1.000  C|G: 0.000  \n\tPJL \tG:0.052  C:0.948\tG|G: 0.000  C|C: 0.896  C|G: 0.104
\n\tSTU \tG:0.015  C:0.985\tG|G: 0.000  C|C: 0.971  C|G: 0.029  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
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printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38884799)|| (snp==17582893))
{
            printf(" \n\n Alleles  G/A, Ancestral: G, Ambiguity code: R, MAF: 0.17 [2]\n Location: 4:38884799 [2] \n SNP ID:
rs17582893 [1] \n GWAS Trait: Suicide attempts in bipolar disorder, Helicobacter pylori serologic status, Self-reported allergy [1] \n
Archaic-like haplotype cluster: The GWAS-identified archaic like SNP, And The SNP differs between core haplotype III and other
modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known   \n\n\n Population  \tAllele
Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tG:0.830  A:0.170\tG|G: 0.706  A|A: 0.045  A|G: 0.249 \n\n AFRICAN  \tG:0.989
A:0.011\tG|G: 0.977  A|A: 0.000  A|G: 0.023  \n\tACB \tG:0.974  A:0.026\tG|G: 0.948  A|A: 0.000  A|G: 0.052  \n\tASW \tG:0.934
A:0.066\tG|G: 0.869  A|A: 0.000  A|G: 0.131  \n\tESN \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000  \n\tGWD \tG:0.991
A:0.009\tG|G: 0.982  A|A: 0.000  A|G: 0.18  \n\tLWK \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000  \n\tMSL \tG:1.000
A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000  \n\tYRI \tG:1.000  A:0.000\tG|G: 1.000  A|A: 0.000  A|G: 0.000     \n\n AMERICAN
\tG:0.839  A:0.161\tG|G: 0.720  A|A: 0.043  A|G: 0.236  \n\tCLM \tG:0.830  A:0.170\tG|G: 0.691  A|A: 0.032  A|G: 0.277  \n\tMXL
\tG:0.883  A:0.117\tG|G: 0.797  A|A: 0.031  A|G: 0.172  \n\tPEL \tG:0.929  A:0.071\tG|G: 0.859  A|A: 0.000  A|G: 0.141  \n\tPUR
\tG:0.745  A:0.255\tG|G: 0.587  A|A: 0.096  A|G: 0.317  \n\n EAST ASIAN\tG:0.692  A:0.308\tG|G: 0.484  A|A: 0.099  A|G: 0.417
\n\tCDX \tG:0.839  A:0.161\tG|G: 0.699  A|A: 0.022  A|G: 0.280  \n\tCHB \tG:0.549  A:0.451\tG|G: 0.301  A|A: 0.204  A|G: 0.495
\n\tCHS \tG:0.695  A:0.305\tG|G: 0.457  A|A: 0.067  A|G: 0.476  \n\tJPT \tG:0.591  A:0.409\tG|G: 0.356  A|A: 0.173  A|G: 0.471
\n\tKHV \tG:0.808  A:0.192\tG|G: 0.636  A|A: 0.020  A|G: 0.343    \n\n EUROPEAN \tG:0.771  A:0.229 \tG|G: 0.608  A|A: 0.066  A|G:
0.326  \n\tCEU \tG:0.813  A:0.187\tG|G: 0.677  A|A: 0.051  A|G: 0.273  \n\tFIN \tG:0.909  A:0.091\tG|G: 0.828  A|A: 0.010  A|G: 0.162
```

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\n\tGBR \tG:0.835  A:0.165\tG|G: 0.681  A|A: 0.011  A|G: 0.308  \n\tIBS \tG:0.678  A:0.322\tG|G: 0.449  A|A: 0.093  A|G: 0.458
\n\tTSI \tG:0.645  A:0.355\tG|G: 0.439  A|A: 0.150  A|G: 0.411  \n\n SOUTH ASIAN\tG:0.813  A:0.187\tG|G: 0.656  A|A: 0.031  A|G:
0.313  \n\tBEB \tG:0.767  A:0.233\tG|G: 0.558  A|A: 0.023  A|G: 0.419  \n\tGIH \tG:0.801  A:0.199\tG|G: 0.641  A|A: 0.039  A|G: 0.320
\n\tITU \tG:0.838  A:0.162\tG|G: 0.716  A|A: 0.039  A|G: 0.245  \n\tPJL \tG:0.823  A:0.177\tG|G: 0.677  A|A: 0.031  A|G: 0.292
\n\tSTU \tG:0.828  A:0.172\tG|G: 0.676  A|A: 0.020  A|G: 0.304  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
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printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
 }
else if ((chr==38885730)|| (snp==2381345))
{
            printf(" \n\n Alleles  C/T, Ancestral: T, Ambiguity code: Y, MAF: 0.43 [2]\n Location: 4:38885730 [2] \n SNP ID: rs2381345
[1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known
\n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tC:0.568  T:0.432\tC|C: 0.331  C|T: 0.474  T|T: 0.194
\n\n AFRICAN  \tC:0.499  T:0.501\tC|C: 0.248  C|T: 0.502  T|T: 0.250  \n\tACB \tC:0.469  T:0.531\tC|C: 0.240  C|T: 0.458  T|T: 0.302
\n\tASW \tC:0.426  T:0.574\tC|C: 0.148  C|T: 0.557  T|T: 0.295  \n\tESN \tC:0.571  T:0.429\tC|C: 0.323  C|T: 0.495  T|T: 0.182
\n\tGWD \tC:0.518  T:0.482\tC|C: 0.248  C|T: 0.540  T|T: 0.212  \n\tLWK \tC:0.455  T:0.545\tC|C: 0.202  C|T: 0.505  T|T: 0.293
\n\tMSL \tC:0.524  T:0.476\tC|C: 0.306  C|T: 0.435  T|T: 0.259  \n\tYRI \tC:0.505  T:0.495\tC|C: 0.241  C|T: 0.528  T|T: 0.231      \n\n
AMERICAN \tC:0.615  T:0.385\tC|C: 0.389  C|T: 0.452  T|T: 0.159  \n\tCLM \tC:0.585  T:0.415\tC|C: 0.309  C|T: 0.553  T|T: 0.138
\n\tMXL \tC:0.656  T:0.344\tC|C: 0.438  C|T: 0.438  T|T: 0.125  \n\tPEL \tC:0.712  T:0.288\tC|C: 0.541  C|T: 0.341  T|T: 0.118  \n\tPUR
\tC:0.538  T:0.462\tC|C: 0.308  C|T: 0.462  T|T: 0.231  \n\n EAST ASIAN\tC:0.590  T:0.410\tC|C: 0.363  C|T: 0.454  T|T: 0.183
\n\tCDX \tC:0.699  T:0.301\tC|C: 0.462  C|T: 0.473  T|T: 0.065  \n\tCHB \tC:0.466  T:0.534\tC|C: 0.223  C|T: 0.485  T|T: 0.291
\n\tCHS \tC:0.590  T:0.410\tC|C: 0.362  C|T: 0.457  T|T: 0.181  \n\tJPT \tC:0.514  T:0.486\tC|C: 0.298  C|T: 0.433  T|T: 0.269  \n\tKHV
\tC:0.697  T:0.303\tC|C: 0.485  C|T: 0.424  T|T: 0.091    \n\n EUROPEAN \tC:0.518  T:0.482 \tC|C: 0.278  C|T: 0.479  T|T: 0.243
\n\tCEU \tC:0.566  T:0.434\tC|C: 0.313  C|T: 0.505  T|T: 0.182  \n\tFIN \tC:0.515  T:0.485\tC|C: 0.303  C|T: 0.424  T|T: 0.273  \n\tGBR
\tC:0.544  T:0.456\tC|C: 0.264  C|T: 0.560  T|T: 0.176  \n\tIBS \tC:0.547  T:0.453\tC|C: 0.280  C|T: 0.533  T|T: 0.187  \n\tTSI \tC:0.425
T:0.575\tC|C: 0.234  C|T: 0.383  T|T: 0.383  \n\n SOUTH ASIAN\tC:0.657  T:0.343\tC|C: 0.423  C|T: 0.468  T|T: 0.108  \n\tBEB
\tC:0.605  T:0.395\tC|C: 0.360  C|T: 0.488  T|T: 0.151  \n\tGIH \tC:0.684  T:0.316\tC|C: 0.456  C|T: 0.456  T|T: 0.087  \n\tITU \tC:0.642
T:0.358\tC|C: 0.412  C|T: 0.461  T|T: 0.127  \n\tPJL \tC:0.646  T:0.354\tC|C: 0.417  C|T: 0.458  T|T: 0.125  \n\tSTU \tC:0.701
T:0.299\tC|C: 0.461  C|T: 0.480  T|T: 0.059  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
 else if ((chr==38889552)|| (snp==1873195))
{
            printf(" \n\n Alleles  C/T, Ancestral: C, Ambiguity code: Y, MAF: 0.20 [2]\n Location: 4:38889552 [2] \n SNP ID: rs1873195
[1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: Seen in the archaic-
like haplotypes III, IV, VII and differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between
core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n
Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tC:0.803  T:0.197\tC|C: 0.653  C|T: 0.301  T|T: 0.047 \n\n
AFRICAN  \tC:0.896  T:0.104\tC|C: 0.800  C|T: 0.192  T|T: 0.008  \n\tACB \tC:0.901  T:0.099\tC|C: 0.812  C|T: 0.177  T|T: 0.010
\n\tASW \tC:0.869  T:0.131\tC|C: 0.754  C|T: 0.230  T|T: 0.016  \n\tESN \tC:0.904  T:0.096\tC|C: 0.818  C|T: 0.172  T|T: 0.010
\n\tGWD \tC:0.938  T:0.062\tC|C: 0.876  C|T: 0.124  T|T: 0.000  \n\tLWK \tC:0.793  T:0.207\tC|C: 0.606  C|T: 0.374  T|T: 0.020
\n\tMSL \tC:0.912  T:0.088\tC|C: 0.824  C|T: 0.176  T|T: 0.000  \n\tYRI \tC:0.940  T:0.060\tC|C: 0.880  C|T: 0.120  T|T: 0.000      \n\n
AMERICAN \tC:0.823  T:0.177\tC|C: 0.692  C|T: 0.262  T|T: 0.046  \n\tCLM \tC:0.814  T:0.186\tC|C: 0.660  C|T: 0.309  T|T: 0.032
\n\tMXL \tC:0.891  T:0.109\tC|C: 0.797  C|T: 0.188  T|T: 0.016  \n\tPEL \tC:0.918  T:0.082\tC|C: 0.835  C|T: 0.165  T|T: 0.000  \n\tPUR
\tC:0.712  T:0.288\tC|C: 0.538  C|T: 0.346  T|T: 0.115  \n\n EAST ASIAN\tC:0.692  T:0.308\tC|C: 0.484  C|T: 0.417  T|T: 0.099
\n\tCDX \tC:0.839  T:0.161\tC|C: 0.699  C|T: 0.280  T|T: 0.022  \n\tCHB \tC:0.549  T:0.451\tC|C: 0.301  C|T: 0.495  T|T: 0.204
```

```
\n\tCHS \tC:0.695  T:0.305\tC|C: 0.457  C|T: 0.476  T|T: 0.067  \n\tJPT \tC:0.591  T:0.409\tC|C: 0.356  C|T: 0.471  T|T: 0.173  \n\tKHV
\tC:0.808  T:0.192\tC|C: 0.636  C|T: 0.343  T|T: 0.020   \n\n EUROPEAN \tC:0.771  T:0.229 \tC|C: 0.604  C|T: 0.334  T|T: 0.062
\n\tCEU \tC:0.818  T:0.182\tC|C: 0.677  C|T: 0.283  T|T: 0.040  \n\tFIN \tC:0.909  T:0.091\tC|C: 0.828  C|T: 0.162  T|T: 0.010  \n\tGBR
\tC:0.835  T:0.165\tC|C: 0.681  C|T: 0.308  T|T: 0.011  \n\tIBS \tC:0.673  T:0.327\tC|C: 0.439  C|T: 0.467  T|T: 0.093  \n\tTSI \tC:0.645
T:0.355\tC|C: 0.430  C|T: 0.430  T|T: 0.140  \n\n SOUTH ASIAN\tC:0.809  T:0.191\tC|C: 0.648  C|T: 0.321  T|T: 0.031  \n\tBEB
\tC:0.767  T:0.233\tC|C: 0.558  C|T: 0.419  T|T: 0.023  \n\tGIH \tC:0.801  T:0.199\tC|C: 0.641  C|T: 0.320  T|T: 0.039  \n\tITU \tC:0.828
T:0.172\tC|C: 0.696  C|T: 0.265  T|T: 0.039  \n\tPJL \tC:0.823  T:0.177\tC|C: 0.677  C|T: 0.292  T|T: 0.031  \n\tSTU \tC:0.819
T:0.181\tC|C: 0.657  C|T: 0.324  T|T: 0.020  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38891028)|| (snp==17582921))
{
            printf(" \n\n Alleles  T/C, Ancestral: C, Ambiguity code: Y, MAF: 0.17 [2]\n Location: 4:38891028 [2] \n SNP ID:
rs17582921 [1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1] \n Archaic-like haplotype cluster: The
GWAS-identified archaic like SNP, Seen in the archaic-like haplotypes III, IV, VII and differs from the other modern-human core
haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other modern human core haplotypes II, V, VI, VIII,
IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL
\tT:0.830  C:0.170\tT|T: 0.704  C|C: 0.044  C|T: 0.252 \n\n AFRICAN  \tT:0.989  C:0.011\tT|T: 0.977  C|C: 0.000  C|T: 0.023  \n\tACB
\tT:0.974  C:0.026\tT|T: 0.948  C|C: 0.000  C|T: 0.052  \n\tASW \tT:0.934  C:0.066\tT|T: 0.869  C|C: 0.000  C|T: 0.131  \n\tESN
\tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000   \n\tGWD \tT:0.991  C:0.009\tT|T: 0.982  C|C: 0.000  C|T: 0.018  \n\tLWK
\tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000   \n\tMSL \tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000   \n\tYRI
\tT:1.000  C:0.000\tT|T: 1.000  C|C: 0.000  C|T: 0.000       \n\n AMERICAN \tT:0.843  C:0.157\tT|T: 0.723  C|C: 0.037  C|T: 0.239
\n\tCLM \tT:0.840  C:0.160\tT|T: 0.702  C|C: 0.021  C|T: 0.277  \n\tMXL \tT:0.891  C:0.109\tT|T: 0.797  C|C: 0.016  C|T: 0.188
\n\tPEL \tT:0.929  C:0.071\tT|T: 0.859  C|C: 0.000  C|T: 0.141  \n\tPUR \tT:0.745  C:0.255\tT|T: 0.587  C|C: 0.096  C|T: 0.317  \n\n
EAST ASIAN\tT:0.692  C:0.308\tT|T: 0.484  C|C: 0.099  C|T: 0.417  \n\tCDX \tT:0.839  C:0.161\tT|T: 0.699  C|C: 0.022  C|T: 0.280
\n\tCHB \tT:0.549  C:0.451\tT|T: 0.301  C|C: 0.204  C|T: 0.495  \n\tCHS \tT:0.695  C:0.305\tT|T: 0.457  C|C: 0.067  C|T: 0.476  \n\tJPT
\tT:0.591  C:0.409\tT|T: 0.356  C|C: 0.173  C|T: 0.471  \n\tKHV \tT:0.808  C:0.192\tT|T: 0.636  C|C: 0.020  C|T: 0.343   \n\n
EUROPEAN \tT:0.772  C:0.228 \tT|T: 0.608  C|C: 0.064  C|T: 0.328  \n\tCEU \tT:0.818  C:0.182\tT|T: 0.677  C|C: 0.040  C|T: 0.283
\n\tFIN \tT:0.909  C:0.091\tT|T: 0.828  C|C: 0.010  C|T: 0.162  \n\tGBR \tT:0.835  C:0.165\tT|T: 0.681  C|C: 0.011  C|T: 0.308  \n\tIBS
\tT:0.673  C:0.327\tT|T: 0.449  C|C: 0.103  C|T: 0.449  \n\tTSI \tT:0.650  C:0.350\tT|T: 0.439  C|C: 0.140  C|T: 0.421  \n\n SOUTH
ASIAN\tT:0.809  C:0.191\tT|T: 0.648  C|C: 0.031  C|T: 0.321  \n\tBEB \tT:0.767  C:0.233\tT|T: 0.558  C|C: 0.023  C|T: 0.419  \n\tGIH
\tT:0.801  C:0.199\tT|T: 0.641  C|C: 0.039  C|T: 0.320  \n\tITU \tT:0.828  C:0.172\tT|T: 0.696  C|C: 0.039  C|T: 0.265  \n\tPJL \tT:0.818
C:0.182\tT|T: 0.667  C|C: 0.031  C|T: 0.302  \n\tSTU \tT:0.824  C:0.176\tT|T: 0.667  C|C: 0.020  C|T: 0.314  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
 }
else if ((chr==38892222)|| (snp==6851685))
{
            printf(" \n\n Alleles  G/T, Ancestral:T, Ambiguity code: K, MAF: 0.24 [2]\n Location: 4:38892222 [2] \n SNP ID: rs6851685
[1] \n GWAS Trait: Helicobacter pylori serologic status, Self-reported allergy [1]\n Archaic-like haplotype cluster: The SNP differs
between core haplotype III and other modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not
Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tG:0.755  T:0.245\tG|G: 0.581  G|T: 0.348
T|T: 0.071 \n\n AFRICAN  \tG:0.787  T:0.213\tG|G: 0.620  G|T: 0.334  T|T: 0.045  \n\tACB \tG:0.797  T:0.203\tG|G: 0.656  G|T: 0.281
T|T: 0.062  \n\tASW \tG:0.779  T:0.221\tG|G: 0.607  G|T: 0.344  T|T: 0.049  \n\tESN \tG:0.823  T:0.177\tG|G: 0.667  G|T: 0.313  T|T:
0.020  \n\tGWD \tG:0.726  T:0.274\tG|G: 0.522  G|T: 0.407  T|T: 0.071  \n\tLWK \tG:0.803  T:0.197\tG|G: 0.636  G|T: 0.333  T|T:
0.030  \n\tMSL \tG:0.824  T:0.176\tG|G: 0.682  G|T: 0.282  T|T: 0.035  \n\tYRI \tG:0.773  T:0.227\tG|G: 0.593  G|T: 0.361  T|T: 0.046
```

```
\n\n AMERICAN \tG:0.797  T:0.203\tG|G: 0.657  G|T: 0.280  T|T: 0.063  \n\tCLM \tG:0.798  T:0.202\tG|G: 0.628  C|T: 0.340  T|T:
0.032  \n\tMXL \tG:0.875  T:0.125\tG|G: 0.766  G|T: 0.219  T|T: 0.016  \n\tPEL \tG:0.900  T:0.100\tG|G: 0.812  G|T: 0.176  T|T: 0.012
\n\tPUR \tG:0.663  T:0.337 \tG|G: 0.490  G|T: 0.346  T|T: 0.163  \n\n EAST ASIAN\tG:0.741  T:0.259\tG|G: 0.562  G|T: 0.359  T|T:
0.079  \n\tCDX \tG:0.892  T:0.108\tG|G: 0.796  G|T: 0.194  T|T: 0.011  \n\tCHB \tG:0.626  T:0.374\tG|G: 0.388  G|T: 0.476  T|T: 0.136
\n\tCHS \tG:0.733  T:0.267\tG|G: 0.524  G|T: 0.419  T|T: 0.057  \n\tJPT \tG:0.601  T:0.399\tG|G: 0.375  G|T: 0.452  T|T: 0.173
\n\tKHV \tG:0.874  T:0.126\tG|G: 0.758  G|T: 0.232  T|T: 0.010  \n\n EUROPEAN \tG:0.717  T:0.283 \tG|G: 0.541  G|T: 0.352  T|T:
0.107  \n\tCEU \tG:0.798  T:0.202\tG|G: 0.646  G|T: 0.303  T|T: 0.051  \n\tFIN \tG:0.843  T:0.157\tG|G: 0.737  G|T: 0.212  T|T: 0.051
\n\tGBR \tG:0.797  T:0.203\tG|G: 0.604  G|T: 0.385  T|T: 0.011  \n\tIBS \tG:0.579  T:0.421\tG|G: 0.355  G|T: 0.449  T|T: 0.196  \n\tTSI
\tG:0.593  T:0.407\tG|G: 0.393  G|T: 0.402  T|T: 0.206  \n\n SOUTH ASIAN\tG:0.736  T:0.264\tG|G: 0.536  G|T: 0.401  T|T: 0.063
\n\tBEB \tG:0.733  T:0.267\tG|G: 0.500  G|T: 0.465  T|T: 0.035  \n\tGIH \tG:0.718  T:0.282\tG|G: 0.534  G|T: 0.369  T|T: 0.097  \n\tITU
\tG:0.750  T:0.250\tG|G: 0.549  G|T: 0.402  T|T: 0.049  \n\tPJL \tG:0.714  T:0.286\tG|G: 0.521  G|T: 0.385  T|T: 0.094  \n\tSTU
\tG:0.765  T:0.235\tG|G: 0.569  G|T: 0.392  T|T: 0.039  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38892759)|| (snp==6835514))
{
        printf(" \n\n Alleles  A/G, Ancestral:G, Ambiguity code: R, MAF: 0.37 [2]\n Location: 4:38892759 [2] \n SNP ID: rs6835514
[1] \n GWAS Trait: Multiple complex diseases, Coronary Artery Disease, Helicobacter pylori serologic status, Self-reported allergy [1]
\n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele Frequency [2]
\tGenotype Frequency [2] \n\n ALL      \tA:0.631  G:0.369\tA|A: 0.415  A|G: 0.432  G|G: 0.153 \n\n AFRICAN  \tA:0.570
G:0.430\tA|A: 0.339  A|G: 0.461  G|G: 0.200  \n\tACB \tA:0.573  G:0.427\tA|A: 0.354  A|G: 0.438  G|G: 0.208  \n\tASW \tA:0.566
G:0.434\tA|A: 0.328  A|G: 0.475  G|G: 0.197  \n\tESN \tA:0.631  G:0.369\tA|A: 0.384  A|G: 0.495  G|G: 0.121  \n\tGWD \tA:0.580
G:0.420\tA|A: 0.372  A|G: 0.416  G|G: 0.212  \n\tLWK \tA:0.434  G:0.566\tA|A: 0.182  A|G: 0.505  G|G: 0.313  \n\tMSL \tA:0.582
G:0.418\tA|A: 0.376  A|G: 0.412  G|G: 0.212  \n\tYRI \tA:0.616  G:0.384\tA|A: 0.370  A|G: 0.491  G|G: 0.139  \n\n AMERICAN
\tA:0.683  G:0.317\tA|A: 0.490  A|G: 0.386  G|G: 0.124  \n\tCLM \tA:0.702  G:0.298\tA|A: 0.468  A|G: 0.468  G|G: 0.064  \n\tMXL
\tA:0.695  G:0.305\tA|A: 0.516  A|G: 0.359  G|G: 0.125  \n\tPEL \tA:0.741  G:0.259\tA|A: 0.565  A|G: 0.353  G|G: 0.082  \n\tPUR
\tA:0.611  G:0.389\tA|A: 0.433  A|G: 0.356  G|G: 0.212  \n\n EAST ASIAN\tA:0.594  G:0.406\tA|A: 0.359  A|G: 0.470  G|G: 0.171
\n\tCDX \tA:0.688  G:0.312\tA|A: 0.441  A|G: 0.495  G|G: 0.065  \n\tCHB \tA:0.495  G:0.505\tA|A: 0.233  A|G: 0.524  G|G: 0.243
\n\tCHS \tA:0.595  G:0.405\tA|A: 0.371  A|G: 0.448  G|G: 0.181  \n\tJPT \tA:0.519  G:0.481\tA|A: 0.298  A|G: 0.442  G|G: 0.260
\n\tKHV \tA:0.687  G:0.313\tA|A: 0.465  A|G: 0.444  G|G: 0.091  \n\n EUROPEAN \tA:0.711  G:0.289 \tA|A: 0.533  A|G: 0.356  G|G:
0.111  \n\tCEU \tA:0.798  G:0.202\tA|A: 0.646  A|G: 0.303  G|G: 0.051  \n\tFIN \tA:0.838  G:0.162\tA|A: 0.727  A|G: 0.222  G|G: 0.051
\n\tGBR \tA:0.786  G:0.214\tA|A: 0.593  A|G: 0.385  G|G: 0.022  \n\tIBS \tA:0.575  G:0.425\tA|A: 0.346  A|G: 0.458  G|G: 0.196
\n\tTSI \tA:0.584  G:0.416\tA|A: 0.383  A|G: 0.402  G|G: 0.215  \n\n SOUTH ASIAN\tA:0.634  G:0.366\tA|A: 0.403  A|G: 0.462  G|G:
0.135  \n\tBEB \tA:0.605  G:0.395\tA|A: 0.360  A|G: 0.488  G|G: 0.151  \n\tGIH \tA:0.646  G:0.354\tA|A: 0.417  A|G: 0.456  G|G: 0.126
\n\tITU \tA:0.618  G:0.382\tA|A: 0.392  A|G: 0.451  G|G: 0.157  \n\tPJL \tA:0.625  G:0.375\tA|A: 0.396  A|G: 0.458  G|G: 0.146
\n\tSTU \tA:0.672  G:0.328\tA|A: 0.441  A|G: 0.461  G|G: 0.098  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38895633)|| (snp==1604834))
{
        printf(" \n\n Alleles  G/A, Ancestral:A, Ambiguity code: R, MAF: 0.44 [2]\n Location: 4:38895633 [2] \n SNP ID: rs1604834
[1] \n GWAS Trait: Multiple complex diseases, Self-reported allergy [1]\n Archaic-like haplotype cluster: Not Known\n Clinical
Assertion Description: Not Known \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tG:0.561
A:0.439\tG|G: 0.323  A|A: 0.200  A|G: 0.476 \n\n AFRICAN  \tG:0.567  A:0.433\tG|G: 0.313  A|A: 0.180  A|G: 0.507  \n\tACB
\tG:0.568  A:0.432\tG|G: 0.312  A|A: 0.177  A|G: 0.510  \n\tASW \tG:0.557  A:0.443\tG|G: 0.295  A|A: 0.180  A|G: 0.525  \n\tESN
```

```
\tG:0.606  A:0.394\tG|G: 0.323  A|A: 0.111  A|G: 0.566  \n\tGWD \tG:0.531  A:0.469\tG|G: 0.310  A|A: 0.248  A|G: 0.442  \n\tLWK
\tG:0.480  A:0.520\tG|G: 0.232  A|A: 0.273  A|G: 0.495  \n\tMSL \tG:0.618  A:0.382\tG|G: 0.376  A|A: 0.141  A|G: 0.482  \n\tYRI
\tG:0.611  A:0.389\tG|G: 0.343  A|A: 0.120  A|G: 0.537  \n\n AMERICAN \tG:0.611  A:0.389\tG|G: 0.386  A|A: 0.164  A|G: 0.450
\n\tCLM \tG:0.606  A:0.394\tG|G: 0.330  A|A: 0.117  A|G: 0.553  \n\tMXL \tG:0.656  A:0.344\tG|G: 0.469  A|A: 0.156  A|G: 0.375
\n\tPEL \tG:0.700  A:0.300\tG|G: 0.518  A|A: 0.118  A|G: 0.365  \n\tPUR \tG:0.514  A:0.486 \tG|G: 0.279  A|A: 0.250  A|G: 0.471  \n\n
EAST ASIAN\tG:0.596  A:0.404\tG|G: 0.361  A|A: 0.169  A|G: 0.470  \n\tCDX \tG:0.715  A:0.285\tG|G: 0.473  A|A: 0.043  A|G: 0.484
\n\tCHB \tG:0.476  A:0.524\tG|G: 0.223  A|A: 0.272  A|G: 0.505  \n\tCHS \tG:0.605  A:0.395\tG|G: 0.371  A|A: 0.162  A|G: 0.467
\n\tJPT \tG:0.510  A:0.490\tG|G: 0.288  A|A: 0.269  A|G: 0.442  \n\tKHV \tG:0.692  A:0.308\tG|G: 0.465  A|A: 0.081  A|G: 0.455  \n\n
EUROPEAN \tG:0.493  A:0.507 \tG|G: 0.268  A|A: 0.282  A|G: 0.449  \n\tCEU \tG:0.561  A:0.439\tG|G: 0.313  A|A: 0.192  A|G: 0.495
\n\tFIN \tG:0.495  A:0.505\tG|G: 0.293  A|A: 0.303  A|G: 0.404  \n\tGBR \tG:0.527  A:0.473\tG|G: 0.264  A|A: 0.209  A|G: 0.527
\n\tIBS \tG:0.500  A:0.500\tG|G: 0.271  A|A: 0.271  A|G: 0.458  \n\tTSI \tG:0.393  A:0.607\tG|G: 0.206  A|A: 0.421  A|G: 0.374  \n\n
SOUTH ASIAN\tG:0.553  A:0.447\tG|G: 0.309  A|A: 0.202  A|G: 0.489  \n\tBEB \tG:0.523  A:0.477\tG|G: 0.291  A|A: 0.244  A|G:
0.465  \n\tGIH \tG:0.592  A:0.408\tG|G: 0.340  A|A: 0.155  A|G: 0.505  \n\tITU \tG:0.505  A:0.495\tG|G: 0.265  A|A: 0.255  A|G: 0.480
\n\tPJL \tG:0.536  A:0.464\tG|G: 0.302  A|A: 0.229  A|G: 0.469  \n\tSTU \tG:0.603  A:0.397\tG|G: 0.343  A|A: 0.137  A|G: 0.520
\n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38896848)|| (snp==974734))
{
        printf(" \n\n Alleles  G/C, Ancestral: G, Ambiguity code: S, MAF: 0.45 [2]\n Location: 4:38896848 [2] \n SNP ID: rs974734
[1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known
\n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tG:0.552  C:0.448\tG|G: 0.311  C|C: 0.207  C|G: 0.482
\n\n AFRICAN  \tG:0.533  C:0.467\tG|G: 0.275  C|C: 0.209  C|G: 0.516  \n\tACB \tG:0.516  C:0.484\tG|G: 0.250  C|C: 0.219  C|G:
0.531  \n\tASW \tG:0.525  C:0.475\tG|G: 0.279  C|C: 0.230  C|G: 0.492  \n\tESN \tG:0.586  C:0.414\tG|G: 0.313  C|C: 0.141  C|G: 0.545
\n\tGWD \tG:0.535  C:0.465\tG|G: 0.265  C|C: 0.195  C|G: 0.540  \n\tLWK \tG:0.449  C:0.551\tG|G: 0.202  C|C: 0.303  C|G: 0.495
\n\tMSL \tG:0.529  C:0.471\tG|G: 0.318  C|C: 0.259  C|G: 0.424  \n\tYRI \tG:0.583  C:0.417\tG|G: 0.306  C|C: 0.139  C|G: 0.556   \n\n
AMERICAN \tG:0.610  C:0.390\tG|G: 0.380  C|C: 0.161  C|G: 0.458  \n\tCLM \tG:0.596  C:0.404\tG|G: 0.309  C|C: 0.117  C|G: 0.574
\n\tMXL \tG:0.656  C:0.344\tG|G: 0.469  C|C: 0.156  C|G: 0.375  \n\tPEL \tG:0.700  C:0.300\tG|G: 0.518  C|C: 0.118  C|G: 0.365
\n\tPUR \tG:0.519  C:0.481\tG|G: 0.279  C|C: 0.240  C|G: 0.481  \n\n EAST ASIAN\tG:0.595  C:0.405\tG|G: 0.359  C|C: 0.169  C|G:
0.472  \n\tCDX \tG:0.710  C:0.290\tG|G: 0.462  C|C: 0.043  C|G: 0.495  \n\tCHB \tG:0.476  C:0.524\tG|G: 0.223  C|C: 0.272  C|G: 0.505
\n\tCHS \tG:0.605  C:0.395\tG|G: 0.371  C|C: 0.162  C|G: 0.467  \n\tJPT \tG:0.510  C:0.490\tG|G: 0.288  C|C: 0.269  C|G: 0.442
\n\tKHV \tG:0.692  C:0.308\tG|G: 0.465  C|C: 0.081  C|G: 0.455   \n\n EUROPEAN \tG:0.493  C:0.507 \tG|G: 0.266  C|C: 0.280  C|G:
0.453  \n\tCEU \tG:0.561  C:0.439\tG|G: 0.313  C|C: 0.192  C|G: 0.495  \n\tFIN \tG:0.495  C:0.505\tG|G: 0.293  C|C: 0.303  C|G: 0.404
\n\tGBR \tG:0.527  C:0.473\tG|G: 0.264  C|C: 0.209  C|G: 0.527  \n\tIBS \tG:0.495  C:0.505\tG|G: 0.262  C|C: 0.271  C|G: 0.467
\n\tTSI \tG:0.397  C:0.603\tG|G: 0.206  C|C: 0.411  C|G: 0.383  \n\n SOUTH ASIAN\tG:0.551  C:0.449\tG|G: 0.305  C|C: 0.202  C|G:
0.493  \n\tBEB \tG:0.523  C:0.477\tG|G: 0.291  C|C: 0.244  C|G: 0.465  \n\tGIH \tG:0.592  C:0.408\tG|G: 0.340  C|C: 0.155  C|G: 0.505
\n\tITU \tG:0.505  C:0.495\tG|G: 0.265  C|C: 0.255  C|G: 0.480  \n\tPJL \tG:0.526  C:0.474\tG|G: 0.281  C|C: 0.229  C|G: 0.490
\n\tSTU \tG:0.603  C:0.397\tG|G: 0.343  C|C: 0.137  C|G: 0.520  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38898436)|| (snp==7688418))
{
        printf(" \n\n Alleles  C/G, Ancestral: C, Ambiguity code: S, MAF: 0.32 [2]\n Location: 4:38898436 [2] \n SNP ID: rs7688418
[1] \n GWAS Trait: Self-reported allergy [1]\n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known
\n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tC:0.678  G:0.322\tC|C: 0.470  C|G: 0.416  G|G: 0.115
```

```
\n\n AFRICAN  \tC:0.703  G:0.297\tC|C: 0.478  C|G: 0.449  G|G: 0.073  \n\tACB \tC:0.703  G:0.297\tC|C: 0.510  C|G: 0.385  G|G:
0.104  \n\tASW \tC:0.697  G:0.303\tC|C: 0.443  C|G: 0.508  G|G: 0.049  \n\tESN \tC:0.747  G:0.253\tC|C: 0.515  C|G: 0.465  G|G: 0.020
\n\tGWD \tC:0.735  G:0.265\tC|C: 0.540  C|G: 0.389  G|G: 0.071  \n\tLWK \tC:0.667  G:0.333\tC|C: 0.444  C|G: 0.444  G|G: 0.111
\n\tMSL \tC:0.694  G:0.306\tC|C: 0.447  C|G: 0.494  G|G: 0.059  \n\tYRI \tC:0.671  G:0.329\tC|C: 0.426  C|G: 0.491  G|G: 0.083  \n\n
AMERICAN \tC:0.725  G:0.275\tC|C: 0.548  C|G: 0.354  G|G: 0.098  \n\tCLM \tC:0.686  G:0.314\tC|C: 0.479  C|G: 0.415  G|G: 0.106
\n\tMXL \tC:0.844  G:0.156\tC|C: 0.719  C|G: 0.250  G|G: 0.031  \n\tPEL \tC:0.876  G:0.124\tC|C: 0.776  C|G: 0.200  G|G: 0.024
\n\tPUR \tC:0.562  G:0.438 \tC|C: 0.317  C|G: 0.490  G|G: 0.192  \n\n EAST ASIAN\tC:0.736  G:0.264\tC|C: 0.563  C|G: 0.345  G|G:
0.091  \n\tCDX \tC:0.909  G:0.091\tC|C: 0.817  C|G: 0.183  G|G: 0.000  \n\tCHB \tC:0.592  G:0.408\tC|C: 0.369  C|G: 0.447  G|G: 0.184
\n\tCHS \tC:0.729  G:0.271\tC|C: 0.524  C|G: 0.410  G|G: 0.067  \n\tJPT \tC:0.596  G:0.404\tC|C: 0.375  C|G: 0.442  G|G: 0.183
\n\tKHV \tC:0.879  G:0.121\tC|C: 0.768  C|G: 0.222  G|G: 0.010  \n\n EUROPEAN \tC:0.523  G:0.477 \tC|C: 0.284  C|G: 0.477  G|G:
0.239  \n\tCEU \tC:0.571  G:0.429\tC|C: 0.323  C|G: 0.495  G|G: 0.182  \n\tFIN \tC:0.515  G:0.485\tC|C: 0.313  C|G: 0.404  G|G: 0.283
\n\tGBR \tC:0.555  G:0.445\tC|C: 0.275  C|G: 0.560  G|G: 0.165  \n\tIBS \tC:0.542  G:0.458\tC|C: 0.280  C|G: 0.523  G|G: 0.196
\n\tTSI \tC:0.439  G:0.561\tC|C: 0.234  C|G: 0.411  G|G: 0.355  \n\n SOUTH ASIAN\tC:0.709  G:0.291\tC|C: 0.497  C|G: 0.423  G|G:
0.080  \n\tBEB \tC:0.674  G:0.326\tC|C: 0.453  C|G: 0.442  G|G: 0.105  \n\tGIH \tC:0.728  G:0.272\tC|C: 0.524  C|G: 0.408  G|G: 0.068
\n\tITU \tC:0.716  G:0.284\tC|C: 0.539  C|G: 0.353  G|G: 0.108  \n\tPJL \tC:0.677  G:0.323\tC|C: 0.458  C|G: 0.438  G|G: 0.104
\n\tSTU \tC:0.740  G:0.260\tC|C: 0.500  C|G: 0.480  G|G: 0.020  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38898512)|| (snp==7665932))
{
        printf(" \n\n Alleles  A/C, Ancestral: A, Ambiguity code: M, MAF: 0.35 [2]\n Location: 4:38898512 [2] \n SNP ID:
rs7665932 [1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description:
Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tA:0.647  C:0.353\tA|A: 0.426  A|C:
0.442  C|C: 0.132 \n\n AFRICAN  \tA:0.675  C:0.325\tA|A: 0.448  A|C: 0.455  C|C: 0.097  \n\tACB \tA:0.688  C:0.312\tA|A: 0.500
A|C: 0.375  C|C: 0.125  \n\tASW \tA:0.680  C:0.320\tA|A: 0.443  A|C: 0.475  C|C: 0.082  \n\tESN \tA:0.722  C:0.278\tA|A: 0.475  A|C:
0.495  C|C: 0.030  \n\tGWD \tA:0.695  C:0.305\tA|A: 0.496  A|C: 0.398  C|C: 0.106  \n\tLWK \tA:0.626  C:0.374\tA|A: 0.404  A|C:
0.444  C|C: 0.152  \n\tMSL \tA:0.665  C:0.335\tA|A: 0.412  A|C: 0.506  C|C: 0.082  \n\tYRI \tA:0.653  C:0.347\tA|A: 0.398  A|C: 0.509
C|C: 0.093          \n\n AMERICAN \tA:0.723  T:0.277\tA|A: 0.542  A|C: 0.363  C|C: 0.095  \n\tCLM \tA:0.686  C:0.314\tA|A: 0.479
A|C: 0.415  C|C: 0.106  \n\tMXL \tA:0.852  C:0.148\tA|A: 0.719  A|C: 0.266  C|C: 0.016  \n\tPEL \tA:0.876  C:0.124\tA|A: 0.776  A|C:
0.200  C|C: 0.024  \n\tPUR \tA:0.553  C:0.447\tA|A: 0.298  A|C: 0.510  C|C: 0.192  \n\n EAST ASIAN\tA:0.664  C:0.336\tA|A: 0.446
A|C: 0.435  C|C: 0.119 \n\n\tCDX \tA:0.801  C:0.199\tA|A: 0.624  A|C: 0.355  C|C: 0.022  \n\tCHB \tA:0.510  C:0.490\tA|A: 0.282
A|C: 0.456  C|C: 0.262  \n\tCHS \tA:0.690  C:0.310\tA|A: 0.457  A|C: 0.467  C|C: 0.076  \n\tJPT \tA:0.572  C:0.428\tA|A: 0.337  A|C:
0.471  C|C: 0.192  \n\tKHV \tA:0.763  C:0.237\tA|A: 0.556  A|C: 0.414  C|C: 0.030      \n\n EUROPEAN \tA:0.522  C:0.478 \tA|A:
0.284  A|C: 0.475  C|C: 0.241  \n\tCEU \tA:0.571  C:0.429\tA|A: 0.323  A|C: 0.495  C|C: 0.182  \n\tFIN \tA:0.515  C:0.485\tA|A: 0.313
A|C: 0.404  C|C: 0.283  \n\tGBR \tA:0.549  C:0.451\tA|A: 0.275  A|C: 0.549  C|C: 0.176  \n\tIBS \tA:0.542  C:0.458\tA|A: 0.280  A|C:
0.523  C|C: 0.196  \n\tTSI \tA:0.439  C:0.561\tA|A: 0.234  A|C: 0.411  C|C: 0.355  \n\n SOUTH ASIAN\tA:0.666  C:0.334\tA|A: 0.440
A|C: 0.452  C|C: 0.108  \n\tBEB \tA:0.610  C:0.390\tA|A: 0.384  A|C: 0.453  C|C: 0.163  \n\tGIH \tA:0.699  C:0.301\tA|A: 0.476  A|C:
0.447  C|C: 0.078  \n\tITU \tA:0.652  C:0.348\tA|A: 0.441  A|C: 0.422  C|C: 0.137  \n\tPJL \tA:0.651  C:0.349\tA|A: 0.417  A|C: 0.469
C|C: 0.115  \n\tSTU \tA:0.706  C:0.294\tA|A: 0.471  A|C: 0.471  C|C: 0.059  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38898776)|| (snp==6531677))
{
        printf(" \n\n Alleles  A/G, Ancestral:G, Ambiguity code: R, MAF: 0.11 [2]\n Location: 4:38898776 [2] \n SNP ID: rs6531677
[1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Seen in the archaic-like haplotypes III, IV, VII and
```

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differs from the other modern-human core haplotypes II, V, VI, VIII, IX, And The SNP differs between core haplotype III and other
modern human core haplotypes II, V, VI, VIII, IX. [1]\n Clinical Assertion Description: Not Known  \n\n\n Population  \tAllele
Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tA:0.114  G:0.886\tA|A: 0.042  A|G: 0.144  G|G: 0.814 \n\n AFRICAN  \tA:0.018
G:0.982\tA|A: 0.002  A|G: 0.033  G|G: 0.965  \n\tACB \tA:0.042  G:0.958\tA|A: 0.010  A|G: 0.062  G|G: 0.927  \n\tASW \tA:0.074
G:0.926\tA|A: 0.000  A|G: 0.148  G|G: 0.852  \n\tESN \tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000  \n\tGWD \tA:0.018
G:0.982\tA|A: 0.000  A|G: 0.035  G|G: 0.965  \n\tLWK \tA:0.015  G:0.985\tA|A: 0.000  A|G: 0.030  G|G: 0.970  \n\tMSL \tA:0.000
G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000  \n\tYRI \tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000   \n\n AMERICAN
\tA:0.180  G:0.820\tA|A: 0.043  A|G: 0.274  G|G: 0.683  \n\tCLM \tA:0.255  G:0.745\tA|A: 0.085  A|G: 0.340  G|G: 0.574  \n\tMXL
\tA:0.141  G:0.859\tA|A: 0.031  A|G: 0.219  G|G: 0.750  \n\tPEL \tA:0.076  G:0.924\tA|A: 0.000  A|G: 0.153  G|G: 0.847  \n\tPUR
\tA:0.221  G:0.779\tA|A: 0.048  A|G: 0.346  G|G: 0.606  \n\n EAST ASIAN\tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000
\n\tCDX \tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000  \n\tCHB \tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000
\n\tCHS \tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000  \n\tJPT \tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000
\n\tKHV \tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000    \n\n EUROPEAN \tA:0.405  G:0.595 \tA|A: 0.179  A|G: 0.451  G|G:
0.370  \n\tCEU \tA:0.500  G:0.500\tA|A: 0.263  A|G: 0.475  G|G: 0.263  \n\tFIN \tA:0.424  G:0.576\tA|A: 0.222  A|G: 0.404  G|G: 0.374
\n\tGBR \tA:0.440  G:0.560\tA|A: 0.143  A|G: 0.593  G|G: 0.264  \n\tIBS \tA:0.355  G:0.645\tA|A: 0.131  A|G: 0.449  G|G: 0.421
\n\tTSI \tA:0.318  G:0.682\tA|A: 0.140  A|G: 0.355  G|G: 0.505  \n\n SOUTH ASIAN\tA:0.016  G:0.984\tA|A: 0.000  A|G: 0.033  G|G:
0.967  \n\tBEB \tA:0.017  G:0.983\tA|A: 0.000  A|G: 0.035  G|G: 0.965  \n\tGIH \tA:0.024  G:0.976\tA|A: 0.000  A|G: 0.049  G|G: 0.951
\n\tITU \tA:0.000  G:1.000\tA|A: 0.000  A|G: 0.000  G|G: 1.000  \n\tPJL \tA:0.036  G:0.964\tA|A: 0.000  A|G: 0.073  G|G: 0.927
\n\tSTU \tA:0.005  G:0.995\tA|A: 0.000  A|G: 0.010  G|G: 0.990  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38899908)|| (snp==12642243))
{
            printf(" \n\n Alleles  T/A, Ancestral:A, Ambiguity code: W, MAF: 0.47 [2]\n Location: 4:38899908 [2] \n SNP ID:
rs12642243 [1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description:
Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tT:0.533  A:0.467\tT|T: 0.293  A|A: 0.227
A|T: 0.480 \n\n AFRICAN  \tT:0.474  A:0.526\tT|T: 0.218  A|A: 0.271  A|T: 0.511  \n\tACB \tT:0.479  A:0.521\tT|T: 0.219  A|A: 0.260
A|T: 0.521  \n\tASW \tT:0.467  A:0.533\tT|T: 0.213  A|A: 0.279  A|T: 0.508  \n\tESN \tT:0.545  A:0.455\tT|T: 0.253  A|A: 0.162  A|T:
0.586  \n\tGWD \tT:0.482  A:0.518\tT|T: 0.230  A|A: 0.265  A|T: 0.504  \n\tLWK \tT:0.338  A:0.662\tT|T: 0.101  A|A: 0.424  A|T:
0.475  \n\tMSL \tT:0.476  A:0.524\tT|T: 0.259  A|A: 0.306  A|T: 0.435  \n\tYRI \tT:0.519  A:0.481\tT|T: 0.250  A|A: 0.213  A|T: 0.537
\n\n AMERICAN \tT:0.595  A:0.405\tT|T: 0.372  A|A: 0.182  A|T: 0.447  \n\tCLM \tT:0.580  A:0.420\tT|T: 0.309  A|A: 0.149  A|T:
0.543  \n\tMXL \tT:0.656  A:0.344\tT|T: 0.469  A|A: 0.156  A|T: 0.375  \n\tPEL \tT:0.700  A:0.300\tT|T: 0.518  A|A: 0.118  A|T: 0.365
\n\tPUR \tT:0.486  A:0.514\tT|T: 0.250  A|A: 0.279  A|T: 0.471  \n\n EAST ASIAN\tT:0.592  A:0.408\tT|T: 0.355  A|A: 0.171  A|T:
0.474  \n\tCDX \tT:0.710  A:0.290\tT|T: 0.462  A|A: 0.043  A|T: 0.495  \n\tCHB \tT:0.476  A:0.524\tT|T: 0.223  A|A: 0.272  A|T: 0.505
\n\tCHS \tT:0.605  A:0.395\tT|T: 0.371  A|A: 0.162  A|T: 0.467  \n\tJPT \tT:0.510  A:0.490\tT|T: 0.288  A|A: 0.269  A|T: 0.442
\n\tKHV \tT:0.677  A:0.323\tT|T: 0.444  A|A: 0.091  A|T: 0.465  \n\n EUROPEAN \tT:0.491  A:0.509 \tT|T: 0.264  A|A: 0.282  A|T:
0.453  \n\tCEU \tT:0.561  A:0.439\tT|T: 0.313  A|A: 0.192  A|T: 0.495  \n\tFIN \tT:0.495  A:0.505\tT|T: 0.293  A|A: 0.303  A|T: 0.404
\n\tGBR \tT:0.527  A:0.473\tT|T: 0.264  A|A: 0.209  A|T: 0.527  \n\tIBS \tT:0.491  A:0.509\tT|T: 0.252  A|A: 0.271  A|T: 0.477  \n\tTSI
\tT:0.393  A:0.607\tT|T: 0.206  A|A: 0.421  A|T: 0.374  \n\n SOUTH ASIAN\tT:0.551  A:0.449\tT|T: 0.305  A|A: 0.202  A|T: 0.493
\n\tBEB \tT:0.523  A:0.477\tT|T: 0.291  A|A: 0.244  A|T: 0.465  \n\tGIH \tT:0.592  A:0.408\tT|T: 0.340  A|A: 0.155  A|T: 0.505  \n\tITU
\tT:0.505  A:0.495\tT|T: 0.265  A|A: 0.255  A|T: 0.480  \n\tPJL \tT:0.526  A:0.474\tT|T: 0.281  A|A: 0.229  A|T: 0.490  \n\tSTU
\tT:0.603  A:0.397\tT|T: 0.343  A|A: 0.137  A|T: 0.520  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38900148)|| (snp==12641669))
```

```
{
        printf(" \n\n Alleles  A/C, Ancestral: C, Ambiguity code: M, MAF: 0.48 [2]\n Location: 4:38900148 [2] \n SNP ID:
rs12641669 [1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description:
Not Known  \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tA:0.517  C:0.483\tA|A: 0.278  A|C:
0.478  C|C: 0.244 \n\n AFRICAN  \tA:0.417  C:0.583\tA|A: 0.168  A|C: 0.498  C|C: 0.334  \n\tACB \tA:0.417  C:0.583\tA|A: 0.177
A|C: 0.479  C|C: 0.344  \n\tASW \tA:0.402  C:0.598\tA|A: 0.148  A|C: 0.508  C|C: 0.344  \n\tESN \tA:0.515  C:0.485\tA|A: 0.222  A|C:
0.586  C|C: 0.192  \n\tGWD \tA:0.425  C:0.575\tA|A: 0.150  A|C: 0.549  C|C: 0.301  \n\tLWK \tA:0.293  C:0.707\tA|A: 0.081  A|C:
0.424  C|C: 0.495  \n\tMSL \tA:0.406  C:0.594\tA|A: 0.188  A|C: 0.435  C|C: 0.376  \n\tYRI \tA:0.449  C:0.551\tA|A: 0.204  A|C: 0.491
C|C: 0.306          \n\n AMERICAN \tA:0.589  T:0.411\tA|A: 0.360  A|C: 0.458  C|C: 0.182  \n\tCLM \tA:0.564  C:0.436\tA|A: 0.277
A|C: 0.574  C|C: 0.149  \n\tMXL \tA:0.648  C:0.352\tA|A: 0.453  A|C: 0.391  C|C: 0.156  \n\tPEL \tA:0.700  C:0.300\tA|A: 0.518  A|C:
0.365  C|C: 0.118  \n\tPUR \tA:0.486  C:0.514\tA|A: 0.250  A|C: 0.471  C|C: 0.279  \n\n EAST ASIAN\tA:0.591  C:0.409\tA|A: 0.353
A|C: 0.476  C|C: 0.171 \n\n\tCDX \tA:0.710  C:0.290\tA|A: 0.462  A|C: 0.495  C|C: 0.043  \n\tCHB \tA:0.476  C:0.524\tA|A: 0.223
A|C: 0.505  C|C: 0.272  \n\tCHS \tA:0.605  C:0.395\tA|A: 0.371  A|C: 0.467  C|C: 0.162  \n\tJPT \tA:0.510  C:0.490\tA|A: 0.288  A|C:
0.442  C|C: 0.269  \n\tKHV \tA:0.672  C:0.328\tA|A: 0.434  A|C: 0.475  C|C: 0.091      \n\n EUROPEAN \tA:0.491  C:0.509 \tA|A:
0.264  A|C: 0.453  C|C: 0.282  \n\tCEU \tA:0.561  C:0.439\tA|A: 0.313  A|C: 0.495  C|C: 0.192  \n\tFIN \tA:0.495  C:0.505\tA|A: 0.293
A|C: 0.404  C|C: 0.303  \n\tGBR \tA:0.527  C:0.473\tA|A: 0.264  A|C: 0.527  C|C: 0.209  \n\tIBS \tA:0.491  C:0.509\tA|A: 0.252  A|C:
0.477  C|C: 0.271  \n\tTSI \tA:0.393  C:0.607\tA|A: 0.206  A|C: 0.374  C|C: 0.421  \n\n SOUTH ASIAN\tA:0.551  C:0.449\tA|A: 0.305
A|C: 0.493  C|C: 0.202  \n\tBEB \tA:0.523  C:0.477\tA|A: 0.291  A|C: 0.465  C|C: 0.244  \n\tGIH \tA:0.592  C:0.408\tA|A: 0.340  A|C:
0.505  C|C: 0.155  \n\tITU \tA:0.505  C:0.495\tA|A: 0.265  A|C: 0.480  C|C: 0.255  \n\tPJL \tA:0.526  C:0.474\tA|A: 0.281  A|C: 0.490
C|C: 0.229  \n\tSTU \tA:0.603  C:0.397\tA|A: 0.343  A|C: 0.520  C|C: 0.137  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38900512)|| (snp==1115259))
{
        printf(" \n\n Alleles  C/A/T, Ancestral:C, Ambiguity code: H, MAF: 0.48 [2]\n Location: 4:38900512 [2] \n SNP ID:
rs1115259 [1]  \n GWAS Trait: Self-reported allergy [1]\n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description:
Not Known \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tC:0.517  T:0.483\tC|C: 0.278  C|T: 0.477
T|T: 0.245 \n\n AFRICAN  \tC:0.416  T:0.584\tC|C: 0.168  C|T: 0.496  T|T: 0.336  \n\tACB \tC:0.417  T:0.583\tC|C: 0.177  C|T: 0.479
T|T: 0.344  \n\tASW \tC:0.402  T:0.598\tC|C: 0.148  C|T: 0.508  T|T: 0.344  \n\tESN \tC:0.510  T:0.490\tC|C: 0.222  C|T: 0.576  T|T:
0.202  \n\tGWD \tC:0.425  T:0.575\tC|C: 0.150  C|T: 0.549  T|T: 0.301  \n\tLWK \tC:0.293  T:0.707\tC|C: 0.081  C|T: 0.424  T|T: 0.495
\n\tMSL \tC:0.406  T:0.594\tC|C: 0.188  C|T: 0.435  T|T: 0.376  \n\tYRI \tC:0.449  T:0.551\tC|C: 0.204  C|T: 0.491  T|T: 0.306  \n\n
AMERICAN \tC:0.589  T:0.411\tC|C: 0.360  C|T: 0.458  T|T: 0.182  \n\tCLM \tC:0.564  T:0.436\tC|C: 0.277  C|T: 0.574  T|T: 0.149
\n\tMXL \tC:0.648  T:0.352\tC|C: 0.453  C|T: 0.391  T|T: 0.156  \n\tPEL \tC:0.700  T:0.300\tC|C: 0.518  C|T: 0.365  T|T: 0.118  \n\tPUR
\tC:0.486  T:0.514 \tC|C: 0.250  C|T: 0.471  T|T: 0.279  \n\n EAST ASIAN\tC:0.591  T:0.409\tC|C: 0.355  C|T: 0.472  T|T: 0.173
\n\tCDX \tC:0.710  T:0.290\tC|C: 0.462  C|T: 0.495  T|T: 0.043  \n\tCHB \tC:0.476  T:0.524\tC|C: 0.223  C|T: 0.505  T|T: 0.272
\n\tCHS \tC:0.605  T:0.395\tC|C: 0.371  C|T: 0.467  T|T: 0.162  \n\tJPT \tC:0.510  T:0.490\tC|C: 0.288  C|T: 0.442  T|T: 0.269  \n\tKHV
\tC:0.672  T:0.328\tC|C: 0.444  C|T: 0.455  T|T: 0.101  \n\n EUROPEAN \tC:0.491  T:0.509 \tC|C: 0.264  C|T: 0.453  T|T: 0.282
\n\tCEU \tC:0.561  T:0.439\tC|C: 0.313  C|T: 0.495  T|T: 0.192  \n\tFIN \tC:0.495  T:0.505\tC|C: 0.293  C|T: 0.404  T|T: 0.303  \n\tGBR
\tC:0.527  T:0.473\tC|C: 0.264  C|T: 0.527  T|T: 0.209  \n\tIBS \tC:0.491  T:0.509\tC|C: 0.252  C|T: 0.477  T|T: 0.271  \n\tTSI \tC:0.393
T:0.607\tC|C: 0.206  C|T: 0.374  T|T: 0.421  \n\n SOUTH ASIAN\tC:0.551  T:0.449\tC|C: 0.305  C|T: 0.493  T|T: 0.202  \n\tBEB
\tC:0.523  T:0.477\tC|C: 0.291  C|T: 0.465  T|T: 0.244  \n\tGIH \tC:0.592  T:0.408\tC|C: 0.340  C|T: 0.505  T|T: 0.155  \n\tITU \tC:0.505
T:0.495\tC|C: 0.265  C|T: 0.480  T|T: 0.255  \n\tPJL \tC:0.526  T:0.474\tC|C: 0.281  C|T: 0.490  T|T: 0.229  \n\tSTU \tC:0.603
T:0.397\tC|C: 0.343  C|T: 0.520  T|T: 0.137  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
```

```
else if ((chr==38902960)|| (snp==6824769))
{
        printf(" \n\n Alleles  T/C, Ancestral:C, Ambiguity code: Y, MAF: 0.49 [2]\n Location: 4:38902960 [2] \n SNP ID: rs6824769
[1] \n GWAS Trait: Multiple complex diseases, Self-reported allergy [1]\n Archaic-like haplotype cluster: Not Known\n Clinical
Assertion Description: Not Known \n\n\n Population  \tAllele Frequency [2] \tGenotype Frequency [2] \n\n ALL      \tT:0.514
C:0.486\tT|T: 0.277  C|C: 0.248  C|T: 0.475 \n\n AFRICAN  \tT:0.408  C:0.592\tT|T: 0.166  C|C: 0.349  C|T: 0.484  \n\tACB \tT:0.411
C:0.589\tT|T: 0.177  C|C: 0.354  C|T: 0.469  \n\tASW \tT:0.385  C:0.615\tT|T: 0.148  C|C: 0.377  C|T: 0.475  \n\tESN \tT:0.515
C:0.485\tT|T: 0.222  C|C: 0.192  C|T: 0.586  \n\tGWD \tT:0.403  C:0.597\tT|T: 0.150  C|C: 0.345  C|T: 0.504  \n\tLWK \tT:0.293
C:0.707\tT|T: 0.081  C|C: 0.495  C|T: 0.424  \n\tMSL \tT:0.394  C:0.606\tT|T: 0.176  C|C: 0.388  C|T: 0.435  \n\tYRI \tT:0.444
C:0.556\tT|T: 0.204  C|C: 0.315  C|T: 0.481  \n\n AMERICAN \tT:0.586  C:0.414\tT|T: 0.354  C|C: 0.182  C|T: 0.464  \n\tCLM
\tT:0.564  C:0.436\tT|T: 0.277  C|C: 0.149  C|T: 0.574  \n\tMXL \tT:0.648  C:0.352\tT|T: 0.453  C|C: 0.156  C|T: 0.391  \n\tPEL
\tT:0.694  C:0.306\tT|T: 0.506  C|C: 0.118  C|T: 0.376  \n\tPUR \tT:0.481  C:0.519 \tT|T: 0.240  C|C: 0.279  C|T: 0.481  \n\n EAST
ASIAN\tT:0.591  C:0.409\tT|T: 0.353  C|C: 0.171  C|T: 0.476  \n\tCDX \tT:0.710  C:0.290\tT|T: 0.462  C|C: 0.043  C|T: 0.495  \n\tCHB
\tT:0.476  C:0.524\tT|T: 0.223  C|C: 0.272  C|T: 0.505  \n\tCHS \tT:0.605  C:0.395\tT|T: 0.371  C|C: 0.162  C|T: 0.467  \n\tJPT \tT:0.510
C:0.490\tT|T: 0.288  C|C: 0.269  C|T: 0.442  \n\tKHV \tT:0.672  C:0.328\tT|T: 0.434  C|C: 0.091  C|T: 0.475  \n\n EUROPEAN
\tT:0.491  C:0.509 \tT|T: 0.264  C|C: 0.282  C|T: 0.453  \n\tCEU \tT:0.561  C:0.439\tT|T: 0.313  C|C: 0.192  C|T: 0.495  \n\tFIN
\tT:0.495  C:0.505\tT|T: 0.293  C|C: 0.303  C|T: 0.404  \n\tGBR \tT:0.527  C:0.473\tT|T: 0.264  C|C: 0.209  C|T: 0.527  \n\tIBS \tT:0.491
C:0.509\tT|T: 0.252  C|C: 0.271  C|T: 0.477  \n\tTSI \tT:0.393  C:0.607\tT|T: 0.206  C|C: 0.421  C|T: 0.374  \n\n SOUTH
ASIAN\tT:0.551  C:0.449\tT|T: 0.305  C|C: 0.202  C|T: 0.493  \n\tBEB \tT:0.523  C:0.477\tT|T: 0.291  C|C: 0.244  C|T: 0.465  \n\tGIH
\tT:0.592  C:0.408\tT|T: 0.340  C|C: 0.155  C|T: 0.505  \n\tITU \tT:0.505  C:0.495\tT|T: 0.265  C|C: 0.255  C|T: 0.480  \n\tPJL \tT:0.526
C:0.474\tT|T: 0.281  C|C: 0.229  C|T: 0.490  \n\tSTU \tT:0.603  C:0.397\tT|T: 0.343  C|C: 0.137  C|T: 0.520  \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England
and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in
Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like
Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2.
Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
else if ((chr==38903573)|| (snp==7664107))
{
        printf(" \n\n Alleles  A/T, Ancestral:T, Ambiguity code: W, MAF: 0.47 [2]\n Location: 4:38903573 [2] \n SNP ID: rs7664107
[1] \n GWAS Trait: Self-reported allergy [1] \n Archaic-like haplotype cluster: Not Known\n Clinical Assertion Description: Not Known
\n\n\n Population  \tAllele Frequency [2] \t      Genotype Frequency [2] \n\n ALL      \tA:0.532  ATT:0.001  T:0.467\tA|A: 0.292
A|ATT: 0.001  A|T: 0.480  T|T: 0.227 \n\n AFRICAN  \tA:0.473  ATT:0.000  T:0.527\tA|A: 0.216  A|ATT: 0.000  A|T: 0.513  T|T:
0.271  \n\tACB \tA:0.484  ATT:0.000  T:0.516\tA|A: 0.229  A|ATT: 0.000  A|T: 0.510  T|T: 0.260  \n\tASW \tA:0.451  ATT:0.000
T:0.549\tA|A: 0.180  A|ATT: 0.000  A|T: 0.541  T|T: 0.279  \n\tESN \tA:0.535  ATT:0.000  T:0.465\tA|A: 0.253  A|ATT: 0.000  A|T:
0.566  T|T: 0.182  \n\tGWD \tA:0.482  ATT:0.000  T:0.518\tA|A: 0.230  A|ATT: 0.000  A|T: 0.504  T|T: 0.265  \n\tLWK \tA:0.359
ATT:0.000  T:0.641\tA|A: 0.111  A|ATT: 0.000  A|T: 0.495  T|T: 0.394  \n\tMSL \tA:0.471  ATT:0.000  T:0.529\tA|A: 0.247  A|ATT:
0.000  A|T: 0.447  T|T: 0.306  \n\tYRI \tA:0.514  ATT:0.000  T:0.486\tA|A: 0.250  A|ATT: 0.000  A|T: 0.528  T|T: 0.222    \n\n
AMERICAN \tA:0.594  ATT:0.000  T:0.406\tA|A: 0.369  A|ATT: 0.000  A|T: 0.450  T|T: 0.182  \n\tCLM \tA:0.585  ATT:0.000
T:0.415\tA|A: 0.319  A|ATT: 0.000  A|T: 0.532  T|T: 0.149  \n\tMXL \tA:0.656  ATT:0.000  T:0.344\tA|A: 0.469  A|ATT: 0.000  A|T:
0.375  T|T: 0.156  \n\tPEL \tA:0.694  ATT:0.000  T:0.306\tA|A: 0.506  A|ATT: 0.000  A|T: 0.376  T|T: 0.118  \n\tPUR \tA:0.481
ATT:0.000  T:0.519\tA|A: 0.240  A|ATT: 0.000  A|T: 0.481  T|T: 0.279  \n  \n\n EAST ASIAN\tA:0.591  ATT:0.003  T:0.406\tA|A:
0.353  A|ATT: 0.006  A|T: 0.470  T|T: 0.171  \n\tCDX \tA:0.710  ATT:0.000  T:0.290\tA|A: 0.462  A|ATT: 0.000  A|T: 0.495  T|T:
0.043  \n\tCHB \tA:0.476  ATT:0.000  T:0.524\tA|A: 0.223  A|ATT: 0.000  A|T: 0.505  T|T: 0.272  \n\tCHS \tA:0.605  ATT:0.010
T:0.386\tA|A: 0.371  A|ATT: 0.019  A|T: 0.448  T|T: 0.162  \n\tJPT \tA:0.510  ATT:0.000  T:0.490\tA|A: 0.288  A|ATT: 0.000  A|T:
0.442  T|T: 0.269  \n\tKHV \tA:0.672  ATT:0.005  T:0.323\tA|A: 0.434  A|ATT: 0.010  A|T: 0.465  T|T: 0.091    \n\n EUROPEAN
\tA:0.491  ATT:0.000  T:0.509\tA|A: 0.264  A|ATT: 0.000  A|T: 0.453  T|T: 0.282  \n\tCEU \tA:0.561  ATT:0.000  T:0.439\tA|A: 0.313
A|ATT: 0.000  A|T: 0.495  T|T: 0.192  \n\tFIN \tA:0.495  ATT:0.000  T:0.505\tA|A: 0.293  A|ATT: 0.000  A|T: 0.404  T|T: 0.303
\n\tGBR \tA:0.527  ATT:0.000  T:0.473\tA|A: 0.264  A|ATT: 0.000  A|T: 0.527  T|T: 0.209  \n\tIBS \tA:0.491  ATT:0.000
T:0.509\tA|A: 0.252  A|ATT: 0.000  A|T: 0.477  T|T: 0.271  \n\tTSI \tA:0.393  ATT:0.000  T:0.607\tA|A: 0.206  A|ATT: 0.000  A|T:
0.374  T|T: 0.421    \n\n SOUTH ASIAN\tA:0.551  ATT:0.000  T:0.449\tA|A: 0.305  A|ATT: 0.000  A|T: 0.493  T|T: 0.202  \n\tBEB
\tA:0.523  ATT:0.000  T:0.477\tA|A: 0.291  A|ATT: 0.000  A|T: 0.465  T|T: 0.244  \n\tGIH \tA:0.592  ATT:0.000  T:0.408\tA|A: 0.340
A|ATT: 0.000  A|T: 0.505  T|T: 0.155  \n\tITU \tA:0.505  ATT:0.000  T:0.495\tA|A: 0.265  A|ATT: 0.000  A|T: 0.480  T|T: 0.255
\n\tPJL \tA:0.526  ATT:0.000  T:0.474\tA|A: 0.281  A|ATT: 0.000  A|T: 0.490  T|T: 0.229  \n\tSTU \tA:0.603  ATT:0.000
T:0.397\tA|A: 0.343  A|ATT: 0.000  A|T: 0.520  T|T: 0.137    \n\n");
printf("\n\n\n   ACB: African Caribbean in Barbados\n   ASW: African Ancestry in Southwest US\n   ESN: Esan in Nigeria\n   GWD:
Gambian in Western Division, The Gambia\n   LWK: Luhya in Webuye, Kenya\n   MSL: Mende in Sierra Leone\n   YRI: Yoruba in
Ibadan, Nigeria\n");
printf("   CLM: Colombian in Medellin, Colombia\n   MXL: Mexican Ancestry in Los Angeles, California\n   PEL: Peruvian in Lima,
Peru\n   PUR: Puerto Rican in Puerto Rico\n");
printf("   CDX: Chinese Dai in Xishuangbanna, China\n   CHB: Han Chinese in Bejing, China\n   CHS: Southern Han Chinese, China\n
JPT: Japanese in Tokyo, Japan\n   KHV: Kinh in Ho Chi Minh City, Vietnam\n");
```

```
printf("   CEU: Utah residents with Northern and Western European ancestry\n   FIN: Finnish in Finland\n   GBR: British in England and Scotland\n   IBS: Iberian Populations in Spain\n   TSI: Toscani in Italy\n");
printf("   BEB: Bengali in Bangladesh\n   GIH: Gujarati Indian in Houston, TX\n   ITU: Indian Telugu in the UK\n   PJL: Punjabi in Lahore, Pakistan\n   STU: Sri Lankan Tamil in the UK\n\n\n");
printf("   REFERENCES\n\n1. Dannemann, M., Andres, A.M., and Kelso, J. (2016). Introgression of Neandertal-and Denisovan-like Haplotypes Contributes to Adaptive Variation in Human Toll-like Receptors. The American Journal of Human Genetics 98,22-33\n2. Ensembl. (2016). Browse a Genome. Retrieved March 9, 2017 from http://www.ensembl.org/index.html\n\n");
}
system("pause");
return 0;
}
```